Volume 14 No. 2 (May-August) : 2022

ISSN: 2582-2675

Journal of Cereal Research

(Formerly Journal of Wheat Research)

JCR

Society for Advancement of Wheat and Barley Research
ICAR-Indian Institute of Wheat & Barley Research
Karnal - 132 001, India

Society for Advancement of Wheat and Barley Research

(Registered under Haryana Registration and Regulation of Societies Act, 2012)
(Registration No.: HR-006-2016-06817)

Advisory Board

H S Gupta
Ravi P Singh
K V Prabhu
B D Singh
R R Hanchinal
B S Mahapatra
Robert Park
S A Patil

Executive Council

President : Gyanendra Pratap Singh, Karnal
Vice President : Gyanendra Singh, Karnal and S V Sai Prasad, Indore
General Secretary : Poonam Jasrotia, Karnal
Joint Secretary : C N Mishra, Karnal
Treasurer : Charan Singh, Karnal
Joint Treasurer : Mamrutha H M, Karnal
Editor-in-chief : Satish Kumar, Karnal

Assoc. Editors : R S Chhokar, Karnal, India
R Abdul Fiyaz, Hyderabad, India
P L Kashyap, Karnal, India
V K Singh, New Delhi, India
Vikas Gupta, Karnal, India
Vishnu Kumar, Jhansi, India
S K Bishnoi, Hisar, India
O P Gupta, Karnal, India
Harbans Bariana, Australia
Mathew Reynolds, Mexico
R Trethowan, Australia
Leonardo A. Crespo Herrera, Mexico
Hadi Pirasteh-Anosheh, Iran
Santosh Kumar, Canada
Chikkappa G. Karjagi, New Delhi, India
Sunish Sehgal, USA
Prem Bahadur Magar, Nepal

Zonal Councillors

Northern Hills Zone : S H Wani, Srinagar
North Western Plains Zone : Harikrishna, New Delhi
North Eastern Plains Zone : Sunita Mahapatra, Kalyani
Central Zone : J B Singh, Indore
Peninsular Zone and Southern Hills Zone : V K Vikas, Wellington

Editorial Board Members : J P Jaiswal, Pantnagar
Sivasamy M, Wellington
B S Tyagi, Karnal
Ranjeet Ranjan Kumar, New Delhi
Dhiman Mukherjee, Kalyani
Amit Kumar, Barapani
P K Singh, New Delhi
Jaspal Kaur, Ludhiana
Prashanth Babu H, New Delhi
Mamrutha H M, Karnal
Pramod Prasad, Shimla
P Venkatesh, New Delhi
Deepak Baranwal, Bihar
Aditya K S, New Delhi
Subash S P, New Delhi

Consulting Editors Overseas

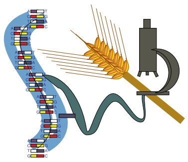
A K Joshi, CIMMYT-India; A Pattanayak, India; Pawan Singh, Mexico; S Sukumaran, Mexico;
S C Bhardwaj, India; Ravish Chatrath, India; Lakshmi Kant, India

For subscription, submission of articles, editorial inquiry and advertisement, please contact:
E-mail: sawbargs@gmail.com; editorinchiefjwr@gmail.com

Volume 14 No. 2 (May-August) : 2022 ISSN: 2582-2675

Journal of Cereal Research

JCR



Society for Advancement of Wheat and Barley Research
ICAR-Indian Institute of Wheat & Barley Research
Karnal - 132 001, India

Contents

Review Articles

Research Articles

Short Communication

Varietal Release

Journal of Cereal Research
Volume 14 (2): 108-128
Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Review Article

On and Off Farm Crop Residue Management: A brief review on Options, Benefits, Drawbacks, Limitations and Policy Interventions

Deepti Singh and Usha Mina*

School of Environmental Sciences, Jawaharlal Nehru University, New Delhi-110067

Article history:
Received: 27 July, 2022
Revised: 04 Sept., 2022
Accepted: 06 Oct., 2022

Citation:
Singh D and U Mina. 2022. On and Off Farm Crop Residue Management: A brief review on Options, Benefits, Drawbacks, Limitations and Policy Interventions. *Journal of Cereal Research* ***14 (2):*** *108-128. http://doi.org/10.25174/2582-2675/2022/123108*

***Corresponding author:**
E-mail: ushamina@mail.jnu.ac.in

Abstract

India ranks as second largest country for agro-based economy having about 1.79 MKM^2 agricultural land that generates approximately 686 Million Tonnes (MT) of gross crop residues including approximately 234 MT surplus residues annually. In 686 MT crop residue, contribution of crop types as well as states is variable. In the present study, the role of crop residue as an important natural and renewable resource along with their on and off farm management options having their own benefits, drawbacks and limitations were discussed. Various terminologies used for crops' residue and methodoloies used to estimate their generation potential were analysed. Different factors regulating the crop residue usage for diverse purposes which affects their end use were identified and listed. As, raw and condensed form of crop residues have different physico-chemical properties and resource value. Various on and off farm crop residue management options including crop residue burning, residue removal, residue retention, residue incorporation, composting, biochar production, livestock feed, mushroom cultivation, biofuel biogas and bioenergy production from different crop residues were compared. Various Government initiatives to minimise and support the unsustainable and sustainable crop residue management options, respectively were reviewed.

Key words: Crop residues, Crop residue generation potential, Crop Residue management option, On and Off farm options.

1. Introduction

In India total agricultural land occupies 1.79 MKM^2 (60.5% of total land area). As per World Bank (2010), agricultural land basically corresponds to the portion of total land which is arable (53.2%). 3.8% and 3.5% arable land is under permanent crops and pasture, respectively. With net area of around 180 Million hectare under the agricultural cultivation and about 140% cropping intensity (Cardoen *et al.,* 2015), India generates huge amount of agricultural residues. Agricultural residues include - livestock residue (both commercial and household livestock) and crop residue (includes non-edible plant parts that are left in the field after the crop being harvested, thrashed or left after pastures grazed including leaves, stalk, stubbles, straws and roots) (FAO, 2014; Lal, 2005).Crop residues are basically the crop parts that remained after all the economic part of the crop has been separated out (Shahane *et. al.,* 2016).

As per the estimations, India generates around 686 Million Tonnes (MT) (Hiloidhari *et al.,* 2014; Singh *et al.,* 2020) of crop residue on farm plus off farm annually. Of total residue generated, field crops such as cereals, pulses, sugarcane and oilseeds contribute 545 MT, 79.8 MT is contributed by fiber crops such as Jute and cotton and 61

MT by horticulture crops such as banana, coconut and areca nut. Under field crops, cereal crops come at the top with 368 MT (i.e. 54%) of residue generation. Among other field crops, sugarcane contributing around 111 MT (16%). 34% of the gross crop residue generated remains as surplus (234.5MT) (Hiloidhari *et al.* 2014) (Table 1).

Table 1. Crop residue generation by different crop types

Crop Name	**Quantity of crop residue generated (In Million Tonnes or MT)**
Field Crops	
Cereals	367.7
Pulses	17.9
Sugarcane	110.6
Oilseeds	48.8
Total	545.0
Fiber crops	
Jute	3.9
Cotton	75.9
Total	79.8
Horticulture crops	
Banana	41.9
Coconut	18.0
Areca nut	1.5
Total	61.0
Gross total	**686**

The crop residue generation potential of different Indian states depends on the type of crop grown, cropping intensity as well as the productivity level. As per the reports, Uttar Pradesh comes at first position in terms of residue generation by contributing 116 MT followed by West Bengal and Andhra Pradesh by contributing 63.26 MT and 57.44 MT. respectively (Jain *et al.,* 2014). However on comparing generated cereal crop residues, Uttar Pradesh (72MT) is the leading state followed by Punjab (45.6MT), West Bengal (37.3MT), Andhra Pradesh (33MT) and Haryana(24.7MT) (Table 2). The sustainable management of this amount of crop residues generated as well as to understand its importance as a natural resource is necessary to get long term benefits (Jain *et al.,* 2014).

Table 2. Crops' residue generated by different states

State	**Cereal crops(MT)**	**Oilseed crops(MT)**	**Fiber crops(MT)**	**Sugarcane (MT)**	**Total(MT)**
Uttar Pradesh	72.02	2.49	0.04	41.13	115.68
West Bengal	37.26	0.95	24.43	0.62	63.26
Andhra Pradesh	33.07	2.5	16.07	5.8	57.44
Punjab	45.58	0.08	9.32	1.76	56.74
Maharashtra	8.75	0.57	19.51	22.87	51.7
Gujarat	8.18	5.06	28.62	5.85	47.71
Haryana	24.73	2.15	7.58	1.93	36.39
Rajasthan	22.19	9.26	2.96	0.15	34.56

Crop residues support diverse ecosystem services (Table 3) and have various competing uses (FAO, 2014) therefore they should not be considered as a waste but as an essential commodity as a natural and renewable resource for providing numerous environmental services and thereby assuring perpetuation of productive agro-ecosystems (Lal, 2004).

Table 3. Ecosystem Services provide by Crop Residues

Type of Ecosystem Services	End use/Example
Regulating services when residues are left on soil	Balancing soil temperature Control Soil Erosion Increase Water holding capacity of soil Carbon sequestration and maintenance of soil structure
Supporting services	Play role in nutrient and water cycling Disease and pest incidence regulation by acting as surface mulch, limits the light and nitrogen availability near soil as well as due to some allelopathic effects supress the emergence of weeds (Singh 2014; Prashanthi and Billa 2020 ;farmpractices.com) The residue mulch prevents the soil which is infected with fungi from splashing up onto the plant foliage(Sinkeviciene et al., 2009; Yordanova and Gerasimova 2016) Protect and promote growth of soil microorganisms and habitat
Provisioning services when crop residues are used as value added products	
If crop residue used as feed	Provide nutrient and energy source to cattle
Nutrient source for plants/crops	After residue decomposition As part of compost As Biochar
Construction materials	Residue based boards, cement material, bricks panels, temporary roof, roof thatching, agrocrete
Energy source	Heat, Electricity, steam
Chemicals	Organic acids, polysaccharides, plastics
Paper pulp	Paper boards

2. Crop residues: Sources and types

The National Agricultural Technology Project (NATP) has placed all Indian agroecosystems under 5 broad categories namely, Arid, Coastal, Hill & Mountain, Irrigated and Rainfed (Saxena *et al.,* 2000) and 14 type of crop production systems. Under each production system, depending upon the cropping system, cropping pattern, cropping intensity and crops productivity, different amount of crop residues being generated. On comparing different production systems, approx. 40%, 15% and 13% of the gross cropped area is under rice - wheat cropping system, other cereal crops(maize, pearl millet and sorghum), oil seeds (groundnut, mustard, soybean) respectively (Figure 1) (Cardoen *et al.,* 2015).

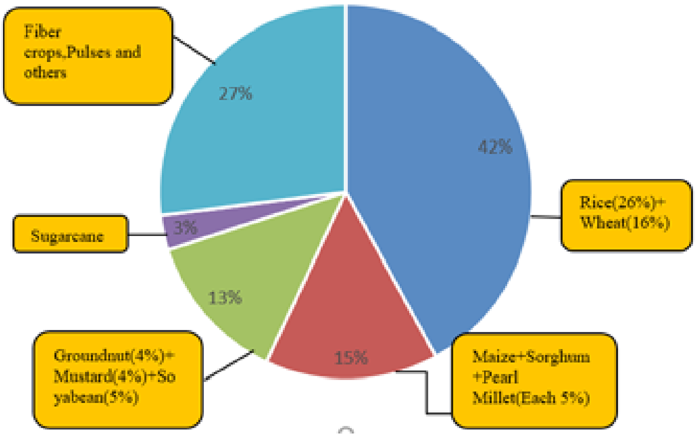


Figure 1. Gross area under cultivation of major crops grown in India

Crop residues generated from different type of crops have been given different names (Hiloidhari *et al.,* 2014) (Table 4). Different crop types (Cereals, oilseeds. Pulses, Sugarcane, horticulture crops and fiber crops) generate variable quantity of on and off farm residues in the states identified as their major producers (Cardoen et.al.,2015) (Table 4).

Table 4. Crop residues: Sources, types, place of generation, quantity and generating states

S.No.	Crop category	Name of Crop Source	Name of residue generated	Place of generation	Quantity of residue generated (MT)	Major producing States
1.	Cereals	Rice/Paddy	Straw	On-Farm	154.0	UP, WB, PB, AP,
		Wheat	Husk	Off-Farm(AtMill)	131.1	OR, HR, TN, CG,
		Maize	Bran	Off-Farm (At Mill)	35.8	BR
		Pearl Millet	De-oiled bran	Off-Farm (At Oil-mill)	24.3	UP, PB, MP, HR,
		Sorghum		On-Farm	17.6	RJ, BR
		Others	Straw	On-Farm	4.9	BR, UP GJ, RJ AP,
			Chaff	Off-Farm (AtMill)		HP, MP, JK, KA,
			Bran	On-Farm		GJ, HR, MH, RJ, UP
				On-Farm		MH, KA, RJ, MP,
			Stover	Off-farm (At Wet Mill)		AP,
			Cobs	On-Farm		TN
			Corn-fibre/Grain	On-Farm		
			hull	Off-farm (At Mill)		
				On-Farm		
			Stalks	On-Farm		
			Cobs	Off-Farm (At Mill)		
			Husk			
			Stalks			
			Cobs			
			Husk			
	Total				367.7	
2.	Oilseeds	Mustard	Stalks	On-Farm	12.7	AS, UP, GJ, RJ, HR,
		and	Seedpod	On-Farm	13.5	JK, MP, , WB
		rapeseed	Meal/Oilcake	Off-Farm(At Oil-Mill)	17.0	MP, MH, RJ, AP,
		Soyabean		On-Farm	3.8	KA
		Groundnut	Stalks	Off-Farm (At Oil -Mill)	1.8	GJ, TN, AP, KA,
		Sunflower	Husk	Off-Farm(At Oil -Mill)		MH
		Others	Meal/Oilcake	On-Farm		KA, AP, MH, BR,
				Off-Farm(At Oil-Mill)		OR, TN
			Stalks	Off-Farm(At Oil -Mill)		
			Shell			
			Meal/Oilcake			
	Total				48.8	
3.	Pulses	Tur(Arhar)	Stalks	On-Farm	7.2	MH, UP, KA, GJ,
			Husk	Off-Farm (At Mill)	6.4	MP, AP
		Gram	Stalks	On-Farm	4.3	MP, UP, RA, MH,
			Husk	Off-Farm(At Mill)		AP, KA
		Others				
	Total				17.9	

4.	Sugarcane	Sugarcane	Tops and leaves Molasses Bagasse Press mud/filter cake Depithed bagasse	On-Farm Off-Farm(Sugar -Mill) Off-Farm(Sugar-Mill) Off-Farm(Sugar -Mill) Off-Farm(Sugar- Mill)	**110.6**	HR, KA, MH, PB, TN, UP
5.	Horticulture crop	Banana Coconut Areca nut	Leaves/ Pseudostems Peels Fronds Husk Shell Meal/Oilcake Coir pith	On-Farm/Plantation Off-Farm(Processing Plant) On-Farm On-Farm Off-Farm (Oil Mill) Off-Farm (Oil Mill) Off-Farm (Processing plant)	41.9 18.0 1.5	MH, TN, KA, GJ, WB, AP, AS OR, BR, AS, KA,GJ KA, KL, TN, AP, OR, MH, GA, AS AS,KR,KA
	Total				61.4	
6.	Fiber crops	Cotton	Stalks Hull/bollshel Gin trash Meal/oilcake	On-Farm Off-Farm (Cotton gin) Off-Farm (Cotton gin) Off-Farm (Oil Mill)	75.9 3.9	AP, GJ, HR, KA, MH, PB, TN WB, AS, OR, BR, AP, TR, MG
		Jute				
	Total				79.8	
	Gross				686.0	

3. Crops' residue generation: Terminologies used and methods for crops residue generation potential estimation

Crop residues are the by-product of crop production system. In literature crops' residue generated on production system is represented throught different terminologies. Similarly crop's residue generation potential is estimated by different methods. The crops residue generated is reported as - Residue to Product Ratio (RPR), Crop to Residue Ratio (CRR), (Gadde *et al.,* 2009; Hiloidhari *et al.,* 2014; Lohan *et al.,* 2018), Gross Crop Residue(CRg), Surplus crop residue (CRs). RPR is also termed as 'yield of crop residue' or straw-to-grain ratio (SGR).It represents the quantity of residue generated for each tonne of crop produced (Equation for calculation of RPR involves the mass of crop residue generated divided by the mass of crop produced) and units are dimensionless(Malik *et al.,* 2019).Inversely CRR corresponds to mass of crop produced divided by mass of residue produced. Some researchers suggested that same crop may have different RPR and CRR value depending upon the portion of crop (Chauhan 2012) (Table 5). For example an RPR range value of 0.416-0.452 for rice is when only top part of rice stem is being cut including 3-5 leaves and leaving the remaining portion in the field (Bhattacharya and Shrestha, 1990) similarly a RPR range value of 1.75-1.87 was reported when the rice stem was being cut at the height of about 2 inches above from the ground (Bhattacharya *et al.,* 1993; Vimal 1979). RPR varies with crop type, varieties, weather conditions, soil fertility, water availability, farming practices, fertilizers, moisture content.

The moisture content of fresh and air-dry crop residue biomass may vary significantly (like the difference of about factor 3 was found in the case of sugarcane bagasse). Estimation of the amount of crop residue generated using a RPR value without considering moisture content may results in inaccurate estimations.

The equation used by Lohan *et al.,* (2018) for the estimation of total residue generated is as follows:

Total crop residue generated (CRR) = The area covered by a particular crop (Ai) Yield of that crop (Yi) Crop to residue ratio of the crop (CRRi)

Table 5. RPR, CRR and Heating values for different crop residues and types

Crop	Residue type	CRR value	RPR value	Heating Value	References
Rice	Straw	1.20	1.5	15.54	Hiloidhari *et al.,* 2011
	Husk	0.16	0.2	15.54	Singh *et al.,* 2008
Wheat	Stalk	-	1.5	17.15	Singh *et al.,* 2008
	Pod	-	0.3	17.39	Singh *et al.,* 2008
	Straw	1.15	-	-	Chauhan , 2012
	Husk	0.16	-	-	Chauhan , 2012
Maize	Cob	0.30	0.2	17.39	Singh *et al.,* 2008
	Stalk	1.88	2	16.67	Singh *et al.,* 2008
Pearl Millet	Cob	0.25	0.33	17.39	
	Husk	0.22	0.3	17.48	Raveendran *et al.,* 1995
	Stalk	1.85	2	18.16	Friedl *et al.,*2005
Mustard and rapeseed	Stalk	1.72	1.8	17.0	Singh *et al.,* 2008
Soyabean	Stalk	-	1.7	16.99	Kis. *et al.,* 2009
Groundnut	Shell	0.26	0.3	15.56	Jekayinfa *et al.,* 2009
	Stalk	1.75	2	14.4	Jekayinfa *et al.,* 2009
Sunflower	Stalk	2.40	3	17.53	
Gram	Stalk	1.08	1.1	16.02	Singh *et al.,* 2008
Tur (Arhar)	Stalk	2.35	2.5	18.58	Singh *et al.,* 2008
Sugarcane	Bagasse	-	0.33	20	Singh *et al.,* 2008
	Top/Leaves	0.06	0.05	20	Singh *et al.,* 2008
Banana	Peel	-	3	17.4	Wilaipon *et al.,*2009
Areca nut	Frond	-	3	18.1	
	Husk	-	0.8	17.9	Pilon *et al.,* 2007
Coconut	Frond	-	4	10	Rahman *et al.,*2006
	Husk	-	0.53	19.4	Minowa *et al.,* 1998
Cotton	Stalk	1.00	3.8	17.4	Jekayinfa *et al.,* 2009
	Husk	-	1.1	16.7	
	Boll shell	-	1.1	18.3	Çağlar *et al.,*2001
Jute	Stalk	-	2	19.7	Asadullah *et al.,* 2008

The **gross crop residue (CRg)** can be defined as the sum total of crop residues produced for a particular crop. CRg for any crop is determined based on three important parameters such as area occupied by the particular crop, crop yield and RPR value for that crop. The formula for calculation using these parameters are as follows:

CRg = $\sum_{i=1}^{n} A \times Y \times RPR$

Here 'CRg' denotes the gross crop residue for n number of crops, in tonnes; and 'A' denotes the area covered by crop, in hectares; 'Y' denotes the yield of crop, in tonnes/hectare and RPR denotes the residue to product ratio the given crop.

Some scientists (Venkatramanan *et al.,* 2021) also used the formula as:

CRg = $\sum_{i=1}^{n} A \times Y \times RPR \times DM$

Where DM is the dry matter fraction of the selected crop.

The **surplus crop residue** of particular crop represents the amount of crop residues that are available for energy production after all the other competing uses such as cooking fuel, cattle feed, roof thatching, composting, animal bedding and others. The formula used to calculate CRs is as follows:

CRs = $\sum_{i=1}^{n} CRg \times SF$

Here 'CRs' denotes the surplus crop residue for n number of crops, in tonnes. CRs contributed by crops in total is around 209-234 MT/year which is only about 30-34% of gross crop residue (Venkatramanan *et al.,*2021; Hiloidhari *et al.,*2014). $\Sigma_{i=1}$

4. Factors regulating Crop residue uses

Crop residues are used in raw as well as in condensed form for various purposes. However crop residues in raw form are bulky, uneven and have low energy density as well as require more volume for storage and transporting this huge volume is a difficult task. Hence to make their handling, storage, transportation and utilization feasible, they are converted into more condensed briquette form

Figure 2. Loose and condensed(briquette)form of crop residues

(Figure 2). Managing a large amount of residue generated is a tedious task and for this the crop residues need to be converted into bales/briquettes for easy transportation. For making this process effective in practice, bailing and briquetting machines should be planted near the agricultural farms and should be accessible to each farmer. The raw as well as condensed form of crop residues have different physical properties(Pathak *et al.,* 1986; Mythili *et al.,* 2013; Vyas *et al.,* 2015; Sapariya *et al.,* 2016; Ecostan machineries) and are listed in Table 6.

Table 6. Physical properties of raw and condensed (briquette) form of crop resides

Residue names	**Bulk Density (Kg/m^3)**		**Moisture content (%) at (80-100 % relative humidity**		**Calorific-value (Mj/Kg)**		**Fixed carbon (%)**		**Volatile C (%)**		**Ash content (%)**	
	Raw form	Briquette	Raw form	Briquette	Raw form	Briquette	Raw form	Briquette	Raw form	Briquette	Raw form	Briquette
Arhar stalks	180	438.70	20.5	-	18.58	16.74	15.12	10.28	82.9	74.92	1.98	10.30
Sugarcane Baggasse	70	675	34.86	5.42	20	19.66	15.86	19.36	79.2	76.12	4.94	-
Cotton sticks	160	641.20	27.05	-	17.05	16.30	15.30	9.64	81.4	75.56	3.30	14.80
Groundnut shell	100	680	-	9.18	20.1	18.83	11.67	18.88	83.9	77.3	3.27	3.75
Maize stalks	50	-	38.08	-	16.70	15.89	17.10	-	79.6	-	3.40	-
Maize cobs	100	-	28.00	-	17.40	-	15.16	-	83.01	-	1.84	-
Rice straw	50	590	36.70	9.77	14.53	14.64	4.66	16.09	69.70	64.44	19.20	24.44
Rice husk	105	-	29.40	12.00	15.50	15.17	12.50	5.00	71.00	63.00	16.5	20.00
Wheat straw	60	591	34.0	-	17.20	17.15	12.30	-	85.73	75.95	8.80	11.75

Some important physical properties of crop residues are briefly discussed here.

Moisture Content (MC): The level of moisture percentage for any crop residue varies significantly depending on their storage and drying processes. The moisture content of crop residue has an important role in the formation of briquettes and subsequently its combustion also. Moisture content in the crop residues for briquetting must be between 8 and 15 % (Kazi and Mankad., 2020).On an average the moisture content of a briquette is 5.55 to 12.33 % (Kpalo and Zainuddin; 2020) The formula for moisture content is as follows:

MC (%) = (W1–W2/W1) x 100

Here, W1 denotes weight of sample taken before drying (in grams) and W2 denotes weight of sample taken after drying (in grams).

Bulk Density (BD): Bulk density is one of the major physical property playing role in designing the logistic system for crop residue handling. The factors affecting the BD may include particle density, shape, size, moisture content and other surface characteristics .Average density of crop residue briquettes ranges from 0.24-0.37 g/cm^3 (Kpalo *et al.,*2019). Different methods are used to estimate BD of briquettes such as geometric method, wax method and water displacement method. According to Rabier *et al.,* (2006), the formula for calculation of BD of briquettes by geometric method is as follows:

Bulk Density = Mass of briquette material / volume of briquette material

Tumbling Resistance: Tumbling resistance is the measure of per cent loss in weight of condensed crop residue form such as briquette subjected to tumbling action for a period of 5 min. Tumbling resistance is measured with the help of tumbling test in a durability tester using the following formula:

Tumbling Resistance (%) = 100 (Percent weight loss)

and Percent weight loss (%) = (W1–W2/ W1)x100%

Here, W1 denotes the weight of crop residue briquette before the tumbling (in grams) and W2 denotes the weight of crop residue briquette after tumbling (in grams).

Resistance to water penetration: It of percentage water absorbed by a crop residue briquette when immersed in water.

% Resistance to water penetration=100–(water gain%)

Water gain by residue (%)=[(W2–W1)/W1] x 100

Where W1 denotes the initial weight of residue, (in grams) W2 denotes the weight of wet residue (in grams).

Volatile Matter: Volatile matter in crop residues is the combination of short and long-chain hydrocarbons, aromatic hydrocarbons, and some sulphur compounds and it is a combination of CO, H2, H2O, CH4, CO2, N2 and O2. Under some conditions particularly when the air is absent, the volatile matter is driven off on heating the given sample to 950°C. Residue with higher content of volatile matter probably provide a high concentration of bio-oil. The higher percentage of volatile matter contributes to increase in calorific value and also produces long flames. The average value of VM for crop residue based briquettes is 68.20 % (Andrew and Gbabo; 2015).

Volatile matter (%) = [(b–c)/a]x100

Where a denotes the initial weight of the sample taken as 1g. b denotes the final weight of the sample after cooling (Heating temperature 107± 3 °C for 1 hour), c denotes the final weight of the sample after cooling (Heating temperature 950 ± 20 °C).

Fixed carbon: The fixed carbon of crop residue represents the amount of char produced during the process of pyrolysis. Fixed carbon in any sample can be determined by subtracting the total percentage of moisture, ash content as well as volatile matter from the initial mass. The formula for the calculation of fixed carbon is as follows:

Fixed Carbon (%) = 100–[Moisture(%)+Ash(%)+VM(%)]

Ash Content: Ash content represents the remaining inorganic residue left after the complete heating of a crop residue sample when all the organic matter and moisture removed particularly in presence of any oxidizing agent**.** Reduction in ash content enhances the calorific value as it is an incombustible matter. Therefore the ash content in any material should be as low as possible. Crop residue briquettes generally have low ash content. The formula for calculation of ash content is as follows:

Ash content (%) = [weight of ash left/ weight of sample taken]/10

Chemical composition of crop residues

Crop residues contains almost one fourth of phosphorus, nitrogen, around three fourth of potassium and half of the sulphur (S) that is up taken by different crops. Besides N, P and K crop residues are reservoir of several other elements also. And this makes the crop residues as a most important and valuable natural resource (Pathak *et al.,* 1986; Sapariya *et al.,* 2016; Singh *et al.,* 2020).The elemental composition of different crop residues are given in Table 7.

Table 7. Selected crops' residues chemical composition

Crop residues	**Chemical Composition (%)**										
	C	**H**	**N**	**Na**	**K**	**P**	**Mg**	**Ca**	**SiO2**	**O**	**S**
Sugarcane Baggasse	48.20 57.20 (B)	6.10 3.98 (B)	0.20 1.84 (B)	0.06	0.51	0.04	0.36	0.14	1.30	44.40 37.78 (B)	0.01
Arhar stalks	53.30	4.70	0.60	0.05	0.57	0.08	0.40	0.11	0.68	-	-
Cotton sticks	51.00	4.90	1.00	0.09	0.61	0.08	0.43	0.12	1.33	43.87	0
Groundnut shell	41.10 16.49 (B)	4.80 16.42 (B)	1.60 0.28 (B)	0.05	1.20	0.12	0.40	0.10	2.52	- 68.79 (B)	-
Maize stalks	41.10	4.20	0.60	0.04	0.42	0.05	0.45	0.08	0.90	-	-
Maize cobs	46.20	4.90	0.60	0.03	0.54	0.07	0.28	0.09	2.00	-	-
Rice straw	36.80	5.00	1.00	0.09	2.50	0.06	0.53	0.08	15.60	40.50	0.02
Rice husk	37.80 45.20 (B)	5.00 5.8 (B)	0.30 1.02 (B)	0.02	0.30	0.03	0.17	0.10	15.77	35.45 47.6(B)	0.03
Wheat straw	43.80	5.40	1.00	0.06	0.78	0.04	0.35	0.10	7.08	-	-

Here 'B' stands for briquettes and other values are for raw form of crop residues

5. Crop residue management options in practice

The crop residues management can be categorised based on the site of generation (Figure 3):

1. On-farm
2. Off –farm

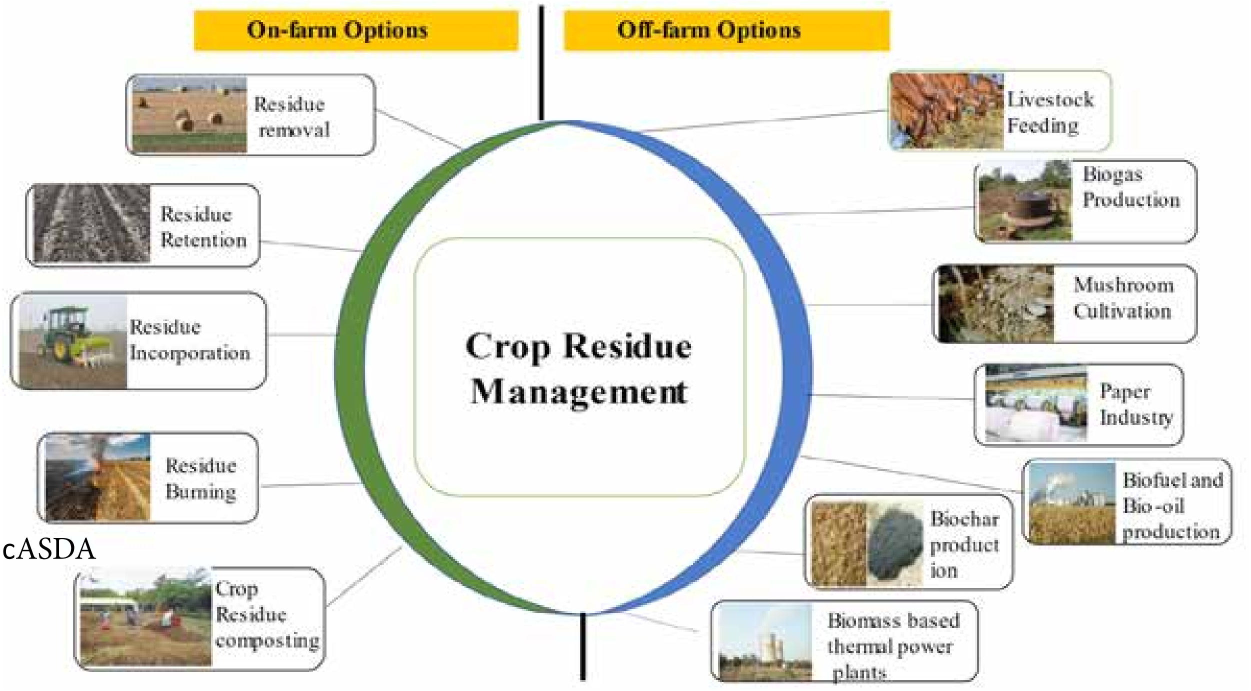


Figure 3. Crop residue management options

5.1. On farm generated residue management options: The management of residues on the point of origin i.e., farmers field itself without the need of transporting them is considered as on farm management. Some common on farm management options are:

- Residue removal
- Residue retention
- Residue uses as mulch
- Residue incorporation
- Residue Burning
- Composting of residues

Residue removal

The crop residues such as straw, husk etc. produced after harvest are removed from the field for various competing purposes. However limited number of studies assessed where, when, and how much of crop residue can be removed without causing serious adverse impacts on soil, NPP, and the environment (Wilhelm *et al.,* 2007). For example it has been reported that in case of corn stover, about 30% to 50% of the total stover produced can be removed without causing severe adverse impacts on soil (Kim and Dale, 2004; Graham *et al.,* 2007). Removal/ bailing/briquetting practice of residues generally being utilised for cattle fodder, as a cooking fuel and stable animal bedding or as raw material in various industrial processes (Lal,. 2008). However residue removal in certain cases can adversely affect soil quality. Hence estimation of sustainable residue removal rates is important to maintain good soil quality (Lal.,2008, Andrews.,2006). For instance, the rates for residue removal should be less when the climate become more warm or humid, when the soil become coarser, when there is more tillage/disturbances in soil (Raffa *et al.,* 2015).

Residue Retention

Leaving the crop residues after harvest as such on the farms ground is called as residue retention. Crop residue retention on the soil surface has been recommended by many agriculture scientists for maintaining soil physico-chemical, and biological properties (Wilhelm *et al.,* 2007). Farming practices that involve reduced/minimum or zero tillage such as conservation agriculture supports a permanent or semi-permanent organic soil covering. Happy seeder and turbo happy seeder machineries are being used to sow the next crop over the surface retained residues in the field (Figure 4).

Figure 4. Sowing of crop seeds through happy seeder in farms having residue retention

Crop residue as surface mulch

Mulching is one of the emerging crop residue management option to avoid burning. It is a conservational management practice in which crop residue (rice/wheat straw) are chopped/shredded into smaller pieces and evenly spread on the ground. For chopping, Super Straw Management System (SSMS) (Figure 5) is attached to the combine harvester and shredding of residues require an added run of mulcher as well as cutter/spreader (mounted onto a tractor) after the harvesting of the field. The field covered with mulch is sown using happy seeder following conservational method that is zero-tillage. It sows wheat in a field covered with mulch.

Figure 5. Super Straw Management System(SMS)machine while chopping and shredding the crop residues in the field creating a surface mulch

Residue incorporation

Residue incorporation can be defined as the use of tillage implements for burying remnant crop residues into soil and has traditionally been used for returning of organic matter back to the soil. This form of tillage buries all superficial crop residues in the soil (Tisdale *et al.,* 1985). Incorporation of residues involve primary tillage by mal board plowing and is the followed by secondary tillage involving disking, harrowing or field cultivating(Figure 6). Another way to incorporate residues is using zero till drill machine or roto- till drill while sowing the wheat crop in rice straw and stubbles. Zero-till which is seed-cum-fertilizer drill has poor efficacy when straw retained on field build up in the seed drill furrow openers that reduces seed sowing efficiency and results in poor seed germination (Sidhu *et al.,* 2015).

Figure 6. Incorporation of crop residues in field through different machineries.
(a. Malboard plow, b. Disk c. Harrow)

Residue burning

Burning of crop residue is an uncontrolled combustion process(Figure 7) which releases CO_2 as a principal component, along with carbon monoxide (CO), un-burnt carbon which has amount of sulphur dioxide (SO_2). Out of 686 MT residue biomass, approximately 16%of crop residues were burnt on fields in which rice and wheat together contribute 62% (Jain *et al.,* 2014). This burning incidents are majorly confined to Indo-Gangetic Plains regions. Studies suggest that Punjab, Uttar Pradesh and Haryana are major potential contributor states for harvesting of cereal crops and on-field burning of their residues. It has been estimated that total 1.95 Million ha area was under paddy residue burning during 2015(Singh *et al.,*2020) in Punjab and Haryana, by different remote sensing agencies in the country (PPCB 2015; Yadav *et al.,* 2015). According to IPCC, over 25% of the total crop residues were burnt on the farm (Jain *et al.,* 2014) and the fraction of crop residue burned ranged from 8–80% for paddy waste across all states. It is the most common and preferred on-farm residue management option for most of the farmers due to cost and time effectiveness as well as shortage of labour, increased mechanisation, destruction of pests and unsuitability of rice straw as cattle feed(Lohan *et. al.,* 2018).

Figure 7. Open burning of crop residues in farmer's paddy fields (a: Before burning, b: After burning)

Crop residues as compost

Composting is a natural process of decomposition by aerobic and anaerobic micro-organisms under controlled conditions and they convert crop residue into a valuable manure or compost with additional advantage in terms of nitrogen, phosphorous sand potassium (NPK) (Mishra *et al.,* 2003). Crop residues are considered as ideal raw material such as animal manure and food waste because of its high organic matter content. It can be made on the farm at very low cost and can be used as organic fertilizer (Bhuvaneshwari *et al.,* 2019; Kaur *et al.,* 2019). Composting involves labour input, but it is not capital intensive and does not require sophisticated infrastructure machinery(Goswami *et al.,*2020).

Researchers have demonstrated successful trials using some microbes (*Aspergillus terreus* MTCC 11778 and *Trichoderma hargianum* MTCC 8230) assisted on-site composting of paddy residues and thereby providing an alternative to most common practice of residue burning(Singh.,2015, Hindustan Times).Other trial demonstrated that bacterial isolate (Pseudomonas) obtained from naturally degrading paddy straw caused the decomposition of paddy straw within 45 days with application of only 5% urea after shortening of straw by using happy seeder machine. In this treatment there was no any requirement to gather the straw in large heap which saves extra space and efforts. Another group of researchers developed and reported microbial consortium based (crop friendly fungi) decomposing capsules known as **PUSA decomposer** for decomposing paddy crop residue (Zaidi, 2021). Four capsules are capable of turning one hectare of farm waste into usable compost. Each capsule costs around 5-10 Rs. Using these capsules, the field retains moisture during decomposition process of agricultural waste, and the soil is enriched with nutrients present in residues and thus minimizing the use of fertilizer.

5.2. Off Farm crop residue management options

There are a number of ways in which the crop residues can be managed ex -situ or off-farm but the common limitations with ex-situ operations are high cost of collection and transportation.

Crop residue for livestock feed

The crop residues are the major feed resources that are available and utilised by smallholder farmers in tropical livestock feeding system. Most of the crop residues are having high nutritional values and are thus suitable for animal feed like wheat straw have high nutritional value and therefore they are collected intensively, stored and then used around the year as feed with sale of surplus. Based on the type of crop, these residues may be either left on the field for grazing of ruminants or may be transported for other livestock feed at market values. In India buffalo are stall-fed with the basal diet called as 'bhusa' that primarily consist of hewed wheat straw. In case of lactating animals this basal diet is given along with supplementation of green fodder and some bi-products of crops. But rice straw is not suitable for livestock feedings because of high silica (6-12%) content and low nutritional contents (Protein 2-7%) (Lohan *et al.*,2018). Also rice straw feeding causes calcium and phosphorous imbalance in cattle (Moellers and Riese,1979). For encouraging the use of rice residue as animal fodder, a pilot project was initiated which involved trials on natural fermentation of rice straw to be used as protein enriched livestock feed and those cattle fed with this feed exhibited a significant improvement in their health and milk production (Kumar *et al.,* 2015).

Crop residue for production of biofuel and bio-oil

Crop residues are rich source of lignin and the production of alcohol from lingo-cellulosic biomass has immense significance. Bioethanol can be blended with petrol and diesel and can thereby reduces the harmful emissions in transport sector. Apart from sugarcane molasses, rice straw can also be the ideal (easily available in plenty amount at cheapest rates) feed stock for biofuel production by converting it into sugary slurries. As per theoretical information the estimates of ethanol production from different kind feedstocks such as corn grain, wheat straw, rice straw, sugarcane bagasse, saw dust etc. vary from 382 to 471 l/t of dry matter (Thorat *et al.,* 2015; Gupta and Dadlani., 2012). This technology is evolving in India but has certain limitations because of some energy and cost intensive conversion steps. Also rice straw is resistant to microbial attacks during the conversion processes because of having phenolic monomers in its structure (Sharma *et al.,* 2018).

Bio-oil is also produced from variety of crop residues by the process involving fast pyrolysis which require temperature of biomass to be raised up to 400-500 ^{0}C within few seconds and it may result a significant change in the process of thermal disintegration. Almost 75% of biomass' dry weight can be converted into condensable vapours. This condensate is allowed to cool quickly and it yields a dark brown coloured viscous liquid which is called as bio-oil. The calorific value of bio-oil ranges from16-20 MJ/kg (Gupta and Dadlani.,2012).

Crop residue for biogas generation

Gasification of crop residues is generally a thermo-chemical process involving the formation of gas due to partial combustion of residues. Crop residues are used in gasifiers for generation of 'Producer Gas'. This gas is being cleaned using bio-filters and then fed into the specially designed engines which are coupled with alternators to produce electricity. One tonne of crop biomass have the capacity to produce 300 kWh of electricity (Koopman *et al.,*1997; Lohan *et al.,* 2018). This technology of gasification can be encountered for successful utilization of crop residues in the form of briquettes and pellets.

Crop residues for mushroom cultivation

Crop residues including rice straw can be used for cultivation of mushrooms. In Punjab rice straw is used as key ingredient for culture of mushroom, but farmers commonly utilize wheat straw as raw material. It is basically used for cultivation of *Agaricus bisporus, Pleuro tusspp., Volvariella and Volvacea*. Around 300, 600,120–150 g of these mushrooms are formed from 1Kg of paddy straw respectively (Kumar *et al.,*2015). Production process involves operations like straw washing and excess water draining, straw cutting and bundle preparations. Presently around 20,000 Metric tonnes of crop residues are being used for cultivation of mushroom solely in Punjab state. Roy *et al.,* (2016) revealed that the estimated cost for using paddy straw as raw material is 7$ per quintal whereas it is 11$ per quintal when using wheat straw as raw material for mushroom cultivation. Thus the use of paddy straw is an economic source for mushroom growers that provides a net saving of 3.75$ per quintal. Paddy straw based mushroom cultivation accounts for 16 % of total production of cultivated mushroom in the world. Straw based mushroom are also a good source of amino acids and can supplement a protein rich diet(Goswami *et al.,*2019). In fact paddy residue mushrooms are easy to grow and require very less space and cost investment.

Crop residues in paper production

Rice and wheat straw are used in combination in the ratio of 40:60 respectively for the production of paper. The sludge thus produced then undergoes bio-methanization process for generation of energy. Paddy residue alone can also an ideal raw material for manufacturing of paper and pulp boards. There are around more than 50 % pulp board mills and paper industries that are utilizing paddy residues as their raw material (Kumar *et al.,*2015).

Crop residues for biochar production

Biochar is a very important C-rich substance which is fine grained and porous product of a thermo-chemical conversion reactions known as 'pyrolysis' which occurs at low temperatures and in an oxygen free (Bhuvaneshwari *et al.,*2019) environment. It has relatively stable biological state that is resistant to microbial decay so it can be considered as one of the important long term carbon sink that can sustain soil productivity, mitigate climate change and can be an emerging option for diverting the residue burning. Biochar produced from crop biomass, when applied to the soil enhances soil fertility,causes reduction in leaching of nutrients and other chemicals to enhance soil carbon, increases fertiliser use efficiency, mitigate soil greenhouse gas emissions and thereby enhances the overall productivity of agricultural system (Chan *et al.* 2008).

Crop residue for energy generation

Crop residues can be utilised to produce energy. In literature it has been reported that currently surplus crop residue is utilized for bio energy generation. The India's bioenergy potential from surplus residues is 4.15 EJ. Among different crops sugarcane bagasse has the potential role in bioenergy generation. Other cereal crops have major role in animal feeding, packaging material apart from energy generation. The bioenergy potential (BE) of any crop is the amount of energy produced by the surplus fraction of crop residues. The formula used for calculation is as follows:

$$\mathrm{BE} = \sum_{i=1}^{n} \boldsymbol{CRs} \times \boldsymbol{HV}$$

Here, 'BE' denotes the bioenergy potential of n crops, in M-Joules; CRs denotes the surplus crop residue, in tonnes and 'HV' denotes the heating value of the crop, in MJ tonnes.

Biomass based power plants prefer to utilise different crop residues like sugarcane trash, cotton stalks, groundnut shell, rice husk, wood chips, mustard stalk and cluster bean straw over the rice straw because of low heating value of rice straw which results in low profit margins (Suramaythangkoor and Gheewala, 2010). Punjab produces around 20–25 Million tonnes rice straw annually which is now a days being utilized in thermal plants. At recent times in Punjab, the boilers using 25–30% rice straw with 70–75% other biomass. A12 MW capacity rice straw power plant demands around 0.12 Million tonnes of straw to produce energy (Singh *et al.,* 2020). It is estimated that on average basis a power industry pays around 900 Rs. per tonne for non-basmati (straw from coarse varieties) and approximately 1500 Rs. for basmati rice (fine grain rice varieties).

Other competing uses of crop residues: Crop residue can also be used for making bedding of cattle, can be used as domestic fuel, cushioning material, packaging of manufactured items such floor tiles, glass etc.

6. Crop residue management options: Benefits, drawbacks and limitations

Though there are diverse on and off farm generated residue management options available at present time for managing the surplus crop residues. But each options have pros and cons both with respect to economic viability, environmental impacts, lack of knowledge, access to machineries to small land holding farmers, costly machineries affecting adoption rate (Table 8 and Table 9).

Table 8. On farm crop residue management options' benefits, drawbacks and limitations

Crops' residue management option (On farm)	Benefits	Drawbacks	Limitations for adoption
Residue Removal	Residue removal from the fields in the form of bales/briquettes make them accessible to various household and industrial uses.	Residue removal sometimes results in low biomass carbon input and decrease in nutrient/elemental cycling (Lal., 2008.)	In some cases logistic issues in transportation of these removed crop residues to longer distances adds to additional costs. (Bhuvaneshwari *et al.,*2019).

		Also it reduces food/energy source as well as habitat for soil biota along with the attendant decline in soil quality((Lal., 2008). Therefore sustainable rates for residue removal should be determined as discussed in section 5.1.	
Residue Retention	Improves soil physico-chemical and biological properties including cation exchange capacity, soil microbial biomass carbon and soil enzyme activities (Wilhelm *et al.,* 1986; Wilhelm *et al.,* 2007; Lohan *et al.,* 2018). Help in carbon sequestration in the soil (Jain *et al.,*2014). With No-Tillage improve water and air quality through reduction in soil erosion (through water and wind), non-point source pollution, sedimentation, and transport of different pollutants into aquatic ecosystems.	Zero till drill has poor efficacy over surface retained residue and thus reduces seed sowing efficiency and results in poor seed germination due to straw build up in seed furrows (Sidhu *et al.,* 2015).	Zero till -drill, happy-seeder consumes high power(> 33.6 kW). Choking of the machine with intense loads of straw(> 7–8 Mg ha—1) occurs sometime. Poor establishment of crops (Sidhu *et al.,* 2015).
Residue Incorporation	Improves soil water retention capacity (Gangwar, et al 2006; Kumar et al 2016). Improves soil structure by reducing bulk density, increasing infiltration rate and soil porosity(Lohan *et al.,* 2018). Enhances soil microbial biomass, alkaline phosphatase and soil dehydrogenase activities (Peter *et al.,* 2014).	Stimulation of CH_4 emissions on short term basis (Singh and Sidhu 2014). Crops suffers N-deficiency due to microbial immobilization of soil and fertilizer N (Singh *et al.,*2005; Goswami *et al.,*2020).	Residue decomposition takes times so significant fallow period is necessary between two successive crops (Goswami *et al.,* 2020). Labour intensive if proper machinery is not available to every farmer (Dobermann and Fairhust 2002). The high C:N ratio of residue needs to be corrected by applying extra fertilizer N at the time of residue incorporation(Singh et al. 2005; Singh *et al.* 2008).
Residue Burning	Controls harmful weeds, soil pest and pathogens (Gupta.,2012; Gupta and Dadlani.,2012). Increases short term availability of exchangeable NH_4^+-N and bicarbonate-extractable P content and Potassium (Gupta and Dadlani.,2012). Easy and time saving option for a narrow window between rice-wheat crops (Jain *et al.,* 2014).	Sudden increase in soil temperature (33.8-42^{0}C) results in death of beneficial microbes(Gupta *et al.,*2004; Gupta and Dadlani.,2012). Long-term burning practice of crop residues decreases total carbon and nitrogen and potentially mineralizable nitrogen in the 0–150 mm soil layer(Gupta et.al., 2004; Singh et.,2010) Degrade air quality and indirectly affects human health.1 tonne of paddy residue burning generates almost 1460 kg carbon dioxide, 3 kg particulate matter, 2 kg of sulphur dioxide ,60 kg carbon mono oxide and 199 kg ash in the air and which consequently (Lohan *et. al.,* 2018). 70%, 7% and 0.66% of C present in paddy straw is released as CO_2, CO and CH_4, respectively upon burning these residues. Around 2.09% of N in straw is emitted as N_2O (Galanter *et al.,* 2000) Support heavy smog problem in adjoining regions during the winter season (Manjeet *et al.,*2019).	No limitations as such.

Composting	Improve soil structure and moisture content and therefore support microbial activity and diversity. Replenish soil carbon stock and restore plant nutrition by adding nutrients from residues to soil.	Results in establishment of suitable habitat for rodent pests and undesirable presence of immobilized residual N(Porichha *et al.,* 2021).	Requires additional chemicals and controlled conditions. Decomposition of residues takes time so more time gap required between two crops (Goswami *et al.,* 2020).

Table 9. Off farm crop residue management options' benefits, drawbacks and limitations

Off farm Crop residue management option	Benefits	Drawbacks	Limitations
Consumption for livestock feed	Source of various nutrients, energy supply and natural support to various food webs.	Enteric fermentation of crop residues in cattle may lead to GHGs emission such as methane(State of Indian Agriculture,2015-16).	Some crop need pre-treatment to be used as fodder which incur extra cost and effort (Kamla *et al.* 2015) Rice straw require extra pre-treatment because it contains silica which has very low digestibility and high palatability (Biswas *et al.* 2006). Rumen micro-organisms' limited ability to digest cell wall polysaccharides (cellulose and hemicellulose)is due to the presence of phenolic and other aromatic compounds such as lignin(Gupta and Dadlani., 2012)in residues.
Biofuel and Bio-oil production	It is best alternative option for fossil fuel consumption and a renewable source of energy. Biomass based biofuels are source to reduce GHGs. By-products of biofuel production such as proteins can be used for animal feed can make a positive contribution to climate change mitigation.	High amount of crop residues are required for biofuel generation and extensive residue removal for this purpose can cause soil losses. Partial removal can be feasible without jeopardizing sustainability provided inputs of K, S, and other nutrients are suitably adjusted to compensate for those removed with residue. (Singh *et al.,* 2014). Also this creates pressure for production of high energy crops That sometimes lead to soil erosion,	The process requires high energy operating conditions, various hydrolytic cellulase enzyme that comes costly,. (Bhagawati *et al.,* 2020). Also lack of natural robust commercial organism which can ferment pentose and hexose sugars simultaneously either individually or in combination with other species poses some basic limitations to this option (Bhagawati *et al.,* 2020).
Biogas production	It's a clean energy source and reduces GHGs emissions. Anaerobic digestion deactivates pathogens and some parasites and reduce the chance of waterborne diseases. Provide healthy cooking alternative in developing areas.	Few studies also reported contradicting facts that in some cases specially during incomplete combustion of biogas some air pollutants such as CO, NO, $CH4$ also releases during production. Therefore correct assessment of these emissions is a key point in social acceptance of this technology (Paolini *et al.,*2018).	Process requires purification of gas for removal of impurities and that need special bio filters that is also not cost effective for every kind of farmers.

Biochar production	Potential option to sequester soil carbon, improve soil quality and promote plant growth (Bhagawati *et al.,* 2020). Enhances nitrogen retention in soil by reduction in leaching and gaseous loss. It also increases phosphorus availability by reducing the leaching process in soil. (Hossain *et al.,* 2020) Improves microbial populations, enzyme activity, soil respiration, and microbial biomass.	Negative effects on some important soil properties including soil available water content, soil salinity, soil erosion (Brtnicky *et al.,* 2021).	The biochar production technology is not economically viable as the products and co-products (Heat energy, bio-oil, H2 gas) involved are costly (Bhagawati *et al.,* 2020). Need to develop low-cost pyrolysis kiln (Bhagawati *et al.,* 2020).
io-energy production	The energy generated is used for heat production, electricity generation.	Residue based energy plants generates large amount of ash waste (Hills *et al.,* 2020) if not managed properly affect air quality of the region.	Crop residues are having low bulk density and low energy yield per unit weight basis and transportation of large volume needed for efficient energy production is a major cost barrier. (Thorat *et al.,*2015). Rice straw having low heating value is less profitable for energy generation Suramaythangkoor and Gheewala,2010).

7. Policy interventions for crop residue management options

The Indian Government and the national agencies are continuously taking step to develop policies and other options in order to manage the crop residues in sustainable way.

i. Ministry of Agriculture & Farmers Welfare for have implemented a Central Sector Scheme (which include 100% Central share) for the period of 2018-2019 and 2019-2020 which is further extended for 2020-2021 in order to support the efforts of the Governments of Uttar Pradesh, Punjab and Haryana and NCT of Delhi for addressing air pollution and to subsidize machinery required for in-situ management of crop residues.

The key components of this scheme are:

- Establish Farm Machinery Banks for Custom Hiring of in-situ crop residue management machinery.
- Financial Assistance to the farmers for Procurement of Agriculture Machinery and Equipment for in-situ crop residue management.
- Information, Education and Communication for awareness on in-situ crop residue management.

ii. The Nature Conservancy (TNC), the largest conservation non-profit in the world, launched a project in 2019 to promote sustainable in situ CRM in the states of Punjab and Haryana to complement the efforts of the government.

iii. The Indian Government directed National Thermal Power Corporation (NTPC) for mixing crop residue pellets(approximately 10%) with coal for the purpose of power generation(Patial *et al.,*2020).

iv. Government of India has adopted two ways to curb the open field burning, under NPMCR,2014(National Policy for Management of Crop Residues).

First one is to give emphasis on developing huge awareness among farmers about the ill effects of residue burning and imposing heavy charges on the famers that still practice burning.

And the second approach is promotion of agricultural equipment that are involved in management of crop residues.

v. NPMCR also brought interventions through extending subsidy for the farmers to hire resource conservation machineries from different Custom Hiring Centers (CHS)/Agriculture Service Centers (ASC),and also promoting the establishment of new CHS/ASC for ensuring availability of different machines to the farmers at the time of crop harvesting. (NMPCR, 2014).

vi. In order to motivate farmers to change residue burning practice, rotavator machine/SSMS was introduced in the NICRA (National Innovations for Climate Resilient Agriculture) villages. This machine chops the harvested crop stalks/ stubbles a into small pieces and then incorporate them in-situ into the soil with varying efficiencies depending upon the left over residue.

vii. Punjab government is promoting 100% rice straw-based power plant in order to set a target for using 1 million tonnes rice straw with 200 MW capacity in coming future (PSCST 2013).

viii. Punjab Government and Gramin Vikas Trust signs MoU for establishing biogas pellets plants for ex-situ management of crop residues in sustainable way by incentivizing ex-situ extraction of residues(The New Indian Express report dated on October 12,2022).

ix. As per latest information Punjab Government is going to supply paddy straw to Kerala where it will be used as dry fodder therefore this will solve the problem of paddy straw management in in Punjab to some extent, where paddy straws are not used as cattle feed(The Tribune, November 24, 2022).

8. Conclusion

It can be said based on the benefits of crop residues that they are not a waste but an important natural resource to be used for various purposes. But still many farmers' community is unaware about the potential uses of crop residues and the revenue generation through it which make them find residue burning the easiest and cost effective option. The surplus amount available in India for crop residues is 234 Mt available for energy generation potential of 4.15Ej. Therefore there should be increased awareness programmes for giving idea about alternative options of crop residue management, machineries and resources involved, their cost-effectiveness, their pros and cons, training programmes to use those different machineries, and handholding to make the permanent switch to in-situ crop residue management options .On-farm management options need to be promoted and research should be strengthened to develop fast residue decomposition promoting microbes consortia so that farmers can utilize residue as organic fertilizer. More custom Hiring Centres should be set up under the scheme to provide easy access of farm machinery on rent to small-scale farmers and also should be made popular through these awareness programmes. Though numerous researches have been done in this field but it is important to convey the findings to the farmers in a convincing and understanding ways such as seminars and visual representations, animations for different aspects of each options. There should be introduction of C-credit schemes to benefit the farmers who use crop residue for conservation agriculture for carbon sequestration and greenhouse gas emissions mitigation. Also a community level approach should be there to reach out as much farmers as possible to spread the information related to crop residue management options and a nexus of stakeholders of different fields not only limited to agriculture should be there to deal with the issue

Author's contribution

Conceptualization of research (DS and UM); Designing of the experiments (DS and UM); Contribution of experimental materials (DS and UM); Execution of field/lab experiments and data collection (DS and UM); Analysis of data and interpretation (DS and UM); Preparation of the manuscript (DS and UM).

Declaration

The authors declare no conflict of interest.

9. References

1. Andrew, N.E. and A. Gbabo. 2015. The physical, proximate and ultimate analysis of rice husk briquettes produced from a vibratory block mould briquetting machine.
2. Andrews, S.S. 2006. Crop residue removal for biomass energy production: Effects on soils and recommendations.
3. Bhagawati, R., S. Paul and A.S. Dambale. 2020. Chapter-5 Farm Waste Management. *AGRONOMY*, p.77.
4. Bhattacharya, S.C., S. Sett and R.M. Shrestha. 1990. Two approaches for producing briquetted charcoal from wastes and their comparison. *Energy*, *15*(6), pp.499-506.
5. Bhuvaneshwari, S., H. Hettiarachchi and J.N. Meegoda. 2019. Crop residue burning in India: Policy challenges and potential solutions. *International journal of environmental research and public health*, *16*(5), p.832.v
6. Biswas, P.K., A Goswami, B.K. Biswas, B.K. Chand and A. Biswas. 2002. Studies on improvement of poor quality paddy straw through urea-molasses-mineral mixture treatment on intake and milk production in cows. *Journal of Interacademicia (India).*

7. Brtnicky, M., R. Datta, J. Holatko, L. Bielska, Z.M. Gusiatin, J. Kucerik, T. Hammerschmiedt, S. Danish, M. Radziemska, L. Mravcova and S. Fahad, 2021. A critical review of the possible adverse effects of biochar in the soil environment. *Science of the Total Environment*, *796*, p.148756.

8. Cardoen, D., P. Joshi, L. Diels, P.M. Sarma and D. Pant. 2015. Agriculture biomass in India: Part 1. Estimation and characterization. *Resources, Conservation and Recycling*, *102*, pp.39-48.

9. Chan, K.Y., L. Van Zwieten, I. Meszaros, A. Downie and S. Joseph. 2008. Agronomic values of greenwaste biochar as a soil amendment. *Soil Research*, *45*(8), pp.629-634.

10. Chauhan, S. 2012. District wise agriculture biomass resource assessment for power generation: A case study from an Indian state, Punjab. *Biomass and Bioenergy*, *37*, pp.205-212.

11. Crop Residues, their Types, Management and Uses, 12, May 2021 Crop Residues, their Types, Management and Uses (farmpractices.com). (Accessed on 20.11.2022).

12. Dobermann, A.T.H.F. and T.H. Fairhurst. 2002. Rice straw management. *Better Crops International*, *16*(1), pp.7-11.

13. EcoStan machineries, Calorific Value of Different Agricultural & Forest Waste (ecostan.com). (Accessed on 2 January 2022).

14. FAO, BEFS Rapid Appraisal., Natural Resources Module., 2014. Agricultural Residues Component.,Crop residue and livestock residue.

15. Friedl, A., E Padouvas, H. Rotter, K. Varmuza, 2005. Prediction of heating values of biomass fuel from elemental composition. *Anal Chim Acta*, 544, pp.191–8.

16. Gadde, B., C. Menke and R. Wassmann. 2009. Rice straw as a renewable energy source in India, Thailand, and the Philippines: Overall potential and limitations for energy contribution and greenhouse gas mitigation. *Biomass and bioenergy*, *33*(11), pp.1532-1546.

17. Gangwar, K.S., K.K. Singh, S.K. Sharma and O.K. Tomar. 2006. Alternative tillage and crop residue management in wheat after rice in sandy loam soils of Indo-Gangetic plains. *Soil and Tillage Research*, *88*(1-2), pp.242-252.

18. Goswami, S.B., R. Mondal and S.K. Mandi. 2020. Crop residue management options in rice–rice system: a review. *Archives of Agronomy and Soil Science*, *66*(9), pp.1218-1234.

19. Graham, R.L., R. Nelson, J. Sheehan, R.D. Perlack and L.L. Wright. 2007. Current and potential US corn stover supplies. *Agronomy Journal*, *99*(1), pp.1-11.

20. Gupta, H.S. and M. Dadlani. 2012. Crop residues management with conservation agriculture: Potential, constraints and policy needs. *New Delhi: Indian Agricultural Research Institute.*

21. Gupta, P.K., S. Sahai, N. Singh, C.K. Dixit, D.P. Singh, C. Sharma, M.K. Tiwari, R.K. Gupta and S.C. Garg. 2004. Residue burning in rice–wheat cropping system: Causes and implications. *Current science*, pp.1713-1717.

22. Gupta, R., 2012. *Causes of emissions from agricultural residue burning in north-west India: evaluation of a technology policy response.* SANDEE.

23. Hills, C.D., N. Tripathi, R.S. Singh, P.J. Carey and, F. Lowry. 2020. Valorisation of agricultural biomass-ash with CO2. *Scientific reports*, *10*(1), pp.1-14.

24. Hiloidhari, M. and D.C. Baruah. 2011. Crop residue biomass for decentralized electrical power generation in rural areas (part 1): Investigation of spatial availability. *Renewable and Sustainable Energy Reviews*, *15*(4), pp.1885-1892.

25. Hiloidhari, M., D. Das and D.C. Baruah. 2014. Bioenergy potential from crop residue biomass in India. *Renewable and sustainable energy reviews*, *32*, pp.504-512.

26. Hossain, M.Z., M.M. Bahar, B. Sarkar, S.W. Donne, Y.S. Ok, K.N. Palansooriya, M.B. Kirkham, S. Chowdhury and N. Bolan. 2020. Biochar and its importance on nutrient dynamics in soil and plant. *Biochar*, *2*(4), pp.379-420.

27. Jain, N., A. Bhatia and H. Pathak. 2014. Emission of air pollutants from crop residue burning in India. *Aerosol and Air Quality Research*, *14*(1), pp.422-430.

28. Jekayinfa, S.O. and V. Scholz. 2009. Potential availability of energetically usable crop residues in Nigeria. *Energy Sources, Part A: Recovery, Utilization, and Environmental Effects*, *31*(8), pp.687-697.

29. Kaur, K., P. Kaur and S. Sharma. 2019. Management of crop residue through various techniques. *Management*, pp.618-620.

30. Kaur, P., G.S. Kocher and M.S. Taggar. 2019. Enhanced bio-composting of rice straw using agricultural residues: an alternate to burning. *International Journal of Recycling of Organic Waste in Agriculture*, *8*(1), pp.479-483.

31. Kim, S. and B.E. Dale. 2004. Global potential bioethanol production from wasted crops and crop residues. *Biomass and bioenergy*, *26*(4), pp.361-375.

32. Kiš, D., B. Sučić, V. Guberac, N. Voća, V. Rozman. and L. Šumanovac. 2009. Soybean biomass as a renewable energy resource. *Agriculturae Conspectus Scientificus*, *74*(3), pp.201-203.

33. Koopmans, A. and J. Koppejan. 1997. Agricultural and forest residues-generation, utilization and availability. *Regional consultation on modern applications of biomass energy*, *6*, p.10.

34. Kpalo, S.Y. and M.F. Zainuddin, 2020. Briquettes from Agricultural Residues; an alternative clean and sustainable fuel for domestic cooking in Nasarawa state, Nigeria. *Energy and Power*, *10*(2), pp.40-47.

35. Kpalo, S.Y., M.F. Zainuddin, H.A. Halim, A.F. Ahmad and Z. Abbas. 2019. Physical characterization of briquettes produced from paper pulp and Mesua ferrea mixtures. *Biofuels*, pp.1-8.

36. Kumar, P. 2015. The Extent and Management of Crop Stubble. *Socioeconomic and Environmental Implications of Agricultural Residue Burning, Springer Briefs in Environmental Science*.

37. Lal, R., 2004. Is crop residue a waste?. *Journal of Soil and Water Conservation*, *59*(6), pp.136A-139A.

38. Lal, R. 2005. World crop residues production and implications of its use as a biofuel. *Environment International*, *31*(4), pp.575-584.

39. Lal, R. 2008. Crop residues and soil carbon. *Proceedings of the Conservation Agriculture Carbon Offset Consultation, Lafayette, IN, USA*, *2330*.

40. Lohan, S.K., H.S. Jat, A.K. Yadav, H.S. Sidhu, M.L. Jat, M. Choudhary, J.K. Peter and P.C. Sharma. 2018. Burning issues of paddy residue management in north-west states of India. *Renewable and Sustainable Energy Reviews*, *81*, pp.693-706.

41. Malik, J.S. and S. Kumar. 2019. Crop Residue Burning: Issue and Management for Climate-Smart Agriculture in NCR Region, India. *Asian Journal of Agricultural Extension, Economics & Sociology*, pp.1-11.

42. Malik, K., J. Tokkas, , R.C. Anand and N. Kumari. 2015. Pretreated rice straw as an improved fodder for ruminants-An overview. *Journal of Applied and Natural Science*, *7*(1), pp.514-520.

43. Manjeet, M.J. and S. Kumar. 2019. Crop Residue Burning: Issue and Management for Climate-Smart Agriculture in NCR Region, India. *Asian J. Agricult. Ext. Econom. And Sociol*, *36*(1), pp.1-11.

44. Minowa, T., T. Kondo and S.T. Sudirjo. 1998. Thermochemical liquefaction of Indonesian biomass residues. *Biomass and Bioenergy*, *14*(5-6), pp.517-524.

45. Misra, R.V., R.N. Roy and H. Hiraoka. 2003. On-farm composting meth-ods. Food and Agriculture Organization of the United Nations. *Land and Water Discussion Paper*, *2*, pp.1-37.

46. Moellers, J. and R. Riese. 1988. Nutritional causes of infertility in dairy cows. *Iowa State University Veterinarian*, *50*(2), p.5.

47. Mythili, R. and P. Venkatachalam. 2013. Briquetting of Agro-residues.

48. Government of India, Ministry of Agriculture & Farmers Welfare Department of Agriculture, Cooperation & Farmers WelfareDirectorate of Economics & StatisticsNew Delhi,National Policy for Management of Crop residues(NMPCR)2014. https://agricoop.nic.in/sites/default/files/NPMCR_1.pdf.(Accessed on 20.01.2022)

49. Open burning of paddy: Bacteria, PAU's small solution to the issue, Hindustan Times, 23.April.2022, Open burning of paddy: Bacteria, PAU's small solution to the issue - Hindustan Times.(Accessed on 20.03.2022).

50. Paolini, V., F. Petracchini, M. Segreto, L. Tomassetti, N. Naja and A. Cecinato. 2018. Environmental

impact of biogas: A short review of current knowledge. *Journal of Environmental Science and Health, Part A*, *53*(10), pp.899-906.

51. Pathak, B.S., A.K. Jain and A. Singh. 1986. Characteristics of crop residues. *Agricultural wastes*, *16*(1), pp.27-35.

52. Patial, M., K. K. Pramanick, A.K. Shukla, A. Thakur, R. Chauhan. 2020. Crop residue: Type, alternative use and National Policies for its management. 10, July. 2020. Crop residue: Type, alternative use and National Policies for its management (ropanonline.com). (Accessed on 18 Dec 2021).

53. Peter J.K., H. Masih, Y. Kumar, A.K. Singh, S. Chaturvedi. 2014. Organophosphate pesticide(Methyl Parathion) degrading bacteria isolated from rhizospheric soil of selected plants and optimization of growth conditions for degradation. *Int J Res*,5:1–13.

54. Porichha, G.K., Y. Hu, K.T.V. Rao and C.C. Xu, 2021. Crop residue management in India: Stubble burning vs. other utilizations including bioenergy. *Energies*, *14*(14), p.4281.

55. PPCB., 2015. Monitoring residue burning through satellite remote sensing. Report prepared by Punjab remote sensing centre, Ludhiana and submitted to Punjab pollution control board Patiala, Punjab, India. Productivity in rice-based cropping systems in the tropics. *Adv Agron* 85 (2005) 269-407.

56. Thakur, R.K., Punjab government, Gramin Vikas Trust signs MoU for establishing biogas pellets plants,The New Indian Express. 12. October. 2022, Punjab government, Gramin Vikas Trust signs MoU for establishing biogas pellets plants- The New Indian Express (Accessed on 21. November. v2022)

57. Punjab to supply paddy straw to Kerala, will be used as dry fodder, The Tribune India, 14. November. 2022. Punjab to supply paddy straw to Kerala, will be used as dry fodder : The Tribune India. (Accessed on 24 November 2022).

58. Rabier, F., M. Temmerman, T. Böhm, H. Hartmann, P.D. Jensen, J. Rathbauer, J. Carrasco and M. Fernández. 2006. Particle density determination of pellets and briquettes. *Biomass and Bioenergy*, *30*(11), pp.954-963.

59. Raffa, D.W., A. Bogdanski and P. Tittonell. 2015. How does crop residue removal affect soil organic carbon and yield? A hierarchical analysis of management and environmental factors. *Biomass and Bioenergy*, *81*, pp.345-355.

60. Raveendran, K., A. Ganesh and K.C. Khilar. 1995. Influence of mineral matter on biomass pyrolysis characteristics. *Fuel*, *74*(12), pp.1812-1822.

61. Roy, P. and M. Kaur. 2016. Economic analysis of selected paddy straw management techniques in Punjab and West Bengal. *Indian Journal of Economics and Development*, *12*(1a), pp.467-471.

62. Sapariya, D.D., K. Parikh and M. Barot. 2016. A Review on Briquette (Biocoal) from Crops Residual as A Feasible Energy Conversion Technology. *International Journal of Engineering Research & Technology (IJERT)*.

63. Saxena, R., S. Pal and P.K. Joshi. 2000. Delineation and characterization of agro-ecoregions.

64. Shahane, A.A. and Y.S. Shivay. 2016. Cereal residues-not a waste until we waste it: A review. *International Journal of Bio-resource and Stress Management*, *7*(1), pp.162-173.

65. Sharma, S., P. Nandal and A. Arora. 2019. Ethanol production from NaOH pretreated rice straw: a cost effective option to manage rice crop residue. *Waste and Biomass Valorization*, *10*(11), pp.3427-3434.

66. Sidhu, H.S., M. Singh, Y. Singh, J. Blackwell, S.K. Lohan, E. Humphreys, M.L. Jat, V. Singh and S. Singh. 2015. Development and evaluation of the Turbo Happy Seeder for sowing wheat into heavy rice residues in NW India. *Field Crops Research*, *184*, pp.201-212.

67. Singh, J., B.S. Panesar and S.K. Sharma. 2008. Energy potential through agricultural biomass using geographical information system–A case study of Punjab. *Biomass and Bioenergy*, *32*(4), pp.301-307.

68. Singh, R., D.B. Yadav, N. Ravisankar, A. Yadav and H. Singh. 2020. Crop residue management in rice–wheat cropping system for resource conservation and environmental protection in

north-western India. *Environment, Development and Sustainability*, *22*(5), pp.3871-3896.

69. Singh, Y. and H.S. Sidhu. 2014. Management of cereal crop residues for sustainable rice-wheat production system in the Indo-Gangetic plains of India. *Proceedings of the Indian National Science Academy*, *80*(1), pp.95-114.

70. Government of India, Ministry of Agriculture & Farmers Welfare Department of Agriculture, Cooperation & Farmers Welfare Directorate of Economics & Statistics New Delhi. State of Indian Agriculture 2015-16, 19. May. 2016, https://eands.dacnet.nic.in/PDF/State_of_Indian_Agriculture,2015-16.pdf. (Accessed on 20.11.2021).

71. Suramaythangkoor, T. and S.H. Gheewala. 2010. Potential alternatives of heat and power technology application using rice straw in Thailand. *Applied Energy*, *87*(1), pp.128-133.

72. The World Bank. 2010. http://data.worldbank.org/indicator/AG.LND.AGRI.ZS/countries?page=2. (Accessed on 10.11.2021).

73. Thorat, T.N., K.K. Agrawal, M.L. Kewat, G. Jha and S. Silawat. 2015. Crop residue management with conservation agriculture for sustaining natural resources. *Jawaharlal Nehru Krishi Vishwa Vidyalaya Research Journal*, *49*(2), pp.125-136.

74. Tisdale, S.L., W.L. Nelson and J.D. Beaton. 1985. *Soil fertility and fertilizers.* Collier Macmillan Publishers.

75. Venkatramanan, V., S. Shah, S. Prasad, A. Singh and R. Prasad. 2021. Assessment of Bioenergy Generation Potential of Agricultural Crop Residues in India. *Circular Economy and Sustainability*, *1*(4), pp.1335-1348.

76. Vyas, D.K., F.G. Sayyad, M.S. Khardiwar and S. Kumar. 2015. Physicochemical Properties of Briquettes from Different Feed Stock. *Current World Environment*, *10*(1), p.263.

77. Wilaipon, P., 2009. The effects of briquetting pressure on banana-peel briquette and the banana waste in Northern Thailand. *American Journal of Applied Sciences*, *6*(1), p.167.

78. Wilhelm, W.W., J.M.F. Johnson, D.L. Karlen and D.T. Lightle. 2007. Corn stover to sustain soil organic carbon further constrains biomass supply. *Agron. J. 99*, 1665–1667

79. Singh, Y., B. Singh and T. J. 2005. Crop residue management for nutrient cycling and improving soil productivity in rice-based cropping systems in the tropics. *Adv Agron 85*,269-407.

80. Yordanova, M. and N. Gerasimova. 2016. Effect of mulching on weed infestation and yield of beetroot (Beta vulgaris ssp. rapaceae atrorubra Krass). *Organic agriculture*, *6*(2), pp.133-138.

81. Zaidi, S., T. 2021. Rice Crop Residue burning and alternative measures by India: A Review. *Journal of Scientific Research Institute of Science, Banaras Hindu University, Varanasi, India,65(1).*

Journal of Cereal Research
Volume 14 (2): 129-138
Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Research Article

Effectiveness of *Thinopyrum ponticum*-derived wheat leaf rust resistance gene, *Lr24* in India - a revisit

Sivasamy Murugasamy[*1], Jayaprakash Paramasivan[1], Vikas Venu Kumaran[1], Subhash Chander Bharadwaj[2], Manjunatha Channappa[1], Rebekah Nisha[1], Shajitha Paneer[1], Agasthikumar Sindhu[1], Vijaishree Sivasamy[3] and John Peter[1]

[1]ICAR-Indian Agricultural Research Institute Regional Station, Wellington, Tamil Nadu -643 231, India
[2]ICAR - Indian Institute of Wheat and Barley Research, Regional Station, Flowerdale, Shimla-171001, India
[3]Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore-3, India

Article history:
Received: 17 Aug., 2022
Revised: 15 Sept., 2022
Accepted: 28 Sept., 2022

Citation:
M Sivasamy, J Paramasivan, VV Kumaran, SC Bharadwaj, M Channappa, R Nisha, S Paneer, A Sindhu, V Sivasamy and J Peter. 2022. Effectiveness of Thinopyrum ponticum-derived wheat leaf rust resistance gene, Lr24 in India - a revisit. *Journal of Cereal Research* ***14 (2):*** *129-138. http://doi.org/10.25174/2582-2675/2022/129000*

***Corresponding author:**
E-mail: iariwheatsiva@gmail.com

Abstract

Leaf or brown rust is one of the most devastating rust diseases in wheat. Development and deployment of resistance wheat cultivars is considered as the most effective, economic and sustainable method of protecting against the yield losses due to leaf rust. Though several alien resistance genes have been reported and utilized, *Thinopyrum ponticum* derived leaf rust resistance gene *Lr24/Sr24* has been proved to be effective for nearly three decades in India. The effectiveness of this gene was validated recently at seedling and adult plant stage. In the sixteen (16) backcrossed inbred lines (BILs) showed resistance reaction to the existing pathotypes. Furthermore, the presence of *Lr24* gene was confirmed in BILs through molecular markers. The results showed that *Lr24* gene conferred all stage resistance to the existing pathotypes of *P. triticina* f.sp. *tritici*. This emphasizes the importance of *Lr24* gene in Indian wheat breeding program and its prolonged protection of wheat crop from leaf rust in India.

Keywords: *Triticum aestivum*, Leaf rust, *Puccinia triticina, Lr24*, All stage resistance (ASR), Back crossed inbred lines (BIL's)

1. Introduction

Leaf or brown rust caused by *Puccinia triticina* Eriks. (*Pt*) is one of the most serious diseases targeting wheat worldwide. *P. triticina* is an obligate parasite that can easily survive in areas with mild temperatures and moist conditions (Figueroa *et al.*, 2017). The upper surface of the leaves is occupied with infectious orange-brown urediniospores (Wegulo and Emmanuel, 2012). These spores can travel hundreds of miles by wind thereby resulting in an endemic outbreak (Bolton *et al.*, 2008). The pathogen exhibits wider adaptability and hence can cause losses upto 70% under favourable climatic conditions (Figueroa *et al.*, 2017). Constant monitoring of leaf rust is crucial in order to keep track of any fluctuation in the pathogen population.

In India, changes in the pathogen population have been so far recorded for 49 pathotypes of *P. triticina* (Tomar *et al.* 2014). Among them, *P. triticina* race 77-1, 77-5, 77-9 and 104-2 are the most virulent pathotypes with more frequency in India (Prasad *et al.*, 2020). The most effective and economical approach to control this disease is deployment of leaf rust resistance genes.

Until now nearly 80 leaf rust resistance genes have been reported in wheat (McIntosh *et al.*, 2017). Of which many of them have been transferred from alien sources such as *Aegilops umbellulata*(*Lr9*), *Thinopyrum ponticum (Agropyron elongatum)* (*Lr19, Lr24*, and *Lr29*), *Aegilops speltoides* (*Lr28, Lr35, Lr36, Lr47* and *Lr51*), *Aegilops ventricosa* (*Lr37*) and

Triticum tauschii (*Lr21*, *Lr22a, Lr32, Lr39, Lr41, Lr42*, and *Lr43*) (MdAktar-Uz-Zaman *et al.*, 2017).

Lr24 derived from *Thinopyrum ponticum* (Podpera) Lu & Wong (syn. *Agropyron elongatum* (Host) Beauv.) is one of the important genes providing resistance to leaf rust for almost three decades in India (Tomar *et al.*, 2014). The spontaneous translocation occurred between the alien donor and chromosome 3D of bread wheat (Gough and Merkle, 1971). *Lr24* is also reported to be closely associated with the stem rust resistance gene *Sr24* (Mago *et al.*, 2005) and also with red grain colour. Later efforts were made to develop stocks with white seeded germplasm (McIntosh, 1995). Since 1993, *Lr24* has been effectively deployed in most Indian released varieties.

Previously, virulence for the resistance gene *Lr24* has been reported in North America (Browder, 1973), Canada (Kolmer, 1991), South America (Singh, 1991), South Africa (Pretorius *et al.*, 1990), Eastern Australia (Park *et al.*, 2002), Nepal (Mishra *et al.*, 2001) and Pakistan (Fayyaz *et al.*, 2008). But, in India, until now, the resistance gene *Lr24* provided all stage resistance (ASR) to all the occurring leaf rust pathotypes of *P. triticina* Eriks. (*Pt*) (Tomar *et al.*, 2014).

In this study, 16 backcross inbred lines (BILs) which were in the background of fifteen Indian wheat varieties were subjected to multi-race seedling tests, field tests and molecular marker detection for two seasons (2019,2020) and its efficacy over the period of years against the prevalent pathotype of *P. triticina* is being reported.

2. Material and Methods

2.1 Plant and Fungal material

Sixteen BILs were developed by introgressing *Lr24* gene through backcross breeding method using Tr380-14*7/3/Ag#14 and DarfKite (white seeded germplasm) as donor parents in the background of eighteen Indian wheat varieties from 1990-2000, continuously maintained and evaluated at ICAR- Indian Agricultural Research Institute (IARI), Regional Station, Wellington, Tamil Nadu, India located at (11^{0}22'47.5"N; 76^{0}46'26.1"E; altitude 1850 AMSL).

As *Lr24/Sr24* genes are tightly linked dominant genes, six to seven backcrosses were made with the respective recurrent parents within a short span of time by raising three experimental crops a year, under natural epiphytotic conditions. The genotypes were evaluated phenotypically and genotypes resembling the respective recurrent parents were selected and selfed for five subsequent generations. The final constituted BILs carrying *Lr24* along with the corresponding recurrent parents and donor (listed in Table 1& 2) were used for this study.

Table 1: Phenotypic validation of Seedling (SRT) and Adult plant resistance response of *Lr24/Sr24* in NILs/back crossed lines, recurrent parent and donors against leaf rust pathotypes during 2019

S. No	Variety	Pedigree/details	SRT Score (IARI, RS, Wellington mixed races)	SRT Score (IIWBR, Shimla)						Field Score (IARI, RS, Wellington)
				12-5	77-2	77-5	77-9	104-2	106	
1	**HW 2001A**	**Sonalika*7//Tr380-14**	**;**	**-**	**;**	**2**	**2**	**2**	**;-**	**0**
2	Sonalika	Recurrent Parent	3+	3+	3+	3+	3+	3+	0;	100S
3	**HW 2002**	**K.sona*6//Tr380-14**	**0**	-	;-	;	-	;	0;	**0**
4	Kalyansona	Recurrent Parent	3+	-	3+	3+	3+	3+	0;	100S
5	**HW 2003**	NI 5439*7//Tr380-14	0	;	;-	;	0;	;-	0;	**0**
6	NI 5439	Recurrent Parent	2+	-	-	3+	;-	-	-	80S
7	**HW 2004**	**C306*6//Tr380-14**	**0**	**0;**	**-**	**-**	**1**	**-**	**-**	**0**
8	C 306	Recurrent Parent	3+	1	3+	2	3+	3+	0;	60S
9	**HW 2006**	**Lok-1*6//Tr380-14**	**0**	;	1	-	-	;	0;	**0**
10	LOK 1	Recurrent Parent	3+	-	-	-	-	-	-	100S
11	**HW 2007**	**HD2329*6//Tr380-14**	**0**	-	2	-	-	-	-	**0**
12	HD 2329	Recurrent Parent	3+	0;	-	0;	3+	0;	0;	80S
13	**HW 2008**	**HD2285*6//Tr380-14**	**0**	-	-	-	-	-	0;	**0**
14	HD 2285	Recurrent Parent	3+	-	-	-	-	-	-	80S
15	**HW 2014**	**Wl 711*6//Tr380-14**	**0**	;	;-	;-	;	;-	-	**0**

16	WL 711	Recurrent Parent	3+	-	-	-	-	3+	0;	100S
17	**HW 2015**	**HUW 234*6//Tr380-14**	**;**	0;	-	;-	;-	0;	0;	**0**
18	HUW 234	Recurrent Parent	3+	;	3+	3	3+	3+	0;	100S
19	**HW 2016**	**PBW 226*6//Tr380-14**	**0**	0;	;	;-	;-	;	0;	**0**
20	PBW 226	Recurrent Parent	3	;	-	3+	3+	;	0;	80S
21	**HW 2017**	**HD 2402*6//Tr380-14**	**0**	0;	;-	0;	;-	;-	;-	**0**
22	HD 2402	Recurrent Parent	3+	;	-	-	-	-	0;	80S
23	**HW 2018**	**HI 1077*6//Tr380-14**	**0**	0;	;-	0;	;-	;	0;	**0**
24	HI 1077	Recurrent Parent	3	0;	3+	;	3+	-	0;	80S
25	**HW 2019**	WH 542*6//Tr380-14	;	0;	0;	;-	;-	;-	0;	**0**
26	WH 542	Recurrent Parent	3	3	0;	3+	3+	3+	0;	80S
27	**HW 2020**	**HS 240*6//Tr380-14**	**0**	**0;**	**;-**	**0;**	**0;**	**0;**	**0;**	**0**
28	HS 240	Recurrent Parent	3+	0;	0;	2	3+	3+	0;	100S
29	**HW 2022**	**WH 147*6//Tr380-14**	0;	;-	;-	0;	;	2	;1	0
30	WH 147	Recurrent Parent	3+	1-2	3+	3+	3+	3-3+	0;	80S
31	DarfKite (Resistant check)	*Lr24/Sr24*	0	0;	0;	0;	-	0;	0;	0

Table 2: Phenotypic validation of Seedling (SRT) and Adult plant resistance response of *Lr24/Sr24* in NILs/back crossed lines, recurrent parent and donors against predominant leaf and stem rust pathotypes during 2020.

S. No.	Wheat Lines	Pedigree/details	SRT Score (IARI, RS, Wellington) mixed races leaf rust pathotypes*	SRT Score IIWBR, Flowerdale Shimla Leaf rust pathotypes			SRT Score IIWBR, Flowerdale Shimla Stem rust pathotypes			Adult plant response under natural epiphytotic conditions at IARI, RS, Wellington
				77-5	77-9	104-2	15-1	40-1	40A	
1	**HW 2002**	**K.sona *6//Tr380-14**	**0**	**;**	**;**	**0;**	**2-**	**3-**	**2-**	**0**
2	**HW 2002A**	**K.sona *6//Tr380-14**	**0**	**;**	**;**	**0;**	**2=**	**3-**	**2-**	**0**
3	Kalyansona	Recurrent Parent	3+	3+	3+	3+	2-	3+	3+	100S
4	**HW 2003**	**NI5439(*7//Tr380-14**	**0;**	**;**	**;**	**;**	**;**	**2=**	**;1**	**0**
5	NI 5439	Recurrent Parent	2+	;	3+	0;	2=	3+	3+	80S
6	**HW 2004**	**C306*6//Tr380-14**	**0**	**12**	**;**	**;**	**;**	**3-**	**2-**	**0**
7	C 306	Recurrent Parent	3+	3+	3+	3+	3+	3+	3+	80S
8	**HW2007**	**HD 2329*6//Tr380-14**	**0**	**;1**	**;1**	**;1**	**0;**	**2=**	**2-**	**0**
9	HD 2329	Recurrent Parent	3+	3+	;1	3+	3+	33+	3+	100S
10	**HW 2008**	**HD 2285*6//Tr380-14**	**0;**	**;1**	**;**	**;**	**;**	**2=**	**2-**	**0**
11	HD 2285	Recurrent Parent	3+	3+	;1	3+	;1	2=	3+	80S
12	**HW 2010**	**J24*6//Tr380-14**)	**0;**	**;**	**;**	**;**	**;**	**2=**	**2-**	**0**
13	J24	Recurrent Parent	3+	3+	3+	3+	3+	33+	3+	100S
14	**HW 2011**	**HD2009*6//Tr380-14**	**0**	**0;**	**;1**	**0;**	**2-**	**2=**	**12-**	**0**
15	HD 2009	Recurrent Parent	2+	3+	3+	3+	2-	3-	2-	80S
16	**HW 2012**	**UP 262*6//Tr380-14**	**0;**	**;**	**;**	**;**	**0;**	**2=**	**2-**	**0**
17	UP 262	Recurrent Parent	2+	3+	;1	3+	2-	33+	3	80S
18	**HW 2015**	**HUW234*6//Tr380-14**	**;**	**;1**	**;**	**0;**	**2-**	**2-**	**2-**	**0**
19	HUW 234	Recurrent Parent	3+	3+	3+	3+	2=	2=	3+	100S
20	**HW 2016**	**PBW226*6//Tr380-14**	**0**	**;**	**;**	**;**	**0;**	**2=**	**2-**	**0**
21	PBW 226	Recurrent Parent	3	;1	12	3+	0;	0;	;	80S
22	**HW 2017**	**HD2402(*Lr24/Sr24*)**	**0;**	**;**	**;**	**;**	**;**	**2=**	**2**	**0**
23	HD 2402	Recurrent Parent	3+	3+	;1	3+	0;	2=	2	80S

24	**HW 2018**	**HI1077*6//Tr380-14**	**0**	**0;**	**;-**	**0;**	**;**	**2=**	**2-**	**0**
25	HI 1077	Recurrent Parent	3	3+	3+	3+	;	2=	2	80S
26	**HW 2019**	**WH 542*6//Tr380-14**	**;**	**;1**	**0;**	**0;**	**0;**	**2=**	**12**	**0**
27	WH542	Recurrent Parent	3+	3+	;1	3	0;	2=	;	80S
28	**HW 2020**	**HS240*6//Tr380-14**	**0**	**;1**	**;1**	**;-**	**2-**	**2=**	**2-**	**0**
29	HS 240	Recurrent Parent	3+	0;	;-	0;	2=	0;	2-	80S
30	**HW 2022**	**WH147*6//Tr380-14**	**0;**	**;-**	**;-**	**0;**	**;**	**2**	**;1**	**0**
31	WH 147	Recurrent Parent	3+	3+	3+	3+	0;	3+	2-	100S
32	Agent	*Lr24/Sr24* (Resistant check)	-	**;**	**;**	**;**	**2=**	**3+**	**2-**	**0**
33	*Tr380-14*	*Lr24/Sr24*	0;	0;	0;	0;	0;	2-	2	0

*Predominant leaf rust races occurring at Wellington are 77-1, 77-5, 77-9 and less frequent ones are 12-4, 12-8, 20, 77-6, 104-1, 162 & 1R31(*Mehtaensis 40 (2) July 20, IIWBR, Shimla*)

DNA isolation and molecular validation of Lr24 gene

The leaf samples were collected from the BILs, recurrent parents and donor from 15 days old seedlings and their DNA was isolated using CTAB method (Murray and Thompson, 1980). Two markers, *Sr*24#12 (Mago *et al.*, 2005) and *SCS73*$_{719}$ (Prabhu *et al.*, 2004) used to molecularly validate the NILs for the presence of *Lr*24 gene along with the recurrent parents and donor parent Tr380-14*7/3/Ag#14 and Darf kite.

The DNA samples were amplified with STS marker *Sr*24#12 and SCAR marker SCS73$_{719}$. The PCR reactions were carried out with 2X Dream Taq PCR master mix (Thermo Fisher Scientific) and 0.4pm forward and reverse primers. For *Sr*24#12, initial denaturation was kept at 94°C for 5mins, and 35 cycles of 94°C for 30s, 55°C for 30s and 72°C for 1min, and the final extension at 72°C for 10min and for *SCS73*$_{719}$ same condition with annealing temperature of 51°C was carried out. The PCR products were resolved with 1.2% agarose gel and documented with gel documentation system (Syngene, Gene Genius Match GGM/D2/F2-1).

2.2 Seedling Resistance Test

The seedling response test (SRT) of molecularly validated 16 BIL's (Lr24) and their corresponding recurrent parents were done with 6 different leaf rust pathotypes viz., 12-5, 77-2, 77-5, 77-9, 104-2 and 106 during 2019 and again 16 different sets of BIL's against three predominantly occurring leaf rust pathotypes 77-5, 77-9 and 104-2 and stem rust pathotypes 15-1, 40-1 and 40A during 2020 at ICAR, Indian Institute of Wheat and Barley Research (IIWBR), Flowerdale, Shimla located at a latitude of 31.088 and longitude 77.186, with an altitude of 2000 m AMSL. Lines were inoculated on 14 day old seedlings with a suspension containing 10 mg spores of leaf rust pathotype using an atomizer and incubated in humid chambers with diffused light at 20–22 °C for 48 hours. After 48 hours they were kept at glass house at 22°C and maintained for symptom development. Symptoms appeared ten days after inoculation and seedling reactions were recorded. Infection response was determined based on the host response to leaf rust using Stakman scale (0-4) (Stakman *et al.,* 1962). Infection types of 0 to 2 were considered as resistant and infection types of 3 to 3+ and more were considered as susceptible.

2.3 Adult plant resistance

The near isogenic lines with their recurrent parents were sown in field at ICAR-IARI, Regional Station, Wellington, Tamil Nadu with spreader rows around the field. Wellington is a natural hotspot for rusts and it survives here though around the year crop cycles, self sown plants and green bridge maintained at the station provides regular supply of rust inoculum to the breeding materials. Rust inoculum was sprayed using aqueous suspension of viable uredospores of prevailing rust pathotypes at two different plant seedling stages, first and fifth leaf (12 and 16 Zadoks scale) (Zadoks et al., 1974). Recommended cultivation practices were followed for raising the crop (Singh et al., 2006). The spreader rows were ensured with maximum susceptibility up to 100S.The adult plant reaction in the field conditions was recorded as per modified Cobb's scale (Peterson *et al.,* 1948) for two consecutive seasons (Kharif 2019 and Rabi 2019-20) as follows: 0- No visible infection, R- Resistant: necrotic areas with or without minute uredia, MR- Moderately resistant: small uredia, surrounded by necrotic areas, MX- Intermediate: variable sized uredia, some with necrosis or chlorosis, MS- Moderately susceptible: medium uredia with no chlorosis present, S- Susceptible: large uredia, no necrosis or chlorosis.

3. Results and Discussion

Among the several leaf rust resistant genes deployed in wheat, *Lr24* is one of the most effective genes conferring high level of resistance to *P.triticina* in India (Tomar *et al.*, 2014). In the recent past, efforts have been made to understand seedling and adult plant resistance provided by *Lr24* gene through transcriptome analysis (Manjunatha, 2015).

Seedling resistance test carried out at ICAR- IIWBR, RS, Flowerdale, Shimla for the 16 BIL's carrying *Lr24* against 6 different pathotypes of leaf rust (12-5, 77-2, 77-5, 77-9, 104-2 and 106) showed resistance reaction. The infection type developed by the BIL's and the corresponding recurrent parents at the seedling stage under greenhouse conditions was recorded and is presented in Table-1and Table-2. The recurrent parents showed susceptible reaction with the infection score ranging from 2 to 3+ against different pathotypes during 2019 and 2020. The donor screened against leaf rust pathotypes exhibited high level of seedling resistance with infection type (IT) '0'.The BILs showed resistant response ranging from 0 to 2 indicating the presence of the gene. The results revealed and confirmed that *Lr24* gene had seedling resistant response to the occurring leaf rust pathotypes in India.

Wellington is an important hotspot for rusts in the southern and peninsular India. The weather conditions in the hills are very congenial for host and pathogens and the rusts are highly destructive throughout the year. A wide spectrum of stem and leaf rust pathotypes are prevalent in this hills (Bahadur 1986; Nayar *et al.*, 1988). The results of the seedling resistance test done at ICAR- IARI, RS, Wellington using mixed pathotypes collected from field was in concordance with the results of at ICAR- IIWBR, RS, Flowerdale, Shimla.

Field screening was carried out at IARI, Regional Station, Wellington, The Nilgiris, Tamil Nadu under natural and artificially created epiphytotic conditions at Wellington for two successive seasons (2019 and 2020). The field reactions of the recurrent parents showed susceptible response with severity ranging from 80-100S, while the BILs and donor parents carrying *Lr24* showed resistant response (0). The scores were tabulated in Table 1&2. This is in agreement with the report stating that *Lr24* is continuing to be effective against the occuring leaf rust pathotypes prevailing in India (Bhardwaj *et al.*, 2021).

These lines were also evaluated against the predominant pathotypes of *P.graminis.* f. sp. *tritici* such as 15-1, 40-1 and 40-A during 2020. The *Lr24* linked stem rust gene *Sr24* recorded susceptible infection types IT 3+ particularly to the race 40-1 for which virulence has been reported in India (Bhardwaj *et al.*, 1990).

Furthermore, DNA isolated from the 16 BIL's and their corresponding recurrent parents were subjected to PCR analysis using the gene specific markers viz., *Sr*24#12 (STS marker) and $SCS73_{719}$ (SCAR marker) during 2019. All the lines carrying *Lr24/Sr24* gene(s) amplified a 500bp positive band for *Sr*24#12 (Fig. 1A and 1B) and 650bp positive band for $SCS73_{719}$ (Fig. 2A and 2B). Whereas, no amplification was seen in the corresponding recurrent parents for both the markers thereby indicating the absence of gene. Further re-confirmation was done during 2020 and all the BILs were amplified with 500bp positive band for *Sr*24#12 (Fig.3 & 4). Molecular validation of *Lr24* gene using two different markers (*Sr24#12* and *SCS73719*) showed that all the 16 BILs carried *Lr24* gene. It confirms that the meticulously planned conventional breeding approaches followed at IARI Regional Station, Wellington to develop the backcross inbred lines were efficient, systematic and successful.

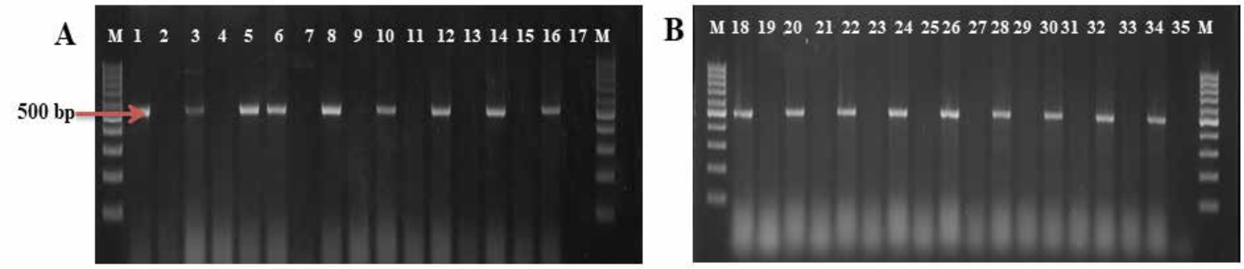


Fig 1: Molecular validation of *Lr24* gene in NIL's with *Sr24*#12marker (2019)

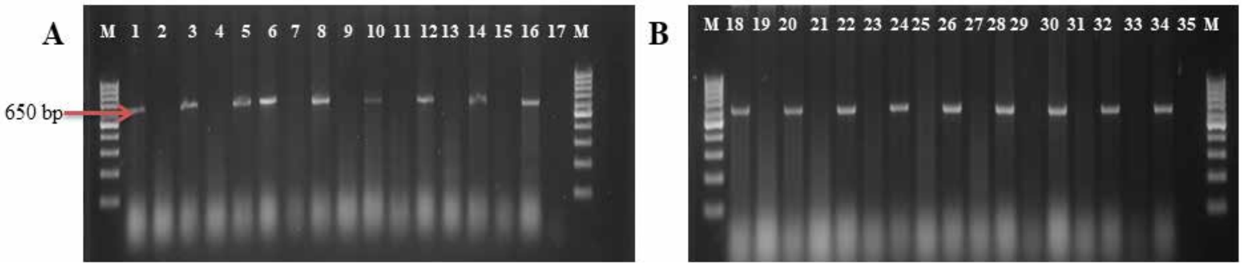


Fig 2: Molecular validation of *Lr24* gene in 16 NIL's with SCS73719marker(2019)

Fig. 1 and Fig. 2: M- 100bp Ladder, 1- Darfkite (Positive control), 2- Sonalika (RP), 3- HW 2001A, 4- Kalyansona(RP), 5- HW 2002, 6-HW 2002A, 7- NI5439(RP), 8- HW 2003, 9- C306(RP), 10- HW 2004, 11- WH147(RP), 12- HW 2005, 13- LOK1(RP), 14- HW 2006, 15- HD2329(RP), 16- HW 2007, 17- NTC, 18- Darfkite, 19- HD 2285(RP), 20- HW 2008, 21- WL711(RP), 22- HW 2014, 23- HUW234(RP), 24- HW 2015, 25- PBW226(RP), 26- HW 2016, 27- HD2402(RP), 28- HW 2017, 29- HI1077(RP), 30- HW 2018, 31- WH542(RP), 32- HW 2019, 33- HS 240(RP), 34- HW 2020, 35- NTC

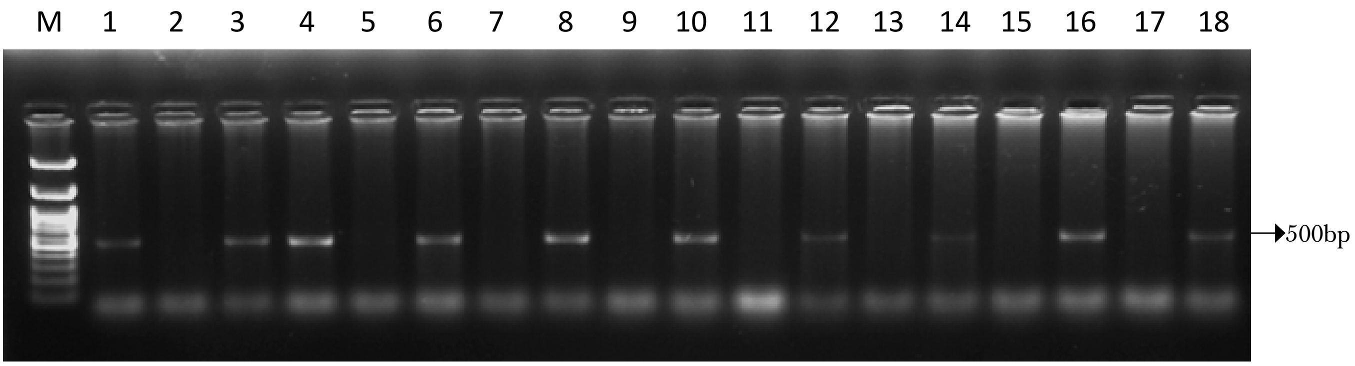


Fig 3: Molecular validation of *Lr24* gene in NIL's with *Sr24*#12marker re-confirmed during 2020

M-100bp Ladder, 1.Tr380-4 (Donor/Positive control), 2. Kalyansona (RP), 3.HW 2002 (Kalyansona * *Lr24/Sr24*), 4. HW 2002A (Kalyansona * *Lr24/Sr24*), 5. NI 5439(RP), 6. HW 2003 (NI 5439 * *Lr24/Sr24*), 7. C 306 (RP), 8.HW 2004 (C 306 * *Lr24/Sr24*), 9.HD 2329(RP), 10.HW 2007 (HD 2329* *Lr24/Sr24),* 11.HD 2285 (RP), 12.HW 2008 (HD 2285 * *Lr24/Sr24*), 13.J24 (RP), 14. HW 2010 (J24**Lr24/Sr24*)

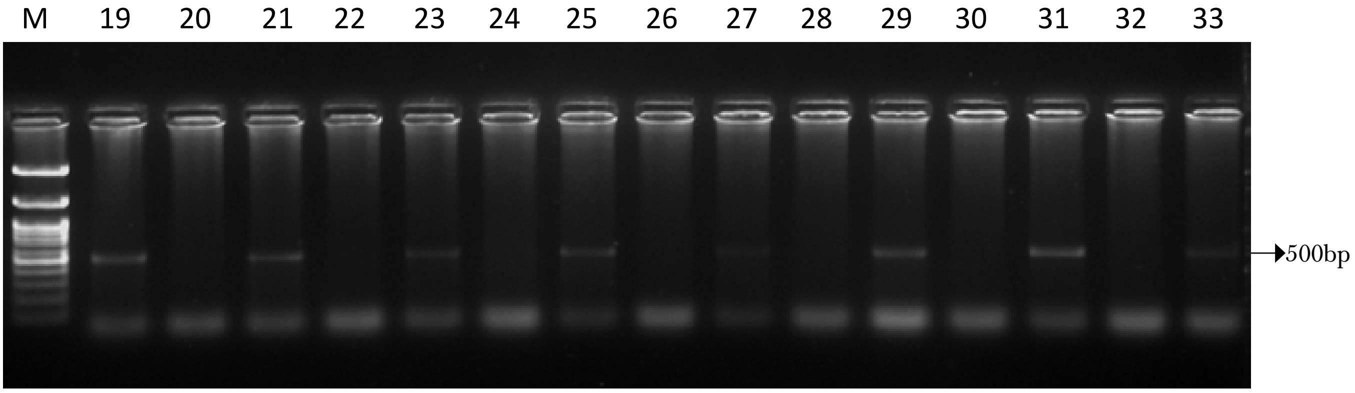


Fig 4: Molecular validation of *Lr24* gene in NIL's with *Sr24*#12marker re-confirmed during 2020

M- 100bp ladder, 19. Tr380-4 (Donor/Positive control), 20.HUW 234(RP), 21.HW 2015(HUW 234 * *Lr24/Sr24*), 22.PBW 226(RP), 23.HW 2016 (PBW 226**Lr24/Sr24*), 24.HD 2402(RP), 25.HW 2017 (HD 2402**Lr24/Sr24*), 26. HI 1077(RP), 27. HW 2018 (HI 1077**Lr24/Sr24*), 28.WH 542(RP), 29.HW 2019(WH 542 * *Lr24/Sr24*), 30.HS 240(RP), 31.HW 2020 (HS 240**Lr24/Sr24*), 32.WH 147(RP), 33. HW 2022 (WH 147**Lr24/Sr24*)

(# RP-Recurrent Parent used as negative control; NTC- Non template control)

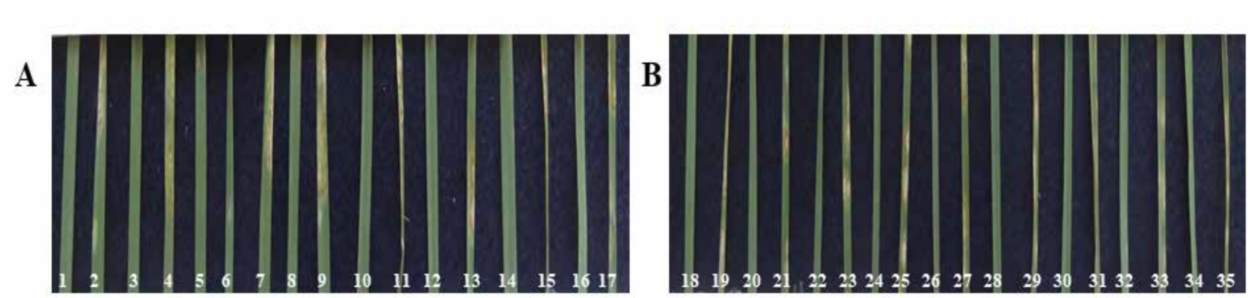


Fig 3: Seedling resistance pattern in NIL's

A: 1- Darfkite, 2- Sonalika, 3- HW 2002, 4- Kalyansona, 5- HW 2002, 6- HW 2002A, 7- NI5439, 8- HW 2003, 9- C306, 10- HW 2004, 11- WH147, 12- HW 2005, 13- LOK1, 14- HW 2006, 15- HD2329, 16- HW 2007, 17- Agralocal; **B:** 18- Drafkite, 19- HD2285, 20- HW 2008, 21- WL711, 22- HW 2014, 23- HUW234, 24- HW 2015, 25- PBW226, 26- HW 2016, 27- HD2402, 28- HW 2017, 29- HI1077, 30- HW 2018, 31- WH542, 32- HW 2019, 33- HS240, 34- HW2020, 35- WH147.

Though virulence to *Lr24* has been reported worldwide, however, *Lr24* still continues to be highly effective in seedling as well as in adult stage to Indian pathotypes of *P.triticina* and virulence for *Lr24* occur in low frequencies in most geographical areas(Huerta-Espino,1992) and Australia (Prasad *et al.*, 2018). Depending on the various climatic zones in India, the following leaf rust resistance genes *Lr9, Lr19, Lr24* and *Lr34* have been strongly recommended for the management of leaf rust pathotypes (Bahadur *et al.*, 1994).

Though *Lr24* provides all stage resistance to the prevailing Indian pathotypes of *P.triticina*, relying on monogene culture has a disadvantage of being overcome by new evolving leaf rust pathotypes. Thus, stacking of single effective genes with other resistant race specific or APR genes might confer long term resistance to leaf rust. Similar works of pyramiding *Lr24+Lr28* (Kumar *et al.*, 2017) and *Lr24+Lr19* (Singh *et al.*, 2017) have been reported.

'Agent' was the first wheat carrying the *Thinopyrum* derived segment with leaf and stem rust resistance gene, *Lr24/Sr24* respectively (Smith *et al.*, 1968). In India the first bread wheat variety DL 784-3 (Vidisha) carrying *Lr24/Sr24* was released in 1993. Since then more than 16 varieties carrying *Lr24/Sr24* have been released and are continuing to be in cultivation in India. The following varieties viz., DL784-3, HW 2004, DL788-2, HW 2045, HD 2781, HI 1500, MP4010, Raj4037, HD2851, HD 2833, HI 1531, COW(W)-1, HD 2888, AKAW3722, AKAW4627 and HW 5207(Pusa Navagiri) all carrying *Lr24/Sr24* have been released for commercial cultivation occupying a total of 15 million ha over a period of 20 years (Tomar *et al.*,2014). The adult plant scoring for leaf rust in the Indian varieties released to different wheat cultivating zones carrying specific leaf rust resistance gene(s) *Lr24/Sr24* is given in **Table 3.** This clearly indicates the effective resistance conferred by the gene. Furthermore, the release of more number of varieties with *Lr24* evidently remarks that the alien translocation 3Ag#3DL does not impair on yield (Singh *et al.*, 2007).

Table 3: Adult plant scoring for leaf rust in the released varieties carrying specific leaf rust resistance gene(s) *Lr24/Sr24* at ICAR-IARI, Regional Station, Wellington

S.No.	Name of the variety	Year and Zone for which released	Adult plant response under natural epiphytotic conditions at IARI, RS, Wellington	
			Leaf Rust	Stem Rust
	DL 784-3 (Vidisha)	1993, NEPZ	0	0
	HW 2004 (Amar)	1995, CZ	0	10MR
	DL 788-2 (Vaishali)	1996, CZ	0	20MS
	HW 2045 (Kaushambi)	2002, NEPZ	0	20MR
	HD 2781 (Aditya)	2002, PZ	0	20MS
	HI 1500 (Amrita)	2002,CZ	0	20M

MP 4010	2002, CZ	0	20MS
RAJ 4037	2003, PZ	0	20MR
HD 2851 (Pusa Vishesh)	2003, DELHI	0	10MS
HD 2833 (Trpti)	2004, PZ	0	10M
NW 1067	2004, UP	0	20MS
HI 1531	2005, CZ	0	20MR
COW(W)1	2005, TN	0	20MS
HD 2888 (Pusa wheat)	2005, NEPZ	0	20MR
AKAW 3722	2005, VIDARBHA	0	20MS
AKAW 4627	2011, PZ	0	20MS
HW 5216 (Pusa Thenmalai)	2012,SHZ	0	0

The deployment of this effective gene complex in Indian released cultivars for more than a decade played pivotal role in checkmating the *P.triticina* pathotypes prevalent in India (Tomar *et al.,* 2014). From this study it is confirmed that *Lr24* gene continued to provide resistance both in seedling as well as adult plant stage against all the occurring leaf rust pathotypes in India for more than three decades.

Acknowledgements

Authors thank Director and Joint Director (Research), ICAR-Indian Agricultural Research Institute**,** (IARI), New Delhi for constant encouragements and support.

Author's contribution

Conceptualization of research (MS); Designing of the experiments (MS, JP, VKV, CM); Contribution of experimental materials (MS); Execution of field/lab experiments and data collection (SCB, RN, SP, AS, SV, JP); Analysis of data and interpretation (MS, RN, SP, JP, VKV); Preparation of the manuscript (MS, RN, SP, JP, VKV).

Declaration

The authors declare no conflict of interest.

4. References

1. Bahadur P. 1986. Physiologic specialization in wheat rust. In: Joshi LM, Singh DV and Srivastava KD (ed) Problems and progress of wheat pathology in south Asia. Malhotra Publishing House, New Delhi: 69-91.
2. Bhardwaj SC, SK Nayar, M Prashar, J Kumar, MK Menon and S Singh. 1990. A pathotype of *Puccinia graminis* f. sp. *tritici* on *Sr24* in India. *Cereal rusts and powdery mildews bulletin.* **18**: 35-38.
3. Bahadur P, DV Singh and KD Srivastava. 1994. Management of wheat rusts- a revised strategy for gene deployment. *Indian Phytopathology.* 47(1):41-47.
4. Bhardwaj SC, S Kumar, OP Gangwar, P Prasad, PL Kashyap, H Khan, S Savadi, GP Singh 289, N Gupta, R Thakur. 2021. Physiologic specialization and genetic 290 differentiation of *Puccinia triticina* causing leaf rust of wheat in the Indian 291 subcontinent during 2016-2019. *Plant Diseases* doi.org/10.1094/PDIS-06-20-1382-RE
5. Browder LE. 1973. Specificity of the *Puccinia recondita* f. sp. *tritici*: *Triticum aestivum* 'Bulagria 88' relationship. *Phytopathology.* **63**: 524-528.
6. Fayyaz M, AR Rattu, I Ahmad, MA Akhtar, AA Hakro and A Mujeeb-Kazi. 2008. Current status of the occurrence and distribution of (*Puccinia triticina*) wheat leaf rust virulence in Pakistan. *Pakistan Journal of Botany.* **40**: 887-895.
7. Figueroa M, K Hammond-Kosack and P Solomon. 2017. A review of wheat diseases - a field perspective. *Molecular Plant Pathology.* **19**. 10.1111/mpp.12618.
8. Gough FJ and OG Merkle. 1971. Inheritance of stem and leaf rust resistance in Agent and Argus cultivars of *Triticum aestivum*. *Phytopathology.* **61***:* 1501-1505
9. Huerta-Espino J. 1992. Analysis of wheat leaf and stem rust virulence on a worldwide basis. PhD thesis, University of Minnesota, St. Paul, MN.
10. Kolmer JA. 1991. Physiologic specialization of *Puccinia recondita f.sp. tritici* in Canada in 1990. *Canadian Journal of Plant Pathology.* **13**: 371-373.
11. Kumar G, RR Hanchinal, S Desai and S Biradar. 2017. Marker Assisted Gene Pyramiding of Leaf Rust Resistance Genes *Lr24* and *Lr28* in the Background

of Wheat Variety DWR 162 (*Triticum aestivum* L.) *International Journal of Current Microbiology and Applied Sciences.* **6(9):** 1883-1893.

12. Mago R, HS Bariana IS Dundas, W Spielmeyer, Lawrence GJ, Pryor AJ and JG Ellis. 2005. Development of PCR markers for the selection of wheat stem rust resistance genes, *Sr24* and *Sr26* in diverse wheat germplasm. *Theoretical and Applied Genetics.* **111**: 496–504.

13. Manjunatha C. 2015. Development of DNA based detection assay for *Puccinia triticina* and gene expression studies during host pathogen interaction. Division of Plant Pathology ICAR-Indian Agricultural Research Institute New Delhi.

14. McIntosh RA, J Dubcovsky, WJ Rogers, C Morris and X Xia. 2017. Catalogue of Gene Symbols for Wheat: 2017 Supplement. Available at: https://shigen.nig.ac.jp/wheat/komugi/genes/macgene/supplement 2017.pdf.

15. McIntosh RA, CR Wellings and RF Park. 1995. Wheat Rusts: An Atlas of Resistance Genes. Melbourne: Csiro Publishing.

16. Md Aktar-Uz-Zaman, Mst Tuhina-Khatun, Mohamed Musa Hanafi and Mahbod Sahebi. 2017. Genetic analysis of rust resistance genes in global wheat cultivars: an overview, *Biotechnology & Biotechnological Equipment.* **31**:3, 431-445.

17. Mishra AN, AP Roelfs and HJ Dubin 2001. Virulence for wheat leaf rust resistance gene *Lr24* in Nepal. Cereal Rusts and Powdery Mildews Bull (www.crpmb.org/ 2001/0920mishra).

18. Murray MG and WF Thompson. 1980. Rapid isolation of high molecular weight plant DNA. *Nucleic Acids Research.* **8 (19):**4321-5.

19. Nayar SK, S Nagarajan and P Bahadur. 1988. Virulence distribution pattern of *Puccinia recondita* f. sp. *tritici* in India during 1983-86. *Plant Disease Research.* **3**: 203-210.

20. Park RF, HS Bariana, CR Wellings and H Wallwork. 2002. Detection and occurrence of a new path type of *Puccinia triticina* with virulence for *Lr*24 in Australia. *Australian Journal of Agricultural Research.* **9**: 1069- 1076.

21. Peterson RF, A Campbell, A Hannah. 1948. A diagrammatic scale for estimating rust intensity on leaves and stems of cereals. *Canadian Journal of Research.* **26(5):**496–500.

22. Prabhu KV, SK Gupta, A Charpe and S Koul. 2004. SCAR marker tagged to the alien leaf rust resistance gene *Lr19* uniquely marking the *Agropyron elongatum*-derived gene *Lr24* in wheat: a revision. *Plant Breeding.* **123**: 417- 420.

23. Prasad P, OP Gangwar, Subodh Kumar and SC Bhardwaj. 2020. Monitoring pathotype distribution of *Puccinia* species on wheat and barley. *Mehtaensis* 40(2): July, 2020

24. Prasad P, Savadi, Siddanna Bhardwaj, Subhash Chander; Kashyap, Prem Lal; Gangwar, Om Prakash; Khan, Hanif; Kumar, Subodh; Kumar, Ravinder; Patil, Virupaksh. 2018. Stage-specific reprogramming of defense responsive genes during *Lr24*-mediated leaf rust resistance in wheat. *Journal of Plant Pathology*, doi:10.1007/s42161-018-00199-x)

25. Pretorius ZA, J LeRoux and SC Drijenpondt, 1990. Occurrence and pathogenicity of *Puccinia recondita* f.sp. *tritici* on wheat in South Africa during 1988. *Phytophylactica* **22** : 225-228

26. Singh B, SMS, Vinod and Singh. 2007. Notification of crop varieties: A bread wheat variety HD 2851. *Indian Journal of Genetics.* **67**: 305-306.

27. Singh M., N Mallick, S Chand. *et al.* 2017. Marker-assisted pyramiding of *Thinopyrum*-derived leaf rust resistance genes *Lr19* and *Lr24* in bread wheat variety HD2733. *Journal of Genetics.* **96**: 951–957.

28. Singh R.P. 1991. Pathogenicity variations of Puccinia recondita f. sp. tritici in wheat growing areas of Mexico during 1988 and 1989. *Plant Diseases.* **75**: 790-794.

29. Singh R, A Kumar, RK Sharma, RS Chhokar, AK Sharma, J Shoran, R Chand and B Mishra. 2006. Wheat production technology for North West plain zone (in Hindi). Extension Bulletin – 22, Directorate of Wheat Research, Karnal.

30. Smith EL, AM Schlehuber, HC Young. 1968. Registration of agent wheat. Jr, Edwards LH. In: *Crop Science.* **8**:511-512.

31. Stakman EC, DM Stewart, WQ Loegring. 1962. Identification of physiologic races of *Puccinia graminis* var *tritici.* Agricultural Research Service E617 United States Department of Agriculture, Washington.

32. Tomar SMS, SK Singh, M Sivasamy and Vinod. 2014. Wheat rusts in India: Resistance breeding and gene deployment- A review. *Indian Journal of Genetics.* **74(2):** 129- 156.

33. Wegulo SN and B Emmanuel. 2012. Rust diseases of wheat. Plant Disease. University of Nebraska–Lincoln Extension, Institute of Agriculture and Natural Resources.

34. Zadoks JC, TT Chang and CF Konzak. 1974. A decimal code for the growth stages of cereals. *Weed Research.* **14**: 415–421.

Journal of Cereal Research
Volume 14 (2): 139-149
Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Research Article

Heterotic capability of five crosses for quantitative traits in bread wheat (*Triticum aestivum* L.) with inbreeding depression studies using generation mean analysis

Darshika Busa[2], Ashwin Pansuriya[1*], Deep Vekaria[1], Chandrakant Singh[1], G. U. Kulkarni[2] and Jagdish Patel[3]

[1] *Wheat Research Station, Junagadh Agricultural University, Junagadh -362001*
[2] *Department of Genetics and Plant Breeding, Junagadh Agricultural University, Junagadh -362001*
[3] *Department of Seed Science and Technology, Junagadh Agricultural University, Junagadh -362001*

Article history:
Received: 04 June, 2022
Revised: 07 Aug., 2022
Accepted: 23 Aug., 2022

Citation:
Busa D, A Pansuriya, DM Vekaria, C Singh, GU Kulkarni and JB Patel. 2022. Heterotic capability of five crosses for quantitative traits in bread wheat (*Triticum aestivum* L.) with inbreeding depression studies using generation mean analysis. *Journal of Cereal Research* ***14 (2):*** *139-149. http://doi.org/10.25174/2582-2675/2022/124049*

****Corresponding author:***
E-mail: agpansuriya@jau.in

Abstract

Six generations, namely P_1, P_2, F_1, F_2, BC_1 and BC_2 of five crosses of bread wheat *viz.*, AKAW 4842 x Raj 4238, AKAW 4924 x RW 5, DBW 39 x MP 3353, GW 11 x DWAP 1540 and GW 455 x UP 2968 were developed to estimate the extent of heterosis and inbreeding depression and underlying genetic causes for different characters in bread wheat. The analysis of variance between families (crosses) revealed that the mean square due to crosses were highly significant for all the characters. The analysis of variance among progenies (generations) within each family (cross) indicated significant differences among six basic generation means for all the characters studied in all the five crosses. In the present study all the crosses depicted significant and positive mid parent heterosis and heterobeltiosis for grain yield per plant and almost all the component traits. Among which crosses AKAW 4842 x Raj 4238, AKAW 4924 x RW 5, GW 11 x DWAP 1540 and GW 455 x UP 2968 depicted negative inbreeding as well as significant and positive mid parent heterosis and heterobeltiosis for grain yield per plant therefore, intermating in F_2 generation may be advantageous for improving particular character for above mentioned crosses. Generally, the character like grain yield per plant governed by fixable additive gene effect can be improved through pedigree selection method.

Keywords: Bread wheat, heterosis, inbreeding depression, generation mean analysis

1. Introduction

Wheat (*Triticum sp.*) is usually accorded a premier place among cereals because of the vast acreage devoted to its cultivation, its high nutritive value and its association with some of the earliest and most important civilizations of the world. *Triticum aestivum* is most extensively grown crop among cereals in the world, grown on more than 17% of the cultivable land and consumed by nearly 40% of the global population. Wheat fulfils 20% of the total food calories and 21% protein in human diet (Bhutto *et al.*, 2016). India, a major contributor to the world wheat production after China witnessed a tremendous increase in production during the last four decades.

Wheat is a unique gift from nature to main kind as it can be moulded into innumerable products like chapattis, breads, cakes, biscuits, pasta and many hot and ready-to-eat breakfast foods. Wheat grain contains crude protein (13.3 %), fat (2.0 %), minerals (1.7 %), fibre (2.3%), other carbohydrates (68.7 %) and water (12 %) (Das, 2008). The uniqueness of wheat in contrast to other cereals is that wheat contains gluten protein, which enables leavened dough to rise by forming minute gas cells and this property enables bakers to produce light breads.

Nature and magnitude of heterosis is one of the important aspects for selection of the right parents for crosses and also helps in identification of superior cross combinations that may produce desirable transgressive segregants in advanced generations especially in self- pollinated crops like wheat. The superiority of hybrids depends on their yield potential over the better released varieties and the extent of heterosis for seed yield. The aim of heterosis analysis is to find out the best combination of crosses giving high degree of useful heterosis and characterization of hybrids for commercial exploitation. Singh and Singh (1984) appears to be most acceptable, both in concept and utilization of heterosis in self-pollinated crops. According to them, one can select a pure breeding line equally good or even better than F_1 hybrid. Therefore, the knowledge of heterosis together with inbreeding depression would help in determination of the parents which produce the best cross combinations having maximum heterosis and minimum inbreeding depression. Inbreeding depression points out whether the vigour observed in the F_1 generation can be fixed or not in later generations through selfing. The information of such estimates is essential to plan efficient breeding programmes as well as selection of parents so as to obtain good segregants for improvement of the crop yield.

2. Materials and methods

The present investigation was carried out on bread wheat (*Triticum aestivum* L.) at Wheat Research Station, Junagadh Agricultural University, Junagadh. The seeds of F_1 generations of five crosses were available from Wheat Research Station, Junagadh Agricultural University, Junagadh. The F_1 as well as 10 parents were sown in the field to generate F_2, BC_1 and BC_2 generations as well as fresh selfed seeds of P_1, P_2 and fresh F_1 during *Rabi* 2018-19 and materials which are developed were evaluated during *Rabi* 2019-20. Wheat Research Station, JAU, Junagadh is located in South Saurashtra Agro Climatic Zone of Gujarat state. Ten parents were used in this experiment *viz.,* AKAW 4842, AKAW 4924, DBW 39, GW 11, GW 455, Raj 4238, RW 5, MP 3353, DWAP 1540 and UP 2968. The experimental material was comprised of five crosses each with six basic generations, *viz.*, P_1, P_2, F_1 (P_1 x P_2), F_2 (F_1 selfed), BC_1 (F_1 x P_1) and BC_2 (F_1 x P_2). Ten diverse parents were selected on the basis of their phenotypic variability for different characters. The seeds of F_1 generations [AKAW 4842 x Raj 4238 (cross 1), AKAW 4924 x RW 5 (cross 2), DBW 39 x MP 3353 (cross 3), GW 11 x DWAP 1540 (cross 4) and GW 455 x UP 2968 (cross 5)] of five crosses were made during *Rabi* 2017-18. The F_1 as well as 10 parents were sown in the field to generate F_2, BC_1 and BC_2 generations as well as fresh selfed seeds of P_1, P_2 and fresh F_1 during *Rabi* 2018-19. The experiment was laid out in Compact Family Block Design with three replications having each row of 3 m length and 22.5 cm row to row distance. Each replication was divided into five compact blocks. The blocks were comprised of six basic generations of each cross. The crosses were assigned to each block and six generations of a cross were relegated to individual plot within the block. The single row plot for P_1, P_2 and F_1; two rows for each BC_1 and BC_2 generations and three rows of F_2 generation were accommodated. The observations were recorded on 10 competitive and randomly selected plants each from P_1, P_2 and F_1; 20 plants each from backcross (BC_1 and BC_2) and F_2 generations in each replication. Various observations taken were days to flowering (DF), days to maturity (DM), plant height (PH), number of effective tillers (TIL), length of main spike (SL; cm), number of spikelets per main spike, grain filling period, number of grains per main spike (NGPS), 100-grain weight (g), grain yield per plant (GY; g plant^{-1}), biological yield per plant (g plant $^{-1}$), and harvest index (HI; %).

The mean values obtained for each character were subjected to analysis of variance using Compact Family Block Design according to the following model as described by Panse and Sukhatme (1985). The standard statistical procedures were used to calculate means and variances of each generation for each character (Singh and Chaudhary, 2004). The crosses which showed significant differences among the different generations for various traits were subjected to generation mean analysis for the detection of digenic interactions and for the estimation of gene effects as suggested by Hayman (1958) and Cavalli (1952). The heterotic effects in term of superiority of F_1 over mid parent values (relative heterosis) as per Briggle (1963) and over better parent (heterobeltiosis) as per Fonseca and Patterson (1968). The inbreeding depression (ID) in F_2 generation was calculated as,

$$\text{Inbreeding depression (\%)} = \frac{\overline{F}_1 - \overline{F}_2}{\overline{F}_1} \times 100$$

Where,

$\overline{F}_1$ = Mean of F_1 generation

$\overline{F}_2$ = Mean of F_2 generation

3. Results and discussion

The analysis of variance for the experimental design for all the different characters studied in five crosses is presented in Table 1. The analysis of variance between families (crosses) revealed that the mean square due to crosses were highly significant for all the characters. The Bartlett's test for homogeneity of error variances of five crosses indicated that the error variances were heterogeneous for plant height, length of main spike, grain filling period, number of grains per main spike, 100 grain weight and biological yield per plants showed by significance of chi-square values and homogeneous for rest of characters *viz.* days to flowering, days to maturity, number of effective tillers per plant, number of spikelets per main spike, grain yield per plant and harvest index as showed by non-significance of chi-square values. The analysis of variance among progenies (generations) within each family (cross) indicated significant differences among six basic generation means for all the characters studied in all the five crosses. Hence, further genetic analysis of generation means and calculation of heterosis and inbreeding were carried out.

3.1 Days to flowering

The results on heterosis and inbreeding depression are presented in table 2. The heterosis over mid parent ranged from -6.88 % (GW 11 x DWAP 1540) to 7.14% (AKAW 4842 x Raj 4238) and were significant and positive in crosses AKAW 4842 x Raj 4238, AKAW 4924 x RW 5, DBW 39 x MP 3353 and GW 455 x UP 2968, while it was significant in desirable direction in cross GW 11 x DWAP 1540. For the purpose of estimation of heterosis over better parent, the parent having less number of days to opening of first flowering was considered as better parent. Heterosis over better parent ranged from -6.09 % (GW 11 x DWAP 1540) to 9.01 % (AKAW 4842 x Raj 4238) and were significant and positive in crosses AKAW 4842 x Raj 4238, AKAW 4924 x RW 5, DBW 39 x MP 3353, and GW 455 x UP 2968, while it was significant negative in cross GW 11 x DWAP 1540. The heterosis over mid parent and better parent was significant and desirable for days to flowering in only GW11 x DWAP. Desirable heterosis for this trait has also been reported by Lal *et al.* (2013), Aware and Padukone (2018) and Khokhar *et al.* (2019). The estimates of inbreeding depression ranged from -3.69 % (GW 11 x DWAP 1540) to 4.98 % (GW 455 x UP 2968) and was significant and positive in crosses AKAW 4842 x Raj 4238, AKAW 4924 x RW 5, GW 11 x DWAP 1540 and GW 455 x UP 2968. Positive and significant inbreeding depression was observed in AKAW 4842 x Raj 4238, AKAW 4924 x RW 5, GW 11 x DWAP 1540 and GW 455 x UP 2968 and is supported by earlier report of Kumar *et al.* (2018).

3.2 Days to maturity

As early maturity is desirable in wheat crop, the early maturing parent was considered as better parent for the calculation of heterobeltiosis. Heterosis over better parent ranged from -0.96 % (GW 455 x UP 2968) to 4.99 % (AKAW 4842 x Raj 4238) and were significant and positive in crosses AKAW 4842 x Raj 4238, AKAW 4924 x RW 5, DBW 39 x MP 3353 and GW 11 x DWAP 1540, while it was negative direction in cross 5. The observed values of inbreeding depression ranged from 0.31 % (AKAW 4924 x RW 5) to 3.97 % (GW 11 x DWAP 1540) and were significant and positive in crosses DBW 39 x MP 3353, GW 11 x DWAP 1540 and GW 455 x UP 2968. Results of the experiment with respect to days to maturity were similar to the findings of Khokhar *et al.* (2019). The crosses DBW 39 x MP 3353, GW 11 x DWAP 1540 and GW 455 x UP 2968 showed significant and positive inbreeding depression and similar result was reported by Kumar *et al.* (2018).

3.3 Plant height

The estimates of heterosis over mid parent ranged from 3.17% (AKAW 4924 x RW 5) to 10.57% (AKAW 4842 x Raj 4238). All the five crosses exhibited significant and positive mid parent heterosis. The dwarf plant was considered as better parent for calculating heterobeltiosis. The estimates of heterosis over better parent varied from 3.33% (AKAW 4924 x RW 5) to 13.53% (AKAW 4842 x Raj 4238) and were significant and positive in all the crosses. The estimates of inbreeding depression ranged from -1.09 % (DBW 39 x MP 3353) to 7.70 % (GW 455 x UP 2968) and was significant and positive in crosses AKAW 4924 x RW 5, GW 11 x DWAP 1540 and GW 455 x UP 2968. None of the crosses depicted significant but negative heterosis for this trait. Similar trend was noticed by Vanpariya *et al.* (2006) and Lal *et al.* (2013). Inbreeding depression for plant height was significant and positive in AKAW 4924 x RW 5, GW 11 x DWAP 1540 and GW 455 x UP 2968 and is supported by earlier report of Aware and Potdukhe (2018) and Kumar *et al.* (2018).

3.4 Number of effective tillers per plant

The estimates of heterosis over mid parent ranged from 2.65% (AKAW 4842 x Raj 4238) to 27.85% (GW 11 x DWAP 1540) and were significant and positive in crosses AKAW 4924 x RW 5, DBW 39 x MP 3353, GW 11 x DWAP 1540 and GW 455 x UP 2968. The estimates of heterosis over better parent varied from 14.02% (GW 455 x UP 2968) to 45.62% (GW 11 x DWAP 1540) and were significant and positive in all the crosses. The estimates of inbreeding depression ranged from -8.02% (AKAW 4842 x Raj 4238) to 14.16 % (DBW 39 x MP 3353) and found significant and positive in crosses 39 x MP 3353 and GW 11 x DWAP 1540. Number of effective tillers per plant is one of the important component traits, which is directly related with increased grain yield per plant. Out of five cross combinations, only cross AKAW 4842 x Raj 4238 resulted in non-significant and positive heterosis and heterobeltiosis, remaining crosses resulted in significant and positive heterosis and heterobeltiosis. Similar findings were reported for this character by Vanpariya *et al.* (2006), Baloch *et al.* (2016), Aware and Potdukhe (2018) and Khokhar *et al.* (2019). Negative inbreeding depression is desirable for this trait. The cross AKAW 4842 x Raj 4238 showed high desirable inbreeding depression. Similar conclusions were drawn by Aware and Potdukhe (2018) and Kumar *et al.* (2018).

3.5 Length of main spike

The estimates of heterosis over mid parent ranged from 4.57% (AKAW 4842 x Raj 4238) to 17.92% (DBW 39 x MP 3353) and were significant and positive in crosses AKAW 4924 x RW 5, DBW 39 x MP 3353, GW 11 x DWAP 1540 and GW 455 x UP 2968. The estimates of heterosis over better parent varied from 7.80% (GW 455 x UP 2968) to 31.06% (DBW 39 x MP 3353) and were significant and positive in all the crosses. The estimates of inbreeding depression ranged from 2.27% (AKAW 4842 x Raj 4238) to 9.55 % (GW 455 x UP 2968) and were significant, positive in crosses AKAW 4924 x RW 5, DBW 39 x MP 3353, GW 11 x DWAP 1540 and GW 455 x UP 2968. For length of main spike, four crosses namely, AKAW 4924 x RW 5, DBW 39 x MP 3353, GW 11 x DWAP 1540 and GW 455 x UP 2968 had significant and positive heterosis over mid parent, while all the five crosses showed significant and positive heterosis over better parent. Vanpariya *et al.* (2006), Khokhar *et al.* (2019) reported significant and positive heterosis for length of main spike. None of the cross showed negative inbreeding depression for length of main spike and is supported by earlier report of Kumar *et al.* (2018).

3.6 Number of spikelets per main spike

The estimates of heterosis over mid parent ranged from 7.53% (AKAW 4842 x Raj 4238) to 14.06% (AKAW 4924 x RW 5) and were significant, positive in crosses AKAW 4924 x RW 5, DBW 39 x MP 3353 and GW 455 x UP 2968. The estimates of heterosis over better parent varied from 10.52% (AKAW 4842 x Raj 4238) to 21.67% (AKAW 4924 x RW 5) and were significant, positive in crosses AKAW 4924 x RW 5, DBW 39 x MP 3353, GW 11 x DWAP 1540 and GW 455 x UP 2968. The estimates of inbreeding depression ranged from -3.16% (DBW 39 x MP 3353) to 10.14 % (AKAW 4842 x Raj 4238) and were significant and positive in cross AKAW 4842 x Raj 4238. Number of spikelets per main spike is an important yield attribute in wheat. For this trait, AKAW 4924 x RW 5, GW 11 x DWAP 1540 and GW 455 x UP 2968 showed significant and positive heterosis over mid parent. All the crosses except cross 1 showed significant and positive heterosis over better parent. Significant and positive heterosis for this character has been reported by Vanpariya *et al.* (2006) and Baloch *et al.* (2016). Negative inbreeding depression is desirable for Number of spikelets per main spike. The crosses DBW 39 x MP 3353 and GW 455 x UP 2968 showed desirable negatively inbreeding depression and similar conclusions were drawn by Aware and Potdukhe (2018) and Kumar *et al.* (2018).

3.7 Grain filling period

The estimates of heterosis over mid parent ranged from -13.31% (GW 455 x UP 2968) to 11.66% (AKAW 4842 x Raj 4238) and were significant and positive in crosses AKAW 4842 x Raj 4238, DBW 39 x MP 3353 and GW 11 x DWAP 1540, while it was negative direction in crosses AKAW 4924 x RW 5 and GW 455 x UP 2968. The estimates of heterosis over better parent varied from -4.44% (AKAW 4924 x RW 5) to 12.38% (AKAW 4842 x Raj 4238) and were significant and positive in crosses AKAW 4842 × Raj 4238, DBW 39 x MP 3353 and GW 11 x DWAP 1540. The estimates of inbreeding depression ranged from -14.25 % (AKAW 4924 x RW 5) to 8.04 % (GW 11 x DWAP 1540) and were significant and positive in crosses 3 and 4. In case of grain filling period, AKAW 4842 x Raj 4238, DBW 39 x MP 3353 and GW 11 x DWAP 1540 showed significant and positive heterosis over mid parent and better parent. The results of heterosis for grain filling period was in close agreement with the findings of Bhatiya (2006). AKAW 4924 x RW 5 and GW 455 x UP 2968 showed significant and negative inbreeding depression. The results are in agreement with the findings of Bhatiya (2006).

3.8 Number of grains per main spike

The estimates of heterosis over mid parent ranged from 3.45 % (AKAW 4842 x Raj 4238) to 14.88% (GW 11 x DWAP 1540) and were significant and positive in GW 11 x DWAP 1540 and GW 455 x UP 2968 crosses. The estimates of heterosis over better parent varied from10.48% (AKAW 4842 x Raj 4238) to 17.25% (GW 11 x DWAP 1540) and were significant and positive in all five crosses. The estimates of inbreeding depression ranged from -0.79 % (GW 455 x UP 2968) to 4.99 % (GW 11 x DWAP 1540) and were non-significant in all five crosses. For number of grains per main spike, GW 11 x DWAP 1540 and GW 455 x UP 2968 showed significant and positive heterosis over mid parent, while all five crosses showed significant and positive heterosis over better parent for this trait. The present findings are in accordance with those of Vanpariya *et al.* (2006), Rasul *et al.* (2008) and Khokhar *et al.* (2019). All the crosses showed non-significant inbreeding depression for this trait and it is in agreement of earlier reports of Aware and Potdukhe (2018) and Kumar *et al.* (2018).

3.9 100 grain weight

The estimates of heterosis over mid parent ranged from 9.52% (AKAW 4842 x Raj 4238) to 25.05% (AKAW 4924 x RW 5). All the five crosses exhibited significant and positive mid parent heterosis. The estimates of heterosis over better parent varied from 12.65% (AKAW 4842 x Raj 4238) to 29.73% (AKAW 4924 x RW 5) and were significant and positive in all five crosses. The estimates of inbreeding depression ranged from -2.35% (GW 11 x DWAP 1540) to 9.03 % (DBW 39 x MP 3353) and was significant and positive in AKAW 4842 x Raj 4238 and DBW 39 x MP 3353. With respect to 100 grain weight, all five crosses were found significant and positive heterosis over mid-parent and better parent. This result is in agreement with the findings of Vanpariya *et al.* (2006) and Rasul *et al.* (2008). The cross GW 11 x DWAP 1540 showed high desirable negative inbreeding depression. Similar conclusions were drawn by Aware and Potdukhe (2018) and Kumar *et al.* (2018).

3.10 Grain yield per plant

The heterosis over mid parent ranged from 10.71% (AKAW 4842 x Raj 4238) to 31.59% (AKAW 4924 x RW 5). All the five crosses depicted significant and positive mid parent heterosis. Heterosis over better parent ranged from 19.68 % (AKAW 4842 x Raj 4238) to 44.03 % (AKAW 4924 x RW 5) and were significant and positive in all five crosses. The estimates of inbreeding depression ranged from -12.04% (AKAW 4924 x RW 5) to 14.32 % (DBW 39 x MP 3353) and found significant and positive in DBW 39 x MP 3353. Grain yield in wheat is one of the most important economic characters and the final product of the multiplicative interaction of contributing traits. It is imperative to know the causes of heterosis for grain yield. All the five crosses depicted significant and positive heterosis over mid parent and better parent for this trait. Significant and positive heterosis for this character has been reported by Vanpariya *et al.* (2006), Rasul *et al.* (2008), Lal *et al.* (2013), Dedaniya *et al.* (2018) and Bajaniya *et al.* (2019). Negative inbreeding depression is desirable for grain yield per plant. The cross GW 455 x UP 2968 showed desirable inbreeding depression and similar conclusions were drawn by Kumar *et al.* (2018).

3.11 Biological yield per plant

The heterosis over mid parent ranged from 1.69% (AKAW 4842 x Raj 4238) to 19.31% (AKAW 4924 x RW 5) and observed significant and positive in crosses AKAW 4924 x RW 5, DBW 39 x MP 3353, GW 11 x DWAP 1540 and GW 455 x UP 2968. Heterosis over better parent ranged from 4.70% (AKAW 4842 x Raj 4238) to 25.38% (AKAW 4924 x RW 5) and noted significant and positive in crosses AKAW 4924 x RW 5, DBW 39 x MP 3353, GW 11 x DWAP 1540 and GW 455 x UP 2968. The estimates of inbreeding depression ranged from -7.30% (AKAW 4842 x Raj 4238) to 6.30% (DBW 39 x MP 3353) and found significant and positive in DBW 39 x MP 3353. For biological yield per plant, four crosses namely, AKAW 4924 x RW 5, DBW 39 x MP 3353, GW 11 x DWAP 1540 and GW 455 x UP 2968 had significant and positive heterosis over mid parent and better parent. Significant and positive heterosis for this character has been reported by Baloch *et al.* (2016). AKAW 4842 x Raj 4238, AKAW 4924 x RW 5, GW 11 x DWAP 1540 and GW 455 x UP 2968 showed negative and significant inbreeding depression for this trait and similar conclusions were drawn by Kumar *et al.* (2018).

3.12 Harvest index

The heterosis over mid parent ranged from 8.63% (AKAW 4842 x Raj 4238) to 13.76% (DBW 39 x MP 3353) for harvest index. All the five crosses had significant and positive mid parent heterosis. Heterosis over better parent ranged from 13.40% (AKAW 4842 x Raj 4238) to 26.17% (DBW 39 x MP 3353) and were significant and positive in all five crosses. The estimates of inbreeding depression ranged from -7.17% (AKAW 4924 x RW 5) to 8.32% (DBW 39 x MP 3353) and it was significant and positive in cross DBW 39 × MP 3353. In case of harvest index, all the five crosses depicted significant and positive heterosis over mid parent and better parent. Vanpariya *et al.* (2006) also reported significant and positive heterosis for harvest index. Negative inbreeding depression is desirable for harvest index. Cross AKAW 4924 x RW 5 showed high desirable negative inbreeding depression and similar findings were reported by Kumar *et al.* (2018).

Table 1 Analysis of variance (mean squares) between families and between progenies within family of six generations for different characters in bread wheat

Source of variation	d.f.	Days to flowering	Days to maturity	Plant height (cm)	No. of effective tillers per plant	Length of main spike	No. of spikelets per main spike
Analysis of variance between families							
Replications	2	0.43	0.04	1.48	0.01*	0.001	0.001
Crosses	4	10.39**	26.01**	11.47**	2.24**	2.42**	1.89**
Error	8	0.23	0.03	0.42	0.002	0.001	0.00
χ^2		NS	NS	S	NS	S	NS
Analysis of variance between progenies within family							
AKAW 4842 x Raj 4238 (Cross 1)							
Replications	2	2.43	0.39	10.21	0.04	0.006	0.0001
Generations	5	7.20**	10.18**	27.73**	4.36**	1.01**	1.56**
Error	10	1.24	0.19	2.81	0.01	0.05	0.005
AKAW 4924 x RW 5 (Cross 2)							
Replications	2	0.62	0.40	1.67	0.03	0.03	0.0001
Generations	5	12.28**	7.77**	13.63**	7.29**	1.63	3.81**
Error	10	0.47	0.32	0.45	0.01	0.01	0.002
DBW 39 x MP 3353 (Cross 3)							
Replications	2	1.48	0.12	7.05	0.003	0.005	0.009
Generations	5	6.71**	8.69**	24.06**	3.92**	3.40**	6.38**
Error	10	0.54	0.07	1.90	0.006	0.002	0.004

			GW 11 x DWAP 1540 (Cross 4)				
Replications	2	2.81	0.006	0.06	0.009	0.0006	0.004
Generations	5	7.20**	20.88**	21.05**	10.06**	1.59**	2.32**
Error	10	0.87	0.14	0.18	0.006	0.0004	0.005
			GW 455 x UP 2968 (Cross 5)				
Replications	2	0.75	0.005	0.05	0.02	0.0005	0.001
Generations	5	7.77**	25.57**	24.32**	1.25**	1.00**	2.72**
Error	10	1.19	0.06	0.07	0.01	0.0007	0.002

Cont…..

Table 1 Contd…..

Source of variation	d.f.	Grain filling period (days)	No. of grains per main spike	100 grain weight (g)	Grain yield per plant (g)	Biological yield per plant	Harvest index (%)
			Analysis of variance between families				
Replications	2	0.69	0.0001	0.0001	0.0001	0.0001	0.012
Crosses	4	24.34**	1.28**	0.16**	25.89**	77.24**	25.57**
Error	8	0.86	0.001	0.0001	0.0001	0.0001	0.004
χ^2		S	S	S	NS	NS	NS
			Analysis of variance between progenies within family				
			AKAW 4842 x Raj 4238 (Cross 1)				
Replications	2	1.83	0.001	0.001	0.0001	0.0005	0.03
Generations	5	25.48**	12.87**	0.22**	10.55**	34.76**	18.41**
Error	10	3.73	0.002	0.001	0.0007	0.0004	0.03
			AKAW 4924 x RW 5 (Cross 2)				
Replications	2	3.21	0.001	0.000	0.0003	0.0001	0.008
Generations	5	37.19**	10.39**	0.95**	24.52**	47.65**	37.79**
Error	10	2.81	0.003	0.0004	0.0003	0.0005	0.02
			DBW 39 x MP 3353 (Cross 3)				
Replications	2	0.01	0.001	0.0004	0.0001	0.0003	0.06
Generations	5	10.90**	7.51**	0.41**	16.93**	11.62**	35.99**
Error	10	0.02	0.002	0.0004	0.0002	0.0006	0.03
			GW 11 x DWAP 1540 (Cross 4)				
Replications	2	12.74	0.002	0.0001	0.0005	0.0001	0.006
Generations	5	89.65**	15.53**	0.37**	18.48**	16.16**	36.82**
Error	10	7.07	0.01	0.0002	0.0002	0.0003	0.02
			GW 455 x UP 2968 (Cross 5)				
Replications	2	7.13	0.01*	0.0003	0.0002	0.0002	0.06
Generations	5	46.07**	17.48**	0.27**	16.21**	19.31**	22.93**
Error	10	4.07	0.002	0.0001	0.0003	0.0004	0.02

* and ** Significant at 5 and 1 per cent levels, respectively

Chi-square for Bartlett's test of homogeneity of error variances,

S= Significant; NS = Non-significant

Table 2 Heterosis over mid parent (MP), heterosis over better parent (BP) and inbreeding depression (ID) for days to flowering, days to maturity, plant height (cm) and number of effective tillers per plant of five crosses in bread wheat

Crosses	**Heterosis (%) over**		**ID (%)**
	MP	**BP**	
Days to flowering			
AKAW 4842 x Raj 4238 (Cross 1)	7.14** ± 0.65	9.01** ± 0.70	3.72** ± 0.72
AKAW 4924 x RW 5 (Cross 2)	3.08* ± 0.64	7.40** ± 0.64	3.69** ± 0.57
DBW 39 x MP 3353 (Cross 3)	2.95* ± 0.62	6.68** ± 0.60	-0.23 ± 0.69
GW 11 x DWAP 1540 (Cross 4)	-6.88** ± 0.57	-6.09** ± 0.58	-3.69** ± 0.59
GW 455 x UP 2968 (Cross 5)	5.24** ± 0.45	8.37** ± 0.63	4.98** ± 0.44
Days to maturity			
AKAW 4842 x Raj 4238 (Cross 1)	3.01** ± 0.51	4.99** ± 0.54	0.93 ± 0.52
AKAW 4924 x RW 5 (Cross 2)	2.55** ± 0.61	3.94** ± 0.74	0.31 ± 0.74
DBW 39 x MP 3353 (Cross 3)	3.10** ± 0.60	4.81** ± 0.93	2.71** ± 0.63
GW 11 x DWAP 1540 (Cross 4)	2.76** ± 0.69	4.32** ± 0.82	3.97** ± 0.60
GW 455 x UP 2968 (Cross 5)	-3.00** ± 0.51	-0.96 ± 0.55	2.06** ± 0.54
Plant height (cm)			
AKAW 4842 x Raj 4238 (Cross 1)	10.57** ± 0.96	13.53** ± 1.07	2.85 ± 1.10
AKAW 4924 x RW 5 (Cross 2)	3.17** ± 0.71	3.33** ± 0.82	5.54** ± 0.76
DBW 39 x MP 3353 (Cross 3)	7.00** ± 1.15	11.07** ± 1.32	-1.09 ± 1.08
GW 11 x DWAP 1540 (Cross 4)	6.94** ± 0.74	9.76** ± 0.88	2.76** ± 0.74
GW 455 x UP 2968 (Cross 5)	7.98** ± 0.69	11.96** ± 1.08	7.70** ± 0.84
No. of effective tillers per plant			
AKAW 4842 x Raj 4238 (Cross 1)	2.65 ± 0.42	21.60** ± 0.51	-8.02* ± 0.44
AKAW 4924 x RW 5 (Cross 2)	27.08** ± 0.37	28.44** ± 0.42	-0.12 ± 0.36
DBW 39 x MP 3353 (Cross 3)	7.54* ± 0.41	17.72** ± 0.48	14.16** ± 0.40
GW 11 x DWAP 1540 (Cross 4)	27.85** ± 0.36	45.62** ± 0.43	12.45** ± 0.34
GW 455 x UP 2968 (Cross 5)	9.44** ± 0.42	14.02** ± 0.52	5.08 ± 0.41

*and ** Significant at 5 and 1 per cent levels respectively.

Cont…..

Table 2 Heterosis over mid parent (MP), heterosis over better parent (BP)and inbreeding depression (ID) for length of main spike (cm), number of spikelets per main spike, grain filling period (days) and number of grains per main spike of five crosses in bread wheat

Crosses	**Heterosis (%) over**		**ID (%)**
	MP	**BP**	
Length of main spike (cm)			
AKAW 4842 x Raj 4238 (Cross 1)	4.57 ± 0.22	10.90** ± 0.22	2.27 ± 0.22
AKAW 4924 x RW 5 (Cross 2)	11.11** ± 0.21	13.46** ± 0.29	6.34** ± 0.19
DBW 39 x MP 3353 (Cross 3)	17.92** ± 0.19	31.06** ± 0.23	8.94** ± 0.20

GW 11 x DWAP 1540 (Cross 4)	14.09** ± 0.20	20.07** ± 0.25	8.41** ± 0.20
GW 455 x UP 2968 (Cross 5)	5.90** ± 0.18	7.80** ± 0.23	9.55** ± 0.20
	No. of spikelets per main spike		
AKAW 4842 x Raj 4238 (Cross 1)	7.53 ± 0.79	10.52 ± 0.91	10.14* ± 0.79
AKAW 4924 x RW 5 (Cross 2)	14.06** ± 0.82	21.67** ± 0.95	6.76 ± 0.83
DBW 39 x MP 3353 (Cross 3)	10.83 ± 0.89	15.74* ± 0.99	-3.16 ± 0.87
GW 11 x DWAP 1540 (Cross 4)	11.89* ± 0.75	15.23** ± 0.91	5.89 ± 0.75
GW 455 x UP 2968 (Cross 5)	10.50* ± 0.73	14.16* ± 0.85	-2.30 ± 0.79
	Grain filling period (days)		
AKAW 4842 x Raj 4238 (Cross 1)	11.66** ± 0.57	12.38** ± 0.59	-0.64 ± 0.60
AKAW 4924 x RW 5 (Cross 2)	-11.64** ± 0.88	-4.44 ± 1.04	-14.25** ± 0.94
DBW 39 x MP 3353 (Cross 3)	5.55** ± 0.69	8.05** ± 0.95	7.48** ± 0.71
GW 11 x DWAP 1540 (Cross 4)	11.61** ± 0.77	12.20** ± 0.85	8.04** ± 0.72
GW 455 x UP 2968 (Cross 5)	-13.31** ± 0.64	-6.58** ± 0.71	-3.59** ± 0.65
	No. of grains per main spike		
AKAW 4842 x Raj 4238 (Cross 1)	3.45 ± 1.60	10.48* ± 1.86	1.09 ± 1.52
AKAW 4924 x RW 5 (Cross 2)	7.85 ± 1.67	14.26** ± 1.91	4.92 ± 1.76
DBW 39 x MP 3353 (Cross 3)	6.66 ± 1.57	11.29* ± 1.63	1.85 ± 1.57
GW 11 x DWAP 1540 (Cross 4)	14.88** ± 1.86	17.25** ± 2.25	4.99 ± 1.73
GW 455 x UP 2968 (Cross 5)	10.05* ± 1.40	15.64** ± 1.51	-0.79 ± 1.62

*and ** Significant at 5 and 1 per cent levels respectively.

Cont…..

Table 2 Heterosis over mid parent (MP), better parent (BP)and inbreeding depression (ID) for 100 grain weight (g), grain yield per plant (g), biological yield per plant (g) and harvest index (%) of five crosses in bread wheat

Crosses	**Heterosis (%) over**		**ID (%)**
	MP	**BP**	
	100 grain weight (g)		
AKAW 4842 x Raj 4238 (Cross 1)	9.52** ± 0.14	12.65** ± 0.17	5.33* ± 0.13
AKAW 4924 x RW 5 (Cross 2)	25.05** ± 0.15	29.73** ± 0.18	3.48 ± 0.13
DBW 39 x MP 3353 (Cross 3)	10.49** ± 0.14	16.59** ± 0.19	9.03** ± 0.13
GW 11 x DWAP 1540 (Cross 4)	10.02** ± 0.15	13.08** ± 0.19	-2.35 ± 0.12
GW 455 x UP 2968 (Cross 5)	16.49** ± 0.16	22.44** ± 0.19	4.53 ± 0.16
	Grain yield per plant (g)		
AKAW 4842 x Raj 4238 (Cross 1)	10.71* ± 0.62	19.68** ± 0.65	-5.69 ± 0.74
AKAW 4924 x RW 5 (Cross 2)	31.59** ± 0.77	44.03** ± 0.77	-12.04 ± 0.84
DBW 39 x MP 3353 (Cross 3)	22.53** ± 0.86	39.13** ± 0.92	14.32** ± 0.91
GW 11 x DWAP 1540 (Cross 4)	21.05** ± 0.68	31.77** ± 0.73	-5.60 ± 0.70
GW 455 x UP 2968 (Cross 5)	17.91** ± 0.71	29.37** ± 0.73	-7.47* ± 0.67

Biological yield per plant (g)			
AKAW 4842 x Raj 4238 (Cross 1)	1.69 ± 0.77	4.70 ± 0.99	-7.30** ± 0.72
AKAW 4924 x RW 5 (Cross 2)	19.31** ± 0.82	25.38** ± 0.96	-4.75* ± 0.89
DBW 39 x MP 3353 (Cross 3)	7.64** ± 0.77	10.06** ± 0.88	6.30** ± 0.78
GW 11 x DWAP 1540 (Cross 4)	6.76** ± 0.76	11.28** ± 0.85	-1.86* ± 0.75
GW 455 x UP 2968 (Cross 5)	5.66** ± 0.80	9.34** ± 0.87	-5.83** ± 0.76
Harvest index (%)			
AKAW 4842 x Raj 4238 (Cross 1)	8.63* ± 1.58	13.40** ± 1.80	1.36 ± 1.80
AKAW 4924 x RW 5 (Cross 2)	10.64* ± 2.03	14.69* ± 2.13	-7.17 ± 2.17
DBW 39 x MP 3353 (Cross 3)	13.76** ± 1.71	26.17** ± 1.83	8.32* ± 1.81
GW 11 x DWAP 1540 (Cross 4)	13.42** ± 1.61	18.53** ± 1.72	-3.69 ± 1.59
GW 455 x UP 2968 (Cross 5)	11.32* ± 1.74	18.06** ± 1.83	-1.32 ± 1.53

*and ** Significant at 5 and 1 per cent levels respectively.

4. Conclusions

Breeding method that can be employed for improvement of a particular character depends upon the type of gene action prevailed in the expression of character. The type and magnitude of gene action may vary for different characters in the same cross and for the same trait in different crosses which necessitates the handling of individual cross in segregating generations in a specific way. Generally, the character governed by fixable additive gene effect can be improved through pedigree selection method. The cases, where high heterosis coupled with negative inbreeding depression prevail, intermating in F_2 generation may be advantageous for improving particular character. In the present study all the crosses depicted significant and positive relative heterosis and heterobeltiosis for grain yield per plant and almost all the component traits. Among which crosses AKAW 4842 x Raj 4238, AKAW 4924 x RW 5, GW 11 x DWAP 1540 and GW 455 x UP 2968 also showed negative inbreeding depression therefore, intermating in F_2 generation may be advantageous for improving particular character for above mentioned crosses. Grain yield per plant and biological yield per plant showed the highest heterosis over mid parent and better parent as well as minimum inbreeding depression over the crosses.

Acknowledgements

Authors thank to Research Scientist (Wheat), Principal and Dean, P.G. Studies and Professor and head (GPB), Junagadh Agricultural University, Junagadh for constant encouragements and support.

Author's contribution

Conceptualization of research (DB and AGP); Designing of the experiments (DB, DMV and CS); Contribution of experimental materials (DB and AGP); Execution of field/lab experiments and data collection (DB); Analysis of data and interpretation (AGP and GUK); Preparation of the manuscript (DB, AGP and JBP).

Declaration

The authors declare no conflict of interest.

5. References

1. Aware SA and NR Potdukhe. 2018. Heterotic capability of eight crosses for quantitative and qualitative traits in wheat (*Triticum aestivum* L.) with inbreeding depression studies. *International Journal of Current Microbiology and Applied Sciences* **6**: 2436-2444.
2. Bajaniya NA, AG Pansuriya, DM Vekaria, C Singh and JM Patel. 2019. Estimation of heterosis in different crosses of durum wheat (*Triticum durum* L.). *International Journal of Chemical Studies* **7**(3): 3833-3839.
3. Baloch M, AW Baloch, NA Siyal, SN Baloch, AA Soomro, SK Baloch and N Gandahi. 2016. Heterosis analysis in F_1 hybrids of bread wheat. *Sindh University Research Journal* **48**(2): 261-264.
4. Bhatiya VJ. 2006. Genetics for slow leaf-rusting and yield related traits in bread wheat (*Triticum aestivum* L.). Unpublished Ph.D. (Agri.) thesis submitted to Junagadh Agricultural University, Junagadh.

5. Bhutto AH, AA Rajpar, SA Kalhoro, A Ali, FA Kalhoro, M Ahmed, S Raza and NA Kalhoro. 2016. Correlation and regression analysis for yield traits in wheat (*Triticum aestivum* L.) genotypes. *Natural Sci*ences **8**(3): 96-104.

6. Briggle LW. 1963. Heterosis in wheat: A Review. *Crop Sciences* **3**(5): 407-412.

7. Cavalli LL. 1952. An analysis of linkage in quantitative inheritance. In "Quantitative Inheritance". Ed. E.C.R. Reeve and C.H. Waddington, HMSO, London. pp. 135-144.

8. Dedaniya AP, AG Pansuriya, DM Vekaria, JT Memon and TA Vekariya. 2018. Estimation of heterosis in different crosses of bread wheat (*Triticum aestivum* L.). *International Journal of Chemical Studies* **6**(3): 3622-3628.

9. Fonseca S and FL Patterson. 1968. Hybrid vigor in a seven-parent diallel cross in common winter wheat (*Triticum aestivum* L.). *Crop Sciences* **8**(1): 85-88.

10. Hayman BI. 1958. The separation of epistatic from additive and dominance variation in generation means. *Heredity* **12**: 371-390.

11. Khokhar AA, WA Jatoi, FG Nizamani, RA Rind, MM Nizamani, HF Wang, A Mehmood and MU Khokhar. 2019. Study of heterosis analysis in F_1 population of bread wheat. *Pure and Applied Biology* **8**(2): 1757-1770.

12. Kumar A, AK Razdan, V Sharma, N Kumar and D Kumar. 2018. Study of heterosis and inbreeding depression for economic and biochemical traits in bread wheat (*Triticum aestivum* L.). *Journal of Pharmacognosy and Phytochemistry* **7**(4): 558-564.

13. Lal C, V Kumar and SR Maloo. 2013. Heterosis and inbreeding depression for some quantitative and heat tolerance characters in bread wheat (*Triticum aestivum* L.). *Journal of Wheat Research* **5**(2): 52-55.

14. Panse VG and PV Sukhatme. 1985. Statistical Methods for Agricultural Workers. Indian Council of Agricultural Research, New Delhi. pp. 381.

15. Rasul I, AS Khan and Z Ali. 2008. Estimation of heterosis for yield and some yield components in bread wheat. *International Journal of Agriculture and Biology* **4**(2): 214-216.

16. Singh M and RK Singh. (1984). A comparison of different methods of half-diallel analysis. *Theoretical and Applied Genetics* **67**: 323-326.

17. Singh RK and BD Chaudary. 2004. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, Ludhiana.

18. Vanpariya LG, VP Chovatia and DR Mehta. 2006. Heterosis for grain yield and its attributes in bread wheat (*Triticum aestivum* L.). *National Journal of Plant Improvement* **82**: 100-102.

Journal of Cereal Research
Volume 14 (2): 150-160
Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Research Article

Heterosis for grain yield and its attributing traits in bread wheat (*Triticum aestivum* L.)

Hilay Dudhat*[1], Ashwin Pansuriya[2], Deep Vekaria[2], Hardik Dobariya[1], Jagdish Patel[3], Chandrakant Singh[2] and I.B. Kapadiya[2]

[1]Department of Genetics and Plant Breeding, College of Agriculture, Junagadh Agricultural University, Junagadh-362 001, Gujarat, India
[2]Wheat Research Station, Junagadh Agricultural University, Junagadh- 362 001, Gujarat, India
[3]Department of seed Science and Technology, Junagadh Agricultural University, Junagadh- 362 001, Gujarat, India

Article history:
Received: 05 July, 2022
Revised: 17 Aug., 2022
Accepted: 03 Sept., 2022

Citation:
Dudhat H, AG Pansuriya, DM Vekaria, H Dobariya, JB Patel, C Singh and IB Kapadiya. 2022. Heterosis for grain yield and its attributing traits in bread wheat (*Triticum aestivum* L.). *Journal of Cereal Research* ***14 (2):*** *150-160. http://doi.org/10.25174/2582-2675/2022/124052*

****Corresponding author:***
E-mail: hilaydudhat@gmail.com

Abstract

The present investigation was undertaken in order to estimate the heterosis for grain yield and its components in bread wheat (*Triticum aestivum* L.) for 13 characters. The crosses were attempted by using line × tester mating design among 8 lines and 4 testers during *rabi* 2019. The resultant 32 hybrids together with 12 parents and 1 standard check (GW 451) were tested using randomized block design with three replications at Wheat Research Station, Junagadh Agricultural University, Junagadh during *rabi* 2020-21. The prominent heterotic effects were observed for grain yield per plant and its components. A total of 3 and 3 hybrids exhibited significant desirable heterobeltiosis and standard heterosis, respectively for grain yield per plant. The heterobeltiosis for grain yield ranged from -47.58 % to 62.72 %, while standard heterosis ranged from -35.06 % to 36.92 %. The cross J 16-08 × GW 366 (62.72%) exhibited the highest desirable heterosis over better parent followed by J 16-08 × GW 11 (28.98%) and J 17-08 × GW 366 (19.39%). The cross J 16-08 × GW 366 (36.92%) exhibited highest significant heterosis towards positive direction over standard check, followed by J 16-08 × GW 11 (17.36%) and GW 513 × GW 11 (11.58%). These hybrids also exhibited desirable heterosis for important yield attributes suggesting that the heterosis for grain yield was associated with heterosis for component characters.

Keywords: Bread wheat, line × tester analysis, heterosis

1. Introduction

Among the world's crops, wheat is pre-eminent both in regard to its antiquity and its importance as a food for mankind. Bread wheat is known to have been grown in the Nile valley by 5000 B.C., and its apparently later cultivation in other regions (e.g., the Indus and Euphrates valleys by 4000 B.C., China by 2500 B.C. and England by 2000 B.C.) indicate that it spread from Mediterranean centers of domestication. The civilizations of West Asia and of the European peoples have been largely based on wheat, while rice has been more important in East Asia. Due to its wide adaptability to diverse climatic conditions and multiple end-uses along with dynamic nature of genomes and polyploidy character, it has become a crop of financial and nutritional importance especially after the emergence of hexaploid wheat (Dubcovsky and Dvorak, 2007).

Wheat belongs to the genus *Triticum* of Poaceae family and believed to be originated from South West Asia

(Lupton, 1987). In fact, there are three natural group of wheat from polyploid series of *Triticum* species viz. *Triticum aestivum* a hexaploid wheat (bread wheat) which is having chromosome number 2n = 42, *Triticum durum*, a tetraploid wheat (macaroni wheat) with chromosome number 2n = 28 and *Triticum dicoccum*, also a tetraploid wheat (emmer wheat) with chromosome number 2n = 28 are presently grown as commercial crop in India, covering about 95, 4 and 1 per cent area, respectively.

The substantial improvement in production is utmost necessary not only to meet ever increasing food requirement for domestic consumption, but also for export to earn foreign exchange. To feed the growing population, the country's wheat requirement by 2050 has been estimated at 140 million metric tonnes and to achieve this target, wheat production has to be increased at the rate of >1per cent annually and this can be achieved through horizontal approach i.e. by increasing area under cultivation or through vertical approach i.e. varietal improvement, which is one of the strongest tools to take a quantum jump in production and productivity under various agro- climatic conditions.

Heterosis breeding is proved to be the potential method of increasing yield in most of the cross pollinated crops but the commercial exploitation of heterosis in self-pollinated crops like wheat is not appreciable owing to technical difficulties involved in sufficient hybrid seed production. For enhancing the genetic yield potential of the varieties and hybrids, the choice of suitable parents for evolving better varieties/hybrids is a matter of great concern to the plant breeders. The nature and magnitude of heterosis help in identifying superior cross combinations that may produce desirable segregants in the advanced generations. The crosses exhibiting high heterosis could be exploited for obtaining transgressive segregants for improvement of yield and yield components.

2. Materials and Methods

Eight lines (females) namely, J 16 - 08, J 18 - 16, J 17 - 08, GW 513, AKAW 4901, HS 626, WH 1216, HD 3086 and four testers (males) i.e. GW 366, GW 11, HI 1544, GW 499 of bread wheat (*Triticum aestivum* L.) were selected on the basis of their phenotypic variability. The crossing programme was carried out during *Rabi* 2019-20 using line × tester mating design. The experimental material consisting of 45 entries, including 12 parents, 32 crosses and 1 standard check were tested in randomized block design with three replications during *Rabi* 2020-21. A single row plot of 2.5 meters was allotted randomly to each entry. The row-to-row and plant-to-plant distance was kept 22.5 cm and 10 cm, respectively. All the recommended cultural practices and plant protection measures were followed to grow healthy crop. Five competitive plants per genotype in each replication were randomly selected for the purpose of recording observations on for 13 characters, *viz.,* days to heading, days to maturity, plant height, flag leaf area, number of effective tillers per plant, length of main spike, number of spikelets per main spike, grain filling period, number of grains per main spike, 100-grain weight, grain yield per plant, biological yield per plant and harvest index. The estimation of heterosis over better parent and over standard check is more realistic. Hence, in the present investigation Heterobeltiosis was calculated as the deviation of F_1 from the better parent (Fonseca and Patterson, 1968) and was expressed in percentage by following formula: and Standard heterosis is per cent increase or decrease over standard check (GW-451) and was calculated by the following formula: where, = Mean performance of F_1 , = Mean value of batter parent of respective cross combination and Mean performance of standard check.

3. Results and Discussion

The analysis of variance (Table 1) depicted significant differences among the genotypes indicating that experimental materials had sufficient genetic variability for all the characters studied. The variance due to genotypes was further partitioned into variance due to parents, hybrids and parents vs. hybrids. The differences among the parents and hybrids were also found highly significant for all the characters studied. The mean squares due to parents *vs.* hybrids were found significant for plant height, number of effective tillers per plant, grain filling period, number of grains per main spike, grain yield per plant and harvest index. Suggesting that the performance of hybrids as a group was different than that of the parents for those characters. The mean squares due to parents *vs.* hybrid were of higher order as against parents and hybrids for number of spikelets per main spike, number of grains per main spike and grain yield per plant. The higher value of parent *vs.* hybrids indicates the presence of heterosis in material under study. This revealed the presence of substantial amount of heterosis in various cross combinations due to effect of directional dominance.

The heterotic effect in negative direction is desirable for days to heading in wheat. The earliest hybrid was HD 3086 × GW 499 (-12.07%) followed by J 17-08 × GW 11 (-11.98%) and AKAW 4901 × GW 499 (-11.41%). Out of 32 hybrids, 14 hybrids manifested significant and desirable (negative) estimate of heterobeltiosis (Table 2). Out of 32 hybrids, none exhibited significant and negative heterosis over standard check (Table 2). Significant negative heterosis for days to heading have also been reported by Dhoot *et al.* (2020). The negative heterosis for days to maturity is considered desirable for earliness in wheat crop. The earliest hybrid was J 16-08 × GW 499 (-6.02%) followed by WH 1216 × GW 366 (-4.62%), J 16-08 × HI 1544 (-3.68%) and AKAW 4901 × GW 499 (-3.68%). Out of 32 hybrids, 5 hybrid recorded significant negative heterosis over better parent (Table 2). None of the hybrids found earlier to standard check variety GW 451 (Table 2). Significant negative heterosis for days to maturity have also been reported by Saren *et al.* (2018).

In wheat, short plant height is desirable trait. The highest desirable heterobeltiosis was recorded by the cross AKAW 4901 × GW 11 (-17.49%) followed by AKAW 4901 × GW 366 (-17.24%) and AKAW 4901 × HI 1544 (-13.66%). Out of 32 hybrids, 12 hybrids manifested significant and desirable (negative) heterosis over better parent for this trait (Table 2). Out of 32 hybrids, none exhibited significant and desirable (negative) heterosis over standard check (Table 2). These results are in conformity with the results obtained by Khokhar *et al.* (2019).

Table 1. Analysis of variance (mean squares) for parents and hybrids for grain yield and its contributing characters in bread wheat

Source	**df**	**Days to heading**	**Days to maturity**	**Plant height**	**Flag leaf area**	**Number of effective tillers per plant**	**Length of main spike**	**Number of spikelets per main spike**
Replications	2	8.32	7.50	19.27	5.95	0.40	0.78	1.47
Genotypes	43	42.26**	18.08**	77.80**	17.77**	9.45**	2.26**	2.53**
Parents	11	80.12**	16.29**	117.11**	13.38**	8.06**	4.08**	3.17**
Hybrids	31	29.68**	18.97**	64.49**	19.90**	10.18**	1.69**	2.28**
Parents vs Hybrid	1	15.55	10.11	57.70*	0.04	2.37*	0.06	3.44
Error	86	4.05	4.70	13.88	1.93	0.59	0.31	1.07

Contd...

Source	**df**	**Grain filling period**	**Number of grains per main spike**	**100 - grain weight**	**Grain yield per plant**	**Biological yield per plant**	**Harvest index**
Replications	2	6.37	7.99	0.18	4.82*	12.76	39.37
Genotypes	43	23.61**	38.59**	0.33**	13.68**	143.02**	119.60**
Parents	11	36.27**	20.29*	0.22**	14.14**	105.47**	64.95**
Hybrids	31	19.21**	41.98**	0.38**	13.41**	160.86**	139.68**
Parents vs Hybrid	1	20.84**	134.82**	0.01	16.90**	3.00	98.22*
Error	86	2.72	8.38	0.07	1.28	7.40	19.83

Table 2. Per cent heterosis in F1s over better parent (H_1) and standard check GW 451 (H_2) for days to heading, days to maturity and plant height

Sr. No.	Hybrids	Days to heading		Days to maturity		Plant height	
		H_1	H_2	H_1	H_2	H_1	H_2
1	J 16-08 x GW366	-7.93**	-1.95	-2.68	3.56*	5.16	26.61**
2	J 16-08 x GW11	6.71*	13.64**	4.01*	10.68**	-1.13	25.94**
3	J 16-08 x HI1544	-4.27	1.95	-3.68*	2.49	4.05	25.28**
4	J 16-08 x GW499	-9.76**	-3.90	-6.02**	0.00	1.93	22.73**
5	J 18-16 x GW366	8.92**	11.04**	2.77	5.69**	9.13*	21.95**
6	J 18-16 x GW11	12.34**	12.34**	0.69	3.56*	-10.60**	13.87**
7	J 18-16 x HI1544	15.58**	15.58**	4.84**	7.83**	9.13*	21.84**
8	J 18-16 x GW499	6.49*	6.49*	0.00	2.85	7.84*	20.51**
9	J 17-08 x GW366	-4.19	3.90	0.00	2.85	23.09**	32.37**
10	J 17-08 x GW11	-11.98**	-4.55	-1.05	1.07	-3.10	23.43**
11	J 17-08 x HI1544	3.59	12.34**	1.74	3.91*	2.54	12.08**
12	J 17-08 x GW499	-8.38**	-0.65	1.05	3.20*	-1.55	7.21
13	GW513 x GW366	0.00	5.84*	1.02	5.34**	-10.54**	17.63**
14	GW513 x GW11	-2.45	3.25	-1.37	2.85	-10.46**	17.74**
15	GW513 x HI1544	-4.91	0.65	-2.39	1.78	-12.48**	15.08**
16	GW513 x GW499	-0.61	5.19*	-0.68	3.56*	-10.54**	17.63**
17	AKAW4901 x GW366	-3.26	15.58**	1.00	7.47**	-17.24**	10.20*
18	AKAW4901 x GW11	-1.09	18.18**	1.67	8.19**	-17.49**	9.87*
19	AKAW4901 x HI1544	-10.33**	7.14*	-2.34	3.91*	-13.66**	14.97**
20	AKAW4901 x GW499	-11.41**	5.84*	-3.68*	2.49	-7.91*	22.62**
21	HS626 x GW366	-2.19	16.23**	1.35	7.12**	3.03	31.93**
22	HS626 x GW11	-3.28	14.94**	2.02	7.83**	8.92*	39.47**
23	HS626 x HI1544	-3.83	14.29**	-1.01	4.63**	-4.16	22.73**
24	HS626 x GW499	-9.29**	7.79**	3.03*	8.90**	-8.57*	17.07**
25	WH1216 x GW366	-7.18**	9.09**	-4.62**	2.85	-1.19	19.40**
26	WH1216 x GW11	-7.18**	9.09**	-3.63*	3.91*	-6.53*	19.07**
27	WH1216 x HI1544	-6.63**	9.74**	-1.32	6.41**	15.23**	39.25**
28	WH1216 x GW499	-7.73**	8.44**	-1.32	6.41**	1.65	22.84**
29	HD3086 x GW366	-6.32*	5.84*	-0.69	2.14	4.51	20.62**
30	HD3086 x GW11	-8.05**	3.90	-2.08	0.71	-12.45**	11.53*
31	HD3086 x HI1544	-4.02	8.44**	0.00	2.85	-1.06	14.19**
32	HD3086 x GW499	-12.07**	-0.65	-2.77	0.00	1.92	17.63**
	SE±	1.62	1.62	1.75	1.75	3.01	3.01

*,** Significant at 5% and 1% levels, respectively

For flag leaf area, the highest significant positive heterosis over better parent was registered by the hybrid WH 1216 × GW 11 (29.20%) followed by GW 513 × GW 499 (15.44%) and HS 626 × GW 499 (14.39%). Out of 32 hybrids, 6 hybrids depicted significant and positive heterosis over better parent (Table 3). The cross WH 1216 × GW 11 (12.63%) exhibited the highest significant and positive heterosis over standard check followed by the cross GW 513 × GW 499 (11.12%) and HS 626 × GW 499 (7.63%). Among 32 hybrids, 3 hybrids showed significant and positive heterosis over standard check (Table 3). Similar findings were reported for this trait by earlier worker Kalimullah (2011).

For number of effective tillers per plant, the highest significant positive heterosis over better parent was recorded by the hybrid J 18-16 × HI 1544 (43.18%) followed by HS 626 × GW 11 (37.67%) and WH 1216 × GW 499 (28.57%). Out of 32 hybrids, 9 hybrids showed significant and positive heterosis over better parent (Table 3). The cross J 16-08 × GW 11 (39.40%) exhibited the highest significant and positive heterosis over standard check followed by the cross HD 3086 × GW 366 (38.83%) and J 16-08 × GW 499 (34.83%). Out of 32, 11 hybrids registered significant and positive heterosis over standard check (Table 3). Similar findings were also reported by earlier worker Motawea (2017).

For length of main spike, the highest desirable heterosis was recorded by the hybrid J 17-08 × GW 11 (11.74%). Out of 32 hybrids, only one hybrid showed significant and positive heterosis over better parent (Table 3).The cross HS 626 × HI 1544 (19.20%) expressed the highest significant positive heterosis over standard check followed by J 16-08 × GW 11 (17.03%) and HD 3086 × GW 499 (17.03%). Out of 32 hybrids, 18 hybrids exhibited significant positive desirable heterosis over standard check (Table 3). The results are in corroboration with those reported earlier by Shahzadi *et al.* (2015).

Table 3. Per cent heterosis in F1s over better parent (H_1) and standard check GW 451 (H_2) for flag leaf area, number of effective tillers per plant and length of main spike

Sr. No.	**Hybrids**	**Flag leaf area**		**Number of effective tillers per plant**		**Length of main spike**	
		H_1	**H_2**	**H_1**	**H_2**	**H_1**	**H_2**
1	J 16-08 x GW366	-2.71	-11.23**	13.31*	25.12**	-1.83	16.67**
2	J 16-08 x GW11	-8.19	-20.99**	26.25**	39.40**	-1.52	17.03**
3	J 16-08 x HI1544	7.19	-7.60*	-29.30**	-21.94**	-3.66	14.49**
4	J 16-08 x GW499	-1.66	-7.48*	22.10**	34.83**	-3.35	14.86**
5	J 18-16 x GW366	-11.96**	-15.15**	-1.47	5.41	1.96	-5.80
6	J 18-16 x GW11	-11.05**	-14.27**	20.18**	12.36*	-14.95**	-13.41**
7	J 18-16 x HI1544	-1.66	-5.17	43.18**	33.86**	-15.84**	-1.81
8	J 18-16 x GW499	6.12	2.28	-4.33	-7.06	4.65	-2.17
9	J 17-08 x GW366	-9.95**	-1.36	18.10**	34.77**	1.81	2.17
10	J 17-08 x GW11	-23.21**	-15.89**	-5.61	7.71	11.74**	13.77**
11	J 17-08 x HI1544	-23.35**	-16.05**	-36.27**	-27.28**	-14.91**	-0.72
12	J 17-08 x GW499	-15.96**	-7.95*	-6.98	6.14	-3.25	-2.90
13	GW513 x GW366	-16.22**	-19.36**	-21.02**	6.73	1.33	10.51*
14	GW513 x GW11	-21.05**	-24.00**	-8.52*	23.62**	-7.97*	0.36
15	GW513 x HI1544	9.87*	5.76	-12.39**	18.39**	-3.42	12.68**
16	GW513 x GW499	15.44**	11.12**	-24.49**	2.05	-1.33	7.61
17	AKAW4901 x GW366	7.71*	3.91	-8.79	6.22	-6.12*	11.23*
18	AKAW4901 x GW11	-18.26**	-21.14**	-29.98**	-18.46**	-9.17*	7.61*

19	AKAW4901 x HI1544	-10.49*	-13.65**	-12.31*	2.12	-14.98**	0.72
20	AKAW4901 x GW499	-1.11	-4.59	-16.42**	-2.67	-1.53	16.67**
21	HS626 x GW366	-8.43*	-16.46**	-4.37	2.30	-7.60*	10.14*
22	HS626 x GW11	11.67*	-7.37*	37.67**	13.86*	-2.43	16.30**
23	HS626 x HI1544	-7.39	-20.17**	-12.69	-27.79**	0.00	19.20**
24	HS626 x GW499	14.39**	7.63*	-25.37**	-27.50**	-12.16**	4.71
25	WH1216 x GW366	2.87	-6.14	0.21	7.20	-3.70	13.04**
26	WH1216 x GW11	29.20**	12.63**	-11.71	-16.71**	-9.57*	6.16
27	WH1216 x HI1544	-16.31**	-27.04**	11.01	4.72	-4.32	12.32**
28	WH1216 x GW499	5.39	-0.84	28.57**	24.90**	-1.23	15.94**
29	HD3086 x GW366	5.38	-0.78	17.77**	38.83**	-8.67*	6.88
30	HD3086 x GW11	-16.40**	-21.29**	-20.25**	-6.00	-15.17**	-0.72
31	HD3086 x HI1544	-3.34	-8.99*	-16.72**	-1.83	-5.26	10.87*
32	HD3086 x GW499	-4.44	-10.03*	-36.79**	-25.48**	0.00	17.03**
	SE±	1.13	1.13	0.62	0.62	0.46	0.46

*,** Significant at 5% and 1% levels, respectively

For number of spikelets per main spike, the highest heterobeltiosis was exhibited by the cross J 16-08 × GW 366 (7.91%). Out of 32 hybrids, only one hybrid registered significant and positive heterosis over better parent (Table 4). The cross J 16-08 × GW 366 (22.42%) exhibited the highest significant positive heterosis over standard check followed by J 16-08 × GW 11 (21.52%) and HS 626 × GW 11 (14.35%). Out of 32 hybrids, 12 hybrids showed significant and positive heterosis over standard check (Table 4). Significant positive heterosis for this character has also been reported by Ahmad *et al.* (2016).

In case of grain filling period, the highest desirable (positive) heterosis was recorded by the hybrid J 16-08 × GW 366 (8.20%). Out of 32 hybrids, only one hybrid manifested significant and desirable heterosis over better parent for this trait (Table 4).The cross J-16-08 × GW 366 (10.92%) exhibited the highest significant positive heterosis over standard check followed by J 16-08 × GW 499 (8.40%) and GW 513 × GW 499 (6.72%). Out of 32 hybrids, 3 hybrids registered significant and desirable heterosis over standard check (Table 4). Significant desirable heterosis for this character has been reported by Thomas *et al.* (2017).

Regarding number of grains per main spike, the highest heterosis over better parent in desirable direction was recorded by the cross GW 513 × GW 366 (24.00%) followed by HS 626 × GW 366 (22.91%) and J 16-08 × GW 366 (22.48%). Nine hybrids expressed significant positive heterosis over better parent (Table 4). The cross HS 626 × GW 366 (29.98%) exhibited the highest heterosis over standard check in desired direction followed by GW 513 × GW 366 (25.30%) and HD 3086 × GW 366 (21.84%). Out of 32 hybrids, 11 exerted significant positive heterosis over standard check (Table 4). These results are in agreement with the earlier studies carried out by Kumar *et al.* (2019).

Table 4. Per cent heterosis in F1s over better parent (H_1) and standard check GW 451 (H_2) for number of spikelets per main spike, grain filling period and number of grains per main spike

Sr. No.	Hybrids	Number of spikelets per main spike		Grain filling period		Number of grains per main spike	
		H_1	H_2	H_1	H_2	H_1	H_2
1	J 16-08 x GW366	7.91*	22.42**	8.20**	10.92**	22.48**	20.98**
2	J 16-08 x GW11	7.11	21.52**	-11.28**	-0.84	5.94	5.76

3	J 16-08 x HI1544	-4.74	8.07	-4.84	-0.84	11.17*	9.80*
4	J 16-08 x GW499	-3.95	8.97*	4.03	8.40**	-1.14	3.51
5	J 18-16 x GW366	0.43	4.04	-11.72**	-5.04	7.58*	5.92
6	J 18-16 x GW11	-5.91	0.00	-21.05**	-11.76**	0.18	0.02
7	J 18-16 x HI1544	1.71	6.73	-10.94**	-4.20	4.53	2.91
8	J 18-16 x GW499	-7.79	-4.48	-14.84**	-8.40**	4.68	9.60*
9	J 17-08 x GW366	-5.71	3.59	-0.82	1.68	17.77**	20.57**
10	J 17-08 x GW11	-0.82	8.97*	-9.02**	1.68	-2.65	-0.33
11	J 17-08 x HI1544	-6.53	2.69	-14.52**	-10.92**	-0.30	2.06
12	J 17-08 x GW499	-8.16*	0.90	-2.42	1.68	2.54	7.35
13	GW513 x GW366	-7.00	7.17	-4.92	-2.52	24.00**	25.30**
14	GW513 x GW11	-12.45**	0.90	-12.78**	-2.52	6.76	7.87
15	GW513 x HI1544	-1.17	13.90**	-6.45*	-2.52	12.22*	13.40**
16	GW513 x GW499	-10.89**	2.69	2.42	6.72*	12.50**	17.78**
17	AKAW4901 x GW366	-7.49*	10.76*	-13.11**	-10.92**	4.33	7.53
18	AKAW4901 x GW11	-10.86**	6.73	-21.05**	-11.76**	0.52	3.60
19	AKAW4901 x HI1544	-11.61**	5.83	-12.10**	-8.40**	2.97	6.12
20	AKAW4901 x GW499	-7.12*	11.21*	-14.52**	-10.92**	0.17	4.87
21	HS626 x GW366	-8.00*	13.45**	-13.11**	-10.92**	22.91**	29.98**
22	HS626 x GW11	-7.27*	14.35**	-19.55**	-10.08**	-8.39*	-3.12
23	HS626 x HI1544	-8.00*	13.45**	-18.55**	-15.13**	6.21	12.31*
24	HS626 x GW499	-14.55**	5.38	-8.06**	-4.20	-6.23	-0.83
25	WH1216 x GW366	-3.66	6.28	-2.46	0.00	-15.81**	-0.36
26	WH1216 x GW11	-2.03	8.07	-17.29**	-7.56*	-7.55*	9.42*
27	WH1216 x HI1544	2.85	13.45**	-6.45*	-2.52	-11.12**	5.20
28	WH1216 x GW499	-2.03	8.07	-12.90**	-9.24**	-21.10**	-6.62
29	HD3086 x GW366	-6.48	3.59	-8.20**	-5.88*	13.40**	21.84**
30	HD3086 x GW11	-8.10*	1.79	-17.29**	-7.56*	-5.18	1.88
31	HD3086 x HI1544	-4.86	5.38	-10.48**	-6.72*	-1.89	5.42
32	HD3086 x GW499	-1.62	8.97*	-0.81	3.36	-0.54	6.86
	SE±	0.83	0.83	1.33	1.33	2.35	2.35

*,** Significant at 5% and 1% levels, respectively

With respect to 100-grain weight, the highest heterosis over better parent in desirable direction was recorded by the cross WH 1216 × GW 499 (13.45%) followed by AKAW 4901 × GW 366 (8.26%) and J 18-16 × HI 1544 (8.24%). Six hybrids depicted significant desirable heterosis over better parent (Table 5). The cross HD 3086 × GW 499 (21.66%) exhibited the highest significant and positive heterosis over standard check followed by HS 626 × HI 1544 (19.53%) and AKAW 4901 × GW 366 (19.13%). Out of 32 hybrids, 12 hybrids showed significant desirable heterosis over standard check (Table 5). Significant desirable heterosis for this character has been reported by Gul *et al.* (2015).

In wheat, grain yield is one of the most important economic characters and the final product of the multiplicative interaction of contributing traits. Therefore, it is imperative to know the causes of heterosis for grain yield. The cross J 16-08 × GW 366 (62.72%) depicted the highest desirable heterosis over better parent followed by J 16-08 × GW 11 (28.98%) and J 17-08 × GW 366 (19.39%). Out of 32 hybrids, 3 hybrids expressed significant positive heterosis over better parent (Table 5). The cross J 16-08 × GW 366 (36.92%) recorded the highest significant heterosis towards positive direction over standard check, followed by J 16-08 × GW 11 (17.36%) and GW 513 × GW 11 (11.58%). Out of 32 hybrids, 3 hybrids showed significant positive desirable heterosis over standard check GW 366 (Table 5). These results were supported by those obtained by Khokhar *et al.* (2019).

Table 5. Per cent heterosis in F1s over better parent (H_1) and standard check GW 451 (H_2) for 100-grain weight and grain yield per plant

Sr. No.	Hybrids	100-grain weight		Grain yield per plant	
		H_1	H_2	H_1	H_2
1	J 16-08 x GW366	-3.43	4.74	62.72**	36.92**
2	J 16-08 x GW11	-8.33*	-4.27	28.98**	17.36**
3	J 16-08 x HI1544	-3.90	1.42	1.42	0.67
4	J 16-08 x GW499	3.33	7.91*	2.71	10.95
5	J 18-16 x GW366	-13.19**	-5.85	-14.13*	-4.95
6	J 18-16 x GW11	-0.53	3.32	-37.85**	-31.21**
7	J 18-16 x HI1544	8.24*	14.23**	-41.33**	-35.06**
8	J 18-16 x GW499	1.45	5.38	-33.81**	-26.73**
9	J 17-08 x GW366	-14.29**	-7.04*	19.39**	10.65
10	J 17-08 x GW11	-14.83**	-13.28**	-11.07	-17.58**
11	J 17-08 x HI1544	-1.20	4.27	-9.73	-10.40
12	J 17-08 x GW499	8.23*	8.14*	-6.14	1.39
13	GW513 x GW366	-9.31*	2.37	-47.58**	-29.14**
14	GW513 x GW11	-7.28*	4.66	-17.45**	11.58*
15	GW513 x HI1544	-5.32*	6.88*	-28.46**	-3.29
16	GW513 x GW499	-7.35*	4.58	-35.81**	-13.23*
17	AKAW4901 x GW366	8.26*	19.13**	-4.66	5.70
18	AKAW4901 x GW11	-5.39*	4.11	-37.70**	-30.93**
19	AKAW4901 x HI1544	-9.34*	-0.24	-35.72**	-28.74**
20	AKAW4901 x GW499	7.61*	18.42**	-18.15**	-9.26
21	HS626 x GW366	-9.64**	0.00	-4.63	-2.49
22	HS626 x GW11	-18.71**	-10.04*	-9.99	-7.97
23	HS626 x HI1544	8.00*	19.53**	-15.58*	-13.68*
24	HS626 x GW499	1.00	11.78**	-7.06	0.40
25	WH1216 x GW366	-2.84	5.38	7.50	-9.54
26	WH1216 x GW11	-3.18	-1.42	-2.22	-11.03
27	WH1216 x HI1544	4.12	9.88*	-7.84	-8.52
28	WH1216 x GW499	13.45**	13.36**	-1.31	6.60
29	HD3086 x GW366	-11.75**	2.13	4.65	8.40
30	HD3086 x GW11	-7.72*	6.80*	-19.90**	-17.03**

31	HD3086 x HI1544	-16.53**	-3.40	-2.19	1.31
32	HD3086 x GW499	5.12	21.66**	-31.84**	-26.37**
	SE±	0.22	0.22	0.93	0.93

*,** Significant at 5% and 1% levels, respectively

Regarding biological yield per plant, the highest heterobeltiosis was recorded by the cross J 17-08 × GW 366 (37.79%) followed by J 16-08 × GW 366 (34.17%) and J 16-08 × GW 11 (29.68%). Out of 32 hybrids, 13 hybrids expressed significant and positive heterosis over better parent (Table 6). The cross GW 513 × GW 11 (52.23%) exhibited the highest significant heterosis over standard check followed by J 16-08 × GW 11 (35.14%) and HS 626 × HI 1544 (34.84%). Twelve hybrids expressed significant positive desirable heterosis over standard check (Table 6). Similar findings have also been reported by Motawea (2017).

Table 6. Per cent heterosis in F1s over better parent (H_1) and standard check GW 451 (H_2) for biological yield per plant and harvest index

Sr. No.	Hybrids	Biological yield per plant		Harvest index	
		H_1	H_2	H_1	H_2
1	J 16-08 x GW366	34.17**	29.92**	0.73	5.53
2	J 16-08 x GW11	29.68**	35.14**	-0.27	-12.88
3	J 16-08 x HI1544	-15.88**	-6.78	19.58*	7.98
4	J 16-08 x GW499	13.58*	9.98	-14.97*	2.30
5	J 18-16 x GW366	-22.48**	-2.81	-6.42	-1.96
6	J 18-16 x GW11	-38.84**	-23.32**	2.49	-9.56
7	J 18-16 x HI1544	-28.74**	-10.65*	-19.02*	-26.87**
8	J 18-16 x GW499	-49.46**	-36.64**	-2.62	17.17*
9	J 17-08 x GW366	37.79**	11.01*	-15.74*	0.43
10	J 17-08 x GW11	-21.52**	-18.21**	-15.25*	1.02
11	J 17-08 x HI1544	-8.43	1.48	-25.65**	-11.38
12	J 17-08 x GW499	17.46**	6.04	-20.16**	-3.93
13	GW513 x GW366	-39.58**	-21.35**	-13.71	-9.60
14	GW513 x GW11	16.95**	52.23**	-29.52**	-26.56**
15	GW513 x HI1544	-20.50**	3.49	-10.31	-6.56
16	GW513 x GW499	-44.94**	-28.33**	1.01	21.54*
17	AKAW4901 x GW366	-21.93**	-9.63	12.18	17.52*
18	AKAW4901 x GW11	-3.54	11.66*	-36.20**	-38.17**
19	AKAW4901 x HI1544	-14.30**	-0.79	-25.61**	-27.90**
20	AKAW4901 x GW499	-1.54	13.98*	-33.47**	-19.96*
21	HS626 x GW366	13.85**	27.54**	-26.83**	-23.34**
22	HS626 x GW11	-14.70**	-4.44	5.65	-2.51
23	HS626 x HI1544	20.36**	34.84**	-30.48**	-35.85**
24	HS626 x GW499	-13.80**	-3.44	-12.70	5.04
25	WH1216 x GW366	14.99*	-2.04	-11.59	-7.39
26	WH1216 x GW11	-27.67**	-24.62**	37.16**	19.82*

27	WH1216 x HI1544	13.96**	26.29**	-19.71*	-27.49**
28	WH1216 x GW499	27.10**	14.74*	-22.39**	-6.62
29	HD3086 x GW366	-14.93**	-13.01*	19.41*	25.10**
30	HD3086 x GW11	25.07**	30.34**	-37.12**	-36.09**
31	HD3086 x HI1544	-16.19**	-7.12	9.03	10.82
32	HD3086 x GW499	15.99**	18.62**	-47.68**	-37.05**
	SE±	2.19	2.19	3.62	3.62

*,** Significant at 5% and 1% levels, respectively

Table 7. Top five standard heterotic hybrids for grain yield per plant along with desirable heterosis for other traits

Heterotic crosses	**Grain yield per plant (g)**	**Per cent heterosis of grain yield per plant over**		**Desirable heterosis for other traits over**	
		Better parent	**Check (GW 451)**	**Better parent**	**Check (GW 451)**
J 16-08 × GW 366	17.60	62.72**	36.92**	DH, NET, NSMS, GFP, NGMS, BYP	NET, LMS, NSMS, GFP, NGMS, BYP
J 16-08 ×GW 11	15.09	28.98**	17.36**	NET,BYP	NET, LMS, NSMS, BYP
GW 513 × GW 11	14.34	-17.45**	11.58*	PH, BYP	NET, BYP
J 16-08 × GW 499	14.26	2.71	10.95	DH, DM, NET, BYP	NET, LMS, NSMS, GFP, 100-GW
J 17-08 × GW 366	14.22	19.39**	10.65	NET, NGMS, BYP	NET, NGMS, BYP

Where, *, ** were significant at 5 % and 1 % levels of probability, respectively.

DH = Days to heading; NET= Number of effective tillers per plant; NGMS= Number of grains per main spike; DM = Days to maturity; LMS= Length of main spike; 100-GW= 100-grain weight; PH = Plant height (cm); NSMS= Number of spikelets per main spike; BYP= Biological yield per plant; FLA= Flag leaf area (cm^2); GFP= Grain filling period; HI = Harvest Index

For harvest index, the highest significant and desirable heterosis over better parent was recorded by the cross WH 1216 × GW 11 (37.16%) followed by J 16-08 × HI 1544 (19.58%) and HD 3086 × GW 366 (19.41%). Out of 32 hybrids, 3 hybrids demonstrated significant and positive heterosis over better parent (Table 7). The cross HD 3086 × GW 366 (25.10%) exhibited the highest significant standard heterosis followed by GW 513 × GW 499 (21.54%) and WH 1216 × GW 11 (19.82%). Out of 32 hybrids, 5 manifested significant and positive heterosis over standard check (Table 7). Similar findings have also been observed by Barot and Patel (2013).

Acknowledgements

Authors thank Director and Joint Director (Research), ICAR-Indian Agricultural Research Institute, (IARI), New Delhi for constant encouragements and support.

Author's contribution

Conceptualization of research (HD and AGP); Designing of the experiments (HD, AGP and IBK); Contribution of experimental materials (AGP, JBP and CS); Execution of field/lab experiments and data collection (DH, AGP and DMV); Analysis of data and interpretation (AGP and HD); Preparation of the manuscript (HD, AGP and IBK).

Declaration

The authors declare no conflict of interest.

References

1. Ahmad E, A Kumar and JP Jaiswal. 2016. Identifying heterotic combinations for yield and quality traits in bread wheat (*Triticum aestivum* L.). *Electronic Journal of Plant Breeding* **7**(2): 352-361.

2. Barot HG and MS Patel. 2013. Line X Tester analysis in bread wheat (*Triticum aestivum* L.). *AGRES – An International e-Journal* **2**(4): 472-483.
3. Dhoot M, H Sharma, VK Badaya and R Dhoot. 2020. Heterosis for earliness and heat tolerant trait in bread wheat (*Triticum aestivum* L.) over the environments. *International Journal of Current Microbiology and Applied Science* **9**(3): 624-630.
4. Dubcovsky J and J Dvorak. 2007. Genome plasticity a key factor in the success of polyploidy wheat under domestication. *Science* **316**, 1862–1866.
5. Fonseca S and FL Patterson. 1968. Hybrid vigour in a seven parent diallel cross in common winter wheat (*Triticum aestivum* L.). *Crop Science* **8**: 85-90.
6. Gul S, MK Aziz, RI Ahmad, S Liaqat, M Rafiq, F Hussain, M Rafiq, and SA Manzoor. 2015. Estimation of heterosis and heterobeltiosis in wheat (*Triticum aestivum* L.) crosses. *Basic Research Journal of Agricultural Science and Review* **4**(5): 151-157.
7. Kalimullah. 2011. Heterosis of certain important yield components in the population of wheat (*Triticum aestivum* L.) crosses. *Electronic Journal of Plant Breeding* **2**(2): 239-243.
8. Khokhar AA, WA Jatoi, FG Nizamani, RA Rind, MM Nizamani, HF Wang, A Mehmood and MU Khokhar. 2019. Study of heterosis analysis in F_1 population of bread wheat. *Pure and Applied Biology* **8**(2): 1757-1770.
9. Lupton FGH. 1987. Wheat Breeding: Its scientific basis. Chapman and Hall ltd., London.
10. Motawea MH. 2017. Estimates of heterosis, combining ability and correlation for yield and its components in bread wheat. *Journal of Plant Production* **8**(7):729 – 737.
11. Nagar SS, P Kumar, C Singh, V Gupta, G Singh and BS Tyagi. 2019. Assessment of heterosis and inbreeding depression for agro-morphological traits in bread wheat. *Journal of Cereal Research* **11**(2): 125-130.
12. Saren D, AB Mandal and C Soren. 2018. Heterosis studies in bread wheat (*Triticum aestivum* L.). *Journal of Agriculture and Veterinary Science* **11**(9): 80-84
13. Shahzadi M, Z Ali, J Farooq, S Hussain and R Bibi. 2015. Heterosis and heterobeltiosis analysis for spike and its related attributes in different wheat crosses (*Triticum aestivum* L.). *Pakistan Journal of Nutrition* **14**(7): 396-400.
14. Thomas N, S Marker, GM Lal and A Dayal. 2017. Study of heterosis for grain yield and its components in wheat (*Triticum aestivum* L.) over normal and heat stress condition. *Journal of Pharmacognosy and Phytochemistry* **6**(4): 824-830.

Journal of Cereal Research
Volume 14 (2): 161-167
Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Research Article

Prevalence of Southern Leaf Blight of Maize in two major maize producing states of India

Vanlalhruaia[1], Sunita Mahapatra[2*], Sunanda Chakraborty[2] and Srikanta Das[2]

[1]Subject Matter Specialist, KVK, Mamit, Mizoram-796421
[2]Department of Plant Pathology, Bidhan Chandra Krishi Vishwavidyalaya, Mohanpur, Nadia, West Bengal-741252.

Article history:
Received: 19 Aug., 2022
Revised: 13 Sept., 2022
Accepted: 04 Oct., 2022

Citation:
Vanlalhruaia S, S Mahapatra, S Chakraborty and S Das. 2022. Prevalence of Southern Leaf Blight of Maize in two major maize producing states of India. *Journal of Cereal Research* ***14* (2):** *161-167. http://doi.org/10.25174/2582-2675/2022/123845*

****Corresponding author:***
E-mail: sunitamahapatra@yahoo.co.in

Abstract

Southern corn leaf blight (SCLB) or Maydis leaf blight, caused by *Bipolaris maydis,* is an important disease of maize in the eastern and north-eastern part of India. Hence, to assess the severity and distribution of the disease in two distinct and major maize growing states i.e. Mizoram and West Bengal were selected. A roving survey was conducted under different agro-climatic conditions during the *kharif* season of 2019 and 2020 in three districts of West Bengal and as well as in Mizoram. The survey results revealed that SCLB was more prevalent in the plains of West Bengal in comparison to hilly areas of Mizoram. The mean SCLB incidence varied from 18.87% in Zemabawk, Mizoram to 63.22% in institutional farm, C-block, of BCKV, West Bengal. The mean disease severity ranged from 10.06 % in Muthi, Mizoram to 22.09% in Instructional Farm, Jaguli, BCKV, West Bengal. Both disease incidence and severity were highest at 99 DAS in all the locations surveyed. Successive surveys of SCLB in the maize growing belts across the country need to be conducted to develop a better understanding about the disease prevalence, intensity and severity under different agro-ecological conditions.

Keywords: *Bipolaris maydis,* disease incidence, Maydis blight, roving survey, *Zea mays.*

1. Introduction

Maize (*Zea mays* L.) is an important staple crop worldwide, with a share of 36% (782 million tons) in the global grain production (Solaimalai *et. al.*, 2020). Owing to its ability to thrive in a wide range of agro-climatic conditions, it is cultivated across 160 countries with acreage of 201 mha (FAOSTAT, 2022). According to Directorate of Economics and Statistics, Ministry of Agriculture (2020), India ranks fourth in terms of area (4%) and seventh in terms of production (2%) globally. In 1950-1951, India produced 1.73 million metric tonnes of maize which increased upto 27.8 million metric tons in 2018-2019 i.e. an almost 16 fold increase (Basandrai *et. al.,* 2020). Maize production in India exceeded 31 million metric tonnes in the fiscal year 2021 (FAOSTAT, 2022). As per the latest data by Indian Institute of Maize Research, Madhya Pradesh and Karnataka have the most area under maize (15%) among Indian states, followed by Maharashtra (10%), Rajasthan (9%), Uttar Pradesh (8%), and others.

In 2020, maize production of West Bengal was 1.64 million tones (Anon,2020). Maize production of West Bengal increased from 0.71 million tonnes in 2017 to 1.64 million tonnes in 2020 growing at an average annual rate of 35.68% (Debnath *et al.,* 2019). It is Mizoram's second most significant cereal crop after rice, and it is farmed as a single crop or in combination with other crops and trees in a variety of agro environments. As per the report published by department of Agriculture, Mizoram, maize is cultivated in an area of 6,946 ha, with a total production of 12,556 metric tones (Anon,2020a). Although production of maize has grown in India, owing to increased area, productivity has decreased from 2,093 to 1,940 kg/ha over the same time period owing to an increase in the exposure to biotic stresses (Singh *et. al.,* 2019).

The crop is known to be infected by a number of pathogens including fungi, bacteria and viruses (Mubeen *et. al.,* 2017). Among the fungal diseases of maize, Southern corn leaf blight (SCLB), caused by the fungus *Bipolaris maydis*, is a serious foliar disease (Aregbesola *et. al.,* 2020; Debnath *et al.*, 2021). Although the disease has been documented in most maize-growing locations around the world, it is most severe in hot and humid tropical and temperate climates. SCLB has emerged as a major disease in the Indian subcontinent and neighboring areas, resulting in a yield loss of almost 35-40% (Bruns, 2017). The disease is found in warm humid temperate to tropical regions with temperatures ranging from 20^0C to 30^0C throughout the cropping season (Debnath *et al.*,2019).

For assessing the severity of a disease, survey is an important tool. In the recent years, roving surveys have gained importance as it provides a wholesome picture of the pathogen abundance in a shorter duration (Thapa *et al.*,2022; Das *et al.*,2022). Further, since roving surveys or mobile surveys are conducted on randomly selected spots, it also helps in better allocation of resources with maximum results.

The present investigation, hence, was carried out as a roving survey to develop a comprehensive idea of the incidence of the disease, the disease severity and extent of the disease spread of southern corn leaf blight of maize under different agro climatic zone of West Bengal and Mizoram.

2. Materials and Methods

A roving method of survey for southern leaf blight of maize was conducted in different agro-climatic conditions under different maize growing districts of West Bengal, viz., Nadia, Murshidabad and North 24-Parganas and in different districts of Mizoram *viz.*, Mamit, Kolasib & Aizawl (Fig. 1), those are also known for hot spot location for southern leaf blight of maize. For West Bengal conditions, Kaveri variety was assessed while traditional maize lines, viz., Mimpui, Mimban, Puakzo, RCM 75 and RCM 76 were assessed in Mizoram. The location (Global positioning system, GPS reading) was also recorded. Zones and districts were chosen based on differences in production (farming) systems, climatic conditions (relative humidity, maximum and minimum temperatures), altitudes, important transportation corridors and vegetation cover (availability of maize crop) (Ramathani *et al.*, 2011). Observations of disease incidence and severity for southern leaf blight of maize were recorded from the field. Ten maize plant stands were randomly picked in the centre of each indicated area and tested for incidence and severity (Nwanosike *et al.*, 2015).

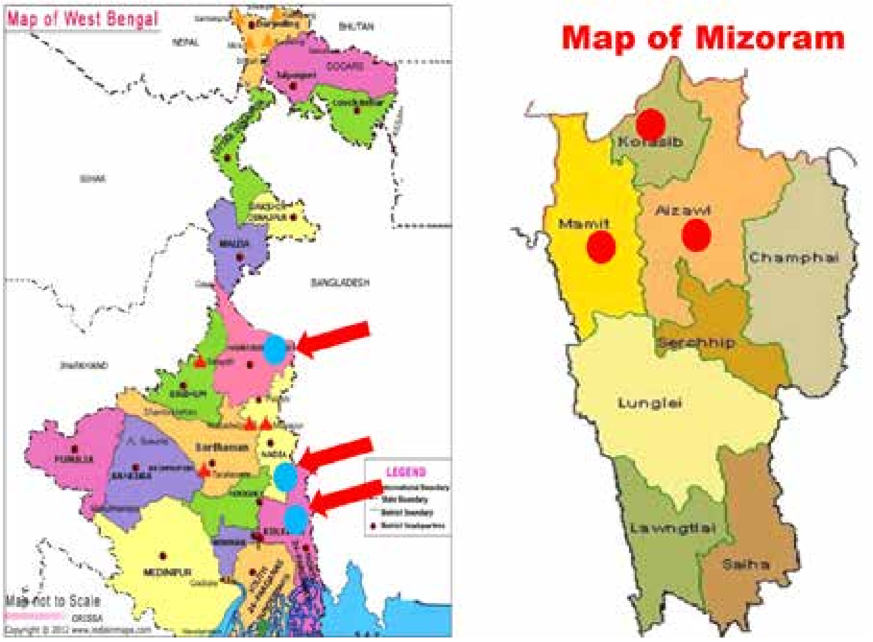


Fig-1: Map of West Bengal and Mizoram showing surveyed areas.

The proportion of plants showing symptoms in the field was used to calculate disease incidence. Disease incidence was recorded at 50, 57, 64, 71, 78, 85, 92 and 99 days after sowing (DAS). The number of plants showing maize leaf spot symptoms within ten randomly selected stands was tallied and expressed as a proportion of the total number of stands per plot using the formula below (Nwanosike *et al.*, 2015).

$$\text{Disease Incidence (\%)} = \frac{\text{No. of infected plants}}{\text{Total no. of plants assessed}} \times 100$$

Disease severity was recorded from 50 days after sowing in 10 plants per square meter in three different spots per plot, avoiding the border areas. The scoring was done at 50, 57, 64, 71, 78, 85, 92 and 99 days after sowing (DAS). It was assessed using the 1-5 standard disease scoring scale (Table 1) recommended by Shekhar and Kumar (2012) and Jakhar *et al.* (2017).

Table 1: Disease scoring scale for southern corn leaf blight disease of maize

Symptoms	Symptoms Severity Grade	Responsive value	Disease Reaction
No symptoms	0	No lesions	Symptom less
Very slight to Slight infection	1	One, two or few scattered lesions on lower leaves.	Highly resistant
Light infection	2	Light infection, Moderate number of lesion on lower Leaves only	Resistant
Moderate infection	3	Abundant lesion on lower leaves, few on middle leaves	Moderately resistant
Heavy infection	4	Lesions abundant on lower and middle leaves, extending to upper leaves	Susceptible
Very heavy infection	5	Lesion abundant on almost all leaves; plants prematurely dry or killed by the disease.	Highly Susceptible

Severity scores were converted to Percent Disease Index (PDI) using the following formula (Wheeler, 1969; Kumar *et al.*, 2011).

$$\text{PDI (\%)} = \frac{\text{Sum of all individual ratings}}{\text{Total no. of leaves examined} \times \text{Maximum rating}} \times 100$$

The Area Under Disease Progress Curve (AUDPC) was calculated using the standard method as recommended by Campbell and Madden (1990)

$$\boldsymbol{Y} = \sum_{i=1}^{n} [(\boldsymbol{X}_i + \boldsymbol{X}_{i+1})/2](\boldsymbol{t}_{i+1} - \boldsymbol{t}_i)$$

Where, Y is the AUDPC, X_i is the disease incidence of the *i*th evaluation, and X_{i+1} is the disease incidence of the $i+1$st evaluation, $t_{i+1} - t_i$ is the number of days between two evaluations.

The data recorded for disease incidence and PDI were recorded and the mean value, Standard error of mean and Critical difference was calculated using SPSS by employing SPSS (version 20.0 SPSS Inc., Chicago IL, USA) software package.

3. Results and Discussion

A roving survey was conducted to know the distribution and severity of SCLB of maize under different agro-climatic conditions during *kharif* season of 2019 and 2020 in West Bengal and Mizoram. Under West Bengal conditions, the survey was conducted in seven locations across three districts, while five locations across three districts of Mizoram were surveyed. It was observed that the disease severity level varied (43.51-100% at 99 DAS) from one locality to another especially between plains of West Bengal and hills of Mizoram, due to diversity in agro-ecological conditions and density of inoculum.

During the survey, typical symptoms of southern leaf blight of maize were observed in the form of lesions on the infected plant. The lesions were tan in colour with buff to brown borders. They begin as small, diamond-shaped spots which later transformed to larger, elongated, dark brown, necrotic lesions within the veins as described by Singh and Srivastava (2012), Kaur *et al.* (2014) and Dai *et al.* (2016).

The mean SCLB incidence varied from 18.87% in Zemabawk (Mizoram) to 63.22% at Instructural farm, C-block, Kalyani (West Bengal). Both disease incidence and severity were highest at 99 days after sowing (DAS) in all the locations surveyed.

The pooled data (Table 2) of both the years revealed the minimum disease incidence at 50 DAS while maximum was recorded at 99 DAS in all the locations surveyed. At 50 DAS, maximum disease incidence was recorded at Instructional Farm at Jaguli 2 (9.31%), statistically *at par* with Instructional Farm at C-Block, Kalyani (8.50%), followed by Instructional Farm at Jaguli 1 (6.17%), farmer's field at Char Jadubati P-1 (5.55%), farmer's field at Char Jadubati P - 2 (5.27%), farmer's field at Jalangi (5.02%) and farmer's field at Bodai (4.73%). The minimum disease incidence recorded at 50 DAS was in the farmer's field at Muthi (1.59%), statistically *at par* with farmer's field at Zemabawk (1.75%), followed by farmer's field at Dialdawk-2 (3.72 %), farmer's field at Dialdawk-1 (3.97%) and farmer's field at Meidum (4.67%) and these were statistically significant with Muthi and Zemabawk. As the disease incidence increases with time and age of the crop, the maximum disease incidence (100%) was recorded at 99 DAS in the Instructional Farm at Jaguli 1 and 2, Instructional Farm at C-Block, Kalyani, farmer's field at Char Jadubati P 1&2, farmer's field at Bodai and farmer's field at Jalangi respectively. At 99 DAS, the minimum disease incidence was recorded from farmer's field at Zemabawk (42.33%), statistically *at par* with farmer's field at Muthi (43.51%), followed by farmer's field at Meidum (69.17%), farmer's field at Dialdawk-2 (72.84%) and farmer's field at Dialdawk-1 (78.26%) which were statistically significant with each other as well as with the first two readings.

Table 2: Prevalence of Southern leaf blight of maize in West Bengal and Mizoram (Pooled mean of two years)

Location	Latitude and Longitude	Disease Incidence of Different DAS (Pooled mean of two years)							
		50	57	64	71	78	85	92	99
Instructional Farm, Jaguli-1, Nadia District	22°56'56"N 88°32'23"E	6.17 (14.38)	15.84 (23.45)	30.92 (33.78)	54.17 (47.39)	77.00 (61.34)	88.17 (69.88)	100.0 (90.0)	100.0 (90.0)
Instructional Farm, Jaguli-2, Nadia District	22°56.885'N 88°32.410'E	9.31 (17.76)	16.50 (23.97)	31.17 (33.94)	54.50 (47.58)	71.17 (57.52)	84.67 (66.95)	100.0 (90.0)	100.0 (90.0)
Instructional Farm, C-Block, Kalyani, Nadia	22°59'21"N 88°27'22"E	8.50 (16.95)	20.58 (26.98)	43.67 (41.36)	59.67 (50.57)	79.33 (62.96)	94.00 (75.82)	100.0 (90.0)	100.0 (90.0)
Char Jadubati P -1, Nadia District	22°59'25"N 88°24'56"E	5.55 (13.63)	11.83 (20.12)	24.78 (29.85)	43.50 (41.27)	62.17 (52.04)	83.83 (66.29)	100.0 (90.0)	100.0 (90.0)
Char Jadubati P - 2, Nadia District	22°59'25"N 88°24'56"E	5.27 (13.27)	10.75 (19.14)	25.58 (30.38)	46.61 (43.06)	64.00 (53.13)	83.33 (65.91)	100.0 (90.0)	100.0 (90.0)
Bodai, North 24-Parganas District	22°48'18"N 88°29'44"E	4.73 (12.56)	11.25 (19.59)	20.36 (26.82)	38.52 (38.36)	56.33 (48.64)	83.67 (66.16)	100.0 (90.0)	100.0 (90.0)
Jalangi, Murshidabad District	24°07'22"N 88°40'55"E	5.02 (12.95)	11.20 (19.55)	21.18 (27.40)	41.32 (40.00)	60.50 (51.06)	81.33 (64.40)	100.0 (90.0)	100.0 (90.0)
Dialdawk-1, Mamit District, Mizoram	23°50'37"N 92°36'07"E	3.97 (11.50)	10.61 (19.01)	19.71 (26.36)	24.77 (29.85)	36.64 (37.25)	46.80 (43.17)	59.41 (50.43)	78.26 (62.21)
Dialdawk-2, Mamit District, Mizoram	23°49'08.20"N 92°36'03.70"E	3.72 (11.12)	9.05 (17.51)	18.07 (25.16)	24.12 (29.41)	34.03 (35.69)	44.45 (41.81)	56.97 (49.01)	72.84 (58.59)
Muthi, Aizawl District, Mizoram	23°46'21.78"N 92°45'43.02"E	1.59 (7.23)	4.67 (12.48)	8.86 (17.32)	13.97 (21.95)	20.42 (26.86)	27.94 (31.91)	34.82 (36.16)	43.51 (41.27)
Zemabawk, Aizawl District, Mizoram	23°44'23"N 92°44'46"E	1.75 (7.59)	4.83 (12.70)	10.00 (18.43)	14.81 (22.63)	19.50 (26.21)	23.17 (28.77)	34.58 (36.02)	42.33 (40.59)
Meidum, Kolasib District, Mizoram	24°10'40.84"N 92°34'55.33"E	4.67 (12.48)	10.72 (19.11)	20.48 (26.90)	30.79 (33.71)	41.83 (40.30)	52.15 (46.23)	60.50 (51.06)	69.17 (56.27)
S.E. (m)±		0.51	0.50	0.49	0.60	0.94	1.31	0.32	0.32
C.D. at 5%		1.51	1.47	1.45	1.76	2.77	3.86	0.95	0.94

Figures in parenthesis are angular transformed values
Note: -DAS: Days After Sowing; AUDPC: Area Under Disease Progress Curve

The pooled data (Table 3) of both the years revealed the minimum disease severity at 50 DAS while maximum was recorded at 99 DAS in all the locations surveyed. At 50 DAS, maximum disease severity was recorded from Instructional Farm at Jaguli-1 (5.02 %) statistically *at par* with Instructional Farm at Jaguli-2 (4.99 %). These were followed by farmer's field at Meidum (3.06 %), Instructional Farm at C-Block, Kalyani (2.93%), farmer's field at Char Jadubati P-1 (2.70%), farmer's field at Char Jadubati P-2 (2.63%), and these were statistically significant with the disease severity from Jaguli 1 and 2 The minimum disease severity at 50 DAS was recorded from farmer's field at Muthi (1.40 %) which was statistically *at par* with farmer's field at Zemabawk (1.50 %), farmer's field at Jalangi (1.63 %), farmer's field at Dialdawk-2 (1.70 %) and farmer's field at Bodai (1.75%). The severity at farmer's field at Dialdawk-1 (2.55%) was statistically significant with Muthi and Zemabawk. The highest disease severity was recorded at 99 DAS in all the locations surveyed (Table 3). At 99 DAS, the maximum disease severity was recorded from farmer's field at Bodai (45.46 %) which is statistically *at par* with farmer's field at Jalangi (45.18 %). These were followed by disease severity in farmer's field at Char Jadubati P-1 (44.60 %), farmer's field at Char Jadubati P-2 (43.66 %), Instructional Farm at C-Block, Kalyani (40.79%), Instructional Farm at Jaguli-1 (38.64%), Instructional Farm at Jaguli-2 (38.10%), and these were statistically significant with Bodai. The minimum disease severity at 99 DAS was reported from farmer's field at Muthi (20.51 %) followed by farmer's field at Zemabawk (22.40 %), farmer's field at Dialdawk-1 (29.43 %) and farmer's field at Meidum (31.78 %) which were statistically significant with each other.

Table 3: Disease Severity at Different DAS (Pooled mean of two years)

Location	**Latitude and Longitude**	**Disease Severity at Different DAS (Pooled mean of two years)**								
		50	**57**	**64**	**71**	**78**	**85**	**92**	**99**	**AUDPC**
Instructional Farm, Jaguli-1, Nadia District	22°56'56"N 88°32'23"E	5.02 (12.94)	9.41 (17.87)	13.37 (21.45)	18.66 (25.59)	23.55 (29.03)	28.13 (32.03)	33.74 (35.51)	38.64 (38.43)	1040.84
Instructional Farm, Jaguli-2, Nadia District	22°56.885'N 88°32.410'E	4.99 (12.90)	8.76 (17.22)	15.33 (23.05)	21.19 (27.41)	25.17 (30.11)	29.49 (32.89)	33.70 (35.49)	38.10 (38.12)	1086.28
Instructional Farm, C-Block, Kalyani, Nadia	22°59'21"N 88°27'22"E	2.93 (9.85)	6.36 (14.61)	10.15 (18.57)	15.18 (22.93)	22.02 (27.98)	29.34 (32.79)	35.49 (36.56)	40.79 (39.69)	982.66
Char Jadubati P -1, Nadia District	22°59'25"N 88°24'56"E	2.70 (9.46)	5.48 (13.53)	8.96 (17.42)	13.25 (21.34)	17.24 (24.53)	24.67 (29.78)	35.55 (36.60)	44.60 (41.90)	901.49
Char Jadubati P - 2, Nadia District	22°59'25"N 88°24'56"E	2.63 (9.33)	6.10 (14.30)	9.26 (17.72)	13.68 (21.71)	17.91 (25.04)	25.61 (30.40)	35.14 (36.36)	43.66 (41.36)	915.94
Bodai, North 24-Parganas District	22°48'18"N 88°29'44"E	1.75 (7.59)	4.23 (11.87)	8.49 (16.94)	16.17 (23.71)	25.79 (30.52)	34.19 (35.78)	40.82 (39.71)	45.46 (42.39)	1073.02
Jalangi, Murshidabad District	24°07'22"N 88°40'55"E	1.63 (7.33)	4.80 (12.65)	8.89 (17.35)	16.00 (23.58)	26.57 (31.03)	34.14 (35.76)	41.63 (40.18)	45.18 (42.23)	1087.96
Dialdawk-1, Mamit District, Mizoram	23°50'37"N 92°36'07"E	2.55 (9.19)	5.90 (14.06)	9.76 (18.20)	14.22 (22.15)	18.45 (25.44)	22.37 (28.22)	26.30 (30.85)	29.43 (32.85)	790.85
Dialdawk-2, Mamit District, Mizoram	23°49'08.20"N 92°36'03.70"E	1.70 (7.48)	5.27 (13.27)	9.54 (17.99)	14.54 (22.41)	19.65 (26.31)	23.82 (29.21)	28.18 (32.06)	32.23 (34.59)	825.69
Muthi, Aizawl District, Mizoram	23°46'21.78"N 92°45'43.02"E	1.40 (6.80)	2.94 (9.87)	5.32 (13.33)	7.98 (16.41)	10.81 (19.19)	14.04 (22.01)	17.46 (24.70)	20.51 (26.93)	486.48
Zemabawk, Aizawl District, Mizoram	23°44'23"N 92°44'46"E	1.50 (7.04)	4.93 (12.83)	8.67 (17.12)	11.57 (19.89)	14.55 (22.43)	17.58 (24.79)	20.50 (26.92)	22.40 (28.25)	628.31
Meidum, Kolasib District, Mizoram	24°10'40.84"N 92°34'55.33"E	3.06 (10.07)	6.28 (14.52)	10.75 (19.14)	18.66 (23.51)	20.59 (26.99)	24.80 (29.86)	28.60 (32.33)	31.78 (34.31)	870.43
S.E.(m)±		0.35	0.33	0.25	0.27	0.26	0.23	0.26	0.28	12.84
C.D. at 5%		1.02	0.97	0.75	0.79	0.76	0.69	0.75	0.82	37.91

Figures in parenthesis are angular transformed values

Note: -DAS: Days After Sowing; AUDPC: Area Under Disease Progress Curve

The pooled maximum area under disease progress curve (AUDPC) was recorded from farmer's field at Jalangi (1087.96) statistically *at par* with Instructional Farm at Jaguli-2 (1086.28), farmer's field at Bodai (1073.02). This is followed by AUDPC in Instructional Farm at Jaguli-1 (1040.84), Instructional Farm at C-Block, Kalyani (982.66), farmer's field at Char Jadubati P-2 (915.94) and farmer's field at Char Jadubati P-1 (901.49). The minimum AUDPC was recorded from farmer's field at Muthi (486.48), followed by farmer's field at Zemabawk (628.31), farmer's field at Dialdawk-1 (790.85), farmer's field at Dialdawk-2 (825.69) and farmer's field at Meidum (870.43) and all of these were statistically significant with each other.

The survey results showed that the disease was more prevalent in the plains of West Bengal *viz,*. Nadia, Murshidabad and North 24-Parganas districts in comparison to hilly are as of Mizoram. The variations in disease incidence and disease severity from location to location may be attributed to the varying climatic factors, different hybrids cultivated, differences in pathogen inoculum density in the field, non-adoption of disease management practices, etc. which affected the growth and development of the disease. The results of this investigation coincided with the findings of Nongmaithem *et al.* (2022) who observed a low incidence of maydis leaf blight (10-20%) in the state of Manipur. During the survey of the fields, it was also observed that most of the fields practiced monocropping with maize as the sole crop, which might lead to an increase in disease inoculum resulting in higher disease incidence (Surendhar *et al.,* 2021).

The findings of the present survey are in accordance with the findings of Debnath *et al.* (2019), who reported SCLB in Murshidabad and Nadia districts of West Bengal. Surveys and surveillance by Harlapur *et al.* (2000) in north Karnataka revealed a moderate intensity of SCLB in the surveyed districts.

Similar trend was also reported by Hulagappa *et al.* (2013), who surveyed the severity of maydis leaf blight of maize in northern Karnataka during Kharif, 2011. They recorded maximum disease severity in Ranebennur (56.26%) while least severity was noticed in Kushtagi (33.88%), indicating the status of the disease in the area.

Conclusion

The plain zones of West Bengal as well as the north eastern states are prone to leaf blight of maize. This roving survey was conducted in three districts of West Bengal and three districts of Mizoram. Among the areas surveyed, the disease incidence as well as severity was found to be lower in the districts of Mizoram as compared to those of West Bengal. Successive surveys of SCLB in the maize growing belts across the country need to be conducted to develop a better understanding of the disease prevalence, intensity and severity under different agro-ecological conditions. This would also help the breeder to recommend zone specific varieties for the sake of the farmers to avoid excessive loss due the disease.

Conflict of interest:

All the authors declare that they do not have any conflict of interest.

Author contribution

All the authors have equally contributed for this review article. SM made the concept of the article, VL, SC and SD wrote according to the concept. SM finally edited and corresponded to the journal

Ethical statement

Not applicable with this article.

4. References

1. Anonymous, 2020(https://knoema.com/atlas/India/WestBengal/topics/Agriculture/Agricultural-Production/Maize-production)
2. Anonymous, 2020a (https://agriculturemizoram.nic.in/pages/agristat.html)
3. Aregbesola E, A Ortega-Beltran, T Falade, G Jonathan, S Hearne, R Bandyopadhyay. A. 2020. Detached leaf assay to rapidly screen for resistance of maize to *Bipolaris maydis*, the causal agent of southern corn leaf blight. *European Journal of Plant Pathology.* **156(1):**133-45.
4. Basandrai AK, D Basandrai and A Mehta. 2020. Sources possessing multiple field resistance to bacterial stalk rot, banded leaf and sheath blight and maydis leaf blight of maize. *Journal of Cereal Research* **12(2)**:160-159.
5. Bruns HA. 2017. Southern corn leaf blight: a story worth retelling. *Agronomy Journal* **109(4):**1218-1224.
6. Campbell CL and Madden LV. 1990. Introduction to Plant Disease Epidemiology. Wiley-Interscience, New York.

7. Dai YL, XJ Yang, L Gan, FR Chen, HC Ruan, YX Du, and ZM Gao. 2016. First report of southern leaf blight caused by *Cochliobolus heterostrophus* on corn (*Zea mays*) in Fujian Province, China. *Plant Disease*, **100**(8):1781
8. Das T, T Sandham,Y Umbrey,S Mahapatra and S Das 2022. An Overview of Fusarium Wilt of Lentil Status in different Districts of West Bengal, India. *Biological Forum – An International Journal*, 14(2): 974-978
9. Debnath D, S Chakraborty and S Mahapatra. 2021. Spot blotch: A journey from minor to major threat of wheat. Journal of Cereal Research 13(3): 255-269. http://doi.org/10.25174/2582- 2675/2022/112851
10. Debnath S, S Chhetri, S Biswas. 2019. Status of maize diseases in southern and western parts of West Bengal. *IJCS.* **7(4):**441-5.
11. FAOSTAT, F. 2022. Available online: http://www. fao. org/faostat/en/# data.
12. Harlapur, SI, CW Mruthunjaya, KH Anahosur, S Muralikrishna. 2000. A report survey and surveillance of maize diseases in North Karnataka. *Karnataka Journal of Agri-cultural Sciences*. **13**(3): 750-751
13. Hulagappa SH, RS Roopa,VM Dore. 2013. Field evaluation of fungicides for management of Maydis leaf blight of maize caused by *Dreschslera maydis* (Nisikado) Subram. and Jain. *Trends-in-Biosciences.* **6**(6): 789-791.
14. Jakhar DS, R Singh, S Kumar, P Singh, and V Ojha 2017. Turcicum leaf blight: A ubiquitous foliar disease of maize (*Zea mays* L.). *International Journal of Current Microbiology and Applied Sciences*, **6**(3): 825-831.
15. Kaur H, KS Hooda and MK Khokhar. 2014. Maydis leaf blight of maize: Historical perspective, impact and present status. *Maize Journal* **3** (1&2): 1-8.
16. Kumar H, T Kawai T, S Akira. 2011. Pathogen recognition by the innate immune system. *International Reviews of Immunology.* **30(1):**16-34.
17. Mubeen S, M Rafique, MFH Munis, HJ Chaudhary. 2017. Study of southern corn leaf blight (SCLB) on maize genotypes and its effect on yield. *Journal of the Saudi Society of Agricultural Sciences.* **16(3):** 210-217.
18. Nongmaithem N, Sanjenbam D, Konsam J, Singh LN, Devi TR. 2022. A report survey and surveillance of maize diseases in Manipur. *The Pharma Innovation Journal.* **11(5):** 557-560.
19. Nwanosike MRO, RB Mabagala, PM Kusolwa. 2015. Disease Intensity and Distribution of *Exserohilum turcicum* Incitant of Northern Leaf Blight of Maize in Tanzania. *International Journal of Pure and Applied Biosciences.* **3(5):**1-13.
20. Ramathani I, M Biruma, T Martin, C Dixelius, P Okori. 2011. Disease severity, incidence and races of *Setosphaeria turcica* on sorghum in Uganda. *European Journal of Plant Pathology.* **131:**383- 392.
21. Shekhar M and S Kumar 2012. Inoculation Methods and Disease Rating Scales For Maize Diseases. Editors: MeenaShekhar and Sangit Kumar, Published by Directorate of Maize Research(ICAR), Pusa Campus, New Delhi. Second Edition, pp 2-6.
22. Singh R and RP Srivastava. 2012. Southern Corn Leaf Blight-an important disease of maize: an extension fact sheet. *Indian Research Journal of Extension Education*, Special Issue (Vol. I), January, 334-337.
23. Singh S, VP Singh, SM Prasad, S Sharma, N Ramawat, NK Dubey, DK Tripathi, DK Chauhan. 2019. Interactive effect of silicon (Si) and salicylic acid (SA) in maize seedlings and their mechanisms of cadmium (Cd) toxicity alleviation. *Journal of Plant Growth Regulation.* **38(4):**1587-97.
24. Solaimalai A, P Anantharaju, S Irulandi, M Theradimani. 2020. *Maize Crop: Improvement, Production, Protection and Post Harvest Technology.* CRC Press.
25. Surendhar M, Y Anbuselvam, JS Johnny. 2021. Status of Rice Brown Spot (Helminthosporium oryza) Management in India: A Review. *Agricultural Reviews*. 1-6.
26. Thapa S, S Mahapatra, D Baral , A Lama, P Shivakoty and S Das.2022. Status of false smut of rice in different districts of West Bengal *Oryza*.59(2).250-254 DOI https://doi.org/10.35709/ory.2022.59.2.5
27. Wheeler, BEJ 1969. An Introduction to Plant Diseases, John Wiley and Sons Limited, London, P. 301.

Journal of Cereal Research
Volume 14 (2): 168-174
Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Research Article

Diversity Analysis in Finger Millet (*Eleusine coracana* L.) Germplasm for Agro-Morphological and Grain Yield Attributing Traits

Maruthamuthu Elangovan[1], Karnam Venkatesh[1], A Annapurna[1], Rajendragouda Patil[1], Ravikiran[1], Sushil Pandey[2] and Chitra Devi Pandey[2]

[1]ICAR-Indian Institute of Millets Research (IIMR), Hyderabad
[2]ICAR-National Bureau of Plant Genetic Resources (NBPGR), New Delhi

Article history:
Received: 29 July, 2022
Revised: 08 Oct., 2022
Accepted: 21 Oct., 2022

Citation:
Elangovan M, K Venkatesh, A Annapurna, R Patil, Ravikiran, S Pandey and CD Pandey. 2022. Diversity Analysis in Finger Millet (*Eleusine coracana* L.) Germplasm for Agro-Morphological and Grain Yield Attributing Traits. *Journal of Cereal Research* ***14 (2):*** *168-174.* *http://doi.org/10.25174/2582-2675/2022/121861*

****Corresponding author:***
E-mail: elangovan@millets.res.in

Abstract

Finger millet (*Eleusine coracana* L.) is an important millet crop grown at large scale in Asia and Africa. Germplasm is the basic source of variation in the crop improvement. An experiment on characterization of 2000 germplasm accessions was conducted in augmented design at ICAR-Indian Institute of Millets Research (IIMR), Hyderabad during Kharif 2017. The multivariate analysis is an important statistical tool which can easily asses the polygenic traits important for breeding program. The PCA analysis showed 14 Principle Components (PCs) to total variability. The first six principal components explained a total of 63.99% of variability with Egan's value of >1. The first two PCs played important role in diversity contribution than other PCs. A total of nine clusters were formed on the bases of Euclidian distance of 14.67% and 85, 63% variation observed within and between clusters. The selection of genotypes from the different clusters will help the breeders to increase variability in their breeding programme

Key words: Genetic diversity, *Eleusine coracana*, Principle Component Analysis, Clusters and Egan's value

1. Introduction

Finger millet (*Eleusine coracana* L.) is popularly known as '*Ragi*' in India. It is an annual millet crop grown mainly in arid and semi-arid region of the world covering Africa and South Asia. Finger millet is tetraploid, self-pollinated and believed to be evolved from wild relative *Eleusine africana* (Sood *et al.* 2017). It is native to Ethiopia and Uganda's highlands (D'Andrea *et al.,* 1999). It is known to with stand 3000 m mean sea level latitude (Bisht and Singh, 2009), contains high level of micronutrients (Iron and Methionine). Finger millet is known to have high drought tolerance and long storability (Keerthana *et al.* 2019).

Variability in the genetic material is the prerequisite for any crop improvement programme. Germplasm is the basic source of natural variation maintained in the gene banks globally. In India, ICAR-National Bureau of Plant Genetic Resource (NBPGR), New Delhi, ICAR-Indian Institute of Millets Research (IIMR), Hyderabad and International Crop Research Institute for Semi-Arid Tropics (ICRISAT), Patancheru are the nodal organisations to maintain Indigenous and Exotic finger millet germplasm. Along with the creation of genetic diversity, it is essential to characterize the germplasm for effective utilization for crop improvement (Upadhyaya *et al.* 2007).

Finger millet is commonly known as nutritious millet as the grains are rich in protein, vitamins, minerals and exceptionally superior in calcium content. It serves as a staple food for rural people in developing countries wherein calcium and anaemia are rampant (Owere *et al.* 2015).

Phenotyping characterization of germplasm accessions and knowing the association between the traits helps in development of high yielding cultivars through crop improvement. Simultaneous improvement of traits depends upon the nature and degree of correlation that exists between traits (Mnyenyembe and Gupta 1998). Many researchers have reported on association and variability of finger millet traits. Mehra (1962) reported that existence of diversity for rachis and raceme width, spikelet and glume length by Metroglyph analysis. There were wide genotypic and phenotypic variations for tiller number, ear numbers and grain weight of 33 cultivars (Goud and Laxmi, 1977). Rao *et al.* (1986) reported the variability of traits, heritability and genetic advance for grain yield among F$_2$ generations of three crosses.

Core sub sets (minicore) have been developed by (Upadhyaya *et al.* 2006, 2007) in finger millet of 5949 germplasm accessions using geographic origin and collected data on 14 quantitative traits. Upadhyaya *et al.* (2007) observed large variability for days to 50 % flowering, plant height and inflorescence length of 909 finger millet germplasm accessions introduced from Southern and Eastern Africa.

Multivariate analysis methods are most useful for characterization, evaluation and classification of large number of accessions assessed for several agronomically important trait (Peeters and Martinelli 1989). Multivariate analysis has been demonstrated to be useful in drawing meaningful information out of large-scale phenotypic characterization of germplasm accessions. Outcome of this analysis can be utilized for identifying accession in the group of desirable traits for crossing, planning efficient germplasm collecting expedition, for establishing of core collection and crop evolution studies. The objective of this study was to phenotypically characterize a set of finger millet germplasm accessions and to estimate the genetic variability.

2. Materials and Methods

The initial experimental material consisted of 2000 finger millet accessions out of which only 1487 were considered for final data analysis as some of them failed to germinate while the other few were having missing data either due to poor seed set or high disease susceptibility. The experiment was conducted at ICAR-Indian Institute of Millets Research (17.3207° N latitude, 78.3959° E longitude and 476.5 meters above msl), Hyderabad India in augmented design during Kharif 2017. Two checks viz., KMR 204 (medium duration variety) and DHFM 78-3 (long duration variety) were repeated after every 100 accessions. Each accession was sown in 1 m long row with 60 cm distance between each row and 10 cm distance maintained between plants. Fertilizers were applied at the rate of 60 kg/ha N, 30 kg/ha P$_2$O$_5$and 30 kg/ha K during the crop growth period. Full dose of P and K whereas half dose of N were applied as basal dose and remaining half of N applied at 20 days after sowing. All necessary package of practices was followed for good crop stand. Regular irrigation was given to maintain sufficient moisture. The crop was protected from weeds, pest and diseases. The data was analysed for Principle Component Analysis (PCA) and Clustering Analysis using Genlex software 14.0.

3. Results and Discussions

3.1 Principal Component Analysis (PCA)

The descriptive statistical (Table 1) analysis reveals the variability within accessions, days to 50 % flowering (0.82) observed with highest variance followed by plant height (0.75) and grain yield (0.70). The yield contributing traits such as number of basal tillers ranged from 1 to 19.33 tillers, plant height (65.00 cm to 185.00 cm), finger length (2.50 cm to 19.57 cm), number of fingers on ear head (3.33 to 17.00), grain yield (1.00 g/plant to 98.00 g/plant) and 100-Seed weight (0.03 g to 3.35 g) also contributed to the overall diversity.

One of the objectives of this study was to use Principal Component Analysis (PCA) to identify representative traits for phenotypic characterization of finger millet. The PCA is a multivariate statistical technique used to simplify and analyse the inter-relationship among a large set of variables in term of a relatively small set of variables or components without losing any essential information of original data set. Total variability can be explained by each component in per cent (%) variation. Thus, it is most useful analysis for genetic improvement of important traits rather than going for all the characters under study. Fenty (2004) reported that PCA depicts the importance of large contributors to total variability at each axis of differentiation and reduce the large set of variables in to smaller sets which summarises the correlations. The total of 14 principle components (PC) contribute to variability of finger millets but cumulative of 63.99 % of variability explained by the first six principle components which were having >1 eigan's values (ranged from 3.17 to 0.18, Figure 1). The first two PCs (22.66 and 10.25%) contribute more towards variability than others. Flag leaf width (cm), Number of leaves and Leaf blade width (cm) were found to be having stronger association with PC1. Patel *et al.,* (2017) reported that first PC contributed 42.81 per cent and second PC was of 18.43 per cent. Each trait has contributed to variability which is explained with cosine value through respective principle components (table 2). The grain yield contributing traits like number of tillers (80.58%) through PC 9, number of fingers on ear head (74.05%) through PC6, finger length (40.59%) through PC 2 and 100-Seed weight (25.66) through PC1 contributed to variability (Table 3). If a single trait associated with a principal component is selected and improved upon will lead to improvement of other traits associated with that PC. The similar trend was supported by Agarwal *et al.,* (2004), Ali *et al.,* (2011), Akatwijuka *et al.,* (2016), Jain and Patel (2016) and Patel *et al.,* (2017).

Table 1: Descriptive statistics of traits studied for characterization of finger millet germplasm during Kharif 2017.

Traits	Mean	Min	Max	SD	Variance	CV (95.0%)
Days to 50% flowering	79.56	33.00	122.00	16.15	260.82	0.82
Number of basal tillers	5.49	1.00	19.33	2.28	5.19	0.12
Flag leaf length (cm)	31.76	10.80	69.30	9.38	87.93	0.48
Flag leaf width (cm)	1.27	0.30	7.50	0.36	0.13	0.02
Number of leaves	17.30	7.00	24.00	1.74	3.03	0.09
Leaf blade length (cm)	56.46	1.80	84.03	7.04	49.63	0.36
Leaf blade width (cm)	1.54	0.90	2.70	0.15	0.02	0.01
Plant height (cm)	119.34	65.00	185.00	14.66	214.92	0.75
Finger length (cm)	8.01	2.50	19.57	2.41	5.79	0.12
Peduncle length (cm)	19.27	2.50	35.10	3.93	15.45	0.20
Number of fingers on ear head	7.75	3.33	17.00	1.47	2.15	0.07
Grain yield (g/plant)	22.88	1.00	98.00	13.67	186.95	0.70
100-Seed weight (g)	0.23	0.03	3.35	0.14	0.02	0.01

Table 2: Eigen's values and variability explained by principle components for 1489 finger millet accessions characterized during Kharif 2017

Source	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11	F12	F13	F14
Eigenvalue	3.17	1.43	1.31	1.06	1.03	1.00	0.95	0.89	0.75	0.72	0.62	0.54	0.39	0.18
Variability (%)	22.66	10.25	9.33	7.58	7.13	7.04	6.78	6.39	5.37	5.13	4.40	3.84	2.81	1.30
Cumulative %	22.66	32.91	42.24	49.81	56.94	63.99	70.77	77.16	82.53	87.66	92.05	95.89	98.70	100.00

Table 3: Percent (squared cosines) contribution of variability from each trait through principle components of finger millet accessions

SN	Traits	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11
1	Days to 50% flowering	0.21 (0.01)	2.73 (0.04)	**44.55** **(0.59)**	0.04 (0.01)	3.33 (0.04)	0.66 (0.01)	0.15 (0.01)	3.64 (0.04)	0.05 (0.01)	37.07 (0.27)	2.06 (0.02)
2	Number of basal tillers	10.17 (0.33)	0.17 (0.01)	0.8 (0.02)	1.27 (0.02)	1.17 (0.02)	0.49 (0.01)	0.59 (0.01)	0.38 (0.01)	**80.58** **(0.61)**	0.2 (0.01)	1.2 (0.01)

3	Flag leaf length (cm)	0.01 (0.01)	0.01 (0.01)	23.24 (0.31)	4.15 (0.05)	15.4 (0.16)	5.69 (0.06)	5.98 (0.06)	**34.85** **(0.32)**	5.09 (0.04)	1.97 (0.02)	3.43 (0.03)
4	Flag leaf width (cm)	**24.28** **(0.77)**	0.5 (0.01)	0.75 (0.01)	0.02 (0.01)	0.01 (0.01)	0.45 (0.01)	0.1 (0.01)	0.17 (0.01)	0.78 (0.01)	1.56 (0.02)	0.47 (0.01)
5	Number of leaves	**15.81** **(0.51)**	0.57 (0.01)	1.38 (0.02)	0.06 (0.01)	0.02 (0.01)	0.2 (0.01)	5.98 (0.06)	8.02 (0.08)	4.44 (0.04)	0.93 (0.01)	0.56 (0.01)
6	Leaf blade length (cm)	3.26 (0.11)	0.15 (0.01)	1.29 (0.02)	0.93 (0.01)	8.3 (0.09)	7.77 (0.08)	**68.9** **(0.66)**	2.23 (0.02)	0.46 (0.01)	0.58 (0.01)	1.16 (0.01)
7	Leaf blade width (cm)	16.53 (0.53)	0.89 (0.02)	0.01 (0.01)	2.08 (0.03)	0.81 (0.01)	0.12 (0.01)	1.06 (0.01)	0.52 (0.01)	6.42 (0.05)	4.38 (0.04)	0.89 (0.01)
8	Plant height (cm)	0.03 (0.01)	0.01 (0.01)	2.21 (0.03)	**46.61** **(0.5)**	37.34 (0.38)	2.77 (0.03)	0.46 (0.01)	0.26 (0.01)	0.03 (0.01)	8.07 (0.06)	0.15 (0.01)
9	Finger length (cm)	1.42 (0.05)	**40.59** **(0.59)**	0.01 (0.01)	0.02 (0.01)	0.88 (0.01)	0.01 (0.01)	2.18 (0.03)	0.13 (0.01)	0.19 (0.01)	7.39 (0.06)	44.01 (0.28)
10	Peduncle length (cm)	0.04 (0.01)	**40.82** **(0.59)**	0.13 (0.01)	0.23 (0.01)	1.75 (0.02)	0.14 (0.01)	0.69 (0.01)	13.12 (0.12)	0.2 (0.01)	1.39 (0.01)	41.46 (0.26)
11	Number of fingers on ear head	0.99 (0.04)	0.02 (0.01)	0.74 (0.01)	1.11 (0.02)	7.89 (0.08)	**74.05** **(0.74)**	13.11 (0.13)	0.17 (0.01)	0.02 (0.01)	0.61 (0.01)	0.73 (0.01)
12	Grain yield (g/plant)	0.22 (0.01)	0.32 (0.01)	16.19 (0.22)	**40.26** **(0.43)**	7.7 (0.08)	6.79 (0.07)	0.68 (0.01)	0.98 (0.01)	1.17 (0.01)	24.1 (0.18)	1.36 (0.01)
13	100-Seed weight (g)	**25.6** **(0.82)**	0.15 (0.01)	0.24 (0.01)	0.01 (0.01)	0.05 (0.01)	0.39 (0.01)	0.07 (0.01)	0.01 (0.01)	0.59 (0.01)	0.06 (0.01)	0.01 (0.01)

Fig 1: Scree plot of principle components for Eigen's value and cumulative variability of finger millet accessions.

3.2 Cluster analysis

Cluster analysis in germplasm is the grouping of a set of accessions in the same cluster which are more similar to each other than to those in other clusters. In present study,1487 accessions were grouped into four broad clusters. There was 14.67 % of variation within the clusters and 85.33 % of variation observed between the clusters. Which indicates that similar accessions were grouped. Selection of the accessions from the different clusters helps to enhance the genetic diversity. There were nine distinct clusters (Figure 2) formed. The cluster IX contained accessions that better performed for flag leaf length, number of leaves, peduncle length and 100-Seed weight. The cluster VIII better performed for number of basal tillers, leaf blade width and finger length. The cluster V was better for flag leaf width and short plant height which indicates that these accessions in cluster V may be used as genetic resources for lodging tolerance. The cluster III was having accessions which better performed for leaf blade length and number of fingers on ear head whereas cluster VI was better for grain yield (Table 4). The accessions from different clusters for different traits should serve as a pool to select parents with desirable attributes for development of better performing finger millet cultivars. Similar study on clustering of finger millet germplasm has been reported by Patel *et al.*, (2017) who found five clusters while Karad and Patil (2010) reported five clusters from 65 finger millet genotypes. Kumar *et al.*, (2010) studied 140 diverse finger millet genotypes which grouped into 10 clusters.

Table 4: Cluster mean for agro-morphological and yield contributing traits of finger millet accessions characterized during kharif 2017

Clusters	**Days to 50% flowering**	**Number of basal tillers**	**Flag leaf length (cm)**	**Flag leaf width (cm)**	**Number of Leaves**	**Leaf blade length (cm)**	**Leaf blade width (cm)**	**Plant height (cm)**	**Finger length (cm)**	**Peduncle length (cm)**	**Number of fingers on ear head**	**Grain yield (g/ plant)**	**100-Seed weight (g)**
I	72.78	5.29	35.84	1.30	16.99	57.50	1.54	116.25	7.72	18.27	7.95	39.87	0.22
II	69.51	5.54	39.40	1.37	16.95	54.79	1.54	129.71	7.95	19.16	7.81	18.15	0.24
III	74.67	5.79	35.07	1.27	17.16	60.18	1.54	116.91	8.41	19.44	7.96	13.96	0.21
IV	98.89	5.34	22.70	1.13	17.66	56.45	1.53	123.74	8.14	19.94	7.66	18.74	0.22
V	66.60	5.41	37.86	1.39	17.60	55.64	1.56	91.76	8.00	19.54	7.49	19.54	0.21
VI	98.98	5.48	22.57	1.11	17.50	54.67	1.55	121.86	8.04	18.07	7.72	47.47	0.24
VII	60.37	5.32	32.89	1.38	17.37	57.43	1.55	118.43	7.55	18.38	7.62	18.57	0.24
VIII	100.76	5.97	24.22	1.11	17.28	55.77	1.57	100.19	8.42	20.52	7.85	26.40	0.22
IX	100.48	5.51	47.17	1.26	17.75	55.04	1.51	144.84	8.13	20.92	7.56	26.48	0.25

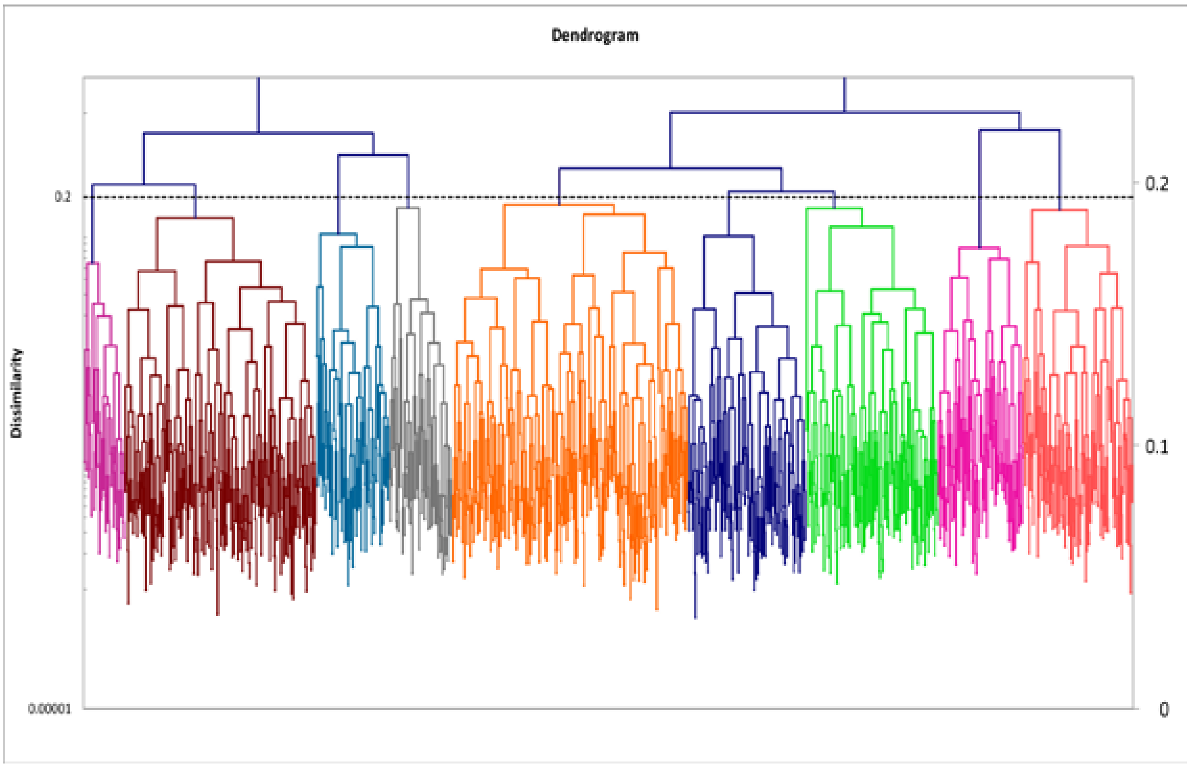


Fig 2: Ward's method of clusters of finger millet accessions characterised during Kharif 2017

Conclusion

There was sufficient variability in the studied finger millet germplasm. Depending upon the diversity in the germplasm the pool grouped into nine clusters. The breeders can make selection of their desirable trait-specific lines as parents for their breeding program from the studied set of germplasm. The following accessions were identified as the best genotypes traitwise among the germplasm for yield and yield related traits *viz*, IC 0475183, IC 0474893, IC 0476432, IC 0475707 and IC 0476381 for early flowering/short days to 50% flowering (< 53 days); IC 0475740, IC 0475629, IC 0475059, IC 0475658 and IC 0476484 for more number of basal tillers (>15); IC 0474962, IC 0475244, IC 0475374, IC 0475858 and IC 0475473 for number of fingers on ear head (>14); IC 0476095, IC 0475125, IC 0474816, IC 0475407 and IC 0476587 for higher grain yield (>84 g/plant) and IC 0477419, IC 0475620, IC 0477078, IC 0475382 and IC 0475193 for more 100-Seed weight (>1.2 g).

4. References

1. Agarwal M, R Singh, and PK Shrotria (2004) Classification of elite sorghum lines by principalcomponent analysis. *IndJ. Agrl.Res.* **38**(1): 55-59.

2. Akatwijuka R, PR Rubaihayo, and TL Odong (2016) Genetic diversity among sorghum landraces of southwestern highlands of Uganda. *Afr. Crop Sci.J.* **24**(2): 179-190.

3. Ali M, K Jabran, SI Awan, A Abbas, MZulkiffal, TAcet, J Farooq, and A Rehman, (2011) Morpho-physiological diversity and its implications for improving drought tolerance in grain sorghum at different growth stages. *Aust. J. Crop Sci.***5**(3): 311-320

4. Fenty, J. (2004). Analyzing distances. *The Stata Journal* **4**(1): 1–26.

5. Ganapathy S, A Nirmalakumari and AR Muthiah (2011) Genetic variability and interrelationship analyses foreconomic traits in finger millet germplasm. *WorldJ. of Agril. Sci.***7** (2): 185-188.Goud J.V. and LAKSHMI. P.V. (1977). Morphological and genetical variabilities for quantitative characters in ragi (*Eleusine coracana*(L.) Gaertn.). *Mysore Journal of Agricultural Sciences.* **11**: 438-443.

6. Jain SK and PR Patel (2016) Genetic Diversity and Principle Component Analyses for Fodder Yield and their Component Traits in Genotypes of Forage Sorghum (*Sorghumbicolor* L. Moench). *Annals of Arid Zone* **55**(1&2): 17-23.

7. Karad SR and JV Patil (2010) Assessment of genetic diversity among of finger millet (*Eleusine coracana* L.) genotypes. *Int. J. of Integrative sciences, Innovation and Technology. Journal,* E-3.

8. Keerthana, K. Chitra, S. Subramanian, A. Nithila, S. and Elangovan, M. (2019). Studies on genetic variability in finger millet [Eleusine coracana (L.) Gaertn] genotypes under sodic conditions. Electronic Journal of Plant Breeding 10(2): 566–569.

9. Kumar D, V Tyagi, B Ramesh, and S Pal, (2010) Genetic diversity in finger millet (*Elusine coracana* L.). *Crop Imp.* **37**(1): 25-28.

10. Mehra, K. (1962). Natural hybridization between *Eleusine coracana* and *E. africana* in Uganda.

11. Mnyenyembe, P. and S Gupta. (1998). Variability for grain yield and related traits in finger millet germplasm accessions from Malawi. *African Crop Science Journal* **6**(3): 317–322.

12. Owere L, P Tongoona, J Derera, and N Wanyera. (2015). Variability and trait relationships among finger millet accessions in Uganda. *Uganda Journal of Agricultural Sciences* **16**(2): 161–176.

13. Patel SN, HE Patiland RC Popat (2017) Genetic diversity study in finger millet (*Eleusine coracana* L.) genotypes: a multivariate analysis approach, *Int. J. Pure App. Biosci.* **5**(5): 183-189.

14. Peeters, J. and J Martinelli. (1989). Hierarchical cluster analysis as a tool to manage variation in germplasm collections. *Theoretical and applied genetics* **78**(1): 42–48.

15. Rao, S. J Mushonga and R Muza. (1986). Collecting in Zimbabwe. *Plant Genetic Resources Newsletter* **67**: 41–43.

16. Sood S, AK Gupta, L Kant and A Pattanayak. (2017). Finger millet (*Eleusine coracana* (L.) Gaertn.) varietal adaptability in North-Western Himalayan region of India using AMMI and GGE biplot techniques. *Electronic Journal of Plant Breeding* **8**(3): 816–824.

17. Upadhyaya HD, C Gowda, H Buhariwalla and J Crouch. (2006). Efficient use of crop germplasm resources: identifying useful germplasm for crop improvement through core and mini-core collections and molecular marker approaches. *Plant Genetic Resources* **4**(1): 25–35.

18. Upadhyaya H, C Gowda and VG Reddy. (2007). Morphological diversity in finger millet germplasm introduced from Southern and Eastern Africa. *Journal of SAT Agricultural Research* **3**(1): 1–3.

Journal of Cereal Research
Volume 14 (2): 175-182
Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Research Article

BK 306: A two-row barley (*Hordeum vulgare* L) as potential source of higher diastatic power and FAN content for malt barley improvement

Dinesh Kumar*, Ramesh Pal Singh Verma, Anil Kumar Khippal, Ajit Singh Kharub, Charan Singh, and Gyanendra Pratap Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal – 132 001, India

Article history:
Received: 27 May, 2022
Revised: 18 Aug., 2022
Accepted: 04, Sep., 2022

Citation:
Kumar D, RPS Verma, AK Khippal, AS Kharub, C Singh and GP Singh. 2022. BK 306: A two-row barley (*Hordeum vulgare* L) as potential source of higher diastatic power and FAN content for malt barley improvement. *Journal of Cereal Research* ***14 (2):*** *175-182. http://doi.org/10.25174/2582-2675/2022/120617*

****Corresponding author:***
E-mail: dinesh.kumar3@icar.gov.in

Abstract

The Indian malt industry has updated the specifications in past few years with respect to the diastatic power of the malt and free amino nitrogen content in the wort. The demand is now for higher values of malt diastatic power for better degradation of starch during the malting and brewing processes. Similarly, higher values of free amino nitrogen (FAN) content are preferred for better yeast growth during the brewing operations. We hereby report a genotype BK 306, which posses' higher diastatic power (average of 107°L) and FAN content (average of 216 ppm) as compared to the prevalent two row malt barley varieties. The genotype can be a potential source for these two traits for malt barley improvement programme of the country.

Key words: Barley, *Hordeum vulgare*, diastatic power, FAN, malt

1. Introduction

Malt is one of the major industrial products of barley and in India approximately 30% of the total barley production is utilized for this purpose (Kumar *et. al.*, 2021). Beer is one of the major products made from barley malt. In terms of volume, the Indian beer market was valued at 5,533.73 Mn ltrs in 2020 and is expected to reach 9,004.74 Mn ltrs by 2025, expanding at a compound annual growth rate (CAGR) of ~10.89% during the 2021 - 2025 period. Urbanization and change in societal perspectives, along with the launch of new low- and no-alcohol variant beer, technological advancements are a few of the significant factors that propel market growth (Source: https://www.globenewswire.com/en/news-release/2021/04/21/2213979/28124/en/ Indian-Beer-Market-Size-and-Growth-Forecasts-2021-2025-Craft-Beer-Forecast-to-Grow-at-a-Rate-of-108-in-Volume-Terms.html, Accessed on 17.01.2022). For making malt, some special physical and biochemical characteristics are desired by the industry and in past few years the demand for barley genotypes with higher malt diastatic power and higher free amino nitrogen (FAN) content in wort has increased.

The diastatic power of barley malt is the collective activity of starch degrading enzymes, which accumulates or gets activated during malting (Gibson *et. al.*, 1995). Higher diastatic power becomes more important, when adjuncts (eg wheat grains, rice flakes etc) are used for brewing and barley malt is used as source of starch degrading enzymes. Normally two row barley is used for malting especially because of higher starch content as compared to the six row type. However, two row row barley has normally lesser diastatic power vis-a-vis the six row barley. Diastatic power, like other quality attributes in barley, has been reported to be determined by a complex interaction of genetic and environmental factors (Arends *et al.*, 1995). Therefore, development of two row barley with higher diastatic power is a major challenge for the Indian malt barley programme (ICAR-IIWBR, 2021).

The nitrogenous compounds available for consumption by growing yeast (serving as catalyst in fermentation) during brewing are known as free amino nitrogen (FAN) plus ammonium ions. FAN can be defined as the sum of the individual wort amino acids and small peptides (di- and tri-peptides) plus ammonium ions. (Pugh *et al.,* 1997). Wort sugar content alone is not a good indicator of yeast fermentation performance (Ingledew, 1977). Therefore, FAN is regarded as the preferable indicator for predicting healthy yeast growth, viability, vitality, fermentation efficiency, and beer quality and stability (Stewart *et al.,* 2013). FAN is the protein degradation product of malted barley and is affected by the malt/ adjunct ratio, mashing schedule, barley variety, and malting conditions (O'Connor-Cox *et al.,* 1989). Therefore, malt barley cultivars having better FAN production capability during malting and mashing are required.

The genotype BK 306 was found to have these both traits of higher diastatic activity and higher FAN content in the preliminary studies conducted during 2019-20 at IIWBR Karnal. Therefore, the present multilocation investigation was carried out to find out the stability of these two traits across the diverse locations.

2. Materials and Methods

2.1 Grain samples

The genotype BK 306 along with the controls (current released malting barley cultivars) DWRUB 52, DWRB 91, DWRB 92, DWRB 101, RD 2849, DWRB 123, DWRB 160 and DWRB 182 was grown in rabi season (mid-November to mid-April) of 2020-21 at Karnal, Hisar, Ludhiana, Durgapura, Pantnagar and Kanpur in augmented design in single replication, with a plot size of 2.5 x 0.60 m^2 at each location. The crop was fertilized with 60 kg N (in 2 equal splits); 20 kg P and 20 kg K and all the other recommended crop management practices including weed, insect/pest were followed as and when required. The crop was harvested and thrashed mechanically; the collected grains were cleaned manually and stored in air tight bags at -20°C till further analysis. Most of the analysis was done as per EBC (2003) procedures until or otherwise stated at respective places.

2.2 Grain physical traits (Test weight, thousand grain weight, Bold grains percentage)

Test weight was estimated by using hectolitre measurement equipment designed by ICAR-IIWBR, Karnal for small grain samples and weighing on electronic balance up to 1 gram's accuracy. The test weight was then expressed as kilogram per hectolitre. For thousand grain weight (TGW), 1000 grains were counted using Contador (Pfeuffer Germany) seed counter and weighed on electronic balance up to two digits in grams. The grain plumpness was measured by using 100-gram grains on Sortimat laboratory grader (Pfeuffer GmbH, Germany) and sieved for three minutes using the sieves of 2.8 mm, 2.5 mm and 2.2 mm. The grains retained on 2.5 mm and above were considered as bold/plump grains. The grains passed through 2.2 mm sieve were designated as thin grains, while the fraction retained on 2.2 mm was considered as intermediate size grain.

2.3 Protein content

The protein content was estimated by near infrared transmittance (NIR) grain analyser (Infratech 1241, FOSS, Denmark). The values were expressed on percent dry weight basis (% dwb).

2.4 Malt preparation

The bold/plump grains (grains >2.5 mm screen) processed on Sortimat (Pfeuffer make laboratory grader) were used for malting in an automatic micro-malting system (Joe White Australia make). The malting cycle involved steeping, germination and kilning stages as per following schedule:

1. Steeping: 8 hours dip in water (temperature 18°C) with continuous aeration 6 hours air rest (temperature 18°C) →10 hours dip in water (temperature 18°C) with continuous aeration
2. Germination: 24 hrs at 18°C→24 hrs at 17°C→24 hrs at 16°C
4. Kilning: 3 hrs at 45°C→3 hrs at 50°C→3 hrs at 55°C→3 hrs at 60°C→3 hrs at 65°C→3 hrs at 70°C→3 hrs at 75°C→3 hrs at 80°C

The malt was taken out from machine after cooling to room temperature and rootlets were removed by hand rubbing. The malt samples were stored in air tight interlocking polythene bags at -20°C till further analysis.

2.5 Malt friability and homogeneity

A 50-gram quantity of malt was used in Friability meter (Pfeuffer, Germany) and machine was run for 8 minutes. The malt powder obtained was weighed on electronic balance to estimate percent friability. Thes malt fractions retained in friability meter mesh were then mixed and put on Sortimat (Pfeuffer, Germany) for one minute and fraction passing through 2.2 mm screen (plus the powdered malt) was considered homogenous malt.

2.6 Wort preparation

The malt flour was prepared in Buhler's laboratory Mill at fine grinding setting and the flour was extracted in EEC make (Australia) mashing bath for 45°C and then at 70°C for a total duration of 120 minutes. The resulting slurry was used to determine wort filtration rate and hot water extract in malt.

2.7 Filtration rate

The slurry obtained after mashing was filtered through Whatman 2555 ½ filter paper and the filtrate obtained in one hour was considered as wort filtration rate (ml/ per hour).

2.8 Hot water extract

The hot water extract or malt extract was determined using Borosil make A grade specific gravity bottles. Fifty ml of wort was kept at 18°C for 20 minutes and specific gravity was measured. The hot water extract or malt extract was computed from standard EBC table and expressed as percent fgdb (fine ground dry basis).

2.9 Diastatic Power

The analysis of diastatic power (D.P.) of malt was done as per the IOB method and expressed in °Linter value as described by Farzaneh *et al.* (2017). In brief starch degradation was done using barley malt powder as enzyme source. The free sugars were estimated through titration using Fehling solutions and methylene blue indicator.

2.10 Free Amino Nitrogen

Free Amino Nitrogen content (FAN) was determined using the method reported by Lie (1973), in brief the colour was developed in the diluted wort sample using ninhydrin and readings were taken spectrophotometrically at 570 nm. Glycine was used as standard for the calculations.

3. Results & Discussion

Barley malt is the major source of nutrition for the yeasts during the fermentation process of in brewing. The sugars and free amino acids constitute the major raw material used by the yeasts, which depends upon the starch content of grain, the starch breaking diastatic enzymes, protein content and the activities of several proteinases in grain and/or malt (Cynthia and Stanley, 2007 and De Schepper *et al.,* 2021). In recent years the brewing industry considers the higher diastatic power and free amino nitrogen as two of the important factors among the several other malt and grain quality criterions. These two parameters and some of other traits in Indian released barley cultivars and genotype BK 306 have been described and discussed in following sections:

3.1 Diastatic Power

The Diastatic Power of barley malt represents the collective activity of four starch-degrading enzymes, namely α-amylase, β-amylase, limit dextrinase, and α-glucosidase (Gibson *et al.,* 1995). The conversion of starch to fermentable products in the endosperm is primarily catalysed by α-amylase, followed by β-amylase, limit dextrinase and α-glucosidase (Bamforth, 2009). Of these enzymes, beta-amylase is laid down during grain filling and alpha-amylase, α-glucosidase and limit dextrinase are synthesised during germination, predominantly in the scutellum and aleurone layers (Arends *et al.,* 1995).

Though the malted barley is the main source in the traditional brewing of beers, but its use has been increasingly substituted by un-malted barley or other raw grain adjuncts (like wheat or rice) in recent years (Cadenas *et al.,* 2021). The incorporation of raw grains is mainly economically driven as the expenditure on malting is evaded. The use of raw grains, however, requires modifications to the brewing process to accommodate the lack of malt enzymes and the differences in structural and chemical composition between malted and raw grains (Kok *et al.,* 2018). Therefore, the barley malt with higher diastatic power is desired by the brewing industry. The genotype BK 306 has been found to have average value of 107-degree Linters (°L in IOB) or 358.5 Windisch-Kolbach units (°WK in EBC; Lintner = (°WK+16)/3.5, which is higher than the most prevalent malt barley varieties DWRUB 52 (96 °L) or DWRB 101 (97 °L) or all the other checks used in this study (Table 1). Diastatic power is considered as a critical parameter of malt quality and normally higher diastatic power is required to get the higher malt extract from the barley grains (Cynthia and Stanley, 2007; Rani and Bhardwaj, 2021). Variation in DP of malt is affected by the complex interaction of genetic variation and environmental factors (Arends *et al.,* 1995). However, as per Fang *et al.,* (2019), diastatic power is mainly determined by genetic factors and easier to improve; thus, the genotype BK 306 can act as donor of this trait in malt barley improvement programme. Three QTLs that significantly increased diastatic power have been mapped on 1H and 4H (Cu *et al.,* 2016). This two-row genotype is progeny from the cross BK9811 / DL472 (F5-50) and having higher diastatic power in two row background can be a material for further genetic and molecular biology studies.

Table 1: Diastatic power (°L) in the malt of genotype BK 306 grown at different locations

Genotype	Hisar	Karnal	Ludhiana	Durgapura	Pantnagar	Kanpur	Average
BK 306	116	102	106	108	106	106	**107**
DWRUB 52 (c)	94	100	106	99	83	94	**96**
DWRB 91 (c)	104	109	109	109	98	102	**105**
DWRB 92 (c)	98	106	102	106	109	104	**104**
DWRB 101 (c)	104	104	96	83	100	96	**97**
RD2849 (c)	100	100	94	98	98	79	**95**
DWRB 123 (c)	111	94	94	96	109	104	**101**
DWRB-160 (c)	111	96	104	99	109	96	**103**
DWRB-182 (c)	109	109	109	90	98	98	**102**

3.2 Free Amino Nitrogen (FAN)

Free amino nitrogen is the only nitrogen source for yeast cell growth and reproduction in the wort and plays major role in metabolite changes during fermentation (Stewart *et al.,* 2013). FAN not only provides nutrition for yeast, but also constitutes the flavor substance of beer. Although higher protein content in the grains can increase the FAN content but leads to a decrease of malt extract (Qi *et al.,* 2005). Therefore, FAN in the wort is generally maintained at 180–220 mg/L (Fang *et al.,* 2019 and references there in). The genotype BK 306 has average FAN content of 216 mg/L or 216 ppm in the wort, which is in desirable range and higher than all the checks used in the study (Table 2). However, some authors have reported different ranges of FAN for optimum yeast growth. Stewart *et al.,* (2017) stated that the amount of FAN needed for the optimum yeast growth is around 130 mg/L. But the industry, especially in India, is asking for higher FAN content *i.e.,* minimum 150 mg/L (ICAR-IIWBR, 2021). Both the amount of proteins and activities of proteinases are important for higher free amino nitrogen content in the wort (Jones and Marinac, 2002; Hill and Stewart, 2019). Mainly endoproteases (primarily cysteine and metallo), carboxypeptidase, dipeptidase take part in proteolysis (Steiner *et al.,* 2012 and references therein).

Table 2: Free Amino Nitrogen (FAN content, in ppm) in the wort of genotype BK 306 grown at different locations

Genotype	Hisar	Karnal	Ludhiana	Durgapura	Pantnagar	Kanpur	Average
BK 306	201	197	206	230	244	217	**216**
DWRUB 52 (c)	192	168	257	174	198	202	**199**
DWRB 91 (c)	183	151	215	173	199	148	**178**
DWRB 92 (c)	186	173	235	187	244	143	**195**
DWRB 101 (c)	200	159	212	188	225	191	**196**
RD 2849 (c)	195	163	186	180	185	124	**172**
DWRB 123 (c)	166	119	202	176	172	140	**162**
DWRB-160 (c)	160	134	163	150	189	125	**154**
DWRB-182 (c)	171	151	218	156	219	140	**176**

3.3 Other grain and malt parameters

BK 306 has average protein content of 12.4% (at nitrogen application of 60 kg/ha), thousand grain weight of 44-gram, test weight of 63 kg/hl, bold grain percentage of 91% (Table 3). The genotype BK 306 has malt friability of 73%, malt homogeneity of 95%, hot water extract of 80 % fgdb and wort filtration rate of 294 ml/hr.

Table 3: Average values of grain and malts traits of genotype BK 306 grown at six locations

Genotype	PC#	TGW#	TW#	BG#	MFB#	MH#	HWE#	WF#
BK 306	12.4	44	63	91	73	95	80	294
DWRUB 52 (c)	12.1	45	64	74	61	92	80	243
DWRB 91 (c)	11.6	60	64	89	62	92	81	225
DWRB 92 (c)	12.6	56	63	97	61	87	79	250
DWRB 101 (c)	11.5	49	66	86	64	93	80	225
RD2849 (c)	12.5	48	65	80	53	84	77	258
DWRB 123 (c)	11.4	51	64	89	57	88	79	213
DWRB-160 (c)	11.5	58	60	92	54	89	79	188
DWRB-182 (c)	12.3	44	60	74	64	90	78	270

PC = Protein content (% dwb); TGW=Thousand grain weight (g); TW=Test weight (kg/hl); BG=Bold grains (retained over 2.5 mm sieve) percentage; MFB= Malt Friability (%); MH= Malt Homogeneity (%); HWE = Hot water extract (%fgdwb); WF = Wort filtration rate (ml/hr)

3.4 Agro morphological characters, yield and disease reaction

The agro-morphological characters have been given in table 4, the yield at different nitrogen levels in Figure 1 and disease reaction has been found as: against stripe rust 5 S* (HS); ACI of 1.3* and against leaf blight 68* (HS) (Directorate of Wheat Research, 2004). The genotype BK 306 responded upto 90 kg nitrogen/hectare and has comparable yields as compared to the released malt barley variety DWRB 101 (Fig 1).

Table 4: Agro morphological traits of genotype BK 306

S. No.	Trait	Observation
1	Growth habit	Erect
2	Stem-Basal Pigmentation	Present
3	Auricle (Flag leaf)-Anthocyanin Pigmentation	Present
4	Upper node Pigmentation	Present
5	Flag leaf attitude	Erect
6	Flag leaf-Waxiness of Sheath	Present
7	Spike emergence	Late
8	Spike type	Two-row
9	Lateral florets (two-row barley)	Developed
10	Spike-Waxiness	Present
11	Spike-colour	Green
12	Spike-attitude	Erect
13	Awn-roughness	Rough
14	Flag leaf length	Long
15	Flag leaf breadth	Narrow
16	Awn-Tip pigmentation	Present
17	Spike-basal sterility	Absent
18	Lemma-pigmentation	Absent
19	Spike length	Medium
20	Plant-height	Tall

21	Peduncle-length	Long
22	Awns	Present
23	Awns-type	Normal
24	Awn-length	Medium
25	Spike-density	Intermediate
26	Grain-hulless	Covered (Hulled)
27	Grain-colour	Yellow
28	Grain-shape	Oblong
29	Grain-size	Medium
30	Grain-surface	Wrinkled
31	Rachilla hairs	Rudimentary
32	Grain-Crease width	Intermediate
33	Flag leaf length	18.1 inches
34	Flag leaf breadth	0.8 inches
35	Spike: Basal sterility	Absent
36	Spike length	8.0 cm
37	Plant height	97.0 cm
38	Peduncle length	29.0 cm
39	Awn length	8.6 cm
40	Days to heading	90
41	Days to maturity	130

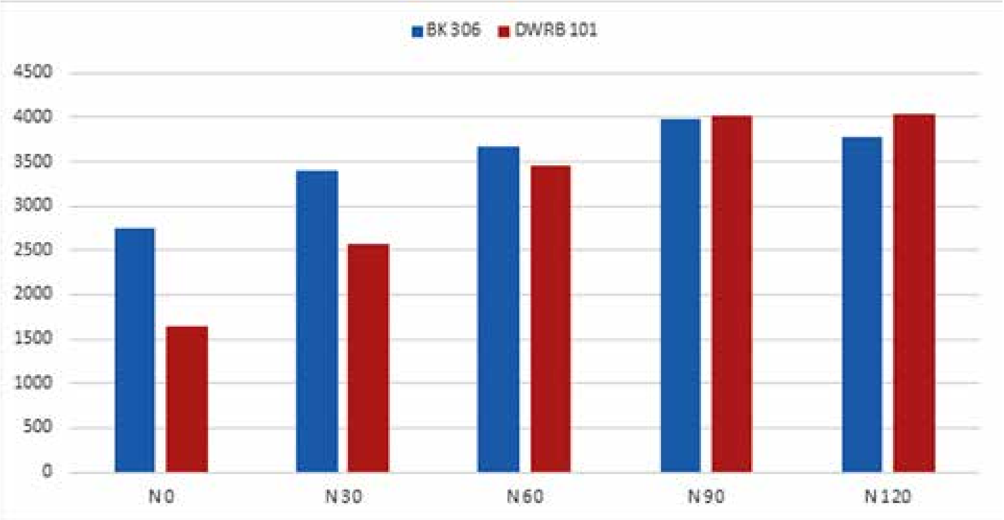


Fig. 1: Yield in kilograms of BK 306 and DWRB 101 at different nitrogen levels (pooled data of two years)

Conclusion

BK 306 can be an excellent source of higher diastatic power and FAN content for the malt barley improvement programme, and it may prove to be a very valuable research material in combination to the disease resistance to stripe rust in good agronomic background.

Conflict of Interest

Authors declare that they have no conflict of interest

Ethical Compliance Statement

NA

Author's Contribution

Dinesh Kumar (Planning & execution of experiment and writing of MS); Ramesh Pal Singh Verma (Breeder of the material, Editing of MS); Anil Kumar Khippal (Evaluation of BK 306 at different nitrogen doses); Ajit Singh Kharub (Evaluation of BK-306 at different nitrogen dotes); Charan

Singh (Recording of Agro-morphological traits of the genotype) and Gyanendra Pratap Singh (Planning and Guidance)

Acknowledgement

The authors are grateful to Indian Council of Agricultural Research (ICAR) for providing all kinds of support in conducting this study. The AICRP centres of Karnal, Hisar, Ludhiana, Durgapura, Pantnagar and Kanpur are thankfully acknowledged for conducting the experiment and supplying the material for quality analysis.

4. References

1. Arends AM, GP Fox, RJ Henry, RJ Marschke and MH Symons. 1995. Genetic and environmental variation in the diastatic power of Australian barley. *Journal of Cereal Science* **21**: 63-70.
2. Bamforth CW. 2009. Current perspectives on the role of enzymes in brewing. *Journal of Cereal Science* **50**: 353–357.
3. Cadenas R, I Caballero, D Nimubona and CA Blanco. 2021. Brewing with Starchy Adjuncts: Its Influence on the Sensory and Nutritional Properties of Beer. *Foods.* **10**:1726.
4. Cu ST, TJ March, S Stewart, S Degner, S Coventry, A Box, D Stewart, B Skadhauge, RA Burton, GB Fincher and J Eglinton. 2016. Genetic analysis of grain and malt quality in an elite barley population. *Molecular Breeding* **36**:129.
5. Cynthia, A, Henson and Stanley H., Duke. 2007. Osmolyte Concentration as an Indicator of Malt Quality. *Journal of the American Society of Brewing Chemists* **65**: 59-62.
6. De Schepper CF, P Michiels, C Buvé, AM Van Loey, CM Courtin. 2021. Starch hydrolysis during mashing: A study of the activity and thermal inactivation kinetics of barley malt α-amylase and β-amylase. *Carbohydrate Polymers* **255**: 117494.
7. Directorate of Wheat Research. 2004. Progress report of the All India Coordinated Wheat & Barley Improvement Project 2003-04. Vol. VI. BARLEY NETWORK. Directorate of Wheat Research, Karnal, India. P. 173.
8. EBC Analytica. 2003. EBC Analysis Committee. Fachverlag Hans Carl, Nurnberg, Germany
9. Fang Y, X Zhang and D Xue. 2019. Genetic Analysis and Molecular Breeding Applications of Malting Quality QTLs in Barley. *Frontiers in Genetics* **10**:352.
10. Farzaneh V, A Ghodsvali, H Bakhshabadi, Z Zare and IS Carvalho. 2017. The impact of germination time on the some selected parameters through malting process. *International Journal of Biological Macromolecules* **94**:663-668.
11. Gibson TS, V Solah, MRG Holmes and HR Taylor. 1995. Diastatic power in malted barley: contributions of malt parameters to its development and the potential of barley grain beta-amylase to predict malt diastatic power. *Journal of The Institute of Brewing* **101**: 277–280.
12. ICAR-IIWBR. 2021. Progress Report of AICRP on Wheat & Barley 2020-21: Barley Improvement. Eds: RPS Verma, AS Kharub, D Kumar, C Lal, J Singh, R Malik, L Kumar, SK Bishnoi, S Kumar, SC Bhardwaj, P Jasrotia, A Verma, AK Sharma, C Singh, S Singh and GP Singh. ICAR-Indian Institute of Wheat and Barley Research, Karnal, India. P. 244.
13. Ingledew WM. 1975. Utilization of wort carbohydrates and nitrogen by *Saccharomyces carlsbergensis. Tech. Q. Master Brew. Assoc. Am.* **12**:146-156. (Original not seen)
14. Jones BL and L Marinac. 2002. The effect of mashing on malt endoproteolytic activities. *Journal of Science of Food and Agriculture* **13**: 858-864.
15. Kok YJ, L Ye, J Muller, DS Ow and X Bi. 2019. Brewing with malted barley or raw barley: what makes the difference in the processes? *Applied Microbiology and Biotechnology* **103:**1059-1067.
16. Kumar D, RPS Verma, AS Kharub and GP Singh. 2021. Industrial evaluation for malting quality of Indian barley varieties. *Journal of Cereal Research* **13**(**3**): 323-327.
17. Lekkas C, AE Hill and GG Stewart. 2014. Extraction of FAN from Malting Barley during Malting and Mashing. *Journal of the American Society of Brewing Chemists* **72**: 6-11.
18. Lie S. 1973. The EBC-ninhydrin method for determination of free alpha amino nitrogen. *Journal of The Institute of Brewing* **79**:37-41.

19. O'Connor-Cox ESC and WM Ingledew. 1989. Wort nitrogenous sources – their use by brewing yeasts: A review. *Journal of the American Society of Brewing Chemists* **47**:102-108.
20. Pugh TA, JM Maurer and AT Pringle. 1997. The impact of wort nitrogen limitation on yeast fermentation performance and diacetyl. *Tech. Q. Master Brew. Assoc. Am.* **34**:185-189. (Original not seen)
21. Qi JC, JX Chen, JM Wang, FB Wu, LP Cao and GP Zhang. 2005. Protein and hordein fraction content in barley seeds as affected by sowing date and their relations to malting quality. *Journal of Zhejiang University of Sciences* **B 6**: 1069–1075.
22. Rani H and RD Bhardwaj. 2021. Quality attributes for barley malt: "The backbone of beer." *Journal of Food Science* **86**:3322–3340.
23. Steiner E, A Auer, T Becker and M Gastl. 2012. Comparison of beer quality attributes between beers brewed with 100% barley malt and 100% barley raw material. *Journal of Science of Food and Agriculture* **92**:803-13
24. Stewart GG, A Hill and C Lekkas. 2013. Wort FAN – its characteristics and importance during fermentation. *Journal of the American Society of Brewing Chemists* **71**:179-185.

Journal of Cereal Research
Volume 14 (2): 183-188
Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Research Article

Assessment of genetic variation and trait inter-relationship in QPM inbred lines in Vindhyan region of Eastern Uttar Pradesh

Ankit Phansal*, Shailesh Marker and Rajesh Aggarwal

Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj-211007, U. P., India.

Article history:
Received: 18 July, 2022
Revised: 29 Aug., 2022
Accepted: 14 Sept., 2022

Citation:
Phansal A., S. Marker and R. Aggarwal. 2022. Assessment of genetic variation and trait inter-relationship in QPM inbred lines in Vindhyan region of Eastern Uttar Pradesh. *Journal of Cereal Research* ***14 (2):*** *183-188. http://doi.org/10.25174/2582-2675/2022/131246*

****Corresponding author:***
E-mail: ankitphansal11@gmail.com

Abstract

The present investigation was carried out to assess genetic variation and trait inter-relationship in QPM inbred lines in Vindhyan region of Eastern Uttar Pradesh for 18 characters during *Rabi* 2018-19. Analysis of variance showed significant differences for all the characters at 1 per cent level of significance, indicating that considerable genetic variability was present among different QPM inbred lines. The less difference between GCV and PCV revealed that there was a very low influence of environment on the expression of various characters. High heritability coupled with high genetic advance as per cent mean was depicted by for cob weight with sheath followed by cob weight without sheath and tassel length. Plant height followed by kernels per row, cob height, cob weight with sheath, tassel length, cobs per plant, cob weight without sheath and cob length showed positive significant correlation with grain yield and days to 50 per cent silking, followed by kernels per row, biological yield, harvest index, tassel length, cob length, anthesis-silking interval, cobs per plant and cob weight without sheath had shown the positive direct effect on grain yield per plant. Therefore, these characters may be used as selection indices for genetic improvement of QPM inbred lines.

Keywords: Genetic variation, Variability parameters, Correlation coefficient, Path analysis, QPM inbreds (*Zea mays* L.).

1. Introduction

Maize (*Zea mays* L.) or 'Queen of cereals' belongs to the family Graminae (2n=2x=20) and is an important staple food of many countries, particularly in the tropics and subtropics. It is the third most important cereal food crop of the world after Rice and Wheat (Poehlman, 2006). It can be grown throughout the year, due to the availability of thermo and photo insensitive varieties. Breeding for improved protein quality maize started in the mid-1960s with the discovery of mutants. The QPM has higher biological value, increased availability and better utilization of niacin, calcium, carbohydrate and carotene. Therefore, it is desirable to replace the present maize hybrids with QPM hybrids which are similar in cultivation, grain yield, potentiality, and tolerance to biotic and abiotic stresses with that of normal maize hybrids.

Genotypic and phenotypic correlation coefficients tell us the association between and among two or more characters. A significant association proposes that such traits could be upgraded concurrently. However, such an improvement depends on phenotypic correlation, additive genetic variance and heritability (Hayes and Smith, 1955). A clear understanding of the association between yield and yield components is necessary for a successful crop improvement programme since grain yield is a complex character and is influenced by several genetic factors interacting with the environment. Correlation coefficient analysis reveals the magnitude and direction of yield components, while path analysis identifies components that directly or indirectly influences yield. Both character association and path analysis help in formulating an effective breeding strategy to further develop productive inbreds in maize. Genetic correlation analysis is a handy technique that elaborates the degree of association among important quantitative traits (Malik *et al.,* 2005).

The estimates of path coefficient analysis are important for a better understanding of the crop. It gives specific measures of the direct and indirect effect of each component character under seed yield (Singh and Singh, 1974). The path analysis provides effective measures of direct and indirect causes of association and depicts the relative importance of each factor involved in contributing to the final product (Jakhar and Kumar, 2017). Coefficient measures the degree and strength of the relationship between the yield and other yield contributing characters which is helpful for the selection of desirable characters under a breeding programme (Falconer, 1989). The measurement correlation of coefficient between the characters is a matter of considerable importance in selection practices which help in the construction of selection indicates and also permit the prediction of correlated response (Lerner, 1985). Therefore, the present study of correlation and path coefficient analysis of various yield-related traits were conducted that would be a valuable aid in selecting and breeding for improved maize hybrids.

Keeping all these facts in view, the present study was planned to evaluate the QPM inbred lines for grain yield and its attributing traits, to assess the genetic variability among QPM inbred lines and to assess correlation and path analysis of yield and yield attributing traits.

2. Materials and methods

The present investigation was carried out at the Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Naini, Prayagraj, U.P. during Rabi 2018-19. The experimental materials comprising of 21 QPM inbred lines including 1 check were grown under RBD with 3 replications. the data were recorded on the 18 pre and post-harvest characters along with morphological characters of the lines i.e. Days to first silk emergence (50%), Days to first tassel emergence (50%), Anthesis-silking interval (Days), Plant height (cm), Cob height (cm), Leaf area index, Tassel length (cm), Number of cobs per plant, Cob length (cm), Cob girth (cm), Cob weight with sheath (g), Cob weight without sheath (g), Number of kernel rows per cob, Number of kernels per row, Grain yield per plant (g), 100 kernel weight (g), Biological yield per plant (g), Harvest index (%). The observations were recorded on five randomly selected plants for all characters except for days to 50% silk emergence and days to 50% tassel emergence where the observation was recorded on a plot basis. The data recorded were subjected to the Analysis of Variance, Genetic Variability parameters, Heritability broad sense, Genetic Advance, Correlation Coefficient Analysis and Path Coefficient Analysis.

3. Results and discussion

The analysis of variance showed significant differences for all traits studied at a 1% level of significance except for anthesis-silking interval, leaf area index and the number of cobs per plant suggesting that the genotypes were genetically variant for each other and provide the scope for breeding. A perusal of mean values of yield and yield contributing characters revealed that QPM inbred line BHU-N4 X QPM-8 (38.09) followed by CML-161 X VL-1056 (35.98), YHPANTH-53 (35.39), BHU-B73-BC2 X BHU-N3 (34.00) were identified as top high yielding QPM inbreds in the present study.

A wide range of phenotypic (Vp) and genotypic variance (Vg) were observed in the experimental material for all the traits studied. The highest variability (Vg and Vp) were recorded for plant height followed by cob weight with sheath, cob weight without sheath, grain yield per plant, cob height, biological yield, days to 50% tasselling, days to 50% silking and harvest index. In the present investigation, it is depicted from Table 1, the values of Phenotypic variance (Vp) and phenotypic coefficient of variation (PCV) were higher than that of genotypic variance (Vg) and genotypic coefficient of variation (GCV) for all the traits studied which indicate that the apparent variation is not only due to genotype but also due to influence of environment. therefore, selection based on phenotype alone can be effective for the improvement of these traits. Similar findings for a genotypic and phenotypic variance were reported by Vashistha *et al.* (2013) and Kapoor and Batra (2015) and for GCV and PCV were reported by Reddy *et al.* (2012) and Hepziba *et al.* (2013).

Table 1. Genetic parameters for 18 quantitative traits of QPM inbred lines.

Characters	**Vg**	**Vp**	**GCV**	**PCV**	**h^2 (bs) %**	**GA**	**GA as % mean**
Days to 50% Tasseling	43.49	49.77	5.84	6.25	87.38	12.70	11.24
Days to 50% silking	42.35	48.63	5.67	6.07	87.08	12.51	10.89
Anthesis-silking interval	0.17	0.53	21.97	38.66	32.29	0.49	25.72
Cob height	75.33	138.59	19.03	25.81	54.36	13.18	28.90
Plant height	495.08	557.17	16.37	17.37	88.86	43.21	31.79
Tassel length	7.73	8.62	9.16	9.68	89.63	5.42	17.87
Leaf area index	0.10	0.16	10.67	13.57	61.73	0.50	17.26
Cobs per plant	0.01	0.02	5.00	8.66	33.33	0.09	5.95
Cob Weight with sheath	425.00	432.19	26.20	26.42	98.34	42.11	53.51
Cob weight without sheath	390.55	426.98	30.04	31.41	91.47	38.94	59.18
Cob length	1.58	2.30	10.27	12.37	68.96	2.15	17.57
Cob girth	0.56	1.22	5.53	8.17	45.79	1.04	7.71
Kernels per row	5.12	7.45	24.37	29.40	68.72	3.86	41.62
Kernel rows per cob	1.39	2.19	8.66	10.86	63.58	1.94	14.22
100 kernel weight	6.5677	8.0891	10.98	12.19	81.19	4.76	20.39
Biological yield	69.7680	102.4791	20.38	24.71	68.08	14.20	34.65
Harvest index	28.052	32.891	6.76	7.32	85.29	10.08	12.86
Grain yield per plant	82.36	116.88	31.29	37.27	70.47	15.69	54.10

Johnson *et al.* (1955) suggested that heritability and genetic advance when calculated together would prove more useful in predicting the resultant effect of selection on phenotypic expression, without genetic advance the estimates of heritability will not be of practical value and emphasized the concurrent use of genetic advance along with heritability. High heritability alone is not enough to make sufficient improvement through selection in genetic advances generation. In the present study, high heritability (>60%) coupled with high genetic advance (>30%) was recorded for cob weight with sheath followed by cob weight without sheath, plant height, grain yield per plant, kernels per row and biological yield. Therefore, indicating a predominance of additive gene effects and the possibilities of effective selection can be conducted based on these traits for the crop improvement program.

High heritability (>60%) with moderate genetic advance (20-30%) was observed for 100 kernel weight. This trait is most probably controlled by both additive and non-additive gene action. This decrease in genetic advance is due to the influence of the environment, hence this trait is less amendable for selection indicates that this character showed intermediate expression for both the additive and dominance gene effect. So, the improvement of this character is possible only through careful directional and restricted selection.

High heritability (>60%) with low genetic advance (10-20%) was observed for tassel length followed by days to 50% tasselling, days to 50% silking, harvest index, cob length, kernel rows per cob and leaf area index. This indicates that role of non-additive gene action in the inheritance of these characters, which revealed the importance of dominance and epistatic effects in the inheritance of these traits and selection would be less effective. Similar findings were reported by Kumar *et al.* (2014) and Mohan and Singh (2014).

The results for correlation coefficient analysis showed that the genotypic correlation coefficient was greater than the phenotypic correlation coefficient for all the traits indication a strong inherent association among these traits.

Grain yield per plant showed positive significant genotypic association with plant height (0.892**) followed by kernels per row (0.753**), cob height (0.615**), cob weight with sheath (0.314*), tassel length (0.311*), cobs per plant (0.299*), cob weight without sheath (0.291*) and cob length (0.275*). Grain yield per plant showed a positive significant phenotypic association with kernel per row (0.787**) followed by plant height (0.402**), cob weight without sheath (0.248*) and biological yield (0.273*). Grain yield per plant showed the positive non-significant phenotypic association with kernel rows per cob (0.224) followed by cob height (0.217), tassel length (0.207), harvest index (0.174), cob weight with sheath (0.169), anthesis-silking interval (0.097), 100 kernel weight (0.083), cob length (0.072), leaf area index (0.029) and cob girth (0.02). Similar findings were reported by Jadhav *et al.* (2014), Prasanna *et al.* (2015) and Bhiusal *et al.* (2017).

Days to 50% silking (11.00) followed by kernels per row (2.146), biological yield (1.969), harvest index (1.535), tassel length (1.359), cob length (1.320), anthesis-silking interval (1.185), cob per plant (0.385) and cob weight without sheath (0.383) had shown the positive direct effect on grain yield per plant at the genotypic level. While, days to 50% tasselling (-10.322) followed by plant height (-1.974), cob girth (-0.752), cob weight with sheath (-0.568), kernel rows per cob (-0.488), 100 kernel weight (-0.436), cob height (-0.197) and leaf area index (-0.008) had shown the negative direct effect on grain yield per plant at the genotypic level. Similar findings were reported by Reddy *et al.* (2016) and Barua *et al.* (2017). Days to 50% silking (198.197) followed by kernels per row (1.052), 100 kernel weight (0.416), kernel rows per cob (0.363), biological yield (0.124), and cob weight with sheath (0.058), harvest index (0.052), leaf area index (0.045), cob girth (0.023) and tassel length (0.004) had shown the positive direct effect on grain yield per plant at the phenotypic level. While days to 50% tasselling (-200.513) followed by an anthesis-silking interval (-200.769), cob weight without sheath (-0.058), cob length (-0.026), cobs per plant (-0.01), cob height (-0.007), and plant height (-0.003) had shown the negative direct effect on grain yield per plant at the phenotypic level. These observations similarly reported by Lingaiah *et al.* (2014).

Traits like 50% silking, 100 kernel weight, kernels per row, kernel rows per cob, biological yield, harvest index, tassel length, cob length, anthesis-silking interval, cob weight with sheath, leaf area index, cob girth, cob per plant and cob weight without sheath show positive direct significant association. Therefore, these traits can be selected for the crop improvement program.

Table 2. Correlation coefficient between grain yield per plant and its components traits in QPM inbred lines at the genotypic and phenotypic level.

	Genotypic correlation coefficient		**Phenotypic correlation coefficient**
Plant height	0.807**	Kernels per row	0.787**
Kernels per row	0.753**	Plant height	0.402**
Cob height	0.615**	Biological yield	0.273*
Cob Weight with sheath	0.314*	Cob weight without sheath	0.248*
Tassel length	0.311*	Grain yield per plant	1
Cobs per plant	0.299*	Kernel rows per cob	0.224
Cob weight without sheath	0.291*	Cob height	0.217
Cob length	0.275*	Tassel length	0.207
Anthesis-silking interval	-0.249*	Harvest index	0.174
Grain yield per plant	1	Cob Weight with sheath	0.169
Cob girth	0.235	Anthesis-silking interval	0.097
Harvest index	0.235	100 kernel weight	0.083
Biological yield	0.231	Cob length	0.072
Kernel rows per cob	0.046	Leaf area index	0.029

Days to 50% Tasseling	0.021	Cob girth	0.02
Days to 50% silking	0.006	Days to 50% silking	-0.062
100 kernel weight	-0.093	Cobs per plant	-0.064
Leaf area index	-0.111	Days to 50% Tasseling	-0.072

Residual for genotypic and phenotypic levels are 0.02520 and 0.03787, while * and ** indicates significance at 5% and 1% level of significance respectively.

Table 3. Path coefficient between grain yield per plant and its components traits in QPM inbred lines at the genotypic and phenotypic level.

	Genotypic path coefficient		**Phenotypic path coefficient**
Days to 50% silking	11	Days to 50% silking	198.197
Kernels per row	2.146	Kernels per row	1.052
Biological yield	1.969	100 kernel weight	0.416
Harvest index	1.535	Kernel rows per cob	0.363
Tassel length	1.359	Biological yield	0.124
Cob length	1.32	Cob Weight with sheath	0.058
Anthesis-silking interval	1.185	Harvest index	0.052
Cobs per plant	0.385	Leaf area index	0.045
Cob weight without sheath	0.383	Cob girth	0.023
Leaf area index	-0.008	Tassel length	0.0043
Cob height	-0.197	Plant height	-0.0025
100 kernel weight	-0.436	Cob height	-0.0067
Kernel rows per cob	-0.488	Cob length	-0.026
Cob Weight with sheath	-0.568	Cob weight without sheath	-0.058
Cob girth	-0.752	Cobs per plant	-0.08
Plant height	-1.974	Anthesis-silking interval	-20.77
Days to 50% Tasseling	-10.322	Days to 50% Tasseling	-200.51

Residual for genotypic and phenotypic levels are 0.05907 and -0.00005 respectively.

Conclusion

It is concluded that considerable genetic variability was observed in different QPM inbred lines. The less difference between GCV and PCV revealed that there was a very low influence of environment on the expression of various characters. High heritability (>60%) coupled with genetic advance as per cent mean (>30%) was depicted for cob weight with sheath (98.34) followed by cob weight without sheath (91.47) and tassel length (89.63). Kernels per row, cob weight with sheath, tassel length, cobs per plant, cob weight without sheath and cob length showed a positive significant correlation and positive direct effect on grain yield. Therefore, these characters may be used as selection indices for genetic improvement of QPM inbred lines.

Author's contribution

Conceptualization of research (AP); Designing of the experiments (AP, SM and RA); Contribution of experimental materials (AP, SM and RA); Execution of field/lab experiments and data collection (AP, SM and RA); Analysis of data and interpretation (AP, SM and RA); Preparation of the manuscript (AP, SM and RA).

Declaration

The authors declare no conflict of interest.

4. References

1. Barua NS, VP Chaudhary and GN Hazarika. (2017). Genetic variability and correlation studies for morphological traits in maize (*Zea mays* L.)

genotypes. *Indian Research Journal of Genetics and Biotechnology*, **9** (1): 38-48.

2. Bhiusal TN, GM Lal, S Marker and GJ Synrem. (2017). Genetic variability and traits association in maize (*Zea mays* L.) genotypes. *Annals of Plant and Soil Research,* **19** (1): 59-65.
3. Falconer DS. (1989). Introduction to quantitative genetics. 3rd Ed. English Language Book Society, Longman.
4. Hayes HK, RI Forrest and DC Smith. (1955). Methods of plant Breeding Correlation and regression in relation to plant breeding. McGraw-Hill Company Inc. 2nd Ed: 439-451.
5. Hepziba SJ, K Geetha and SM Ibrahim. (2013). Evaluation of genetic diversity, variability, character association and path analysis in diverse inbreds of maize (*Zea mays* L.). *Electronic Journal of Plant Breeding,* **4** (1): 1067-1072.
6. Jadhav RS and A Sarkar. (2014). Studies on Genotypic Variation and Character Association in Maize (*Z. may*s L.) Hybrids Grown Under Different Moisture Regimes in Terai Region of West Bengal. *Journal of Agricultural Science and Technol*ogy, **1** (1): 20-24.
7. Jakhar DS, R Singh and A Kumar. (2017). Studies on Path Coefficient Analysis in Maize (*Zea mays* L.) for Grain Yield and Its Attributes. *International Journal of Current Microbiology and Applied Sciences,* (6): 2851-2856.
8. Johnson HW, HF Robinson and RE Comstock. (1955). Genotypic and phenotypic correlation in soybean and their implication in selection. *Journal of Agronomy,* 477-483.
9. Kapoor R and C Batra (2015). Genetic variability and association studies in maize (*Zea mays* L.) for green fodder yield and quality traits. *Electronic Journal of Plant Breeding,* **6** (1): 233-240.
10. Kumar GP, VN Reddy, SS Kumar and PV Rao. (2014). Genetic Variability, Heritability and Genetic Advance Studies in Newly Developed Maize Genotypes (*Zea mays* L.). *International Journal of Pure and Applied Bioscience,* **2** (1): 272-275.
11. Lerner, M. (1985). The genetic basis of selection. John Willey and Sons, New York, p122.
12. Lingaiah N, GP Kumar and V Venkanna. (2014). Character Association and Path Analysis for Yield Contributing and Physiological Parameters for Grain Yield in Maize (*Zea mays* L.). *International Journal of Pure and Applied Bioscience,* **2** (1): 118-121.
13. Malik HN, SI Malik, M Hussain, SUR Chughtai and HI Javed. (2005). Genetic correlation among various quantitative characters in maize (*Zea mays* L.) hybrids. *Journal of Agriculture and Social Science,* **1** (3): 262–265.
14. Mohan L and Singh O. (2014). Studies of variability using morphological and quality traits in Quality Protein Maize (*Zea mays* L.). *Electronic Journal of Plant Breeding,* **5** (3): 526- 530.
15. Poehlman JM. (2006). Breeding Field Crops. 5th Edn. The AVI Publishing Company Incorporated, Westport, Connecticut.
16. Prasanna SV, V. K. and DR Babu. (2015). Character association and path analysis of grain yield and yield components in Maize (*Zea mays* L.) *Electronic Journal of Plant Breeding,* **6** (2): 550- 554.
17. Reddy VR and F Jabeen. (2016). Narrow sense heritability, correlation and path analysis in maize (*Zea mays* L.). *Sabrao Journal of Breeding and Genetics,* **48** (2): 120-126.
18. Reddy VR, F Jabeen, MR Sudarshan and AS Rao. (2012). Studies on genetic variability heritability, correlation and path coefficient analysis in maize (*Zea mays* L.) over locations. *International Journal of Applied Biology and Pharmaceutical Technology,* **4** (1): 195-199.
19. Singh, DD and D Singh. (1974). Correlation in Indian Colza *Brassica campestris* L., var. Sarsonprain. *Indian Journal of Agricultural Sciences,* **44** (3): 142-144.
20. Vashistha A, NN Dixit, D Sharma, S K, S Marker (2013). Studies On heritability and genetic advance estimates in Maize genotypes. *Bioscience Discovery,* **4** (2): 165-168

Journal of Cereal Research
Volume 14 (2): 189-197
Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Research Article

Combining ability study on yield and its contributing traits in maize (*Zea mays* L.)

Prashant Sharma[*1] and Uttam Chandel[2]

[*1]*Department of Genetics and Plant Breeding, CSK Himachal Pradesh Krishi Vishwavidayalaya, Palampur, Himachal Pradesh, India*
[2]*CSKHPKV SAREC, Kangra, Himachal Pradesh, India*

Article history:
Received: 27 Apr., 2022
Revised: 16 Sept., 2022
Accepted: 09 Oct., 2022

Citation:
Sharma P and U Chandel. 2022. Combining ability study on yield and its contributing traits in maize (*Zea mays* L.). *Journal of Cereal Research* ***14 (2):*** *189-197. http://doi.org/10.25174/2582-2675/2022/131247*

Corresponding author:
E-mail: pras1609@gmail.com

Abstract

Experimental material consisted of 25 lines, 2 testers and their 50 crosses along with standard checks *viz.,* Palam Sankar Makka-2 and PSCL 4640 were evaluated using Randomized Block Design with two replication during *Kharif* 2020. Genotype mean square was significant for days to 50% tasseling, days to 50% silking, days to 75% brown husk, ear height (cm), plant height (cm), ear length (cm), ear circumference (cm), kernel rows/cob, kernels/row, 1000-kernel weight (g), shelling (%) and grain yield (q/ha) which indicated the presence of sufficient genetic variability in the material studied. Also the ratio of GCA variance to SCA variance was less than unity for all traits indicated preponderance of non-additive gene action. Among lines, KI-3 exhibited higher grain yield followed by KI-7 and CML 140. These lines also exhibited highest significant GCA effect for grain yield and were identified as promising parents. KI-7 × LM 13, CML 140 × LM 13, CML 139 × LM 13, CML 162 × LM 13 and KI-3 × LM 14 exhibited maximum SCA effect for most of traits. These promising cross combinations need to be evaluated in multi-location trials over the years to assess their suitability in different agro-climatic zones of the State.

Keywords: Maize, GCA, SCA, Combining ability, gene action

1. Introduction

Maize (*Zea mays* L.) is the world's third largest grain crop after wheat and rice mainly grown in temperate highlands, tropical as well as in sub-tropical regions. Maize (2n=20) is a C_4 plant which belongs to tribe *Maydae* of family *Poaceae.* It is a highly cross pollinated crop due to which special efforts are required to maintain its genetic purity. It is a tall, monoecious, short day plant having determinate type of growth habit. Development of hybrids in maize includes various steps that starts with development of inbred lines, their evaluation, crossing selected inbred lines and hybrid production. Selection of right inbred line will lead to production of superior hybrids. For this detailed evaluation of existing germplasm/newly developed elite lines for their potential use in future breeding programmes is required. Combining ability is the measure of the genotype values based on their progeny performance in a definite mating system (Allard, 1960). Combining ability analysis help in selection of most promising parents which can produce superior hybrids when a number of lines are involved. It helps in understanding the nature and magnitude of gene action involved. The nature of gene action involved may be additive and additive × additive which is due to general combining ability or it may be non-additive which is due to specific combining ability. The nature of gene action is important factor in determining effective breeding programme. The presence of non-additive gene action is pre requisite for hybrid development programme. Various statistical tools are available to estimate combining ability. Line × Tester analysis method as developed by Kempthorne in 1957, is used in most breeding programmes as it allows estimation of combining ability, gene effect studies and selection of desirable parents and crosses. Since there is no information available on combining ability and gene action of the newly developed maize inbreds, therefore the present investigation was undertaken involving 25 lines, 2 testers and their 50 crosses along with 2 standard checks to estimate combining ability and gene action involved.

2. Material And Methods

Experimental material consisted of 25 lines, two testers and their 50 hybrids along with two standard checks *viz.,* Palam Sankar Makka-2 and PSCL 4640 were evaluated in a Randomized Block Design during *Kharif* 2020 with an objective to understand the nature of gene actions involved in inheritance of different traits and estimate combining ability effects for yield and its contributing traits. List of inbred lines, testers and standard checks used is presented in Table 1. The genotypes were evaluated at Experiment Farm, Shivalik Agriculture Research and Extension Centre, Kangra for various maturity, physiological, yield and its contributing characters. Observations were recorded based upon the performance of 10 competitive plants and average was worked out except for days to 50% tasseling, days to 50% silking and days to 75% brown husk, observations were recorded on plot basis. Standard package of practices were followed and plant protection measures were taken whenever required. The results obtained were subjected to statistical analysis as per method suggested by Kempthorne, 1957 and Panse and Sukhatme, 1984.

Table 1: Details of inbred lines and testers used as parents along with checks

Symbol/Code	**Inbred line**	**Source/Pedigree**
	A) Lines	
L_1	CML 33	ICAR-IIMR, WNC, Hyderabad
L_2	CML 117	--do--
L_3	CML 138	--do--
L_4	CML 139	--do--
L_5	CML 140	--do--
L_6	CML 162	--do--
L_7	CML 163	--do--
L_8	CML 292	--do--
L_9	CML 295	--do--
L_{10}	CML 338	--do--
L_{11}	CML 411	--do--
L_{12}	CML 426	--do--
L_{13}	CML 439	--do--
L_{14}	CML 451	--do--
L_{15}	CML 452	--do--
L_{16}	CML 494	--do--
L_{17}	CM 212	VPKAS, Almora
L_{18}	V 335	--do--
L_{19}	V 340	--do--
L_{20}	V 405	--do--

L_{21}	HKI-1040	ICAR-IIMR, Karnal
L_{22}	HKI-1105	--do--
L_{23}	CM 502	--do--
L_{24}	KI-3	CML161/CML165-B-B-B-4-B-B
L_{25}	KI-7	CML165-B-B-B-1-B-B
	B) Testers	
T_1	LM 13	PAU, Ludhiana
T_2	LM 14	--do--
	C) Checks	
C_1	Palam Sankar Makka-2	CSKHPKV, Palampur
C_2	PSCL 4640	Bayers

3. Result and Discussions

The analysis of variance for twelve characters of twenty five lines, two testers and their fifty crosses under study is presented in Table 4.1. Genotype mean square was significant for all traits which indicated presence of sufficient amount of genetic variability among genotypes. Similar results were also obtained earlier by Petrovic et al. (1998); Alam et al. (2008); Patil et al. (2012). Mean squares was further partitioned into crosses mean square, parent mean square and crosses vs parent mean square.

Crosses mean square was significant for most characters under study except shelling (%) indicated wider difference among crosses and hence possibility of selection for identification of desired crosses. Among parents, mean square due to lines was found to be significant for all traits except for shelling (%), whereas, mean square due to testers was found to be significant for most characters except for days to 50% silking, days to 50% tasseling, shelling (%) and days to 75% brown husk indicated presence of sufficient genetic variability among parents. Similar results were reported by Ram *et al.* (2015); Patil *et al.* (2012); Negi *et al.* (2018); Chandel *et al.* (2019).

Analysis of Variance for combining ability revealed that variance due to lines was greater than variance due to testers for kernel rows/cob, days to 50% tasseling, days to 50% silking, days to 75% brown husk, shelling (%) and grain yield. This indicated greater contribution of lines towards GCA. Whereas, variance due to testers was found greater than variance due to lines for ear height, plant height, ear length, ear circumference, kernels/row and 1000-kernel weight indicated greater contribution of testers towards GCA. Also GCA variance to SCA variance ratio was less than unity for all traits expressing greater importance of non-additive gene effects. This also highlighted the utilization of hybrid breeding scheme for enhancing productivity.

Estimates of GCA effect revealed that none of the lines and testers had proved significant for all traits studied. L_5, L_{24}, L_{25} were overall good general combiners ability for most characters studied. L_5 exhibited highest GCA effect for ear circumference, kernel rows/cob, kernels/row, 1000-kernel weight and grain yield. Also, lines *viz.,* L_6 and L_3 had highest GCA effect for days to 50% tasseling and days to 50% silking. L_{25} exhibited highest GCA effect for ear height, plant height and ear length. L_{24} exhibited significant GCA effects for all characters studied except ear height and plant height. Among testers, T_1 was good general combiner for ear length, kernel rows/cob, ear circumference, 1000-kernel weight, grain yield and kernels/row, whereas, T_2 was good general combiner for plant height, ear height. Iqbal *et al.* (2007); Reddy *et al.* (2011); Patil *et al.* (2012); Chaurasia *et al.* (2020) had also reported good general combiners for similar traits.

Studies on specific combining ability indicated that none of the crosses had proved significant for all traits. Possible combinations of parental GCA effect such as "high × high", "high × low", "average × low", "low × low" and "low × high" were involved in crosses with high SCA effect. This indicated presence of non-additive gene effect, especially in "high × low", "average × low" and "low × low" cross combinations. Studies on specific combining ability indicated that $L_{25} \times T_1$ exhibited highest combining ability for grain yield (high × high) and ear circumference (high × high), $L_{24} \times T_2$ exhibited highest combining ability

Table 2: Analysis of variance for yield and its contributing traits (maturity, physiological, yield and its contributing traits)

Characters	Replication	Genotypes	Cross	Line	Tester	Line × tester	Parents	Crosses v Parent	Error
Degree of freedom	1	76	49	24	1	24	26	1	76
Days to 50% tasseling	30.02	15.99**	9.81**	17.54**	0.36	2.48**	17.99**	266.53**	1.11
Days to 50% silking	30.91	16.71**	10.59**	18.27**	0.49	3.34**	16.97**	315.35**	1.59
Days to 75% brown husk	43.66	27.33**	24.04**	41.70**	4.84	7.17**	19.09**	403.05**	1.66
Ear height (cm)	0.52	644.78**	67.53**	57.03**	252.81**	70.31**	403.39**	35205.94**	16.90
Plant height (cm)	27.43	2437.07**	236.77**	210.06**	948.64**	233.82**	1470.38**	135386.11**	44.07
Ear length (cm)	1.14	24.83**	2.91**	2.80**	10.11**	2.73**	7.78**	1541.65**	0.16
Ear circumference (cm)	0.24	4.70**	1.09**	1.12**	2.99**	0.98**	1.46**	266.00**	0.03
Kernel rows per cob	0.18	9.17**	1.81**	2.12**	3.02**	1.46**	2.44**	544.84**	0.08
Kernels per row	2.67	71.25**	34.04**	33.13**	88.54**	32.68**	22.86**	3152.55**	0.31
1000-kernel weight (g)	68.88	5989.69**	865.57**	875.09**	1883.56**	813.64**	1830.20**	365218.39**	20.21
Shelling (%)	30.91	28.22**	12.76	16.89	4.36	8.98	28.74**	772.52**	11.24
Yield (q/ha)	14.61	1275.20**	136.90**	151.75**	387.53**	111.61**	365.00**	80717.22**	2.62

* significant at 5% level; ** significant at 1% level

Table 3: Analysis of variance for combining ability (maturity, physiological, yield and its contributing traits)

Source of Variation	Days to 50% tasseling	Days to 50% silking	Days to 75% brown husk	Ear height (cm)	Plant height (cm)	Ear length (cm)	Ear circum-ference (cm)	Kernel rows/ cob	Kernels/ row	1000-kernel weight	Shelling (%)	Grain Yield (q/ha)
σ^2l	3.76	3.73	8.63	-3.31	-5.94	0.01	0.03	0.16	0.11	15.36	1.97	10.03
σ^2 t	-0.04	-0.05	-0.04	3.65	14.29	0.14	0.04	0.03	1.11	21.38	-0.09	5.51
σ^2 gca	0.09	0.09	0.22	-0.03	0.04	0.00	0.00	0.00	0.01	0.69	0.05	0.34
σ^2 sca	0.60	0.81	2.68	27.18	95.64	1.28	0.47	0.68	16.21	395.52	3.20	53.95
σ^2 gca/ σ^2 sca	0.162	0.119	0.084	-0.001	0.000	0.002	0.003	0.007	0.001	0.002	0.016	0.006

Table 4: Estimates of general combining ability (maturity, physiological, yield and its contributing traits)

	Days to 50% tasseling	Days to 50% silking	Days to 75% brown husk	Ear height (cm)	Plant height (cm)	Ear length (cm)	Ear circum-ference (cm)	Kernel rows /cob	Kernels/ row	1000-kernel weight (g)	Shelling (%)	Grain yield (q/ ha)
Lines												
L_{1}	1.47 *	1.61 *	3.02 **	-3.89	-6.85 *	-0.49 *	0.35 **	0.66 **	0.83 **	13.24 **	-1.18	3.38 **
L_{2}	1.22 *	1.36 *	1.52 *	-6.39 **	-12.10 **	0.01	0.26 **	0.46 **	1.01 **	6.99 **	-0.08	2.58 **
L_{3}	-3.78 **	-3.64 **	-4.98 **	-3.14	-5.10	0.54 *	0.68 **	0.71 **	3.38 **	16.49 **	2.95 **	5.98 **
L_{4}	-0.28	-0.64	-1.98 **	-2.39	-6.85 *	0.89 **	0.78 **	1.11 **	4.13 **	18.74 **	-1.78 *	8.83 **
L_{5}	-0.28	-0.39	-0.98	0.36	2.15	1.34 **	1.00 **	1.46 **	5.48 **	24.99 **	-1.00	11.16 **
L_{6}	-3.78 **	-3.64 **	-6.98 **	2.61	6.65 *	0.96 **	0.63 **	0.51 **	3.91 **	10.99 **	1.07	6.44 **
L_{7}	-3.03 **	-3.64 **	-5.98 **	1.86	1.90	-0.41 *	-0.10	0.46 **	0.61 *	6.99 **	2.50 **	1.96 *
L_{8}	-3.03 **	-2.89 **	-2.98 **	-0.14	3.90	-0.74 **	-0.25 *	-0.24	-1.09 **	-5.76 *	0.35	-2.29 *
L_{9}	-0.03	-0.14	1.02	0.36	-2.10	-0.01	0.16	0.06	0.43	5.49 *	-2.15 **	1.44
L_{10}	0.72	0.36	1.02	-7.39 **	-14.10 **	-0.46 *	-0.57 **	-0.74 **	-2.42 **	-14.76 **	-0.40	-5.55 **
L_{11}	3.47 **	3.61 **	5.02 **	-5.14 *	-9.10 **	-0.06	-0.07	-0.29	-1.24 **	-3.01	1.00	-2.42 *
L_{12}	0.97	0.86	1.02	1.61	6.40	-0.44 *	-0.12	-0.24	-1.27 **	-3.01	0.10	-2.80 **
L_{13}	3.97 **	4.36 **	6.02 **	-5.89 **	-9.85 **	-0.76 **	-0.52 **	-0.64 **	-1.79 **	-13.51 **	1.90 *	-6.20 **
L_{14}	1.47 *	1.36 *	2.02 **	2.61	0.15	-0.39	-0.30 **	-0.24	-1.39 **	-2.26	2.92 **	-2.93 **
L_{15}	-0.78	-0.89	0.02	3.36	7.15 *	-0.91 **	-0.27 **	-0.44 **	-1.59 **	-10.51 **	-1.23	-3.17 **
L_{16}	-0.28	-0.64	-1.98 **	0.86	0.15	-0.84 **	-0.12	-0.49 **	-1.72 **	-10.01 **	1.92 *	-2.81 **
L_{17}	-0.03	-0.14	1.02	0.36	-0.10	1.04 **	0.31 **	-0.04	1.88 **	10.99 **	0.62	3.13 **
L_{18}	0.72	1.11	3.02 **	2.86	4.65	-0.56 **	-0.15	0.16	-1.39 **	-4.51	-3.90 **	-2.22 *
L_{20}	-0.28	-0.14	0.02	4.11 *	8.40 *	-0.39	-0.54 **	-0.84 **	-3.42 **	-18.51 **	-1.43	-5.74 **
L_{21}	-1.53 **	-1.14	-1.98 **	-0.64	0.15	-0.46 *	-0.62 **	-0.89 **	-3.57 **	-20.26 **	2.22 **	-7.69 **
L_{22}	0.72	0.61	2.02 **	2.61	6.40	-0.94 **	-0.90 **	-1.14 **	-3.84 **	-22.26 **	-3.43 **	-9.89 **
L_{23}	3.22 **	3.36 **	2.02 **	5.86 **	10.90 **	-0.34	-0.67 **	-0.94 **	-3.72 **	-21.01 **	-3.75 **	-7.90 **
L_{24}	-2.03 **	-1.89 **	-3.98 **	-0.39	-2.60	1.66 **	0.70 **	1.06 **	4.88 **	23.99 **	2.22 **	11.14 **

L_{25}	-0.78	-0.39	1.02	7.36 **	13.40 **	1.96 **	0.71 **	1.01 **	3.93 **	20.24 **	1.50	9.32 **
						Testers						
T_1	0.06	0.07	0.22	1.59 **	3.08 **	0.32 **	0.17 **	0.17 **	0.94 **	4.34 **	0.21	1.97 **
T_2	-0.06	-0.07	-0.22	-1.59 **	-3.08 **	-0.32 **	-0.17 **	-0.17 **	-0.94 **	-4.34 **	-0.21	-1.97 **

Table 5: Estimates of specific combining ability (maturity, physiological, yield and its contributing traits)

Crosses	**Days to 50% tasseling**	**Days to 50% silking**	**Days to 75% brown husk**	**Ear height (cm)**	**Plant height (cm)**	**Ear length (cm)**	**Ear circumferance (cm)**	**Kernel rows per cob**	**Kernels per row**	**1000-kernel weight**	**Shelling (%)**	**Yield (q/ ha)**
$L_1 \times T_1$	1.19 ns	1.43 ns	0.78 ns	-1.09 ns	-0.33 ns	-0.34 ns	-0.17 ns	-0.02 ns	-0.87 *	-1.84 ns	0.92 ns	-1.62 ns
$L_1 \times T_2$	-1.19 ns	-1.43 ns	-0.78 ns	1.09 ns	0.33 ns	0.34 ns	0.17 ns	0.02 ns	0.87 *	1.84 ns	-0.92 ns	1.62 ns
$L_2 \times T_1$	-0.56 ns	-0.32 ns	-0.72 ns	-1.09 ns	-2.08 ns	0.21 ns	0.18 ns	0.38 ns	1.51 **	11.91 **	-0.98 ns	2.07 ns
$L_2 \times T_2$	0.56 ns	0.32 ns	0.72 ns	1.09 ns	2.08 ns	-0.21 ns	-0.18 ns	-0.38 ns	-1.51 **	-11.91 **	0.98 ns	-2.07 ns
$L_3 \times T_1$	0.94 ns	1.18 ns	2.78 **	2.16 ns	2.42 ns	0.83 **	0.45 **	0.43 ns	3.08 **	11.41 **	1.24 ns	3.61 *
$L_3 \times T_2$	-0.94 ns	-1.18 ns	-2.78 **	-2.16 ns	-2.42 ns	-0.83 **	-0.45 **	-0.43 ns	-3.08 **	-11.41 **	-1.24 ns	-3.61 *
$L_4 \times T_1$	-1.56 ns	-1.82 ns	-2.22 *	-4.59 ns	-9.83 *	1.68 **	0.50 **	0.63 **	3.73 **	12.66 **	0.52 ns	6.13 **
$L_4 \times T_2$	1.56 ns	1.82 ns	2.22 *	4.59 ns	9.83 *	-1.68 **	-0.50 **	-0.63 **	-3.73 **	-12.66 **	-0.52 ns	-6.13 **
$L_5 \times T_1$	0.44 ns	0.93 ns	0.78 ns	2.16 ns	3.67 ns	1.33 **	0.38 **	0.08 ns	2.63 **	1.41 ns	1.74 ns	4.51 **
$L_5 \times T_2$	-0.44 ns	-0.93 ns	-0.78 ns	-2.16 ns	-3.67 ns	-1.33 **	-0.38 **	-0.08 ns	-2.63 **	-1.41 ns	-1.74 ns	-4.51 **
$L_6 \times T_1$	-0.06 ns	0.18 ns	0.78 ns	0.91 ns	0.17 ns	1.11 **	0.70 **	0.83 **	4.66 **	21.91 **	-1.48 ns	7.44 **
$L_6 \times T_2$	0.06 ns	-0.18 ns	-0.78 ns	-0.91 ns	-0.17 ns	-1.11 **	-0.70 **	-0.83 **	-4.66 **	-21.91 **	1.48 ns	-7.44 **
$L_7 \times T_1$	-1.31 ns	-1.32 ns	-2.22 *	4.16 ns	8.42 ns	0.03 ns	0.38 **	0.38 ns	0.11 ns	6.91 *	-0.16 ns	1.21 ns
$L_7 \times T_2$	1.31 ns	1.32 ns	2.22 *	-4.16 ns	-8.42 ns	-0.03 ns	-0.38 **	-0.38 ns	-0.11 ns	-6.91 *	0.16 ns	-1.21 ns
$L_8 \times T_1$	0.69 ns	1.43 ns	0.78 ns	7.66 **	10.42 *	0.16 ns	0.23 ns	0.48 *	1.21 **	8.66 *	-0.71 ns	2.36 ns
$L_8 \times T_2$	-0.69 ns	-1.43 ns	-0.78 ns	-7.66 **	-10.42 *	-0.16 ns	-0.23 ns	-0.48 *	-1.21 **	-8.66 *	0.71 ns	-2.36 ns

$L_{9} \times T_{1}$	-0.31 ns	-0.32 ns	-1.22 ns	4.16 ns	10.42 *	-0.87 **	-0.67 **	-0.62 **	-3.92 **	-21.09 **	0.69 ns	-7.19 **
$L_{9} \times T_{2}$	0.31 ns	0.32 ns	1.22 ns	-4.16 ns	-10.42 *	0.87 **	0.67 **	0.62 **	3.92 **	21.09 **	-0.69 ns	7.19 **
$L_{10} \times T_{1}$	0.44 ns	0.68 ns	0.78 ns	-2.59 ns	-6.08 ns	-0.37 ns	0.00 ns	0.18 ns	-0.37 ns	0.66 ns	-2.36 *	0.03 ns
$L_{10} \times T_{2}$	-0.44 ns	-0.68 ns	-0.78 ns	2.59 ns	6.08 ns	0.37 ns	-0.00 ns	-0.18 ns	0.37 ns	-0.66 ns	2.36 *	-0.03 ns
$L_{11} \times T_{1}$	-0.81 ns	-1.07 ns	-1.22 ns	-2.34 ns	-5.08 ns	-0.12 ns	0.40 **	0.63 **	1.36 **	14.41 **	0.64 ns	4.35 **
$L_{11} \times T_{2}$	0.81 ns	1.07 ns	1.22 ns	2.34 ns	5.08 ns	0.12 ns	-0.40 **	-0.63 **	-1.36 **	-14.41 **	-0.64 ns	-4.35 **
$L_{12} \times T_{1}$	0.69 ns	0.68 ns	0.78 ns	3.41 ns	6.42 ns	-0.49 ns	-0.75 **	-1.02 **	-3.32 **	-23.09 **	-1.06 ns	-8.47 **
$L_{12} \times T_{2}$	-0.69 ns	-0.68 ns	-0.78 ns	-3.41 ns	-6.42 ns	0.49 ns	0.75 **	1.02 **	3.32 **	23.09 **	1.06 ns	8.47 **
$L_{13} \times T_{1}$	-0.31 ns	-0.32 ns	-0.22 ns	-3.09 ns	-3.33 ns	-0.42 ns	0.15 ns	0.28 ns	1.21 **	5.41 ns	-0.21 ns	3.30 *
$L_{13} \times T_{2}$	0.31 ns	0.32 ns	0.22 ns	3.09 ns	3.33 ns	0.42 ns	-0.15 ns	-0.28 ns	-1.21 **	-5.41 ns	0.21 ns	-3.30 *
$L_{14} \times T_{1}$	-0.31 ns	-0.32 ns	-0.22 ns	0.41 ns	7.17 ns	-0.69 *	-0.77 **	-1.22 **	-3.39 **	-23.84 **	-0.23 ns	-8.93 **
$L_{14} \times T_{2}$	0.31 ns	0.32 ns	0.22 ns	-0.41 ns	-7.17 ns	0.69 *	0.77 **	1.22 **	3.39 **	23.84 **	0.23 ns	8.93 **
$L_{15} \times T_{1}$	0.44 ns	-0.07 ns	-0.22 ns	-3.34 ns	-8.83 ns	-0.27 ns	-0.40 **	-0.62 **	-2.94 **	-12.09 **	-0.18 ns	-4.84 **
$L_{15} \times T_{2}$	-0.44 ns	0.07 ns	0.22 ns	3.34 ns	8.83 ns	0.27 ns	0.40 **	0.62 **	2.94 **	12.09 **	0.18 ns	4.84 **
$L_{16} \times T_{1}$	-1.56 ns	-1.32 ns	-2.22 *	-8.84 **	-16.33 **	-0.84 **	-0.55 **	-0.57 *	-2.77 **	-13.09 **	0.27 ns	-5.13 **
$L_{16} \times T_{2}$	1.56 ns	1.32 ns	2.22 *	8.84 **	16.33 **	0.84 **	0.55 **	0.57 *	2.77 **	13.09 **	-0.27 ns	5.13 **
$L_{17} \times T_{1}$	0.69 ns	0.68 ns	0.78 ns	7.16 *	12.42 **	1.33 **	0.78 **	0.88 **	4.38 **	25.91 **	1.17 ns	7.92 **
$L_{17} \times T_{2}$	-0.69 ns	-0.68 ns	-0.78 ns	-7.16 *	-12.42 **	-1.33 **	-0.78 **	-0.88 **	-4.38 **	-25.91 **	-1.17 ns	-7.92 **
$L_{18} \times T_{1}$	-0.06 ns	-0.57 ns	-1.22 ns	-3.84 ns	-6.83 ns	-0.67 *	-0.67 **	-1.02 **	-3.14 **	-20.09 **	0.54 ns	-7.44 **
$L_{18} \times T_{2}$	0.06 ns	0.57 ns	1.22 ns	3.84 ns	6.83 ns	0.67 *	0.67 **	1.02 **	3.14 **	20.09 **	-0.54 ns	7.44 **
$L_{19} \times T_{1}$	-0.31 ns	-0.57 ns	-0.22 ns	-1.59 ns	-2.58 ns	0.13 ns	0.33 *	0.43 ns	0.78 *	7.16 *	3.07 **	3.13 *
$L_{19} \times T_{2}$	0.31 ns	0.57 ns	0.22 ns	1.59 ns	2.58 ns	-0.13 ns	-0.33 *	-0.43 ns	-0.78 *	-7.16 *	-3.07 **	-3.13 *
$L_{20} \times T_{1}$	1.44 ns	1.68 ns	1.78 ns	-0.09 ns	-0.08 ns	-0.24 ns	-0.12 ns	-0.12 ns	-0.87 *	-3.59 ns	-2.58 *	-1.25 ns
$L_{20} \times T_{2}$	-1.44 ns	-1.68 ns	-1.78 ns	0.09 ns	0.08 ns	0.24 ns	0.12 ns	0.12 ns	0.87 *	3.59 ns	2.58 *	1.25 ns

$L_{21} \times T_1$	0.19 ns	0.18 ns	1.78 ns	0.66 ns	0.67 ns	-0.42 ns	-0.25 ns	-0.17 ns	-0.92 **	-3.84 ns	-2.48 *	-1.28 ns
$L_{21} \times T_2$	-0.19 ns	-0.18 ns	-1.78 ns	-0.66 ns	-0.67 ns	0.42 ns	0.25 ns	0.17 ns	0.92 **	3.84 ns	2.48 *	1.28 ns
$L_{22} \times T_1$	0.44 ns	-0.07 ns	-0.22 ns	-4.09 ns	-7.58 ns	-0.19 ns	-0.22 ns	-0.22 ns	-0.94 **	-3.84 ns	1.17 ns	-2.07 ns
$L_{22} \times T_2$	-0.44 ns	0.07 ns	0.22 ns	4.09 ns	7.58 ns	0.19 ns	0.22 ns	0.22 ns	0.94 **	3.84 ns	-1.17 ns	2.07 ns
$L_{23} \times T_1$	-0.06 ns	-0.32 ns	1.78 ns	-4.84 ns	-7.08 ns	-0.24 ns	-0.20 ns	-0.22 ns	-0.82 *	-4.09 ns	1.99 ns	-2.15 ns
$L_{23} \times T_2$	0.06 ns	0.32 ns	-1.78 ns	4.84 ns	7.08 ns	0.24 ns	0.20 ns	0.22 ns	0.82 *	4.09 ns	-1.99 ns	2.15 ns
$L_{24} \times T_1$	0.19 ns	-0.07 ns	-0.22 ns	7.91 **	12.92 **	-1.79 **	-0.52 **	-0.42 ns	-5.17 **	-15.59 **	-2.53 *	-4.83 **
$L_{24} \times T_2$	-0.19 ns	0.07 ns	0.22 ns	-7.91 **	-12.92 **	1.79 **	0.52 **	0.42 ns	5.17 **	15.59 **	2.53 *	4.83 **
$L_{25} \times T_1$	-0.56 ns	-0.57 ns	-1.22 ns	0.66 ns	0.92 ns	1.16 **	0.83 **	0.73 **	4.73 **	17.66 **	1.04 ns	9.13 **
$L_{25} \times T_2$	0.56 ns	0.57 ns	1.22 ns	-0.66 ns	-0.92 ns	-1.16 **	-0.83 **	-0.73 **	-4.73 **	-17.66 **	-1.04 ns	-9.13 **

for ear length (high × low) and kernels/row (high × low). Similarly, $L_3 \times T_2$ (high × low) for days to 75% brown husk, $L_4 \times T_1$ for days to 50% tasseling (average × low) and days to 50% silking (average × low), $L_{16} \times T_2$ for plant height (low × high) and ear height (low × high), $L_{16} \times T_1$ (average × low) for days to 50% tasseling, $L_{14} \times T_2$ (low × low) for kernel rows/cob, $L_{17} \times T_1$ (high × high) for 1000-kernel weight and $L_{19} \times T_1$ (low × low) for shelling (%). Similar results were also reported earlier by Petrovic et al. (1998); Uddin et al. (2008); Niyonzima et al. (2015).

Author's contribution

Conceptualization of research (PS); Designing of the experiments (PS and UC); Contribution of experimental materials (PS and UC); Execution of field/lab experiments and data collection (PS and UC); Analysis of data and interpretation (PS and UC); Preparation of the manuscript (PS and UC).

Conflict of Interest

Author declares that they have no conflict of interest

References

1. Alam AKMM, S Ahmed, M Begum and MK Sultan. 2008. Heterosis and combining ability for grain yield and its contributing characters in maize. *Bangladesh Journal of Agricultural Research* 33(3): 375-379.
2. Allard RW. 1960. Principle of Plant Breeding. John Wiley and Sons. p 154.
3. Chandel U, D Kumar and SK Guleria. 2019. Combining ability effects and heterotic grouping in newly developed early maturing yellow maize (*Zea mays* L.) inbreds under sub-tropical conditions. *Electronic Journal of Plant Breeding* 10(3): 1049-1059.
4. Chaurasia NK, RBP Nirala and B Singh. 2020. Combining ability and heterosis studies in maize (*Zea mays* L.) under *kharif* season. *International Journal of Current microbiology and Applied Sciences* 9(11): 2576-2586.
5. Iqbal AM, FA Nehvi, SA Wani, R Qadir and ZA Dar. 2007. Combining ability analysis for yield and yield related traits in maize (*Zea mays* L.). *International Journal of Plant Breeding and Genetics* 1(2): 101-105.
6. Kempthorne O. 1957. An Introduction to Genetic Statistics. John Wiley and Sons. p 143.

7. Negi M, DC Baskheti and Rajani. 2018. Combining ability analysis of maize inbred lines from line × tester mating design under two plant population deity. *International Journal of Current Microbiology and Applied Sciences* 7(6): 3539-3550.

8. Niyonzima JP, TE Nagaraja, HC Lohithaswa, MS Uma, R Pavan, F Niyitanga and A Kabayiza. 2015. *International Journal of Agronomy and Agricultural Research* 7(1): 61-69

9. Panse VG and PV Sukhatme. 1984. Statistical methods for agricultural workers. Indian Council of Agricultural Research, New Delhi. P.381

10. Patil AE, SU Charjan, SR Patil, RN Udasi, MR Puttawar and AB Palkar. 2012. Studies on heterosis and combining ability analysis in maize (*Zea mays* L.). *Association of Soils and Crops Research Scientists* 22(1): 129-138.

11. Patil AE, SU Charjan, SR Patil, RN Udasi, MR Puttawar and AB Palkar. 2012. Studies on heterosis and combining ability analysis in maize (*Zea mays* L.). *Association of Soils and Crops Research Scientists* 22(1): 129-138

12. Petrovic Z, UN Sadu, N Sad and P Fakultet. 1998. Combining abilities and mode of inheritance of yield and yield components in maize (*Zea mays* L.). *Scientia Agricola* 48(1): 63-65

13. Ram L, R Singh, SK Singh and RP Srivastava. 2015. Heterosis and Combining ability studies for quality protein maize. *Journal of Crop Breeding and Genetics* 1(2): 8-25

14. Uddin MS, M Amiruzzaman, SA Bagum, MA Hakim and MR Ali. 2008. Combining ability and heterosis in maize (*Zea mays* L.). *Bangladesh Journal of Genetics and Plant Breeding* 21(1): 21-28.

Journal of Cereal Research
Volume 14 (2): 198-203
Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Short Communication

Effect of integrated nutrient management in rice on vegetative growth and economic profitability of wheat under long term rice-wheat cropping system

Shivani Ranjan*, Sanjay Kumar, Swaraj Kumar Dutta, Sumit Sow and Mainak Ghosh

Department of Agronomy, Bihar Agricultural University, Sabour, Bhagalpur, Bihar, India- 813 210

Article history: Received: 24 July., 2022 Revised: 18 Aug., 2022 Accepted: 27 Aug., 2022

Citation: Ranjan S, S Kumar, SK Dutta, S Sow and M Ghosh. 2022. Effect of integrated nutrient management in rice on vegetative growth and economic profitability of wheat under long term rice-wheat cropping system. *Journal of Cereal Research* ***14 (2):*** *198-203. http://doi.org/10.25174/2582-2675/2022/125999*

****Corresponding author:*** *E-mail: ranjanshivani54@gmail.com*

Keywords: farm yard manure, integrated nutrient management, net return, wheat, yield

Wheat (*Triticum aestivum*) is one of the principal cereal crops and is the second most important staple food after rice in India. Globally, wheat is grown in an area of 222.21 Mha with a production and productivity of 779.03 Mt and 3510 kg ha^{-1}, respectively (USDA, 2022). Generalized recommendations currently followed with respect to NPK fertilizers alone are leading towards depletion of nutrients, poor soil quality and thus application of proper balanced nutrients should be followed. Under the present situation, the concept of balanced fertilization cannot be limited to N, P and K alone. It should include application of all the essential plant nutrients required for high agricultural productivity. Nutrient applied either through chemical fertilizers, organic manure, crop residues or biofertilizers cannot meet the entire nutrient need of a crop in modern intensive agriculture (Darjee *et al.*, 2022). Rather, these need to be used in an integrated manner following a management technology that is integrated nutrient management which is practicable, economically viable, socially acceptable and ecologically sound (Patra *et al.*, 2022; Ullah *et al.*, 2021). Combined use of organic and chemical fertilizers significantly improved crop yield over the recommended dose of inorganic fertilizers alone (Saha *et al.*, 2018; Sarwar *et al.*, 2021). Application of organic manure helps to overcome the deficiency of micronutrients, which is due to the continuous use of high-analysis chemical fertilizers (Singh and Saini, 2021). Integrated use of organic manures and inorganic fertilizers has gained immense importance for sustaining crop production.

The field experiment was conducted at the research farm of Bihar Agricultural University, Sabour, Bhagalpur during the *rabi* season of the year 2020-2021. Since a permanent experiment was carried out in the experimental plot for the last thirty-six years (since 1984) only rice and wheat were grown in *kharif* and *rabi* seasons respectively, over the years followed by fallow in *zaid.* The initial physicochemical properties of the experimental plot were: pH (7.40), electrical conductivity (0.29 dS m^{-1}), organic carbon (0.46%), available N (194 kg ha^{-1}), available P (23 kg ha^{-1}) and available K (155 kg ha^{-1}). The experiment was laid out in randomized block design (RBD) with three replications and 11 treatment combinations. The treatments were: T_1: Control (No fertilizer, no organic manure) in both rice and wheat., T_2: 50% RDF (recommnded dose of fertilizers) in both rice and wheat., T_3: 50% RDF in rice and 100% RDF in wheat., T_4: 75% RDF in both rice and wheat.,T_5: 100% RDF in both rice and wheat., T_6: 50% RDF and 50% N through FYM (farm yard manure) in rice and 100% RDF in wheat., T_7: 75% RDF and 25% N through FYM in rice and 75% RDF in wheat.,

T_8: 50% RDF and 50% N through wheat straw in rice and 100% RDF in wheat., T_9: 75% RDF and 25% N through wheat straw in rice and 75% RDF in wheat., T_{10}: 50% RDF and 50% N through GM (green manure) in rice and 100% RDF in wheat and T_{11}: 75% RDF and 25% N through GM in rice and 75% RDF in wheat. The recommended dose of fertilizer (RDF) was 120 kg N, 60 kg P_2O_5 and 40 kg K_2O per hectare, and fertilizers were applied as per treatment in all the treatments except control. The research trial was conducted on the wheat variety 'HD-2967'. The seeds of wheat cultivars were sown at a row spacing of 20 cm. The dimension of each treatment plot was about 8.5m × 4.95m. The data were statistically analyzed by using "ANOVA" (Analysis of Variance) technique on randomized block design (RBD). For each character, the standard error of mean (SEm) and least significant difference (LSD) at the 5% level of significance were calculated.

The growth attributes namely plant height, LAI (green manure) and number of tillers/m^{-2} differed significantly due to different integrated nutrient management practices (Table 1). Application of 50% RDF and 50% N through FYM in rice and 100% RDF in wheat (T_6) showed best performance in terms of plant height and number of tillers/m^{-2}. This showed residual effect of substitution of 50% inorganic N by FYM in rice on succeeding wheat. It was also relevant to notice that even other organic sources, i.e. wheat straw and green manure substituting for 50% RDF in rice and application of 100% RDF in wheat were equally productive, but was superior to application of 100% RDF in inorganic forms to both the crops. This shows the importance of organic source of nutrients in growth and development of crops. FYM was found more efficient in increasing the availability of nutrients. It is due to its fast nutrient conversion rate from organic to inorganic form (Puniya *et al.*, 2019). Wheat straw decomposes slowly as it contains higher amount of polysaccharides, waxes and silica. Although, *Sesbania aculeata* gets easily decomposed but FYM was found more effective than it. It is due to less total organic matter content on per unit nutrient basis of *Sesbania aculeata.* Therefore, these positive effects of FYM over wheat straw and green manuring with *Sesbania aculeata* resulted in its higher efficacy.

Table 1. Effect of integrated nutrient management practices on plant height (cm), LAI at maturity and number of tillers m^{-2} of wheat at different days after sowing

Treatment	Plant height	LAI	Number of tillers m^{-2}				
			30 DAS	60 DAS	90 DAS	120 DAS	At harvest
T_1	65.4	0.49	74	153	191	194	192
T_2	93.6	1.77	144	284	299	294	280
T_3	98.5	2.26	183	364	379	374	340
T_4	98.2	1.93	169	331	341	336	320
T_5	99.1	2.24	180	346	356	351	343
T_6	100.4	2.43	204	414	431	426	377
T_7	99.2	2.35	186	390	407	399	359
T_8	100.1	2.36	198	406	419	412	356
T_9	98.6	2.01	164	344	356	348	327
T_{10}	100.3	2.40	195	406	429	421	368
T_{11}	99.6	2.30	180	369	379	372	340
SEm(±)	1.4	0.17	5.6	10.9	10.6	10.5	9.5
CD (P=0.05)	4.2	0.51	16.5	32.2	31.2	31.1	28.2

Results showed that yield attributes such as number of earhead/m^{-2}, number of grains/earhead, length of earhead and 1000 grain weight differed significantly due to different integrated nutrient management practices (Table 2). Incorporation of organic matter has improved soil properties which has resulted in increased availability and uptake of nutrients. Due to accelerated uptake of nutrients, there was improvement in yield attributes. Application of 50% RDF and 50% N through FYM in rice and 100% RDF in wheat (T_6) recorded the highest value of yield attributes. The biomass yield of different treatments in this study showed that it was highest with the application of 50% RDF and 50% N through FYM in rice and 100% RDF in wheat (T_6) which was significantly superior over the rest of the treatments. The reason behind this can be the supply of essential nutrients by FYM throughout the entire crop growth period (Kavinder *et al.*, 2019; Jat *et al.*, 2021). Treatments involving substitution of 50% inorganic N by FYM and application of 50% RDF in rice followed by 100% RDF in wheat increased biomass yield by 25.3% over application of 100% RDF in both the crops (T_5). Application of other organic sources, i.e., wheat straw or green manuring in rice followed by 100% RDF in wheat also performed better than T_5 in respect of biomass yield. This can be due to the cumulative residual effect of organic manures over the years (Guo *et al.*, 2016). FYM is more effective than other organic sources due to its ability of improving physical and chemical properties of soil leading to proper crop growth and development (Kumari *et al.*, 2017).

Table 2. Effect of integrated nutrient management practices on biomass yield and yield attributes and economics of wheat

Treatment	**Number of earhead m^{-2}**	**Number of grains/ earhead**	**Length of earhead (cm)**	**1000 grain weight (g)**	**Biomass yield (t ha^{-1})**	**Cost of cultivation (₹ ha^{-1})**	**Net returns (₹ ha^{-1})**	**Benefit: Cost ratio**
T_1	185	21	5.44	28.0	2.32	31073	-7118	-0.23
T_2	269	30	7.29	34.6	5.62	34103	24019	0.70
T_3	328	35	9.53	35.4	8.61	37133	51928	1.40
T_4	307	31	7.53	35.6	6.99	35618	36568	1.03
T_5	328	34	9.55	35.1	8.33	37133	48660	1.31
T_6	363	42	12.09	36.8	10.37	37133	69795	1.88
T_7	347	37	10.45	36.3	8.74	35618	56641	1.59
T_8	345	40	11.48	36.9	9.21	37133	57661	1.55
T_9	319	32	9.91	35.4	7.96	35618	46474	1.30
T_{10}	356	41	11.99	36.6	9.50	37133	60702	1.63
T_{11}	327	36	10.37	35.9	8.87	35618	55764	1.57
SEm(±)	10.44	1.50	0.27	0.75	0.45	-	4301.37	0.12
CD (P=0.05)	30.79	4.44	0.79	2.22	1.33	-	12689.03	0.36

The relationship between data of biomass yield and growth attributes (plant height and number of tillers/m^{-2}) was developed by regression analysis taking Y (plant height and number of tillers m^{-2} as dependent variables) and X (biomass yield as an independent variable) (Fig.1 and 2). Regression studies revealed a close linear relationship between biomass yield and plant height ($Y = 4.144X + 63.144$; $R^2 = 0.819$); biomass yield and number of tillers m^{-2} ($Y = 23.06X + 145.96$; $R^2 = 0.977$). It suggests that application of inorganic fertilizer along with organic sources of nutrients can enhance growth and biomass yield in wheat (Bharali *et al.*, 2017; Kakraliya *et al.*, 2017; Kumar *et al.,* 2019).

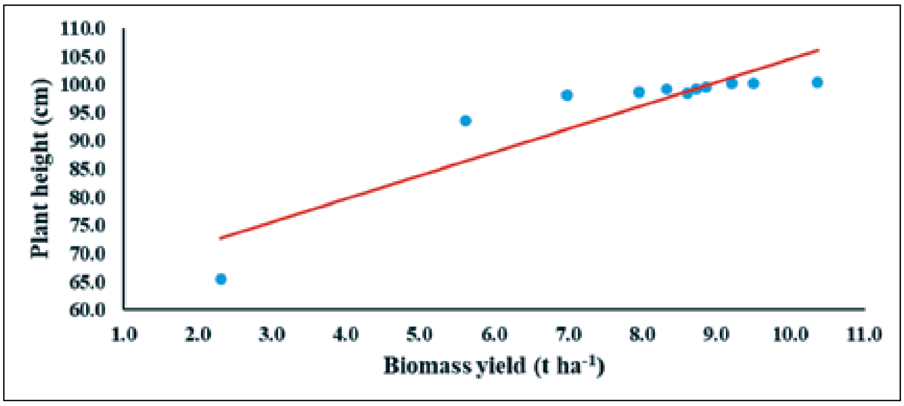


Fig 1. Relationship between plant height and biomass yield of wheat

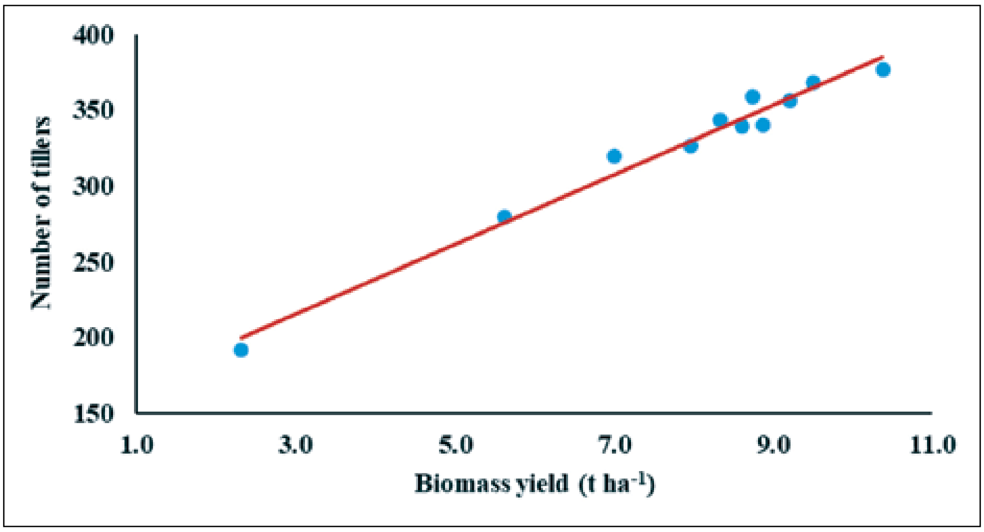


Fig 2. Relationship between number of tillers m^{-2} and biomass yield of wheat

Economic analysis reveals that the net returns and B:C ratio of wheat differed noticeably in different nutrient management options (Table 2) and that was directly related to the price of the crop produced and the cost incurred on nutrient inputs under different treatments. Variable cost was involved with the source of nutrient input in different treatments. Data showed that net return and B:C ratio in terms of wheat were higher with the application of 50% RDF and 50% N through FYM in rice and 100% RDF in wheat (T_6) which was significantly superior over the rest of the treatments. Treatments involving substitution of 50% inorganic N by FYM and application of 50% RDF in rice followed by 100% RDF in wheat increased net return by 43% over application of 100% RDF in both the crops (Fig. 3). The treatment showing a higher yield eventually resulted in increased profitability. The result confirmed that higher yield under the organic nutrient source treatments have been the reason behind its cost effectiveness (Yadav, 2003; Jat *et al.*, 2021).

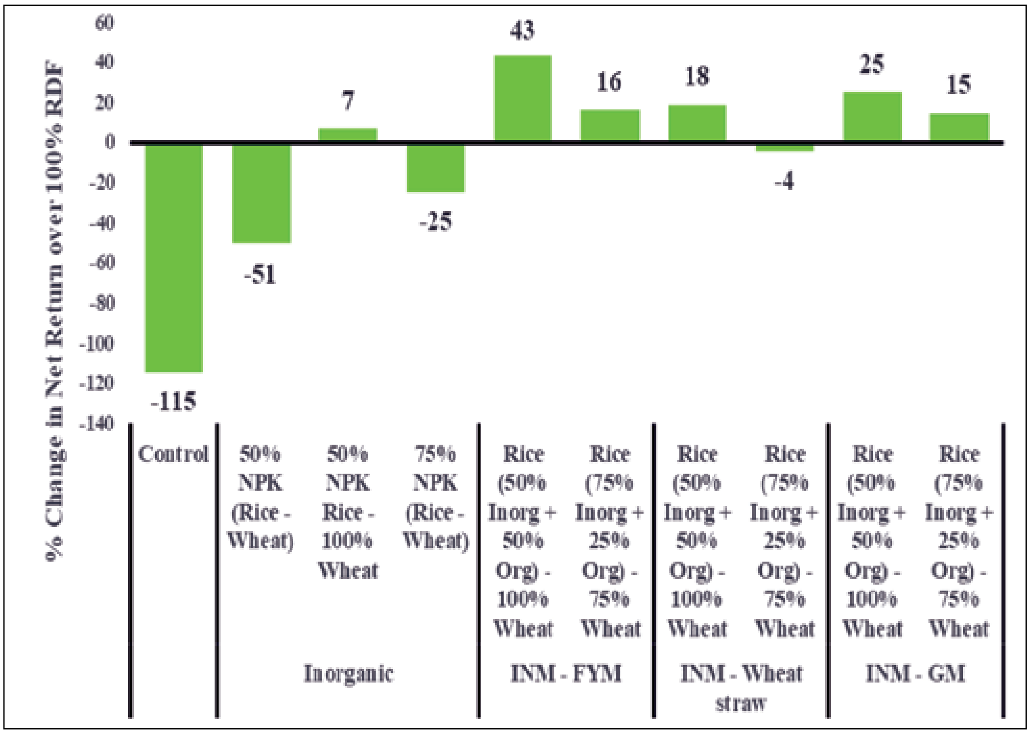


Fig 3. Wheat profitability as influenced by long term INM over conventional nutrient management practices

The results of 36 years long-term experiment concluded that farmers may adopt substitution of 50% inorganic N either through FYM or wheat straw or green manuring with *Sesbania aculeata* and 50% RDF in rice followed by 100% RDF in wheat for improving growth as well as profitability of wheat in the rice-wheat cropping system.

Acknowledgement

The authors are thankful to the Bihar Agricultural University, Sabour, Bhagalpur for providing necessary facilities during the entire research work.

Compliance with ethical standards: NA

Conflict of interest: No

Authors' contribution:

This article is fully based on M.Sc. research work of the first author (SR) under the supervision of SK as major advisor. SR collected the data. Designing of experiment and analysis by SR, SK and SKD. All the authors provided critical feedback and helped in preparation of the manuscript.

References

1. Ali M, F Khan, S Subhanullah, W Ahmad, M Ishaq and M Saeed. 2018. Enhancing wheat productivity and soil physical properties of water eroded agricultural land through integrated nutrient management. *Soil and Environment,* **37**(1): 21-27.
2. Bharali A, KK Baruah, P Bhattacharyya and D Gorh. 2017. Integrated nutrient management in wheat grown in a northeast India soil: Impacts on soil organic carbon fractions in relation to grain yield. *Soil and Tillage Research,* **168**:81–91.
3. Darjee S, M Shrivastava, S Langyan, G Singh, R Pandey, A Sharma, A Khandewal and R Singh. 2022. Integrated nutrient management reduced the nutrient losses and increased crop yield in irrigated wheat. *Archives of Agronomy and Soil Science*, https://doi.org/10.1080/03650340.2022.2084535.
4. Guo L, G Wu, Y Li, C Li, W Liu, J Meng, H Liu, X Yu and G Jiang. 2016. Effects of cattle manure compost combined with chemical fertilizer on topsoil organic matter, bulk density and earthworm activity in a wheat-maize rotation system in eastern China. *Soil and Tillage Research,* **156**:140–47.
5. Jat ML, PC Chaplot, DD Bairwa, SN Meena and BC Dhayal. 2021. Effects of integrated nutrient management on yield and economics of barley (*Hordeum vulgare*). *Indian Journal of Agronomy,* **66** (4): 425-429.
6. Kakraliya SK, N Kumar, S Dahiya, S Kumar, DD Yadav and M Singh. 2017. Effect of integrated nutrient management on growth dynamics and productivity trend of wheat (*Triticum aestivum* L.) under irrigated cropping system. *Journal of Plant Development Sciences,* **9**(1): 11–15.
7. Kavinder, VS Hooda, YP Malik, Devraj, Harender and Kavita. 2019. Effect of Farm Yard Manure and Nitrogen Application on Growth and Productivity of Wheat under Long Term Experimental Conditions. *Current Journal of Applied Science and Technology,* **35** (4):1-7.
8. Kumar S, G Sandhu, SS Yadav, V Pandey, O Prakash, A Verma, SC Bhardwaj, R Chatrath and GP Singh. 2019. Agro-morphological and Molecular Assessment of Advanced Wheat Breeding Lines for Grain Yield, Quality and Rust Resistance. *Journal of Cereal Research* **11**(2): 131-139.
9. Kumari R, S Kumar, R Kumar, A Das, R Kumari, CD Choudhary and RP Sharma. 2017. Effect of long - term integrated nutrient management on crop yield, nutrition and soil fertility under rice-wheat system. *Journal of Applied and Natural Science,* **9**(3): 1801-1807.
10. Patra A, VK Sharma, DJ Nath, TJ Purakayastha, M Barman, S Kumar, KA Chobhe, A Dutta and AS Anil. 2022. Impact of long term integrated nutrient management (INM) practice on aluminium dynamics and nutritional quality of rice under acidic Inceptisol. *Archives of Agronomy and Soil Science*, **68**(1): 31-43.
11. Saha S, B Saha, M Ray, SK Mukhopadhyay, P Halder, A Das, S Chatterjee and M Pramanick. 2018. Integrated nutrient management (INM) on yield trends and sustainability, nutrient balance and soil fertility in a long-term (30 years) rice-wheat system in the Indo-Gangetic plains of India. *Journal of Plant Nutrition,* **41**(18): 2365-2375.

12. Sarwar N, Atique-ur-Rehman, O Farooq, A Wasaya, M Hussain, AM El-Shehawi, S Ahmad, M Brestic, SF Mahmoud, M Zivcak and S Farooq. 2021. Integrated nitrogen management improves productivity and economic returns of wheat-maize cropping system. *Journal of King Saud University – Science,* **33**(5): 101475.

13. Singh P and SP Saini. 2021. Micronutrients availability in soil–plant system as influenced by long-term integrated nutrient management under rice–wheat cropping. *Journal of Plant Nutrition,* **45** (3): 457-470.

14. USDA. 2022. United States Department of Agriculture Global Market Analysis, Circular Series. 27p.

15. Ullah A, A Nawaz, M Farooq and KHM Siddique. 2021. Agricultural Innovation and Sustainable Development: A Case Study of Rice–Wheat Cropping Systems in South Asia. *Sustainability*, **13** (4): 1965.

16. Yadav RL. 2003. Assessing on-farm efficiency and economics of fertilizer N, P and K in rice–wheat systems in India. *Field Crops Research,* **81**: 39–51.

Journal of Cereal Research
Volume 14 (2): 204-210
Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Short Communication

Effect of Tillage and Herbicides on Weeds and Yield of Maize (*Zea mays* L.)

Dinesh Choudhary[1], Rajender Singh Chhokar[1], Subhash Chander Gill[1], Shiv Ram Samota[1]*, Nitesh Kumar[1] and Girdhari Lal Yadav[2]

[1]ICAR-Indian Institute of Wheat & Barley Research, Karnal – 132001 (India)
[2]Department of Agronomy, MJRP, Jaipur

Article history: Received: 04 Apr., 2022 Revised: 19 Sept., 2022 Accepted: 07 Oct., 2022

Citation: Choudhary D, RS Chhokar, SC Gill, SR Samota, N Kumar and GL Yadav. 2022. Effect of Tillage and Herbicides on Weeds and Yield of Maize (Zea mays L.). *Journal of Cereal Research* ***14 (2):*** *204-210. http://doi.org/10.25174/2582-2675/2022/121970*

****Corresponding author:*** *E-mail: shivram10051995@gmail.com*

Maize (*Zea mays* L.) is an important widely adapted food, feed and industrial utilities crop. Although, numerous factors are responsible for limiting the productivity and production of maize crop but among them, weed infestation is major one. The wider row spacing and slow initial growth of maize crop make it more vulnerable to weed competition. Further, during *Kharif* season, frequent rains provide the conducive environment for emergence and growth of diverse weed flora comprising of grasses, broad-leaved and sedges leading to severe yield reductions. Yield reductions of as high as, 90% have been reported depending upon the type and intensity of weed flora (Massinga *et al.,* 2003). For achieving optimum maize yield, effective weed control measures are absolutely needed. Moreover, intensive tillage practices contribute greatly to high energy and labour costs, resulting in low economic returns. These issues can be tackled with adoption of resource conservation technologies (RCTs) such as zero tillage and conservation tillage (Sharma *et al.,* 2005). However, tillage and residue management can influence the weeds abundance because of change in microclimate. A very few studies have been done in respect of effect of different tillage and herbicide options for maize crop. Therefore, it is of immense importance to determine the influence of these changing agronomic practices on weed dynamics, so as to develop the efficient weed management strategies.

A field study consisting of three tillage options as main plot (Zero tillage, zero tillage + residue retention of 6 t ha^{-1}, conventional tillage) and six weed control treatments in sub-plots (Pre-emergence atrazine at 1000 g ha^{-1}, tembotrione at 110 g ha^{-1}, atrazine + tembotrione at 800 + 90 g ha^{-1}, atrazine + tembotrione +bentazone at 800 + 90 + 960 g ha^{-1}, atrazine + tembotrione + halosulfuron at 800 + 90 + 67.5 g ha^{-1} and weedy check) was conducted during *Kharif* 2019 at the Resource Management Research Farm, of ICAR-Indian Institute of Wheat and Barley Research (IIWBR), Karnal, Haryana. The soil was sandy loam in texture, slightly alkaline (pH 8.5, EC 0.12 dS m^{-1}), low in available N (173.4 kg/ha) and medium in available P_2O_5 (14.82 kg/ha) and K_2O (140.09 kg/ha). Maize hybrid S7750 was sown at 60 cm x 20 cm spacing using Turbo Happy Seeder at seed rate of 20-25 kg/ha. Except tillage and weed control treatments, all other agronomic practices such as fertilizer application, irrigation management and plant protection measures were taken as per standard recommendations. The observations on crop biomass, cob weight, grain yield and stover yield were taken. The data on weed density and dry matter were taken at 45 and 75 days after sowing (DAS) by using quadrate of size 50 cm × 50 cm at two places in each plot and then the observed values were multiplied by 2 to convert into per square metre. The data on weed density and dry matter accumulation of weeds were subjected to square root transformation {√(x+1)} before statistical analysis. Weed control efficiency (WCE) was calculated by subtracting dry weight of treatment plot from dry weight of weeds in unweeded control and by dividing it with dry weight of unweeded control. Differences among treatment means were determined using ANOVA and when the F test was significant, means were compared with LSD test at 5 per cent level of significance.

Effect on weeds

Results revealed that among grass weeds, the crop establishment methods significantly affected the dry weights of *Echinochloa colonum, Dactyloctenium aegypticum* and *Digitaria sanguinalis* (Table 1). The dry weights of these weeds were less with zero tillage + residue (ZT + R) treatment compared to two other crop establishment methods (CT and ZT). At 45 DAS, the dry weights of *E. colonum, D. aegypticum* and *D. sanguinalis* were 0.4, 27.6 and 2.5 g/m^2 in ZT, 0.7, 9.0 and 0.4 g/m^2 in ZT+R and 2.9, 21.9 and 11.3 g/m^2 in CT, respectively. Weed control treatments also had significant effect on all the major grass weeds. In comparison to untreated control, all the herbicide treatments caused significant reductions in dry weight of all the grass weeds at 45 DAS except atrazine for *D. aegypticum and D. sanguinalis* dry weights. All the three tank-mix herbicide treatments were at par among themselves. Between two solo herbicide treatments *i.e.,* atrazine and tembotrione, the latter was significantly superior for control of *D. aegypticum* and *Digitaria sanguinalis.* However, for control of *Echinochloa* spp. both the treatments were statistically similar. The significant effect of crop establishment methods was observed on dry weight of *Digera arvensis, Trianthema portulacastrum,* and *Cyperus rotundus.* In general, the lowest weed dry weights were found in ZT with residue retention. This conservation agriculture treatment was significantly superior to CT method for reducing the dry weight of *D. arvensis, T. portulacastrum* and *C. rotundus.* The dry weight of major broad-leaved weed, *T. portulacastrum* recorded under ZT, ZT+R and CT was 23.9, 5.2 and 14.2 g/m^2, respectively. Whereas, *C. rotundus* dry weight under ZT, ZT+R and CT were 17.2, 4.4 and 46.3 g/m^2, respectively. Also, in comparison to untreated control, the various herbicide treatments significantly reduced the dry weight of major broad-leaved weeds namely *D. arvensis, and T. portulacastrum* (Table 1). Application of atrazine alone at 1000 g ha^{-1} was very effective in controlling *D. arvensis.* Tembotrione alone at 110 g ha^{-1} was also effective in controlling *D. arvensis. D. arvensis* and *P. niruri* dry weight did not significantly differ among various herbicide treatments. *T. portulacastrum* and *C. rotundus* control with the tank-mix combinations was better than solo application of either atrazine or tembotrione. Application of atrazine + tembotrione + halosulfuron caused maximum reduction in dry weight of *C. rotundus* (6.3 g/m^2) and was significantly superior to all other weed control treatments. However, atrazine + tembotrione + bentazone (21.3 g/m^2) tank-mix treatment was statistically at par with the application of atrazine + tembotrione + halosulfuron tank mixture. The total weed dry weight was also significantly less with the treatment having ZT with residue retention of 6 t ha^{-1} compared to ZT and CT crop establishment method. The total weeds dry weight recorded under ZT, ZT+R and CT was 79.0, 29.5 and 146.1 g/m^2. The ZT without residue retention was also superior to CT in reducing the total weed dry weight. Among weed control treatments, all the herbicidal treatments significantly lowered the weed dry weight than weedy check treatment. However, the two and three herbicides tank mixture treatments were better than the alone application of either atrazine or tembotrione. Among three herbicides tank mixture treatments, the maximum reduction in weed dry weight was observed with the combination of atrazine + tembotrione + halosulfuron at 800 + 90 + 67.5 g ha^{-1}. The weed control efficiency at 45 DAS was the highest with application of tank mixture of atrazine + tembotrione + halosulfuron at 800 + 90 + 67.5 g ha^{-1} followed by atrazine + tembotrione at 800 + 90 g ha^{-1} and atrazine + tembotrione + bentazone at 800 + 90 + 960 g ha^{-1}. The effective weed control with application of atrazine (Sahoo *et al.,* 2016) and tembotrione (Rana *et al.,* 2017) in maize has also been earlier reported.

At 75 DAS also, ZT + R had lower grass weed dry weight except *Commelina benghalensis.* Statistically, it was significantly superior to CT in reducing the dry weight of *E. colona* and *D. sanguinalis*. Among grass weeds, *D. aegypticum* dry weight recorded in ZT, ZT+R and CT treatments was 9.1, 5.6 and 6.9 g/m^2, respectively. The dry weights of *D. sanguinalis* in ZT+R, ZT and CT were 2.1, 1.2 and 12.9 g/m^2, respectively (Table 2). Weed

Table 1. Effect of crop establishment methods and weed control treatments on weed dry weight in maize at 45 DAS

Treatment	*E. crus-galli*	*E. colonum*	*D. aegypticum*	*Digitaria sanguinalis*	Commelina benghalensis	*D. arvensis*	*T. portulacastrum*	*C. rotundus*	Other weeds	Total weeds	Weed control efficiency (%)
Tillage options											
Zero tillage (ZT)	1.5 (2.0)	1.1 (0.4)	3.8 (27.6)	1.6 (2.5)	1.6 (3.4)	1.6 (4.1)	4.7 (23.9)	4.0 (17.2)	1.5 (2.3)	7.6 (79.0)	6.6
Zero tillage (ZT) + residue 6 t ha^{-1}	1.1 (0.5)	1.2 (0.7)	2.5 (9.0)	1.1 (0.4)	1.7 (4.1)	1.2 (1.0)	2.1 (5.2)	2.1 (4.4)	1.5 (4.0)	4.4 (29.5)	6.7
Conventional tillage (CT)	1.4 (2.2)	1.5 (2.9)	3.0 (21.9)	2.8 (11.3)	1.6 (3.9)	2.4 (12.6)	3.5 (14.2)	6.5 (46.3)	4.3 (27.3)	11.2 (146.1)	6.9
LSD at 5%	NS	0.262	0.490	0.408	NS	0.607	1.750	1.143	NS	1.842	-
Weed control											
Atrazine at 1000 g ha^{-1}	1.1 (0.5)	1.3 (0.9)	7.0 (50.7)	3.1 (12.5)	1.0 (0.0)	1.0 (0.2)	3.1 (12.9)	5.4 (33.3)	2.8 (16.0)	10.3 (118.4)	5.6
Tembotrione at 110 g ha^{-1}	1.1 (0.3)	1.2 (0.5)	1.7 (2.9)	1.6 (3.0)	1.0 (0.1)	1.2 (0.6)	2.7 (8.2)	6.1 (43.9)	2.8 (13.1)	7.8 (68.2)	7.0
Atrazine + tembotrione at 800+90 g ha^{-1}	1.0 (0.0)	1.0 (0.0)	1.0 (0.1)	1.0 (0.0)	1.1 (0.5)	1.1 (0.3)	2.6 (7.1)	3.8 (18.7)	1.9 (6.9)	4.9 (32.1)	9.0
Atrazine + tembotrione + bentazone at 800+90+960 g ha^{-1}	1.1 (0.3)	1.0 (0.0)	1.0 (0.0)	1.0 (0.0)	1.0 (0.2)	1.0 (0.1)	3.3 (12.2)	3.2 (12.3)	1.7 (4.5)	4.4 (25.2)	9.9
Atrazine + tembotrione + halosulfuron at 800+90+67.5 g ha^{-1}	1.1 (0.2)	1.0 (0.1)	1.1 (0.3)	1.0 (0.0)	1.0 (0.0)	1.0 (0.0)	3.1 (10.4)	2.4 (6.3)	2.3 (12.1)	4.0 (22.6)	9.0
Weedy Check	2.8 (8.1)	2.4 (6.6)	7.7 (63.2)	3.3 (12.8)	4.7 (21.9)	5.2 (34.3)	5.8 (35.8)	4.2 (21.3)	3.2 (14.8)	15.0 (242.8)	0.0
LSD at 5%	0.355	0.366	0.703	0.496	0.42	0.682	0.926	0.839	NS	1.142	-

Data were subjected to square root transformation $(\sqrt{x+1})$ for statistical analysis and original values are in parentheses

Table 2. Effect of crop establishment methods and weed control treatments on weed dry weight in maize at 75 DAS

Treatment	*E. crus-galli*	*E. colonum*	*D. aegypticum*	*Digitaria sanguinalis*	*Commelina benghalensis*	*D. arvensis*	*T. portulacastrum*	*C. rotundus*	*Physalis minima*	Other weeds	Total weeds	Weed control efficiency (%)
Tillage options												
Zero tillage (ZT)	1.7 (3.0)	1.3 (1.2)	2.5 (9.1)	1.5 (2.1)	1.9 (8.1)	1.4 (2.3)	1.8 (2.8)	1.8 (2.9)	2.0 (7.5)	1.3 (1.8)	5.3 (40.8)	74.8
Zero tillage (ZT) + residue 6 t ha^{-1}	1.1 (0.6)	1.1 (0.4)	2.1 (5.6)	1.3 (1.2)	2.0 (6.8)	1.1 (0.7)	1.1 (0.5)	1.1 (0.5)	1.6 (3.6)	1.0 (0.2)	3.4 (20.0)	78.6
Conventional tillage (CT)	1.6 (3.5)	1.6 (3.3)	2.2 (6.9)	2.8 (12.9)	1.9 (7.5)	1.7 (4.6)	2.1 (4.9)	2.9 (9.2)	2.2 (8.4)	2.2 (6.2)	7.1 (67.4)	72.0
LSD at 5%	NS	0.353	0.302	0.342	NS	NS	NS	1.151	NS	NS	1.053	-
Weed control												
Atrazine at 1000 g ha^{-1}	1.1 (0.3)	1.37 (1.0)	4.5 (19.9)	3.6 (16.8)	1.0 (0.0)	1.0 (0.0)	1.3 (1.1)	2.03 (4.0)	1.1 (0.3)	1.5 (2.6)	6.6 (46.1)	73.4
Tembotrione at 110 g ha^{-1}	1.1 (0.5)	1.27 (0.9)	1.4 (1.5)	1.1 (0.5)	1.0 (0.2)	1.0 (0.0)	1.4 (1.4)	2.9 (10.8)	1.0 (0.2)	1.9 (4.3)	4.1 (20.3)	89.7
Atrazine + tembotrione at 800+90 g ha^{-1}	1.0 (0.0)	1.0 (0.0)	1.0 (0.1)	1.0 (0.2)	1.1 (0.5)	1.0 (0.0)	1.6 (2.3)	2.0 (4.6)	1.2 (0.6)	1.4 (2.2)	2.9 (10.5)	95.0
Atrazine + tembotrione + bentazone at 800+90+960 g ha^{-1}	1.1 (0.5)	1.0 (0.0)	1.0 (0.0)	1.0 (0.0)	1.1 (0.3)	1.0 (0.0)	1.7 (2.7)	1.4 (1.4)	1.2 (0.8)	1.3 (1.8)	2.6 (7.4)	96.3
Atrazine + tembotrione + halosulfuron at 800+90+67.5 g ha^{-1}	1.3 (0.9)	1.0 (0.0)	1.0 (0.1)	1.0 (0.0)	1.0 (0.0)	1.0 (0.0)	1.4 (1.3)	1.5 (1.5)	1.3 (1.0)	1.4 (1.9)	2.5 (6.7)	96.4
Weedy Check	3.3 (11.9)	2.6 (8.0)	4.6 (21.5)	3.4 (15.0)	6.5 (43.8)	3.7 (15.2)	2.5 (7.4)	1.7 (2.9)	5.8 (36.1)	1.7 (3.6)	12.6 (165.4)	0.0
LSD at 5%	0.457	0.406	0.489	0.559	0.588	0.386	0.613	0.609	0.685	NS	0.844	-

Data were subjected to square root transformation ($\sqrt{x+1}$) for statistical analysis and original values are in parentheses control treatments had significant effect on all the major grass weeds. In comparison to untreated control, all the herbicide treatments caused significant reductions in the dry weight of all the grass weeds except *D. aegypticum* and *D. sanguinalis* dry weight with atrazine application at 1000 g/ha. Tank mix combination of atrazine + tembotrione + bentazone or atrazine + tembotrione + halosulfuron caused complete kill of all the grass weeds except *E. crus-galli.* The significant effect of crop establishment methods was observed on *C. rotundus* dry weight. In general, the lowest weed dry weights were found in ZT with residue retention. The dry weight of *C. rotundus* recorded under ZT, ZT+R and CT were 2.9, 0.5 and 9.2 g/m^2, respectively. Also, the various herbicide treatments in comparison to untreated control significantly reduced the dry weights of four major broad-leaved weeds namely *D. arvensis, P. niruri, T portulacastrum,* and *P. minima* as well as sedge weed *C. rotundus*. Application of atrazine at 1000 g ha^{-1} was very effective in controlling *D. arvensis.* Tembotrione alone at 110 g ha^{-1} was also effective in controlling *D. arvensis and P. minima.* However, tank mix combination of atrazine + tembotrione was at par with three-way combinations of atrazine + tembotrione + bentazone 800 + 90 + 960 g ha^{-1} as well as atrazine + tembotrione + halosulfuron 800 + 90 + 67.5 g ha^{-1}. The tank mixture of atrazine + tembotrione + bentazone and atrazine + tembotrione + halosulfuron were significantly superior to other herbicide treatments in reducing the *C. rotundus* dry weight. The total weed dry weight at 75 DAS was also significantly less with the ZT +R treatment compared to ZT and CT crop establishment method. The total weeds dry weight recorded under ZT, ZT+R and CT was 40.8, 20.0 and 67.4 g/m^2. Zero tillage without residue retention was also superior to CT in reducing the total weed dry weight. Among weed control treatments, all the herbicidal treatments significantly reduced the weed dry weight over weedy check treatment. However, the two and three herbicides tank mixture treatments were better than the alone application of either atrazine or tembotrione. Among three herbicide tank mixture treatments, the maximum reduction in weed dry weight was observed with the combination of atrazine + tembotrione + halosulfuron at 800 + 90 + 67.5 g ha^{-1}. Among tillage practices, ZT+R recorded highest WCE (78.6 %) followed by ZT and CT. The weed control efficiency was the highest with application of tank mixture of atrazine + tembotrione + halosulfuron at 800 + 90 + 67.5 g ha^{-1} followed by atrazine + tembotrione + bentazone at 800 + 90 + 960 g ha^{-1} as compared to alone application of either atrazine or tembotrione. Our results showed the positive effect of straw mulch for controlling different weed species in maize as compared to no mulch treatment. Similarly, various research workers (Sarwar *et al.,* 2013; Shah *et al.,* 2014; Dutta *et al.,* 2016; Chhokar *et al.*, 2020) also observed that straw mulch recorded lesser weed infestation in comparison to no mulch.

Table 3: Effect of tillage options and weed control treatments on plant height, biomass, cob weight, grain yield, stover yield, net returns and B C ratio of maize.

Treatment	Biomass (q/ha)	Grains/ cob (no.)	Grain yield (q/ha)	Stover yield (q/ha)	Net returns (Rs ha^{-1})	B C ratio
Tillage options						
Zero tillage (ZT)	293.7	454	82.5	159.4	114341	2.4
Zero tillage (ZT) + residue 6 t ha^{-1}	311.5	471	85.3	173.7	119851	2.5
Conventional tillage (CT)	262.9	451	78.4	134.4	104086	2.1
LSD at 5%	16.5	15.33	3.5	12.7	6609	0.1
Weed control						
Atrazine at 1000 g ha^{-1}	287.2	448	79.6	153.9	110310	2.4
Tembotrione at 110 g ha^{-1}	297.9	470	82.7	160.2	113870	2.4
Atrazine + tembotrione at 800+90 g ha^{-1}	298.9	479	85.7	160.5	119453	2.5
Atrazine + tembotrione + bentazone at 800+90+960 g ha^{-1}	302.1	479	86.6	164.8	119824	2.4
Atrazine + tembotrione + halosulfuron at 800+90+67.5 g ha^{-1}	300.5	481	87.1	162.88	118954	2.3
Weedy Check	249.4	397	70.7	132.86	94143	2.1
LSD at 5%	10.05	12.83	3.60	8.09	6599	0.14

Effect on crop performance

The effect of tillage options and herbicide treatments on crop performance is shown in Table 3. Out of three tillage options, ZT + residue 6 t ha^{-1} recorded the maximum crop biomass (310.96 q/ha) and was followed by ZT (293.72 q/ha) and CT (262.93 q/ha). The crop grown using conventional tillage practice recorded minimum biomass. The differences were significant only between ZT+R and CT treatments and the crop biomass accumulated under ZT without residue was statistically at par with ZT with residue. This may be attributed to the fact that mulch helped in controlling the weeds and changed the microclimatic conditions near plant base leading to better growth of roots and more availability of nutrients leading to higher dry matter accumulation. Among weed control treatments, the maximum crop biomass (302.16 q/ha) was found in tank mix application of atrazine + tembotrione + bentazone at 800 + 90 + 960 g ha^{-1} and was followed by atrazine + tembotrione + halosulfuron at 800 + 90 + 67.5 g ha^{-1} with biomass accumulation of 300.58 q/ha. In comparison to untreated control (249.47 q/ha), all the herbicide treatments showed significant superiority in biomass accumulation. Among herbicide treatments, only application of atrazine 1000 g ha^{-1} registered significantly lesser biomass compared to rest of herbicide application treatments.

Among three tillage practices, significantly higher number of grains/cob observed in ZT + R. Better grains per cob recorded under ZT + R system compared to that of CT method might be due to fewer weed infestation as well as the better soil physio-chemical properties. Similarly, the improved maize yield with conservation tillage practices has been reported by various workers (Memon *et al.,* 2013). Among various weed control treatments, the highest number of grains/cob (481) were recorded with the application of atrazine + tembotrione + halosulfuron at 800 + 90 + 67.5 g ha^{-1}, which was found to be at par with all chemicals except atrazine at 1000 g ha^{-1}. The better yield attributes under herbicide treated plots were due to significant reduction in weed competition as evident from weed dry weights data leading to better growth and development of maize plants. Similar results were reported by Chhokar *et al.*, (2020).

The maximum (173.75 q/ha) and minimum (134.43 q/ha) stover yields were recorded with ZT + R and CT, respectively. Zero tillage with and without residue had significantly higher stover yield compared to CT. The maximum and minimum maize grain yields were also recorded with the ZT +R (85.32 q/ha) and CT (78.45 q/ha) treatment, respectively. The ZT with and without residue produced significantly more maize grain yield than produced with CT treatment. Statistically ZT+R and ZT were not different for the grain yield. Earlier researchers (Shah *et al.,* 2014; Dutta *et al.*, 2016) also reported higher grain and stover yield in mulch treatments as compared to no mulch.

Among various weed control treatments, untreated weedy check produced the lowest stover yield (132.86 q ha^{-1}) and it was significantly inferior to all the herbicide treatments. The application of tank mix combination of atrazine + tembotrione + bentazone 800 + 90 + 960 g ha^{-1} resulted in the highest stover yield of 164.89 q ha^{-1} followed by 162.88 q/ha obtained with application of atrazine + tembotrione + halosulfuron at 800 + 90 + 67.5 g ha^{-1}. Weedy check treatment recorded significantly the lowest grain yield of 70.73 q ha^{-1} and it was due to higher weed infestation. Walia *et al.* (2005) also observed significant reduction in grain yield of maize due to weed competition. While, Rana *et al.* (2017) also found significant increase in grain yield with application of tembotrione. Among herbicide treatments, tank mix combinations treatments *i.e.* atrazine + tembotrione, atrazine + tembotrione + bentazone and atrazine + tembotrione + halosulfuron were statistically at par among themselves but significantly better to standard treatment of atrazine alone application. The three groups of herbicide combinations were significantly better yielder compared to alone application of either atrazine or tembotrione. Higher grain yield in these treatment combinations could be attributed to drastic decrease in weed population and dry matter accumulation by weeds, thereby better crop growth and yield attributes. These findings were in accordance with the findings of Swetha *et al.* (2015), Sarwar *et al.* (2013) and Chhokar *et al.* (2019).

Economics

Net returns and benefit cost ratio differed significantly due to different tillage and weed control treatments (Table 3). Among tillage options, zero tillage with residue recorded the maximum net returns (RS 119851). The highest B C ratio was obtained with ZT+R (2.57) followed by ZT (2.47). The CT had the lowest net returns and benefit cost ratio. The higher net returns under ZT+R mulch treatment was attributed to higher grain and stover yield as well as lower cost of cultivation compared to CT system. Shah *et al.* (2014) also reported that straw mulch treatments recorded significantly higher net returns than no mulch treatment. Thus, improved profitability was recorded with the adoption of no-till system.

Among the weed control treatments, maximum net returns (Rs 119824/ha) and benefit cost ratio (2.53) were under atrazine + tembotrione + bentazone and atrazine + tembotrione, treatments, respectively. The higher net return under these weed control treatments was attributed to better weed control efficiency and higher grain and stover yield of maize as compared to unweeded check. Rana *et al.* (2017) also reported that maximum benefit cost ratio was obtained with application of tembotrione.

Based on this study, it can be concluded that for achieving effective weed control, and higher maize yield and profitability, combinations of conservation tillage (zero tillage + 6 t ha^{-1} residue) with tank mixture of either atrazine + tembotrione + halosulfuron at 800 + 90 + 67.5 g ha^{-1} or atrazine + tembotrione + bentazone at 900 + 90 + 960 g ha^{-1} as post-emergence can be adopted.

Acknowledgement

Authors are highly thankful to the support and facilities provided by the Director ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India during the conduct of this research.

Author's contribution

Conceptualization of research (DC and RSC); Designing of the experiments (DC, RSC and SRS); Contribution of experimental materials (RSC, SCG and NK); Execution of field/lab experiments and data collection (DC, SRS and GLY); Analysis of data and interpretation (RSC and SCG); Preparation of the manuscript (DC, RSC and SRS).

Conflicts of Interest

The authors declare no conflict of interest.

References

1. Chhokar RS, RK Sharma, SC Gill and GP Singh. (2020). Tank-mix application of p-hydroxyphenylpyruvate dioxygenase (HPPD) inhibiting herbicide (mesotrione, tembotrione or topramezone) with atrazine improves weed control in maize (*Zea mays* L.). *Journal of Research in Weed Science*, 3 (4): 556-581.
2. Chhokar RS, RK Sharma, SC Gill and RK Singh. (2019). Mesotrione and atrazine combination to control diverse weed flora in maize. *Indian Journal of Weed Science*, 51 (2): 145-150.
3. Dutta D, TL Thentu and D Duttamudi. (2016). Effect of weed-management practices on weed flora, soil micro-flora and yield of baby corn (*Zea mays*). *Indian Journal of Agronomy*, 61 (2): 210-216.
4. Massinga RA, RS Currie and TP Trooien. (2003). Water use and light interception under Palmer amaranth (*Amaranthus palmeri*) and corn competition. *Weed Science*, 51 (4): 523-531.
5. Memon SQ, MS Mirjat, AQ Mughal, N Amjad, and KA Ibupoto. (2013). Comparison of energy and yield parameters in maize crop. *Fuel (Diesel)*, 50: 47-8.
6. Rana SS, D Badiyala, N Sharma, R Kumar and P Pathania. (2017). Impact of tembotrione on weed growth, yield and economics of maize (*Zea mays L.)* under mid hill conditions of Himachal Pradesh. *Pesticide Research Journal*, 29 (1): 27-34.
7. Sahoo TR, MK Lal, UK Hulihalli and RK Paikaray. (2016). Effect of sequential application of herbicides on microbial activities and yield of maize. *Research on Crops*, 17 (4): 685-690.
8. Sarwar MA, N Akbar, HMR Javeed, MA Shehzad, A Mehmood and HT Abbas. (2013). Response of zero tilled wheat crop to different mulching techniques in a semiarid environment. *International Journal of Advanced Research*, 1 (9): 768-776.
9. Shah FU, GM Sajid and SU Siddiqui. (2014). Evaluation of mulching materials as integrated weed management component in maize crop. *Pakistan Journal of Agricultural Research*, 27 (2): 118-128.
10. Sharma AR, R Singh and SK Dhyani. (2005). Conservation tillage and mulching for optimizing productivity in maize-wheat cropping system in the outer western Himalayan region–a review. *Indian Journal of Soil Conservation*, 33 (1): 35-41.
11. Swetha K, M Madhavi, G Pratibha and T Ramprakash. (2015). Weed management with new generation herbicides in maize. *Indian Journal of Weed Science*, 47 (4): 432-433.
12. Walia US, LS Brar and B Singh. (2005). Recommendations for weed control in field crops. *Research Bulletin, Department of Agronomy, Agrometerology and Forestry, PAU Ludhiana*. pp. 5.

Journal of Cereal Research

Volume 14 (2): 211-214

Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Short Communication

Performance of pearl millet (*Pennisetum glaucum* L.) as affected by weed control measures

Shiv Ram Samota, Shish Pal Singh and Hansraj Shivran

College of Agriculture, Swami Keshwanand Rajasthan Agricultural University, Bikaner 334006

Article history: Received: 17 Aug., 2022 Revised: 04 Sept., 2022 Accepted: 11 Sept., 2022

Citation: Samota SR, SP Singh and H Shivran. 2022. Performance of pearl millet (*Pennisetum glaucum* L.) as affected by weed control measures. *Journal of Cereal Research* ***14 (2):*** *211-214. http://doi.org/10.25174/2582-2675/2022/121969*

****Corresponding author:*** *shivram10051995@gmail.com*

Pearl millet (*Pennisetum glaucum* L.) is an important nutritious millet crop of India. Its nutritious grain forms the important component of human diet and stover forms the principal maintenance ration for ruminant livestock during the dry season. It is a drought tolerant cereal having the maximum potentiality of grain production in adverse climatic conditions (Acharya *et al*., 2017). As pearl millet is grown predominantly in warm rainy season, heavy infestation of weeds deprives the crop of vital nutrients, moisture, light and space leading to heavy reduction in grain yield. Yield reduction to the tune of 55 per cent has been recorded in pearl millet due to heavy weed infestation (Banga *et al.,* 2000). Whereas, Das and Yaduraju (1995) have reported 72 per cent yield loss in pearl millet due to heavy weed infestation. The field should be kept free from weeds at least for the first 25-30 days after sowing (DAS). The predominant methods of weed management are inter-culturing and hand weeding in pearl millet. The use of herbicides has revolutionized weed management and reduces the cost of cultivation. Among herbicides, atrazine as pre-emergence is a broad-spectrum widely used herbicide in pearl millet. Chhokar *et al.,* 2021 have reported the better efficacy of atrazine applied as post emergence compared to pre-emergence. There is a need to evaluate the efficacy of atrazine under both pre- and post- emergence applications in pearl millet also. Keeping these in views under consideration both pre- and post-emergence applications of atrazine were evaluated to find out the best option for weed management. Experiment was laid out in Randomised Block Design with three replications having twelve treatments *viz*., weedy check, weed free, two hand hoeing at 20 and 40 DAS, two hand wheel hoeing at 20 and 40 DAS, atrazine 0.125 kg/ha pre-emergence (PE), atrazine 0.250 kg/ha (PE), atrazine 0.500 kg/ha (PE), atrazine 0.100 kg/ha post-emergence (PoE) at 20 DAS, atrazine 0.200 kg/ha (PoE) at 20 DAS, atrazine 0.300 kg/ha (PoE) at 20 DAS, 2,4-D 0.300 kg/ha (PoE) at 30 DAS and 2,4-D 0.500 kg/ha (PoE) at 30 DAS. Soil of the experimental field was loamy sand with alkaline in nature and low in organic carbon (0.08 %) and available N (78 kg/ha) and medium in available P_2O_5 (22 kg/ha) and available K_2O (210 kg/ha). Pearl millet variety "HHB- 67" was sown at 45 cm x 15 cm row to row and plant to plant spacing using seed rate of 4 kg/ha. All other agronomic practices were adopted as per recommendation. Observations were recorded on plant height, plant dry weight and number of tillers, chlorophyll content (Arnon, 1949). After threshing, winnowing and cleaning, the produce of each net plot was weighed and expressed in grain yield as kg ha^{-1}. Nitrogen (Snell and Snell, 1959) and Phosphorus (Jackson, 1973) content in grain and straw of pearl millet was also estimated. The total N and P uptake was computed from N and P concentration in grain as well as stover multiplying by their corresponding yield (q/ha.).

The effect of various weed control treatments on crop growth and weeds are given in Table 1 and 2. The maximum plant height of pearl millet was recorded under weed free treatment which was statistically at par with all other weed control treatments except weedy check. All the weed control treatments significantly increased dry matter accumulation at harvest compared to weedy check (888.6 g/m^2).

Table 1. Effect of weed control on growth, chlorophyll, yield attributes and grain yield of pearl millet

Treatment	Plant height (cm) at harvest	Dry matter accumulation (g m^{-2}) at harvest	Chlorophyll content (mg g^{-1}) at 50 DAS	Effective no. of tillers plant^{-1}	Length of ear head (cm)	Grain weight ear head^{-1} (g)	Grain yield (kg ha^{-1})
Weedy check	152.3	888.6	2.83	1.41	23.7	8.29	1313
Weed free	185.3	1505.7	3.06	2.97	28.5	10.61	2480
Two hand hoeing 20 and 40 DAS	175.7	1342.8	3.08	2.49	27.0	9.53	2333
Two hand wheel hoeing 20 and 40 DAS	172.3	1303.3	2.94	2.32	26.7	9.89	2283
Atrazine 0.125 kg ha^{-1} (PE)	171.9	1160.1	2.88	2.08	25.5	9.89	1973
Atrazine 0.250 kg ha^{-1} (PE)	178.1	1248.9	2.92	2.09	25.8	9.81	2027
Atrazine 0.500 kg ha^{-1} (PE)	181.7	1451.4	2.99	2.80	27.2	8.63	2420
Atrazine 0.100 kg ha^{-1} (PoE) At 20 DAS	171.3	1145.3	2.93	2.06	25.4	9.88	1960
Atrazine 0.200 kg ha^{-1} (PoE) At 20 DAS	174.7	1219.3	3.03	2.19	25.8	10.10	2180
Atrazine 0.300 kg ha^{-1} (PoE) At 20 DAS	170.4	1273.7	3.06	2.40	25.9	9.16	2150
2,4-D 0.300 kg ha^{-1}(PoE) at 30 DAS	173.3	1293.4	3.68	2.60	26.7	8.74	2210
2,4-D 0.500 kg ha^{-1}(PoE) at 30 DAS	179.0	1362.5	3.74	2.90	27.2	8.32	2387
CD (P=0.05)	16.59	197.2	0.34	0.46	2.30	1.67	414

The highest plant dry matter (1505.7 g/m^2) was recorded under weed free treatment which was found statistically similar with two hand hoeing, atrazine 0.500 kg ha^{-1} PE, 2,4-D 0.500 kg ha^{-1}. These treatments were responsible for the considerable reduction in weed population and fresh weight of weeds. It further enhanced the availability of resources to the crop rather than to the weeds (Sharma and Jain, 2003). Two hand hoeing and two hand wheel hoeing treatments also increased yield due more growth of roots and increase aeration in soil causing higher uptake of nutrients by crop as suggested by Singh *et al.* (2006). Chlorophyll content in leaves was significantly influenced due to different weed control treatments. The treatment 2,4-D 0.500 kg ha^{-1} recorded the maximum chlorophyll content (3.74 mg g^{-1}) which was significantly higher over weedy check (2.83 mg g^{-1}). The data further indicated the increase in chlorophyll content due to weed free treatment, 2,4-D 0.300 and 0.500 kg ha^{-1} was 8.1, 30.0 and 32.2 per cent, respectively, over weedy check. Maximum grain, straw and biological yield was recorded under weed free being at par with atrazine 0.5 kg ha^{-1} PE followed by 2,4-D 0.500 kg ha^{-1}, 2,4-D 0.300 kg ha^{-1} and atrazine 0.200

Table 2. Effect of weed control on nutrient uptake by crop and nutrient removal by weeds and weed index

Treatment	**Total nutrient uptake by crop (kg ha^{-1})**		**Total nutrient removal by weeds (kg ha^{-1})**		**WI (%)**
	N (kg ha^{-1})	**P (kg ha^{-1})**	**N (kg ha^{-1})**	**P (kg ha^{-1})**	
Weedy check	46.20	10.28	88.83	1.71	88.8
Weed free	96.62	22.56	0.00	0.00	0.0
Two hand hoeing 20 and 40 DAS	88.65	19.79	6.29	0.11	6.3
Two hand wheel hoeing 20 and 40 DAS	80.17	17.60	8.61	0.14	8.6
Atrazine 0.125 kg ha^{-1} (PE)	74.50	16.48	25.68	0.33	25.7
Atrazine 0.250 kg ha^{-1} (PE)	75.17	17.59	22.37	0.37	22.4
Atrazine 0.500 kg ha^{-1} (PE)	93.49	21.03	2.48	0.10	2.5
Atrazine 0.100 kg ha^{-1} (PoE) At 20 DAS	74.17	15.84	26.53	0.21	26.5
Atrazine 0.200 kg ha^{-1} (PoE) At 20 DAS	79.15	18.16	13.76	0.17	13.86
Atrazine 0.300 kg ha^{-1} (PoE) At 20 DAS	81.14	19.45	15.35	0.16	15.4
2,4-D 0.300 kg ha^{-1}(PoE) at 30 DAS	89.88	18.06	12.22	0.63	12.2
2,4-D 0.500 kg ha^{-1}(PoE) at 30 DAS	96.36	18.15	3.91	0.46	3.9
CD (P=0.05)	17.26	4.85	1.01	0.22	-

kg ha^{-1} PoE. It might be due to reduction in weed density and dry weight, which allocated the available resources to the crop. These enhanced the yield attributes which further contributed in enhancement of the grain yield. Maximum yield in 2,4-D treated plot might be due to enhancement of chlorophyll content, growth, dry matter and reduced the weed competition to crop. The results so obtained for straw corroborate with the finding of Suryavanshi *et al.* (2012) and Pathak *et al.* (2015). The yield attributing characters *viz.* effective tillers plant^{-1}, length of ear head (cm) and grain weight ear head^{-1} were significantly improved under various weed control treatments as compared to weedy check and the effect was more pronounced with weed free closely followed by atrazine @ 0.500 kg ha^{-1} PE and 2,4-D @ 0.500 kg ha^{-1}. This was attributed to minimum infestation of weeds together with lesser competition for growth promoting resources. Thus, reduced crop-weed competition resulted into overall improvement in crop growth as reflected by plant height and dry weight consequently resulted into better development of reproductive structure and translocation of photosynthates into the sink. The results corroborated with the findings of Kaur and Singh (2006) and Rao *et al.* (2009). The maximum ear head length (28.5 cm) was observed under the weed free treatment which was statistically at par with two hand hoeing, two hand wheel hoeing, atrazine 0.500 kg ha^{-1} PE, 2,4-D 0.300 and 0.500 kg ha^{-1}. The maximum grain weight ear head^{-1} (10.61 gm) was observed under the weed free treatment which was statistically at par with two hand hoeing, two hand wheel hoeing, atrazine 0.500 kg ha^{-1} PE, 2,4-D 0.300 and 0.500 kg ha^{-1}. All the weed control treatments exerted significant influence on grain yield. The maximum grain yield was observed under the atrazine 0.500 kg ha^{-1} PE (2420 kg ha^{-1}) treatment which was statistically at par with two hand hoeing, two hand wheel hoeing, atrazine 0.250 kg ha^{-1} PE, atrazine 0.200 kg ha^{-1} PoE, atrazine 0.300 kg ha^{-1} PoE, 2,4-D 0.300 and 0.500 kg ha^{-1}. Atrazine 0.500 kg ha^{-1} PE, 2,4-D 0.300 and 0.500 kg ha^{-1} increased the grain yield to the extent of 84.3, 81.8 and 68.3 per cent, respectively over weedy check.

The results showed that weed control measures effectively reduced crop-weed competition for nutrient uptake. All weed control treatments significantly increased N and P uptake by grain and stover of pearl millet over weedy check. Weed free treatment resulted in significantly highest total uptake of N (96.62 kg ha^{-1}) and P (22.56) followed by atrazine 0.500 kg ha^{-1} having N (93.49 kg ha^{-1}) and P (21.03). All weed control treatments significantly reduced nitrogen and phosphorus uptake by the weeds compared to weedy check. It might be due to lesser weed competition in these treatments which enhanced the availability of the nutrients *viz*., N & P to the main crop. Among herbicide treatments, the lowest N and P uptake by weeds was recorded under application of atrazine 0.500 kg ha^{-1} and it was followed by 2,4-D 0.500 kg ha^{-1}.

The lowest and highest weed index was recorded under weed free (0%) and weedy check (88.8 %), respectively as given in Table 2. Among the herbicides, the lowest weed index of (2.5 %) was recorded with application of atrazine 0.500 kg ha^{-1} PE followed by 2,4-D 0.500 kg ha^{-1} (3.9 %), two hand hoeing (6.39 %) and two hand wheel hoeing (8.6 %).

Based on this study it can be concluded that atrazine 0.500 kg ha^{-1} applied as PE was superior in reducing the weed infestation and improving the crop growth, and grain yield of pearl millet. The second best option was application of 2,4-D 0.500 kg ha^{-1}. Therefore, under the scarcity of manual labour, these herbicide options can be used for weed control in pear millet.

Acknowledgement

Authors are thankful to the Professor and Head, Department of Agronomy, SK Rajasthan Agricultural University, Bikaner, Rajasthan, India for providing necessary facilities.

Author's contribution

Conceptualization of research (SRS); Designing of the experiments (SRS, SPS and HS); Contribution of experimental materials (SRS, SPS and HS); Execution of field/lab experiments and data collection (SRS, SPS and HS); Analysis of data and interpretation (SRS, SPS and HS); Preparation of the manuscript (SRS, SPS and HS).

Declaration

The authors declare no conflict of interest.

References

1. Acharya ZR, MD Khanapara, VB Chaudhari and DD Jalpa. 2017. Exploitation of heterosis in pearl millet [*Pennisetum glaucum* (L.) R. Br.] for yield and its component traits by using male sterile line. *International Journal of Current Microbiology and Applied Sciences* **6**(12): 750-759.
2. Arnon DI. 1949. Copper enzymes in isolated chloroplasts, polyphenoxidase in beta vulgaris. *Plant Physiology* **24**: 1-15.
3. Banga RS, A Yadav, RK Malik, SK Pahwa and RS Malik. 2000. Evaluation of tank mixture of acetachlor and atrazine or 2,4-D-Na against weeds in pearl millet. *Indian Journal of Weed Science* **32**: 194-198.
4. Chhokar, RS, RK Sharma, SC Gill and GP Singh. 2021. Tank-mix application of p-hydroxyphenylpyruvate dioxygenase (HPPD) inhibiting herbicide (mesotrione, tembotrione or topramezone) with atrazine improves weed control in maize (*Zea mays* L.). *Journal of Research in Weed Science* ***3***(4):556-581.
5. Das TK and NT Yaduraju. 1995. Crop weed competition studies in some *kharif* crops: nutrient uptake and yield reduction. *Annals of Plant Protection Sciences* **3**(2): 95-99.
6. Jackson ML 1973. Soil Chemical Analysis, Prentice Hall, Pvt. Ltd. New Delhi, 239-241.
7. Kaur A and VP Singh. 2006. Weed dynamics as influenced by planting methods, mulching and weed control in rainfed hybrid pearl millet [*Pennisetum glaucum* L.]. *Indian Journal of Weed Science* **38**(1&2): 135- 136.
8. Pathak PK, S Singh, RS Rinwa and S Singh. 2015. Efficacy of different weed control methods in spring planted maize. *Haryana Journal of Agronomy* **31** (1&2): 92-97.
9. Rao AS, M Ratnam and TY Reddy. 2009. Weed management in zero-till sown maize. *Indian Journal of Weed Science* **41**(1-2): 46-49.
10. Sharma OL and NK Jain. 2003. Integrated weed management in pearl millet. *Indian Journal of Weed Science* **35**(1 &2): 134-135.
11. Singh RV, MK Kaushik and HR Singh. 2006. Integrated weed management in pearl millet under rainfed conditions of *NWPZ of U.P. Crop Research* **32**(1): 18-20.
12. Snell FD, CT Snell and CA Snell. 1959. *Colorimetric Methods of Analysis. Vol 2A: Organic-II.* D Van Nostrand Company.
13. Suryavanshi M, BS Kadam, DM Veer, US Kudtarkar, SM More and BG Gaikawad. 2012. Influence of weed management practices on cane yield, quality and weed density of ratoon sugarcane. *In:* Proceedings of the Biennial Conference on Weed Threat to Agriculture, Biodiversity and Environment pp. 108.

Journal of Cereal Research
Volume 14 (2): 215-218
Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Short Communication

Identification of promising sources of barley (*Hordeum vulgare* L) for malt beta-glucanase activity and wort beta-glucan content

Dinesh Kumar*, Ramesh Pal Singh Verma, Lokendra Kumar, Vishnu Kumar and Gyanendra Pratap Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal – 132 001, India

Article history: Received: 26 July, 2022 Revised: 28 Aug., 2022 Accepted: 04 Sep., 2022

Citation: Kumar D, RPS Verma, L Kumar, V Kumar and GP Singh. 2022. Identification of promising sources of barley (*Hordeum vulgare* L) for malt beta-glucanase activity and wort beta-glucan content. *Journal of Cereal Research* ***14 (2):*** *215-218.* *http://doi.org/ 10.25174/2582-2675/2022/121749*

****Corresponding author:*** *dinesh.kumar3@icar.gov.in*

Keywords: Barley, malt, wort, beta glucanase, beta glucans

Malt is one of the major industrial products from barley, which is further utilized mainly for beer production. The malt producing industry requires certain minimum quality parameters in the barley to get higher recovery and better quality (Kumar *et al.,* 2013). India is one of the emerging markets for barley malt consumption for brewing and nutraceuticals and thus needs malting varieties meeting the international standards. However, the shorter grain filling period in sub-tropical plains of India as compared to the temperate European climates is a major challenge to get the best quality under Indian conditions. Since most of the parameters are governed by genotype, growing environment and cultural practices, but its most important to breed malting barley genotypes with superior quality under Indian climatic conditions (Kumar *et al.*, 2017). Several genotypes have been bred in India with better quality, higher grain yield and disease resistance (Kumar *et al.*, 2014). Improvement being a continuous process, currently one of the major objectives of the Indian malt barley improvement programme is to breed genotypes with lower wort beta glucans. The higher beta glucans content in grain reduces water uptake during steeping; while in wort it adversely affects filtration rate and quality of malt extract. The ideal malt barley variety should have lower grain beta glucans coupled with higher malt beta glucanase activity, to get lower values of wort beta glucans. Malt beta glucanase is the major enzyme which breaks down beta glucans in endosperm cell walls and its higher activity is always desirable. This study was carried out to identify the potential sources of higher malt beta glucanase and lower wort beta glucans in barley genotypes.

A total of nine genotypes were grown in rabi season (mid-November to mid-April) at Karnal, Hisar, Ludhiana, Pantnagar, Durgapura and Kanpur during 2020-21 with plot size of 2.5 x 0.46 m^2 (two rows of 2.5 m each). The crop was fertilized with 60 kg N (in 2 split); 30 kg P and 30 kg K. The grain samples from each location were received and stored in air tight bags at -20°C till further analysis.

The bold/plump grains (grains retained on 2.5 mm screen of Sortimat, the EBC approved grain uniformity analyser from Pfeuffer Germany) were taken for malting purpose. The malt was prepared in an automatic micro-malting system (Joe White Australia) following the below steeping, germination and kilning schedule.

1. Steeping: 8 hours dip in water (temperature 25°C) with continuous aeration, followed by 16 hours air rest (temperature 18°C) and again 6 hours dip in water (temperature 18°C) with continuous aeration
2. Germination: 24 hrs at 18°C→18 hrs at 17°C

3. Kilning: 2 hrs at 30°C→ 2 hrs at 45°C→2 hrs at 50°C→1 hr at 55°C→1 hr at 60°C→16 hr at 65°C →1 hr at 70°C →1 hr at 75°C →1 hr at 80°C

The malt was taken out from machine after cooling to room temperature and rootlets removed by gentle hand rubbing. The malt samples were then stored in air tight interlocking plastic bags at -20°C till further analysis. The malt was grounded by an EBC approved Buhler's laboratory Mill at fine grinding setting and powdered malt flour was extracted in IEC make (Australia) mashing bath for 45°C for 30 minutes and then at 70°C for 90 minutes, making a total duration of 120 minutes. The resulting slurry was filtered through Whatman 2555 ½ filter papers and wort was collected and stored at -20°C till further analysis. Beta glucanase activity in the malt was estimated using Megazyme Assay Kit (Megazyme Ireland Ltd.) following the method of McCleary and Shameer (1987). Mixed linkage (1→3; 1→4)-β-D-glucans in grain and wort was measured using Megazyme Assay Kit (Megazyme Ireland Ltd.) following the method of McCleary and Nurthen (1986). The data was analysed with CropStat 7.2.

The higher levels of beta glucans in barley grain may lead to poor modification of the grain as incomplete degradation of endosperm cell wall may hinder the diffusion of enzymes required for degradation of kernel reserves (Habschied *et al.,* 2020). Therefore, barley genotypes with lower grain beta glucans are considered ideal to get better malt extract values. Besides the beta glucans content in the grain, the activity of beta glucanase, which usually develops during grain germination, should be high, to further reduce the wort beta glucan content. (Habschied *et al.*, 2020). For breeding improved malt barley varieties, sources of these traits need to be identified. In this preliminary investigation, the genotype ICARDA-11 (382 U/kg malt); ICARDA-9 (379 U/kg malt) and DWRB 197 (374 U/kg malt) have been found to have higher beta glucanase activity (Table 1). Wang *et al.* (2004) reported a range of 313 to 490 U/kg of malt beta glucanase activity and suggested that besides selecting for lower beta glucans genotypes, it's also important to have material with higher malt beta glucanase activity. In our study average values for beta glucanase were close to 400U/kg in the genotypes ICARDA-9 and ICARDA-11, and at Durgapura it was well above 450 for these two genotypes. Han *et al.* (1995) reported genes Glb1 and Glb2 on chromosome 1H and 7H, are encoding for (1,3;1,4)-β-glucanases.

Table 1: Activity of Beta-Glucanase (Units/kg) in malt of different barley genotypes

Genotype	Karnal	Hisar	Ludhiana	Durgapura	Pantnagar	Kanpur	Average
ICARDA-5	198	241	187	229	287	226	**228**
ICARDA-9	384	316	318	492	415	346	**379**
ICARDA-11	380	360	382	487	369	315	382
BK 306	345	315	390	333	337	238	**326**
DWRB 197	386	354	350	373	429	354	**374**
DWRUB 52 (c)	260	279	309	308	239	280	**279**
DWRB 101 (c)	175	186	197	263	256	140	**203**
DWRB-182 (c)	167	264	257	299	240	167	232
DWR 37 ©	195	223	208	269	272	272	**240**
Average	**277**	**282**	**289**	**339**	**316**	**260**	
LSD 5%							46

The higher values of beta-glucan may lead to poor lautering performance and affect the colloidal stability of the beer. For brewers, the total β-glucan content in wort should be less than 200 ppm (Davis 2006), while there are no specific limits for beta glucan in malt, as they consider it in the final product to be used for brewing. In this study, we recorded two genotypes i.e., ICARDA-9 (153 ppm) and ICARDA-11 (117 ppm), with average values well below 200 ppm in the wort (Table 2). The genotype ICARDA-11 was more consistent as it scored less than 200 ppm at all the locations. It becomes more important as the genotype is six row type (Table 2). Genotypes BK 306 and ICARDA 5 recorded average wort beta glucan values very close to 200 ppm, but the former had higher beta glucanase activity bringing down wort beta glucan from more higher grain beta glucan, while the second has poor beta glucanase activity, though it has lowest grain beta glucan. Similarly, DWRB 197 had wort beta glucans value of 347 ppm (close or lower than the checks), but has clearly depicted the role of higher beta glucanase activity in degradation of grain beta glucans, which was highest in grain (Table 3). This study has further verified the earlier reported trait of this genotype (Kumar *et al.* 2020) and identified clearly contrasting genotypes for beta glucan contents and beta glucanase activity.

Table 2: Wort Beta-Glucan content (ppm) in different barley genotypes

Genotype	Karnal	Hisar	Ludhiana	Durgapura	Pantnagar	Kanpur	Average
ICARDA-5	382	178	275	344	78	166	**237**
ICARDA-9	327	139	277	93	33	50	**153**
ICARDA-11	198	92	167	101	39	107	**117**
BK 306	423	169	228	79	142	171	**202**
DWRB 197	737	288	392	350	194	120	**347**
DWRUB 52 (c)	552	397	404	392	261	280	**381**
DWRB 101 (c)	471	370	602	447	232	176	**383**
DWRB-182 (c)	368	325	432	441	234	321	**353**
DWR 37 ©	683	856	633	462	269	239	**524**
Average	460	313	379	301	165	181	
LSD 5%							115

Table 3: Grain Beta Glucan content (% dwb) in different barley genotypes

Genotype	Karnal	Hisar	Ludhiana	Durgapura	Pantnagar	Kanpur	Average
ICARDA-5	3.9	3.6	4.3	4.1	3.3	3.8	**3.8**
ICARDA-9	3.0	3.7	4.2	4.3	3.7	4.4	**3.9**
ICARDA-11	4.4	4.3	4.1	4.2	4.0	4.1	**4.2**
BK 306	4.3	3.8	4.4	4.7	4.5	4.5	**4.4**
DWRB 197	6.4	6.3	6.6	6.4	6.5	5.9	**6.4**
DWRUB 52 (c)	4.2	5.4	4.4	5.2	5.1	5.3	**4.9**
DWRB 101 (c)	4.4	5.4	5.9	5.0	5.1	5.0	**5.1**
DWRB-182 (c)	4.2	4.2	4.4	4.7	4.0	4.0	**4.3**
DWR 37 ©	4.4	4.8	4.8	5.0	5.4	4.8	**4.9**
Average	4.4	4.6	4.8	4.8	4.6	4.6	
LSD 5%							0.4

Table 4: Parentage of test genotypes

Genotype	Parentage	Row type
ICARDA-5	LEGACY/4/TOCTE//GOB/HUMAI10/3/ATAH92/ALELI/5/ARUPO/K8755// MORA (ICARDA PYT-15-41)	2
ICARDA-9	J09049 F3 10/030552 (ICARDA PYT 15-93)	2
ICARDA-11	SEN/5/LEGACY/4/TOCTE//GOB/HUMAI10/3/ATAH92/ALELI (ICARDA PYT-15-50)	6
BK 306	BK9811 / DL472 (F5 -50)	2
DWRB 197	DWRUB52/DWR84	2

Conclusion

The genotypes ICARDA-11, ICARDA-9 and DWRB 197 have been found to have higher malt beta glucanase activity and ICARDA-11 and ICARDA-9 with lowest wort beta glucans content. These genotypes may serve as potential sources of these traits in Indian malt barley improvement programme towards bringing down the wort beta glucan content as well as for further biochemical and molecular studies on basic aspects of malt quality under sub-tropical climates.

Conflict of Interest

Authors declare that they have no conflict of interest

Ethical Compliance Statement

NA

Author's Contribution

Dinesh Kumar (Conceptualization, planning, experimentation and writing); Ramesh Pal Singh Verma (Conceptualization, planning and major editing); Lokendra Kumar (Breeder of DWRB); Vishnu Kumar 197 (Planning and editing): Gyanendra Pratap Singh (Overall Supervision)

Acknowledgement

The authors are grateful to Indian Council of Agricultural Research (ICAR) for providing all kinds of support in conducting this study. All the cooperating centres for conducting the experiment and supplying the material. Sh. Rampal, Technical Assistant, deserves sincere acknowledgement for the excellent technical assistance for the study.

References

1. Davis N. 2006. Malt and malt products. In Brewing– New Technologies, 1st ed.; Bamforth, C.W., Ed.; Woodhead Publishing Ltd.: Cambridge, UK, pp. 68–101.
2. Habschied K, A Lalić, D Horvat, K Mastanjević, J Lukinac, M Jukić and V Krstanović. 2020. β-Glucan degradation during malting of different purpose barley varieties. *Fermentatio*n **6**: #21.
3. Han F, SE Ullrich, S Chirat, S Menteur, L Jestin, A Sarrafi, PM Hayes, BL Jones, T K Blake, DM Wesenberg, A Kleinhofs and A Kilian. 1995. Mapping of β-glucan content and β-glucanase activity loci in barley grain and malt. *Theoretical and Applied Genetics* **91**: 921–927
4. Kumar D, V Kumar, RPS Verma, AS Kharub and I Sharma. 2013. Quality parameter requirement and standards for malt barley. *Agricultural Reviews* **34**: 313-317.
5. Kumar V, RPS Verma, D Kumar, AS Kharub and I Sharma. 2014. Association of malting quality attributes under timely and late sown conditions in barley (*Hordeum vulgare* L.). *Journal of Wheat Research* **6**:167-170.
6. Kumar D, S Narwal, RPS Verma and AS Kharub. 2017. Genotypic and growing location effect on grain β-glucan content of barley under sub-tropical climates. *Indian Journal of Genetics and Plant Breeding* 77: 235-241.
7. Kumar D, RPS Verma, V Kumar, L Kumar, Rampal and GP Singh. 2020. DWRB 197: An interesting material for barley beta glucan degradation studies. Wheat & Barley Newsletter, ICAR-IIWBR, Karnal Vol. 14 (2): 16-18.
8. McCleary BV and EJ Nurthen. 1986. Measurement of (1-3)(1-4)-β-D-glucan in malt, wort and beer. *Journal of Institute of Brewing* **92**: 168-173.
9. McCleary BV and I Shameer. 1987. Assay of malt β-glucanase using azo barley glucan: an improved precipitant. *Journal of Institute of Brewing* **93**: 87-90.
10. Wang J, G Zhang, J Chen and F Wu. 2004. The changes of beta glucan content and beta glucanase activity in barley before and after malting and their relationships to malt qualities. *Food Chemistry* **86**: 223-228.

Journal of Cereal Research
Volume 14 (2): 219-222
Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Varietal Release

HI 1634 (Pusa Ahilya), high yielding bread wheat variety tolerant to terminal heat stress conditions of Central Zone

Sakuru Venkata Sai Prasad[*1], Jang Bahadur Singh[1], Divya Ambati[1], Rahul Madhav Rao Phuke[1], Thorehalli Linganna Prakasha[1], Akilesh Nandan Mishra[1], Kailash Chandra Sharma[1], Anil Kumar Singh[1], Dalip Kumar Verma[1], Gyanendra Pratap Singh[2], Jai Bhagwan Sharma[3], Pradeep Kumar Singh[3], Harikrishna[3], Ram Kumar Sharma[3], Naresh Kumar[3], Rajbir Yadav[3], Kiran Bapusaheb Gaikwad[3], Sanjay Kumar[3], Prasantha Babu Hanumanthappa[3], Raghunandan Katlutkor[3], Vaibhav Kumar Singh[3], Murugasamy Sivasamy[4], Tapas Ranjan Das[3], Dharam Pal[5], Anju Mahendru Singh[3], Neelu Jain[3], Manjeet Kumar[3], Paramasivan Jayaprakash[4], Venu Kumaran Vikas[4], Madhu Patial[5], Ram Niwas Yadav[6] and Kumble Vinod Prabhu[7]

[1] *ICAR-IARI, Regional Station, Indore, M.P*
[2] *ICAR-Indian Wheat and Barley Research Institute, Karnal*
[3] *ICAR-Indian Agricultural Research Institute, New Delhi*
[4] *ICAR-IARI, Regional Station, Wellington, Tamil Nadu*
[5] *ICAR-IARI, Regional Station, Shimla*
[6] *ICAR-IARI, Regional Station, Karnal*
[7] *PPVFRA, Government of India, New Delhi*

Article history: Received: 11 July, 2022 Revised: 17 Aug., 2022 Accepted: 02 Sept., 2022

Citation: Prasad SVS, JB Singh, D Ambati, RM Phuke, TL Prakasha, AN Mishra, KC Sharma, AK Singh, DK Verma, GP Singh, JB Sharma, PK Singh, Harikrishna, RK Sharma, N Kumar, R Yadav, KB Gaikwad, S Kumar, PB Hanumanthappa, R Katlutkor, VK Singh, M Sivasamy, TR Das, D Pal, AM Singh, N Jain, M Kumar, P Jayaprakash, VK Vikas, M Patial, RN Yadav and KV Prabhu. 2022. HI 1634 (Pusa Ahilya), high yielding bread wheat variety tolerant to terminal heat stress conditions of Central Zone. *Journal of Cereal Research* ***14 (2):*** *219-222. http://doi.org/10.25174/2582-2675/2022/118676*

****Corresponding author:*** *E-mail: sprasad98@gmail.com*

Increasing wheat area under late sown conditions in the states *viz.,* Madhya Pradesh, Gujarat and Rajasthan of central zone is observed due to potato and cotton cultivation during *kharif* season (Khan *et al.,* 2010). Terminal heat stress occurs when mean temperature during grain filling stage goes above 31°C leads to reduced grain filling rate, photosynthetic capacity and rate of assimilate translocation in turn effecting grain number, grain size, spikelets/spike, grains per spike and grain quality (Bala *et al.,* 2014 & Mondal *et al.,* 2013). To meet the growing demand of farmers for varieties suitable to be sown under late conditions by the development of short duration varieties with high yield and resistance to black and brown rusts along with tolerance to terminal heat stress has become one of the important objectives for wheat breeders.

Development and Notification of HI 1634: HI 1634 was developed from cross GW 322/PBW 498 made during 2008-09 at ICAR-Indian Agricultural Research Institute, Regional Station, Indore and further handled following modified pedigree method. It was released by Central Sub-Committee on Crop Standards, Notification and Release of Varieties for Agricultural Crops, Government of India vide notification No. S.O. 500 E dated 29.01.2021 for commercial cultivation under late sown irrigated conditions of central wheat growing zone of India.

Yield superiority and adaptability of HI 1634: Pooled analysis of yield data over three years of co-ordination indicated that HI 1634 showed mean yield of 51.6 q/ha (weighted mean among 39 locations) and potential yield of 70.6 q/ha in Gwalior during *rabi* 2019-20 under irrigated, late sown conditions (IIWBR, 2020). It showed significant yield advantage of 3.6%, 4.9%, 4.9% and 8.9% over the checks HD 2932, HD 2864, MP 3336 and MP 4010, respectively. It has ranked first six times for higher yield among the test varieties over three years of testing (Table 1). Pooled analysis of the data showed that mean yield of HI 1634 (50.88 q/ha) was significantly superior than the two checks HD 2864 (47.32 q/ha) and MP 3336 (45.73 q/ha) under three sowing conditions. Significant increase in grains/ear head and 1000 grain weight up to 31.8% and 7.6% respectively over all the checks had contributed to the superior yield of HI 1634.

Table 1: Summarized yield data of coordinated trials in Central Zone

Items	**Year of testing**	**No. of trials**	**Proposed variety**	**Check Varieties**				**CD**
			HI 1634	**HD 2932**	**HD 2864**	**MP 3336**	**MP 4010**	
Mean yield (q/ha)	NIVT (2017-18)	7	48.1	41.4	40.7	-	-	1.9
	AVT I (2018-19)	16	52	51.1	48.8	47.2	47.4	1.3
	AVT II (2019-20)	16	52.8	52.2	53.3	51.2	-	1.2
	Weighted Mean		51.6	49.8	49.2	49.2	47.4	
% increase / decrease over the checks & qualifying variety	NIVT (2017-18)			16.2*	18.2*			
	AVT I (2018-19)			1.8	6.6*	10.2*	9.7*	
	AVT II (2019-20)			1.2	-0.9	3.1		
	Overall Weighted Mean			3.6	4.9	4.9	8.9	
Frequency in the first top non-significant group	NIVT (2017-18)		2/7	2/7	1/7	-	-	
	AVT I (2018-19)		10/16	6/16	2/16	3/16	2/16	
	AVT II (2019-20)		12/16	10/16	12/16	7/16	-	
	Pooled for three years		**24/39**	**18/39**	**15/39**	**10/32**	**2/16**	
1st Rank among varieties over the locations				**6/39**	**4/39**	**0/39**	**3/32**	**0/16**

* Significantly superior

Resistance to major disease and pests: Evaluation of HI 1634 in various pathological nurseries showed that it has multiple disease resistance viz., resistance to all three rusts and other diseases (Table: 2). Seedling tests were conducted for two years at ICAR-IIWBR, Shimla for testing its resistance against bread wheat virulent leaf rust pathotypes *viz.,* 77, 12, 104 and 162 groups and stem rust pathotypes *viz.,* 40 and 117 groups. Based on comparison of seedling reactions, "Pusa Ahilya" is postulated to have stem rust resistance gene *Sr31+* and leaf rust resistance gene *Lr26+*. In addition, it showed good levels of resistance to leaf blight (46), Karnal bunt (4.4), *Fusarium* head blight (3), loose smut (22.3), foot rot (5.3) and flag smut (2.7). It was not showing incidence of any of the major insect pests as per the AICRP on Wheat and Barley reports (ICAR-IIWBR, 2020a).

Table 2: Reaction to major diseases during 2018-19 and 2019-20

Disease Reaction	**HI 1634**		**Checks**							
			HD 2932		**HD 2864**		**MP 3336**		**MP 4010**	
	18-19	19-20	**18-19**	**19-20**	**18-19**	**19-20**	**18-19**	**19-20**	**18-19**	**19-20**
					Black (Stem) Rust					
HS	5MS	5MR	20MS	20S	10S	10S	40S	30MS	10MS	-
ACI	1.0	0.3	8.4	11.3	2.8	2.5	15.3	9.4	2.2	-

Brown (Leaf) Rust										
HS	10S	20S	40S	20S	40S*	60S*	40S*	80S	5S	-
ACI	1.4	3.1	19.4	38.8	6.5	7.6	8.1	26.5	0.7	-
Powdery Mildew (0-9)										
HS	5	6	5	9	7	6	7	9	7	-
AV	3	3	3	4	4	4	5	5	5	-
Leaf Blight (dd)										
HS	89	89	89	89	79	89	99	89	79	-
AV	46	46	56	46	57	56	57	56	57	-
Karnal bunt (%)										
HS	6.1	12.5	13.5	10.0	12.2	8.6	10.1	13.3	15.7	-
AV	3.8	4.4	4.5	3.6	7.3	4.0	4.2	4.1	9.0	-
Flag Smut (%)										
HS	7.5	6.8	4.8	7.5	7.1	7.5	6.6	6.3	5.3	-
AV	2.7	4.6	2.1	2.5	2.1	2.5	2.0	2.1	1.7	-
Loose Smut (%)										
HS	-	42.2	-	42.2	-	37.4	-	46.6	-	-
AV	-	22.3	-	30.9	-	12.6	-	18.3	-	-

HS = Highest score, ACI = Average coefficient of infection, AV: Average

Grain quality: High grain appearance score and test weight for HI 1634 (6.9 & 81.8 kg/hl) compared to other test varieties indicate that grain was bold, lustrous and non-shriveled. HI 1634 showed high grain hardness index (81.4), protein content (12.1%) and protein quality (*Glu* score of 8/10) for high molecular weight subunits (Table 3 & ICAR-IIWBR, 2020b). End product analysis conducted at ICAR IIWBR lab indicated that HI 1634 is suitable for *chapatti* making (7.86) along with sedimentation value of 44.8 ml, wet gluten (27.6%), dry gluten (8.8%) and gluten Index (70). Values of HI 1634 indicated its suitability for bread making (Gil et al., 2011). It has good levels of essential micronutrients like iron (39.4 ppm) and zinc content (36.6 ppm) making it rich in nutritional qualities.

Table 3: Data on Quality traits of HI 1634

Quality Parameters	**HI 1634**	**Check Varieties**			
		HD 2932	**HD 2864**	**MP 3336**	**MP 4010**
Nutritional Quality					
Protein (%)	**12.1**	12.5	12.1	12.3	12.7
Fe (ppm)	**37.9**	36.6	38.7	38.1	39.8
Zn (ppm)	**36.0**	35.4	35.0	38.1	39.9
HMW subunits					
Glu-D1	5+10	2+12	2+12	2+12	-
Glu-A1	**2***	2*	1	2*	-
Glu-B1	**7**	17+18	7+8	7+8	-
Glu-1 Score	8	8	8	8	-
Grain Characteristics					
Grain appearance (1-10)	**6.9**	6.5	6.3	6.6	6.7
Test weight (kg/hl)	**81.8**	80.7	82.1	82.3	82.7

Grain Hardness index	81.4	70.8	73.8	71.0	69.4
Sedimentation value (ml)	**44.8**	52.3	43.9	44.2	45.6
Wet Gluten (%)	**27.6**	30.4	29.2	33.0	
Dry Gluten (%)	**8.8**	9.6	9.2	10.1	
Gluten Index	**70**	83	81	56	
End Product evaluation					
Chapati Quality	**7.86**	7.61	7.53	7.72	-
Bread Loaf Volume (ml)	**483**	535	491	471	-
Bread Quality (Max. Score – 10)	**5.64**	6.45	5.36	5.05	-
Biscuit Spread Factor	**6.73**	6.88	6.60	6.62	-

Based on the three years national Co-ordinated trials by AICRP on wheat and Barley, the genotype was proposed for identification in 2020 during All India Wheat workers meet and was released by the Central Sub-Committee on Crop Standards, Notification and Release of Varieties for Agricultural Crops and notified vide S.O. 500 E, dated 29.1.2021 for commercial cultivation under irrigated, late sown conditions of the Central Zone, which is the potential area for wheat crop and comprises states like Madhya Pradesh, Chhattisgarh, Gujarat, Rajasthan (Kota and Udaipur Divisions), and Western Uttar Pradesh (Jhansi Division). In nutshell, the high yield potential variety HI 1634 coupled with stress tolerance to terminal heat and plasticity for sowing time with resistance to major insect pests, stem and leaf rusts makes this variety a suitable choice for the farmers of Central Zone of the country. Pusa Ahilya will help to sustain the livelihood of the farmers and consumer's preferences in addition to increasing its area in the central wheat growing zone to fetch higher price.

Acknowledgment

The article is based on CVRC release and notification and authors are highly thankful to the Director and PIs of ICAR-IIWBR and co-operators of AICW&BIP for their contribution.

References

1. Bala S, B Asthir and N Bains. 2014. Effect of terminal heat stress on yield and yield attributes of wheat. *Indian Journal of Applied Research* 4(6): 1–2.
2. ICAR-IIWBR. 2020c. Director's Report of AICRP on Wheat and Barley 2019-20. ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. Pp.76.
3. ICAR-IIWBR. 2020a. Progress Report of AICRP on Wheat and Barley 2019-20, Crop Improvement Eds: Gyanendra Singh, BS Tyagi, Arun Gupta, SK Singh et al., ICAR- Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. Pp.196.
4. ICAR-IIWBR. 2020b. Progress Report of AICRP on Wheat and Barley 2019-20, *Crop Protection* Eds: Sudheer Kumar, Poonam Jasrotia, Prem Lal Kashyap, Ravindra Kumar and Gyanendra Pratap Singh. ICAR- Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. Pp. 226.
5. Khan MB, M Ghurchani, M Hussain and K Mahmood. 2010. Wheat seed invigoration by pre-sowing chilling treatments. *Pakistan Journal of Bot*any 42:1561-1566.
6. Mondal S, RP Singh, J Crossa, J Huerta-Espino, I Sharma, R Chatrath, GP Singh, VS Sohu, GS Mavi, VSP Sukuru, IK Kalappanavar, VK Mishra, M Hussain, NR Gautam, J Uddin, NCD Barma, A Hakim and AK Joshi. 2013. Earliness in wheat: a key to adaptation under terminal and continual high temperature stress in South Asia. *Field Crops Research* 151: 19–26.

Journal of Cereal Research
Volume 14 (2): 223-228
Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Varietal Release

HD 3298: Biofortified, climate-resilient, high-yielding wheat variety for very late sown conditions of North-Western Plains of India

Rajbir Yadav[1*], Kiran Bapusaheb Gaikwad[1], Manjeet Kumar[1], Gyanendra Pratap Singh[2], Ram Kumar Sharma[1], Pradeep Kumar Singh[1], Naresh Kumar[1], Prashanth Babu Hanumanthappa[1], Vinod[1], Anju Mahendru Singh[1], Murugasamy Sivasamy[3], Peru Nallathambi[3], Vaibhav Kumar Singh[1], Sakuru Venkata Sai Prasad[4], Sanjay Kumar[1], Ram Niwas Yadav[5], Dharam Pal Walia[6], Jai Bhagwan Sharma[1], Ambrish Sharma[1], Jang Bahadur Singh[4], Neelu Jain[1], Shailendra Kumar Jha[1], Venu Kumaran Vikas[3], Madhu Patial[6], Tapas Ranjan Das[1], Niharika Mallick[1], Divya Ambati[4], Harikrishna[1], Raghunandan Katlutkor[1], Rahul Madhav Rao Phuke[4], Mahender Singh Saharan[1], Paramasivan Jayaprakash[3], Thorehalli Linganna Prakasha[4] and Kumble Vinod Prabhu[7]

[1] *ICAR-Indian Agricultural Research Institute, New Delhi, India*
[2] *ICAR-Indian Institute of Wheat and Barley Research, Karnal, India*
[3] *ICAR-Indian Agricultural Research Institute, Regional Station, Wellington, India*
[4] *ICAR-Indian Agricultural Research Institute, Regional Station, Indore, India*
[5] *ICAR-Indian Agricultural Research Institute, Regional Station, Karnal, India*
[6] *ICAR-Indian Agricultural Research Institute, Regional Station, Shimla, India*
[7] *Protection of Plant Varieties and Farmers' Rights Authority, New Delhi*

Article history: Received: 14 Aug., 2022 Revised: 29 Sept., 2022 Accepted: 16 Oct., 2022

Citation: Yadav R, Gaikwad K B, Kumar M, Singh G P, Sharma R K, Singh P K, Kumar N, Babu P, Vinod, Singh A M, Sivasamy M, Nallathambi P, Singh V K, Prasad S V S, Kumar S, Yadav R N, Walia D P, Sharma J B, Sharma A, Singh J B, Jain N, Jha S K, Vikas V K, Patial M, Das T R, Mallick N, Ambati D, Niranjana M, Harikrishna, Raghunandan K, Phuke R, Saharan M S, Jayaprakash P, Prakasha T L, Prabhu K V. 2022. HD 3298: Biofortified, climate-resilient, high-yielding wheat variety for very late sown conditions of North-Western Plains of India. *Journal of Cereal Research* ***14 (2):*** *223-228. http://doi.org/10.25174/2582-2675/2022/123981*

****Corresponding author:*** *rajbiryadav@yahoo.com*

Wheat is one of the most important crops for global food security; in the year 2020-21, wheat was grown on 221.8 million ha of land with a production of around 775.83 million tonnes. In India, wheat production reached ever highest figure of 109.5 million tonnes from a 31.36 million-hectare area (USDA 2021). The development of high-yielding, climate-resilient wheat varieties, and improved agronomic practices have led to significant wheat production in India. However, the pace of developing high-yielding, biofortified wheat varieties is a little bit slow.

Wheat contains low levels of the essential micronutrients iron and zinc. Therefore, a major target in wheat biofortification programs is the improvement of iron (Fe) and zinc (Zn) content in the grain. In India, recent estimates reflect an unacceptably low consumption of iron among women aged more than 18 years, and 51–83% of pregnant women are deprived of the recommended daily allowance of iron (Shankar et al 2017). Thus, it is not surprising that India has the highest number of women with anemia globally and has significant economic implications for the nation's development (Rai et al 2018). In India, the most productive zone of wheat cultivation is the North-Western Plains Zone (NWPZ) which is also referred to as the 'food bowl of India'. In this zone, two biofortified wheat varieties viz., WB 02 and HPBW 01 having 40.0 ppm iron content were released in 2017 (Gaikwad et al 2021). The new wheat variety HD 3298 having 43.1 ppm iron and 12.12 % protein content is suitable for the very late sown conditions of the North-Western Plains Zone (NWPZ) that comprises the areas of Punjab, Haryana, Delhi, Rajasthan (except Kota and Udaipur divisions), Western Uttar Pradesh (except Jhansi division), parts of Jammu and Kashmir (Jammu and Kathua districts), and parts of Himachal Pradesh (Una district and Paonta valley) and Uttrakhand (Tarai region). In addition to its biofortification traits, this variety is high-yielding and has tolerance to terminal heat stress.

HD 3298 is developed from an indigenous two-way cross consisting of CL1449/PBW343 as the female parent and CL882/HD2009 as the male parent. The modified bulk-pedigree method was adopted from F_2-F_5 generations, followed by a single plant selection in the F_6 generation to develop the line. Shuttle breeding facilities at two regional stations for rust screening and generation advancement were utilized. At ICAR-Indian Agricultural Research Institute (ICAR-IARI), Regional Station, Wellington, the breeding material was screened for leaf and stem rust; and, for stripe rust screening, the regional station of ICAR-Indian Institute of Wheat and Barley Research (ICAR-IIWBR), located at Lahaul Spiti, Himachal Pradesh was utilized. During 2016-17, this entry was evaluated in common varietal trials of ICAR-Indian Agricultural Research Institutes (IARI) across three locations. Based on its superior performance, this entry was promoted to the Special Varietal Trials under the All India Coordinated Research Project (AICRP) on Wheat and Barley.

During 2017-18, this entry was evaluated in Special trials for very late sown conditions (SPL-VLS) under the All India Coordinated Research Project (AICRP) on Wheat and Barley as HD 3298. The entry was evaluated at seven locations in randomized block design in four replications with a plot size (14.4 m^2) under irrigated very late-sown (VLS) conditions against checks DBW 71, DBW 14, WR 544. The recommended sowing time for the VLS trial is 1-15th January. During 2018-19, HD 3298 was evaluated under the same very late sown conditions at 7 locations with the same checks; this trial was termed as SPL-Advanced Varietal Trial I (SPL-AVT-I). During 2019-20 in AVT-II, the genotype was evaluated at 18 locations under late sown conditions. Due to administrative reasons, the VLS trial was discontinued and the entry was evaluated under late sown (LS) conditions in SPL-AVT II. In SPL-AVT II, five varieties viz., HD 3059, WH 1021, WH 1124, DBW 173, and PBW 771 were used as checks. In advanced varietal trials (AVTs) the entry and checks were evaluated in randomized block design with four replications and plot sizes of 14.4 m^2. Data on yield and yield contributing traits, reactions to major diseases and insect pests, grain, and nutritional quality traits were recorded. The entry was also characterized in terms of Distinctness, Uniformity, and Stability traits as per the guidelines for varietal identification in wheat (UPOV 2017, www.upov.int).

HD 3298 and the check varieties were artificially screened for stripe rust, leaf rust, and other important diseases like leaf blight, Karnal bunt throughout the yield evaluation process, and Powdery Mildew, Flag smut, and loose smut in AVT I. The average coefficient of infection (ACI) for both the rusts was calculated by multiplying disease severity and constant values of infection type. The constant values for infection types were used based on the following: R = 0.2, MR = 0.4, M = 0.6, MS = 0.8 and S = 1.0. The seedling resistance test against 16 races of stripe rust and 21 races of leaf rust was carried out for gene postulation using pathotype matching techniques (ICAR-IIWBR 2019a, 2020a). HD 3298 was also evaluated for timely, late, and very late sown conditions at 10 locations of NWPZ against five check varieties viz., HD 3059, WH 1021, WH 1124, DBW 173, and PBW 771 (Anonymous 2020). Quality attributes such as grain appearance score, hectolitre weight, protein%, sedimentation value, grain hardness, Chapati quality, bread loaf volume, bread quality, biscuit spread factor, wet and dry gluten %, gluten index, Fe and Zn content, and high molecular weight subunits were determined as per standard procedures and protocols and the data was made available by ICAR-Indian Institute of Wheat and Barley Research, Karnal, India under AICRP (Anonymous 2018, ICAR-IIWBR 2019b, 2020b).

Performance Characteristics

Varietal descriptors

HD 3298, a spring wheat variety with semi-spreading growth habit, flowers in around 72 and 84 days, matures in 103 and 122 days under VLS and LS conditions respectively and is classified as an early maturity group.

This variety attains a height of 85 and 94 cm under VLS and LS conditions respectively (ICAR-IIWBR 2018, 2019c, 2020c). It has lustrous, amber-colored oblong-shaped grains with having semi-hard texture. Thousand-grain weight under VLA and LS conditions is 32.5 and 39 gm respectively. The variety has green foliage and waxy attributes at the time of ear emergence. The ears are tapering, medium-long in length with medium grain density. The ear and awns turn white at the time of maturity. The non-pubescent glumes have sloping shoulder shape with long beak lengths. The grains have medium crease width and depth. The brush hair is shorter in length with a weak profile.

Yield evaluation

In the two years (SPL-VLS and SPL-AVT I) of testing under VLS conditions, on the weighted mean basis, HD 3298 out yielded (39.0 q ha^{-1}) the checks WR 544 (30.9 q ha^{-1}), DBW 14 (35.5 q ha^{-1}), DBW 71 (36.6 q ha^{-1}). In terms of yield gain, it comes at 26.3, 10.1, and 6.6 percent, respectively (Table 1). HD 3298 also out-yielded contemporary test entry which has been recently released for cultivation like PBW 757, HD 3271, and HI 1621 by 7.3, 4.3, and 2.4 percent, respectively under VLS conditions (Table 1). Out of the total of 14 locations during two years of testing under VLS conditions in NWPZ, 8 times it appeared statistically superior group which established its genetic superiority and wide adaptability. Potential yield realized for HD 3298 (47.4 q ha^{-1}) is much higher in comparison to checks DBW 71 (42.8 q ha^{-1}), DBW 14 (40.5 q ha^{-1}), WR 544 (41.0 q ha^{-1}) and recently released varieties PBW 757 (42.5 q ha^{-1}), HD 3271 (45.5 q ha^{-1}) and HI 1621 (43.1 q ha^{-1}) under VLS conditions (Table 1). Since the very late sown trial was terminated, in the third year, it was tested under late sown condition and was able to outperform three checks namely, HD 3059, WH 1021, and WH 1124 (Table 2).

Table 1: Yield performance of HD 3298 in VLS yield trials of AICRP (2017-19)

Item	**Year of testing**	**No. of trials**	**HD 3298**	**Checks**			**Recently Released Varieties**			**CD**
				DBW 71	**DBW 14**	**WR 544**	**PBW 757**	**HD 3271**	**HI 1621**	
Mean yield (q ha^{-1})	2017-18 (VLS)	7	38.0	35.7	35.8	31.2	35.9	35.9	37.9	1.1
	2018-19 (VLS)	7	40.0	37.5	35.1	30.6	36.8	38.9	38.3	1.2
	Weighted mean		39.0	36.6	35.5	30.9	36.4	37.4	38.1	
% Increase over check	2017-18 (VLS)	7		6.4	6.1	21.8	5.8	5.8	0.3	
	2018-19 (VLS)	7		6.7	14.0	30.7	8.7	2.8	4.4	
	Weighted mean			6.6	10.1	26.3	7.3	4.3	2.4	
Yield potential q ha^{-1} (VLS)			47.4	42.8	40.5	41.0	42.5	45.5	43.1	
Statistically superior group		14	8/14	2/14	2/14	0/14	5/14	7/14	6/14	

Table 2: Yield performance of HD 3298 in LS yield trial of AICRP (2019-20)

Item	**Year of testing**	**No. of trials**	**HD 3298**	**Checks**					**CD**
				HD 3059	**WH 1021**	**WH 1124**	**DBW 173**	**PBW 771**	
Mean yield (q ha^{-1})	2019-20 (LS)	18	47.4	46.3	39.0	44.9	49.1	49.7	0.8
% increase or decrease over check	2019-20 (LS)	18		2.4	21.5	5.6	-3.5	-4.6	

Wider adaptation

HD 3298 is suitable for sowing from timely to very late sown conditions. The potential yield of 79.61 q ha^{-1} (VLS) and 67.58 q ha^{-1} (LS) realized at one of the testing sites 'Sriganganagar' in the state of Rajasthan under agronomy trials, is the highest among all the checks under normal and late sown conditions (Anonymous 2020). Agronomy trial indicates its strong plasticity value as it has appeared first or second rank at several locations under timely, late, and very late sown conditions. Among 30 data sets of location by date of seeding in the agronomy trial, it has appeared 14 times in the statistically significant group against less than 10 times of WH 1021 and WH 1124, 10 times of DBW 173, 13 times of HD 3059, and 15 times of PBW 771, which indicates its superiority across location and time of seeding (Anonymous 2020).

Resistance to multiple diseases

HD 3298 exhibited a high level of resistance against both stripe rust and leaf rust both under natural and artificial epiphytotic conditions. Mean ACI was recorded 0.6 (natural) and 8.1(artificial) for stripe rust and 3.6 (artificial) for leaf rust (Table 3). Against two new highly virulent races of stripe rust i.e. 238S119 and 110S119, it has shown 5 MS and TR responses, respectively at the adult plant stage. HD 3298 is resistant against the prevalent races of stripe rust namely 46S119, 110S84, and 78S84 at the seedling stage and therefore likely to be resistant at all stages (ICAR-IIWBR 2020a). It showed a high level of resistance against Karnal bunt (3.75%). It also exhibited a high level of resistance against powdery mildew (3), foliar head blight (3), and flag smut (1.2%) under artificially inoculated conditions in the VLS production environment.

Table 3: Evaluation of HD 3298 along with checks for multiple diseases

Diseases	HD 3298	DBW 71	DBW 14	WR 544	PBW 757	HD 3271	HI 1621
Rusts	ACI	ACI	ACI	ACI	ACI	ACI	ACI
Stripe rust (natural)	0.6	2.5	5.6	26.0	1.1	2.5	3.6
Stripe rust (artificial)	8.1	8.15	24.15	57.6	10.3	9.1	6.25
Leaf rust (artificial)	3.6	6.7	5.0	11.2	3.0	3.7	9.9
Gene postulation							
Stripe rust	Yr2+	NA	Yr2+	NA	R	NA	NA
Leaf rust	Lr23+	NA	Lr23+	Lr13+1+	R	Lr23+	Lr13
Stem rust	R	R	Sr28+11+2+	Sr28+8a+2+	Sr2+	Sr11+2+	Sr28+
Other diseases (Artificial screening)							
Karnal bunt %	3.7	6.5	4.9	6.4	2.8	5.5	5.6
Flag smut %	1.2	3.3	0.6	2.1	2.9	4.9	2.8
Foliar head blight %	3	4	4	4	3	4	3

Grain and nutritional quality attributes

HD 3298 is superior in Iron content (43.1 ppm-VLS condition) in comparison to all checks (Table 4). Under LS conditions, HD 3298 has 39.3 ppm Fe content which is also higher than the rest of the checks. This variety has also a good level of protein content (12.12%) estimated under VLS conditions over the two years. The quality of protein is also good as indicated by a perfect Glu score of 10. This iron and protein-rich, variety is therefore very important for the nutritional food security of India. We believe that this variety will become popular among the farmers because of its higher yield under normal to very late sown and terminal heat stress conditions. Once this variety reaches into Public Distribution System in the coming years, it will certainly help in eliminating the problem of iron deficiency to some extent. This variety also has a good chapatti score (7.78). The other quality parameters of the variety are acceptable as per the prescribed standards (ICAR-IIWBR 2020b).

Table 4: nutritional quality traits of HD 3298

Parameters	Year of testing	HD 3298	Checks			Recently released varieties		
			DBW 71	DBW 14	WR 544	PBW 757	HD 3271	HI 1621
Fe (ppm)	2017-18	42.7	40.5	43.1	42.8	39.1	36.1	36.2
	2018-19	43.4	39.5	36.6	43.3	39.3	36.6	36.8
Mean		**43.1**	40.0	39.9	43.1	39.2	36.4	36.5
Zn (ppm)	2017-18	40.0	39.5	40.3	43.7	38.2	34.7	35.4
	2018-19	39.2	38.5	40.0	46.2	42.2	37.6	38.2
Mean		39.6	39.0	40.2	45.0	40.2	36.2	36.8

Heat stress tolerance studies

In NWPZ, the timely and late sown crop often suffers terminal heat stress during the growth period leading to yield loss. To identify the terminal heat-tolerant genotypes a Multi-location Heat Tolerance trial (MLHT) trial is conducted. This trial was conducted over a total of 15 localtons comprised of 4 locations each in NWPZ, NEPZ, and CZ respectively and 3 in PZ to identify the temperature stress-tolerant lines among AVT genotypes (ICAR-IIWBR 2020c). Heat Sensitivity Index (HSI) is calculated using the formula HSI=(1-YD/Yi)/(1-XD/Xi) Where YD and Yi are the grain yield for each genotype under heat stress and control conditions respectively. XD and Xi are the means of all study genotypes grain yield under heat stress and control conditions respectively. HD 3298 showed a Heat Sensitivity Index of 1 in NWPZ indicating its tolerance to heat stress (ICAR-IIWBR 2020c).

Notification and seed production

Wheat variety HD 3298 was released and notified by the central sub-committee on crop standards, notification and release of varieties *vide* notification in the official gazette number S.O. 500 (E), dated 29th of January, 2021. The ICAR–Indian Agricultural Research Institute, New Delhi is the maintainer of this cultivar and the producer of the nucleus and breeder seeds.

Reference

1. Anonymous. (2018). Progress Report of All India Coordinated Research Project on Wheat and Barley 2017-18, Vol. IV, Wheat Quality. Indian Institute of Wheat and Barley Research Karnal, India. P-.
2. Anonymous. (2020). Progress Report of All India Coordinated Research Project on Wheat and Barley 2019-20, Vol. II, Resource Management. ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. P. 183.
3. Gaikwad KB, S Rani, M Kumar, V Gupta, PH Babu, NK Bainsla and R Yadav. (2020). Enhancing the Nutritional Quality of Major Food Crops Through Conventional and Genomics-Assisted Breeding. *Frontiers in Nutrition*, **7**:533453.
4. ICAR-IIWBR. (2018). Progress Report of AICRP on Wheat and Barley 2017-18, Crop Improvement. ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. p. 206.
5. ICAR-IIWBR. (2019a). Progress Report of All India Coordinated Wheat and Barley Improvement Project 2018-19, Crop Protection. ICAR- Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. Pp. 214.
6. ICAR-IIWBR. (2019b). Progress Report of All India Coordinated Research Project on Wheat and Barley 2018-19, Wheat Quality. ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. P-161.
7. ICAR-IIWBR. (2019c). Progress Report of AICRP on Wheat and Barley 2018-19, Crop Improvement. ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. p. 201.
8. ICAR-IIWBR. (2020a). Progress Report of All India Coordinated Wheat and Barley Improvement Project 2019-20, Crop Protection. ICAR- Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. Pp. 226.

9. ICAR-IIWBR. (2020b). Progress Report of All India Coordinated Research Project on Wheat and Barley 2019-20, Wheat Quality. ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. P-161.

10. ICAR-IIWBR. (2020c). Progress Report of AICRP on Wheat and Barley 2019-20, Crop Improvement. ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. p.197.

11. Rai RK, WW Fawzi, A Barik and A Chowdhury. (2018). The burden of iron-deficiency anaemia among women in India: how have iron and folic acid interventions fared? *WHO South-East Asia journal of public health* **7**(1): 18-23.

12. Shankar B, S Agrawal, AR Beaudreault, L Avula, R Martorell, S Osendarp, D Prabhakaran and MS Mclean. (2017). Dietary and nutritional change in India: implications for strategies, policies, and interventions. *Annals of the New York Academy of Sciences.* **1395**(1):49–59.

13. UPOV 2017. https://www.upov.int/edocs/tgdocs/en/tg003.pdf

14. USDA 2021. https://apps.fas.usda.gov/psdonline/circulars/production.pdf

JOURNAL OF CEREAL RESEARCH
Guidelines to authors

The Journal of Cereal Research is published four monthly (April, August & December) by the Society for Advancement of Wheat and Barley Research (SAWBAR). On meeting the style and requirements of the journal the following types of material are considered for publication.

Review article, each issue of journal will have at least one and maximum two review articles to cover different areas of specialization. The review article up to 25 typed pages should necessarily have a title, brief abstract, key words, introduction and then relevant headings to cover the information provided in the article. The review articles, showing lacunae in research and suggesting possible lines of future work are mostly invited from eminent scientists. The research article or note submitted for publication should have a direct bearing on wheat/ barley research or open up new grounds for productive research. Articles and notes relating to investigation in a narrow but specialized branch of wheat and barley may also form an appropriate material for this journal.

Research articles, not exceeding up to 20 typed pages, including references, tables, etc. based on original research data invariably of two years and not older than five years should be exclusive for the journal, should present a connected picture of investigation and should not be split into parts. Complete information of M.Sc./Ph.D. thesis should preferably be given in a sequential articles (s).

Short communication, not more than total 10 typed pages, which deal with (i) research results that are complete but do not warrant comprehensive treatment, (ii) description of new materials or improved techniques or equipment, with supporting data and (iii) a part of thesis or study. Short communication should not have any abstract and sections but can have tables and figures. There should be a summary paragraph at the end just before references.

Instructions for authors : (a) indicate period (years) of study, (b) article should preferably be submitted soon after completion of study, (c) articles on genetics and plant breeding and on plant crops should be based on data of minimum 2 years, (d) contribution involving a former or present student must clarify that it is not based / based on complete M.Sc. thesis, or complete or a part of the Ph.D. thesis, indicating its year of submission.

Title, should be short, specific and informative, it should be phrased to identify the content of the article and include the nature of the study and the technical approach, essential for key-word indexing and information retrieval.

Affiliation, should follow immediately below the authors after a line space, smaller font than the authors and be italic. The information on corresponding author should include email, phone and fax numbers.

A short title, not exceeding 35 letters should also be provided for running headlines.

Abstract, written in complete sentences, should not have more than 300 words. It should contain a very brief account of the material, methods, results, discussion and conclusion, so that the reader need not refer to the article except for details. It should not have references to literature, Illustrations and tables.

Key words, 4-5 keywords to shortlist, refer and index the article.

Introduction, brief and limited to the statement of the problem or the aim and scope of the experiment. The review of recent literature should be pertinent to the problem.

Materials and methods, should have relevant details of study, experimental design and techniques used. Where the methods are known, citation of the standard work is sufficient, Mean results with the relevant standard errors should be presented rather than detailed data. The statistical methods used should be clearly indicated.

Results and discussion, should be combined and are supported by brief but adequate tables and/or graphic or pictorial materials, wherever necessary. The discussion should relate to the limitations or advantages of the author's study in comparison with the earlier work and relevant literature should be discussed critically. Self-explanatory tables should be typed on separate sheets, with appropriate titles. The tables should fit in the normal layout of the page. All weights and measurement must be in SI (metric) unit and standard acronym (kgha^{-1}, tha^{-1} etc.) must be used. Tables and illustrations (up to 20% of text) should not reproduce the same data.

Numbering, the headings and subheading in the article should be numbered (e.g. 1. Introduction 2. Materials and methods and 3. Results and discussion. The subheading (s), if any, under the main heading should also be numbered as 1.1, 1.2 and so on). Headings should be bold, while sub heading should be normal and italic.

Line drawings, should be clearly drawn on A-4 size paper using black/colour waterproof ink on smooth, tough paper. Minor points of style should be noted carefully. Good quality photographs, relevant to the study, preferably in jpg format should be unmounted and printed on glossy paper. Colour photographs may be sent for better identification or differentiation of different parts of the object. Line-drawings and photographs should have legends (typed). Original artwork should accompany 2 copies.

Acknowledgment, a short para to acknowledge the financial and other support for the study.

References, for citing references recent issue of the journal should be consulted, ensuring that the names and dates in the text and in the reference section correspond. Each citation should have the names of the author(s), initials, year of publication, full title of the article, name of the journal (without abbreviation), volume, preferably the issue (within parentheses), and complete page-range (not merely the first page). Complete name of publisher and place of publication of books should be given. For proceedings/ other publications complete details should be given.

Releases / Genetic stocks of not more than two typed pages, only as running text without abstract, tables, figures and references. Author(s) and affiliation(s) should be given at the end.

All articles are sent to referees for scrutiny, and authors should comply and incorporate comments/suggestions to improve the article. Articles should be **type-written** in double space throughout (including by-line, abstract, references and tables) with a 4cm margin at the top, bottom and left. All articles following journal format and after checking for typographical errors should be submitted online along with duly signed article certificate using link: epubs.icar.org.in/ejournal/index.php/JWR.

Proof reading, will be online using track changes and all queries/comments marked in the article must be answered point wise. Proofs are supplied for a check-up of the correctness of type-setting and facts. Excessive alterations by author at the stage of proof reading will be charged.

Colour **printing,** desirous authors need to pay @ Rs. 4000/- (Rupees four thousand only) for four pages or parts of at the time of acceptance.

Memberships, all contributing authors must be members (Life/Annual) of SAWBAR and will receive soft copy of the issue.