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Research Article

Early Maturing Wheat Genotypes for Better Integration in Rice-Wheat Cropping Systems in Kashmir Valley of Western Himalayas

Reyazul Rouf Mir[1,2]* Mukesh Rathore[1], Nikita Aggarwal[1], Farkhandah Jan[1], Safoora Shafi[1], Mohd. Tahir[1], Mohd. Anwar Khan[1], Mohd. Ashraf Bhat[1], Parvaze Ahmad Sofi[1] and Asif Bashir Shikari[1]

[1]*Division of Genetics and Plant Breeding, Faculty of Agriculture, SKUAST-Kashmir-190025, India*
[2]*Centre for Crop and Food Innovation, State Agricultural Biotechnology Centre, Food Futures Institute, Murdoch University, Murdoch, WA, Australia*

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Corresponding author:
E-mail: imrouf2006@gmail.com

Abstract

Wheat is one of the most important crops for ensuring sustainable food production in the Himalayan region of the Kashmir Valley. However, a major challenge for wheat growers in the valley is that wheat typically matures by the end of June, which delays rice cultivation. To overcome this constraint, developing early maturing wheat varieties that vacate land by May end or June first week for rice has long been a key breeding objective in the region. Achieving a successful wheat–rice crop rotation can significantly enhance crop production and contribute to food security, ultimately helping make the Himalayan region self-sufficient. To address this challenge, we have evaluated more than 10,000 wheat genotypes over the past decade and successfully identified/developed 20 early-maturing wheat genotypes. These 20 genotypes and two regional checks (Shalimar Wheat-1 and Shalimar Wheat-2) making the total 22 genotypes, were evaluated across five cropping seasons (2020–2025) under temperate field conditions at Wadura, SKUAST-Kashmir. Eight key agro-morphological traits including days to 50% flowering, days to maturity, plant height, spike length, spikelets per spike, grains per spike, thousand-grain weight and grain yield were recorded. Considerable phenotypic variation was recorded across all traits. Genotypes WW-103, WW-101, and WW-102 consistently exhibited the earliest flowering and maturity, with WW-103 being the earliest one achieving the highest yield (4.69 t ha^{-1}) and outperforming the checks. The WW-103/ SKAU-70/SKAU-WW103/Shalimar wheat-04 showed strong potential as early-maturing, high-yielding candidate suitable to the Kashmir Valley's cold-prone climate and for strengthening rice–wheat cropping system adoption.

Keywords: Early maturity, High yield, Kashmir Valley, Rice-wheat cropping system, Wheat

1. Introduction

Wheat (*Triticum aestivum* L.) plays a pivotal role in global food and nutritional security, contributing nearly 20% of the world's dietary calories and proteins (WHO, 2023). As a staple crop for approximately 30-32% of the global population, it nourishes more than 2.5 billion people across 89 nations, including India (CGIAR, 2025; Jan *et al.,* 2025a). India is the second-largest wheat producer globally, after China, achieving a record production of ~115.3 million tonnes in 2024–2025 (CGIAR, 2025; Jan *et al.,* 2025b). Wheat is primarily cultivated in the northern plains such as Uttar Pradesh (31.27%), Madhya Pradesh (19.97%), Punjab (15.69%), Haryana (9.90%), Rajasthan (8.58%), and Bihar (6.34%), which together contribute about 91.75% of the country's total wheat output (Discover India 2025). The crop is predominantly grown during the winter season (October to March), when average temperatures range between 10–15 °C. However, wheat is also cultivated across diverse ecologies, including tropical, subtropical, temperate, and cold regions, extending up to 67°N latitude in Jammu and Kashmir (J&K).

The Union Territory (UT) of J&K comprises two distinct agro-climatic zones: the temperate Himalayan Kashmir region and the Sub-Himalayan Jammu region, experiences a hot and humid subtropical climate. Wheat is grown on ~281.87 thousand hectares across the UT, with an average yield of 19.33 q/ha (Qammer *et al.,* 2022). Cultivation is largely confined to the subtropical Jammu region, while only ~1,300 ha is under wheat in the Kashmir Valley (Mahdi *et al.,* 2025). While the total cultivation area and production have shown an increasing trend in recent years, the average productivity has declined (Qammer *et al.,* 2022). Due to persistent food deficits, J&K remains heavily dependent on Punjab and Haryana for grain imports, an unsustainable scenario for long-term food security (Ganaie *et al.,* 2017). Agriculture forms the backbone of the region's economy, and the mountainous terrains, especially the Kashmir Valley, are highly fragile and acutely vulnerable to climatic fluctuations. Consequently, the agricultural sector faces significant challenges from various biotic and abiotic stresses, especially concerning wheat production (Gull *et al.,* 2024; Mahdi *et al.,* 2025; Aggarwal *et al.,* 2025). Among the abiotic stresses, extreme weather events driven by climate change have become increasingly frequent, leading to episodes of severe cold stress in unacclimated plants (Chang *et al.,* 2021). The optimal temperature for wheat growth is ~22/14 °C (day/night) (Pradhan *et al.,* 2015). Wheat is particularly sensitive to cold stress during multiple developmental stages, including germination, early seedling growth, and reproductive development (Hassan *et al.,* 2021; Jan *et al.,* 2023; Singh *et al.,* 2024).

The Kashmir Valley, a fragile cold-arid ecosystem in the Western Himalayas (Chevuturi *et al.,* 2018), is highly suitable for realizing higher yields of wheat due to winter precipitation from December to April coinciding with critical growth stages (Kour *et al.,* 2012). However, the most critical issue for wheat cultivation in the Kashmir Valley is that wheat typically occupies land for about eight months (October to June), leaving little time for rice cultivation and making a rice–wheat cropping system (RWCS) difficult to implement. The introduction of early-maturing varieties such as Shalimar Wheat-1 (2004) and Shalimar Wheat-2 (2011), Shalimar Wheat-3 (2022) by SKUAST-K raised hopes for RWCS adoption, but growers expect better varieties than these three varieties to fit well into the wheat-rice cropping system. Consequently, most growers remain confined to rice monocropping due to the lack of suitable early-maturing wheat varieties. Therefore, continuous breeding efforts are being made to develop early-maturing, high-yielding wheat genotypes with enhanced resistance to both biotic and abiotic stresses. We run extensive programs focused on germplasm evaluation, characterization, and trait discovery for key attributes such as cold tolerance, leaf blight resistance, stripe rust resistance, and yield improvement in wheat (Jan *et al.,* 2023; Aggarwal *et al.,* 2025; Jan *et al.,* 2025a, Jan *et al.,* 2025b). Recently, several promising wheat genotypes, including WW-101, WW-102, and WW-103, along with dozens of others, have been identified by the Division of Genetics and Plant Breeding, SKUAST-K. These genotypes are expected to improve wheat area, RWCS adoption and hence doubling food production and farmers income in the Kashmir Valley. These varieties generally mature in the last week of May to first week of June under hot and dry conditions, providing farmers sufficient time to prepare fields for rice, unlike earlier releases.

To address a critical research gap arising from the non-availability of early-maturing and high-yielding germplasm in the Kashmir Valley, an initiative was undertaken with the following objective: (i) to evaluate the genetic variability of thousands of wheat genotypes in the last decade and identify/develop early maturity wheat genotypes, (ii) to identify and recommend promising early maturing genotypes best suited for cultivation in the Kashmir Valley to support efficient RWCS adoption, (iii) evaluation and trait characterization of a set of early maturing wheat genotypes in different environments, (iv) recommendation of best candidates (early maturing and high yield) for developing and releasing as wheat varieties in Kashmir Valley.

2. Materials and Methods

2.1 Experimental Site

The field experiments were conducted at the Research Farm of the Division of Genetics and Plant Breeding, Faculty of Agriculture (FoA), Wadura Campus, SKUAST-Kashmir. The site located in the temperate agro-climatic zone of J&K at 34°17' N latitude, 74°33' E longitude and an altitude of 1,594 m above mean sea level. The soil is classified as a typical Inceptisol with a clay loam texture, moderate fertility, and good water-holding capacity, characteristic of the valley's alluvial deposits.

2.2 Planting Material

The planting material utilized in the present study was developed/selected through multi-year screening of a large number (>10,000 lines). These germplasm lines were procured from various national and international institutes, including the National Bureau of Plant Genetic Resources (NBPGR), New Delhi; Punjab Agricultural University (PAU), Ludhiana; Borlaug Institute for South Asia (BISA), Ludhiana; and the Indian Institute of Wheat and Barley Research (IIWBR), Karnal. Initial large-scale evaluations of this germplasm were conducted over multiple seasons under temperate field conditions. Based on consistent performance across environments, lines exhibiting stable early maturity, superior agronomic performance, and desirable yield-related traits were progressively shortlisted. From this multi-year selection process, a final set of 20 early-maturing and genetically diverse wheat genotypes was selected for the present study (Figure 1). Two local check varieties, SW-1 and SW-2, released by SKUAST-Kashmir, were included as regional controls for comparative evaluation.

2.3 Experimental Design

The genotypes were phenotyped across five consecutive cropping seasons (2020–2025). Sowing was carried out between October 15 to 20 in all environments/years. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each experimental plot measured 6 m × 1.2 m, with a row-to-row spacing of 22 cm and plant-to-plant spacing of 10 cm. Standard agronomic practices were followed. Pest and disease were managed chemically, while weeds were controlled both manually and chemically to ensure a healthy crop throughout the growing season. During November to February, the region experiences a sudden and significant decrease in temperature, during which wheat undergoes dormancy and remains in its early developmental stages. Average maximum and minimum temperatures and humidity for each environment are presented in Figure 2.

Fig. 1: Field views of large-scale germplasm evaluation (>10,000 lines) conducted over multiple years to identify early-maturing and high yielding wheat genotypes.

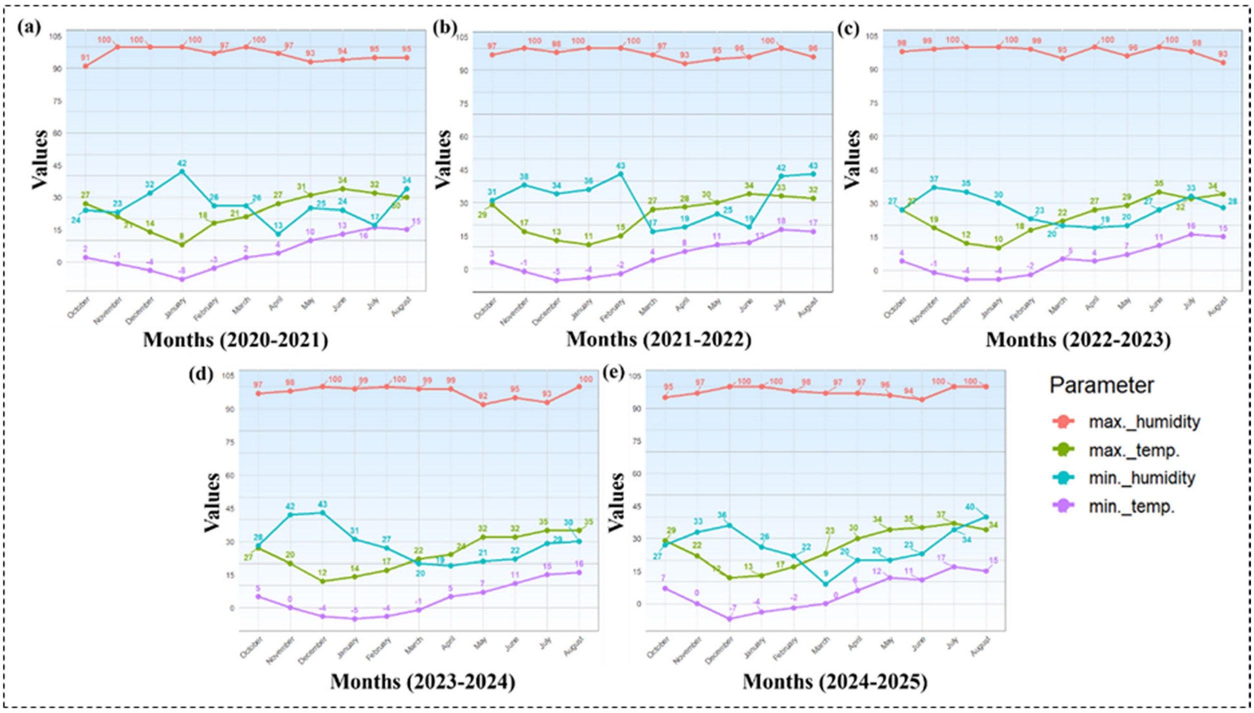

Fig. 2: Monthly trends of temperature and humidity over five wheat-growing seasons (2020–2025). Panels (a–e) represent individual seasons: (a) 2020–2021, (b) 2021–2022, (c) 2022–2023, (d) 2023–2024, and (e) 2024–2025. The graphs display maximum temperature (green line), minimum temperature (purple line), maximum humidity (red line), and minimum humidity (blue line) across months.

2.4 Phenotypic Evaluation for Yield and Related Traits

For each of the five (5) field trials, the phenotypic data were recorded on the following 8 agronomic traits; Days to 50% flowering (DTF) was calculated as days from the date of sowing until 50% of the spikes within a plot had emerged from the flag leaf sheath. Days to 50% maturity (DTM) was recorded when the majority of plants in the plot showed a complete loss of green colour from the flag leaf. Plant height (PH) was recorded at physiological maturity in cm as the average of randomly selected five plants from the central area of each plot. Height was measured from the soil surface to the spike tip excluding awns. Spike length (SL) was determined in cm as the average length of 5 main spikes, measured from the spike base to the tip, excluding awns. Number of spikelets per spike (SNS) was measured as the average number of spikelets present on the main 5 same spikes. Grains per spike (GPS) was calculated as the average of grain number present on the main 5 same spikes. Grain yield (YPP) was calculated at harvest from the total grain weight obtained from each plot and converted to a per-hectare basis (t ha^{-1}). Thousand-grain weight (1000GW) was recorded by weighing 1000 grains in grams (g) post-harvest at physiological maturity.

2.5 Phenotypic Data Analysis

A combined analysis of variance (ANOVA) was performed for all studied traits to assess the main effects of genotype (G), environment (E), and their genotype × environment (G×E) interaction using a multilocation trial model (Littell *et al.,* 1996). To further investigate G×E interactions and identify stable performing genotypes, AMMI analysis was carried out using the adjusted mean values of DTF and YPP (Crossa 1990). AMMI analysis was performed using the AMMI package in R. The AMMI model is expressed as:

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{N} T_n \gamma_{in} \delta_{jn} + \varepsilon_{ij}$$

Where Y_{ij} is the yield of the i^{th} genotype (i = 1,.,I) in the j^{th} environment (j = 1,.,J); μ is the grand mean; g_i and e_j are the genotype and environment deviations from the grand mean, respectively; T_n is the eigenvalue of the PC analysis axis n; γ_{in} and δ_{jn} are the genotype and environment principal component scores for axis n; N is the number of principal components retained in the model and ε_{ij} is the error term.

The AMMI stability value (ASV) was calculated, with smaller ASV scores representing greater stability across environments. Descriptive statistics and genetic variability parameters were estimated using RBD-R (Randomized Block Design with three replications) analysis in R software, based on pooled data across five environments. Mean comparisons among genotypes were done by further analysis of the significant data through Least Significant Difference (LSD) test at 5% probability level. Additionally, Pearson correlation coefficients and principal component analysis (PCA), were also performed using R software (version 4.4.2).

3. Results and Discussion

3.1 Phenotypic Trait Variation

Characterization of genetic variation for earliness and yield related components are considered very important targeted traits for expanding wheat cultivation in the Valley (Rashid *et al.,* 2025). As grain yield is a complex polygenic trait, therefore, section based on associated traits could prove more fruitful for the development of superior genotypes (Shi e*t al.,* 2017; Yousaf *et al.,* 2018). In this context, the present study evaluated a diverse set of early wheat genotypes for eight key yield-related traits under the challenging climatic conditions of Wadura, Kashmir. The sowing window of October 15–20 was adopted, as this period is widely recommended for temperate Kashmir and has been shown to favour optimal crop establishment and higher yield attributes compared to delayed sowing (Dar *et al.,* 2018; Dar *et al.,* 2020). Sowing within this window ensures that the crop completes early vegetative growth before entering the reproductive phase during a gradual rise in temperature, thereby facilitating proper grain development and maturity. Recent studies have demonstrated that timely sowing significantly improves phenological synchronization, grain filling, and yield performance, whereas delayed sowing exposes the crop to higher temperatures during the reproductive phase, leading to shortened reproductive duration and reduced yield (Liu *et al.,* 2023; Salaria *et al.,* 2024). The combined ANOVA (Table 1) revealed significant variation due to genotype (G), environment (E) except for SL and 1000GW, and genotype-environment interaction (G × E) for all studied traits, indicating that trait expression was influenced by G, E, and G × E effects. All parameters exhibited a broad range of phenotypic variations, confirming their polygenic inheritance.

Table 1: Combined Analysis of Variance (ANOVA) of 20 wheat genotypes with two checks (SW-1, SW-2) evaluated across five environments for days to flowering (DTF), days to maturity (DTM), plant height (PH), spike length (SL), spikelet number per spike (SNS), grains per spike (GPS), grain yield (YPP), and thousand-grain weight (1000GW). *Significance levels:* *** = highly significant at $p \leq 0.001$, ** = significant at $p \leq 0.01$, and * = significant at $p \leq 0.05$; NS = non-significant; DF: Degree of Freedom; ENV: Environment; Rep: Replication.

Source	DF	DTF	DTM	PH	SL	SNS	GPS	1000GW	YPP
Genotype	21	1124***	582***	545***	41.4***	58.2***	180***	111***	0.725**
ENV	4	130***	110**	296***	1.4^{NS}	10.6***	65***	37.9^{NS}	1.45**
Rep	2	153***	217**	1284***	276***	165***	343***	900***	16.7***
Genotype: ENV	84	25.4*	34.3*	15.02*	8.65***	12.3***	23.3***	27.9***	0.266*
Residuals	218	21.1	31.5	15.1	0.625	1.73	4.43	14.5	0.339

Significance levels: *** = highly significant at $p \leq 0.001$, ** = significant at $p \leq 0.01$, and * = significant at $p \leq 0.05$; NS = non-significant.

The observed pooled environment -based variation for each trait was as follows: DTF (171.71-207.05) with a mean of 189.13, DTM (224.73-258.60) with a mean of 243.97, PH (106.96-137.31 cm) with a mean of 118.84 cm, SL (8.44-16.93 cm) with a mean of 11.83 cm, SNS (15.83-26.44) with a mean of 19.70, GPS (40.77-54.76) with a mean of 47.72, YPP (3.21-4.69 t ha^{-1}) with a mean of 3.89 t ha^{-1}, and 1000GW (40.39-52.79 g) with a mean of 46. 54 g. The pooled DTF, DTM, PH, SL, SNS, GPS, YPP and 1000GW values recorded for the two checks were as follows: SW-1 (195.79, 244.27, 115.45, 10.72, 18.28, 46.67, 3.68 and 47.60) and SW-2 (188.45, 240.37, 119.72, 11.71, 18.73, 48.42, 3.83, and 50.39) (Table 2). The presence of substantial variability provides ample opportunity to identify superior genotypes for further breeding. Comparable ranges of phenological and yield variability have been reported in temperate Himalayan and other high-altitude wheat environments, emphasizing the importance of exploiting G x E interactions (GEI) for enhancing local adaptation (Pant *et al.,* 2023; Rana *et al.,* 2023; Rana 2024; Sharma *et al.,* 2025).

Based on the performance of studied traits, several genotypes were identified outperformed the check varieties in both earliness and yield. Notably, genotype WW-103 recorded the earliest flowering (171.71 days) and maturity (224.73 days), followed by WW-101 (174.79 and 227.04 days) and WW-102 (178.44 and 229.89 days). This variation may be attributed to differences in genetic backgrounds and the specific environmental cues required by each genotype to complete its life cycle (Yanagi 2024). For plant height, the tallest genotypes were WW-109 (129.88 cm) and WW-118 (127.73 cm), whereas WW-103 exhibited a comparatively shorter stature (106.95 cm), which is desirable for lodging resistance. In addition to this, WW-103 also exhibited superior spike architecture (highest spike length, spikelets per spike, grains per spike, and 1000-grain weight), which contributed to its highest mean yield (4.69 t ha^{-1}), followed by WW-101 (4.26 t ha^{-1}) and WW-102 (4.06 t ha^{-1}), making these genotypes promising candidates for breeding programs and perfect fit for rice-wheat cropping system of the Kashmir Valley.

The G × E interaction for DTM and YPP was further explored using the AMMI model, which integrates additive main effects with multiplicative interaction effects and is widely used for stability analysis in multi-environment trials (Singh *et al.,* 2020; Yue *et al.,* 2022). The AMMI analysis revealed that the G × E interaction and the first four interaction principal component axes (IPCAs) were highly significant for both traits (Table 3). For DTM, IPCA1 accounted for 46.2% of the total GEI variation, followed by IPCA2 (28.1%), IPCA3 (18.3%), and IPCA4 (7.4%). The first three IPCAs together explained 92.6% of the total GEI variation, indicating that the AMMI model effectively captured the interaction structure governing maturity response across environments.

Similarly, for YPP, IPCA1, IPCA2, IPCA3, and IPCA4 explained 42.8%, 23.4%, 17.8%, and 15.9% of the total GEI variation, respectively. The cumulative contribution of the first three IPCAs (84.0%) suggests that yield performance was strongly influenced by genotype-specific responses to environmental variability, reinforcing the necessity of stability analysis in varietal selection.

To translate these statistical patterns into breeding-relevant conclusions, genotype stability was further quantified using the AMMI Stability Value (ASV), where lower ASV values indicate greater stability across environments (Mullualem et al., 2024). For DTM, genotype WW-103 exhibited the lowest ASV (0.37), followed by WW-101 (0.44) and WW-102 (0.47), reflecting high stability in maturity across environments. In contrast, genotypes such as SW-2 (ASV = 3.10), WW-114 (3.05), and WW-115 (2.97) showed high ASV values, indicating strong G × E interaction effects and unstable phenological responses.

For YPP, WW-103 again recorded the lowest ASV (0.10) in combination with the highest mean yield (4.69 t ha^{-1}), clearly identifying it as the most stable and high-yielding genotype across environments. Genotypes WW-102 (ASV = 0.12) and WW-101 (ASV = 0.13) also displayed low ASV values combined with above-average yields, suggesting broad adaptability. Conversely, genotypes WW-119 (ASV = 1.23), WW-113 (1.16), and WW-117 (1.02) showed high ASV values, reflecting greater sensitivity to environmental fluctuations and limited stability (Table 4 & Figure 3).

Reflecting these findings, the Division of Genetics and Plant Breeding, Faculty of Agriculture, SKUAST-Kashmir, has proposed the release of one early-maturing and high-yielding genotypes (WW-103/SKAU-WW103/SKAU-70), which physiologically mature by the last week of May and have already undergone successful multilocation trials (Table 3 & Figure 4).

Table 2: Pooled performance of 20 wheat genotypes with two checks (SW-1, SW-2) evaluated across five environments for days to flowering (DTF), days to maturity (DTM), plant height (PH), spike length (SL), spikelet number per spike (SNS), grains per spike (GPS), grain yield (YPP), thousand-grain weight (1000GW) and physiological maturity date (PMD). Values followed by different lowercase letters within a column indicate significant differences among genotypes according to the appropriate multiple comparison test ($p \leq 0.05$). Higher-ranked letters (e.g., "a") represent superior performance, while lower-ranked letters (e.g., "j", "k") denote comparatively lower trait values.

S. No.	Genotype	DTF	DTM	PH (cm)	SL (cm)	SNS	GPS	YPP (t h^{a-1})	1000GW (g)	PMD
1	SW-1	195.79^{bcd}	244.27^{cdef}	115.45^{cdefg}	10.72^{fghi}	18.28^{fgh}	46.67^{defg}	3.68^{bcde}	47.60^{abcde}	15-Jun
2	SW-2	188.45^{cdefgh}	240.37^{efg}	119.72^{bcdef}	11.71^{def}	18.73^{ef}	48.42^{bcde}	3.83^{bcde}	50.39^{abc}	11-Jun
3	WW-101	174.79^{lij}	227.04^{h}	109.65^{fg}	14.50^{b}	22.82^{b}	50.66^{bc}	4.26^{ab}	45.85^{abcde}	29-May
4	WW-102	178.44^{hij}	229.89^{fg}	111.80^{efg}	13.21^{c}	21.66b^{c}	50.04^{bc}	4.09^{abc}	51.48^{ab}	31-May
5	WW-103	171.70^{j}	224.73^{i}	106.95^{g}	16.93^{a}	26.43^{a}	54.76^{a}	4.68^{a}	52.79^{a}	27-May
6	WW-104	188.52^{cdefgh}	244.45^{cdef}	116.69^{cdefg}	14.59^{b}	22.87^{b}	51.27^{b}	4.08^{abcd}	43.88^{bcde}	15-Jun
7	WW-105	185.91^{cdefgh}	244.08^{cdefg}	115.51^{cdefg}	8.44^{j}	15.82^{k}	40.77^{i}	3.87^{bcde}	42.72^{cde}	15-Jun
8	WW-106	205.74^{a}	252.87^{b}	121.91^{abcde}	12.74^{cd}	17.67^{fghij}	49.58^{bc}	3.36^{de}	45.54^{abcde}	24-Jun
9	WW-107	180.57^{ghij}	247.040^{cd}	118.65^{bcdef}	11.71^{def}	16.93^{hijk}	41.51^{i}	3.675^{bcde}	47.53^{abcde}	18-Jun
10	WW-108	190.68^{cdefg}	247.66^{c}	119.94^{abcdef}	12.83^{cd}	21.15^{c}	46.12^{efg}	4.02^{a}	47.88^{abcde}	18-Jun
11	WW-109	185.36^{defgh}	240.83^{efg}	129.88^{a}	11.74^{def}	20.55^{cd}	47.88^{cdef}	3.21^{e}	48.83^{abcd}	12-Jun
12	WW-110	193.06^{cdef}	245.60^{cde}	115.65^{cdefg}	9.44^{ij}	16.36^{jk}	48.61^{bcde}	4.06^{abcd}	46.75^{abcde}	16-Jun
13	WW-111	207.05$_{a}$	258.59^{a}	119.55^{bcdef}	10.47^{fghi}	17.77^{fghi}	49.58^{bc}	3.85^{bcde}	49.83^{abcd}	30-Jun
14	WW-112	184.63^{efghi}	241.79^{defg}	116.92^{cdefg}	11.30^{efg}	18.68^{ef}	48.96^{bcd}	3.83^{bcde}	48.01^{abcde}	13-Jun
15	WW-113	189.055^{cdefg}	242.62^{cdefg}	125.68^{abc}	10.46^{fghi}	21.42^{c}	45.57^{fg}	3.65^{bcde}	48.63^{abcde}	14-Jun
16	WW-114	189.63^{cdefg}	241.74^{defg}	124.43^{abcd}	9.83^{hi}	19.70^{de}	44.11^{gh}	3.55^{bcde}	46.82^{abcde}	13-Jun
17	WW-115	183.48^{fghi}	248.02^{c}	119.52^{bcdef}	12.59^{cde}	21.52^{bc}	49.46^{bcd}	4.05^{abcd}	42.82^{cde}	19-Jun
18	WW-116	194.61^{bcde}	245.46^{cde}	114.77^{defg}	10.21^{ghi}	17.29^{ghij}	45.27^{fgh}	3.64^{bcde}	45.18^{abcde}	16-Jun
19	WW-117	186.22^{cdefgh}	240.29^{efg}	124.16^{abcd}	13.61^{bc}	21.73^{bc}	50.45^{bc}	4.18^{abc}	45.56^{abcde}	11-Jun
20	WW-118	187.17^{cdefgh}	238.52^{g}	127.73^{ab}	12.48^{cde}	20.75^{cd}	49.43^{bcd}	4.03^{abcd}	43.56^{bcde}	10-Jun
21	WW-119	196.32^{bc}	247.72^{c}	123.36^{abcd}	9.50^{ij}	16.69^{ijk}	42.80^{hi}	3.53^{cde}	40.38^{e}	19-Jun
22	WW-120	203.58^{ab}	255.66^{ab}	116.45^{cdefg}	11.21^{efgh}	18.52^{efg}	47.82^{cdef}	3.77^{bcde}	41.82^{de}	27-Jun

Table 3: AMMI analysis of variance for days to maturity and grain yield (YPP) of 20 wheat genotypes with two checks (SW-1, SW-2) evaluated across five environments.

Source	Df	Sum Sq_ DTM	Sum Sq_ YPP	Mean Sq_ DTM	Mean Sq_YPP	Proportion _DTM	Proportion_ YPP	Accumulated_ DTM	Accumulated_ YPP
ENV	4	219.00	0.36	54.80	0.09	NA	NA	NA	NA
GEN	21	12600.00	27.70	599.00	1.32	NA	NA	NA	NA
GEN: ENV	84	2920.00	36.10	34.80	0.43	NA	NA	NA	NA
PC1	24	1350.00	15.50	56.20	0.65	46.2	42.8	46.2	42.8
PC2	22	822.00	8.46	37.40	0.39	28.1	23.4	74.3	66.3
PC3	20	536.00	6.44	26.80	0.32	18.3	17.8	92.6	84.1
PC4	18	217.00	5.75	12.00	0.32	7.4	15.9	100	100

Table 4: Stability parameters from AMMI model for days to maturity and grain yield of 20 wheat genotypes with two checks (SW-1, SW-2) evaluated across five environments.

Genotypes	IPCA1_DTM	IPCA2_ DTM	IPCA1_YPP	IPCA2_YPP	ASV_DTM	ASV_YPP	Rank_DTM_ Stability	Rank_YPP_ Stability	Overall_ Rank
SW-1	-1.14	0.71	0.02	-0.13	1.62	0.13	15	9	11
SW-2	-2.41	-0.37	0.13	-0.13	3.11	0.22	22	8	12
WW-101	0.35	0.34	0.17	-0.09	0.48	0.13	1	2	3
WW-102	0.42	-0.78	-0.06	0.10	0.44	0.13	4	1	2
WW-103	-0.06	-0.36	0.04	-0.22	0.37	0.10	2	3	1
WW-104	0.30	-0.58	-0.61	0.28	0.70	0.87	7	19	9
WW-105	-0.30	0.96	0.09	-0.10	1.03	0.15	12	4	7
WW-106	-1.57	-0.61	0.10	-0.13	2.10	0.18	17	5	19
WW-107	1.33	-0.82	-0.30	0.29	1.89	0.50	16	15	22
WW-108	-0.24	-0.85	-0.07	0.18	0.91	0.21	10	6	5

WW-109	0.38	0.20	-0.14	-0.11	0.52	0.21	6	7	8
WW-110	0.64	-0.32	-0.02	0.54	0.89	0.54	9	16	13
WW-111	-0.38	-0.70	0.17	0.04	0.85	0.24	8	10	15
WW-112	0.21	1.30	-0.09	0.22	1.33	0.25	13	11	10
WW-113	0.61	1.20	0.85	0.17	1.43	1.16	14	21	20
WW-114	2.37	0.26	-0.26	-0.20	3.05	0.40	21	13	17
WW-115	0.72	-2.53	-0.06	0.74	2.69	0.75	19	17	18
WW-116	0.08	0.08	-0.09	-0.05	2.14	0.25	18	12	6
WW-117	0.39	-0.12	-0.48	-0.78	0.52	1.02	3	20	4
WW-118	-2.19	0.98	-0.54	-0.15	2.97	0.75	20	18	14
WW-119	-0.06	0.63	0.89	-0.24	0.64	1.23	5	22	21
WW-120	-0.47	-0.32	0.25	-0.25	0.68	0.42	11	14	16

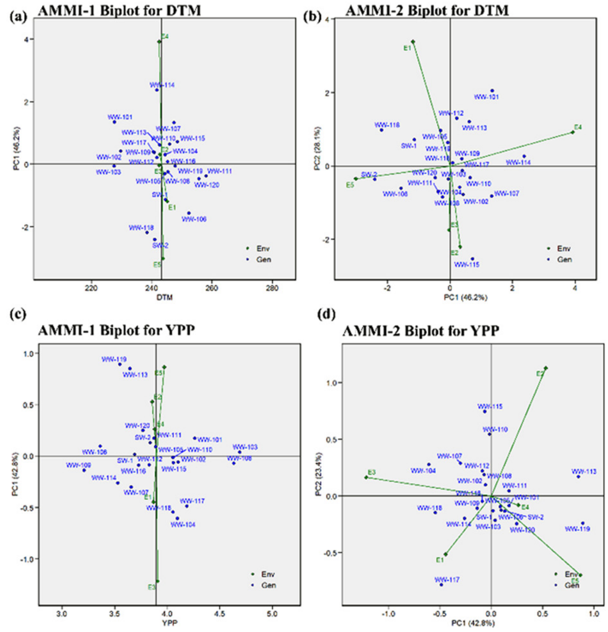

Fig. 3: AMMI-1 and AMMI-2 model biplots for days to maturity and grain yield (YPP) of 20 wheat genotypes with two checks (SW-1, SW-2) evaluated across five environments.

3.2 Estimation of Variance Components and Heritability

Estimates of the variance components and heritability in broad sense, computed using pooled data from the 5 test environments are presented in Table 5. Accordingly, PCV estimate revealed a much wider variation that ranged from 2.52% in DTM to 16.58% in SL. Similarly, GCV also showed wide variations and ranged from 2.47% in DTM to 12.41% in SL. The PCV estimates were higher than the corresponding GCV values for all the traits, indicating the joint contribution of genetic and environmental effects on trait expression (Ahmad and Gupta, 2023). The wide variability and the predominance of genotypic variance over environmental variance for most traits contributed to high heritability estimates, ranging from moderate to high i.e., 76.97 % to 97.37 %. 1000GW being the most heritable trait (97.37 %), followed by DTM (96.95%), GPS (94.31%), DTF (93.88%), PH (89.37%), SNS (86.00%), SL (84.48%) and YPP (76.97) (Table 5). High heritability for 1000GW, DTF, DTM, PH, SNS and SL, and moderate heritability for grain yield, have also been reported by other researchers (Gaur, 2019; Geneti *et al.,* 2022; Akbarzai *et al.,* 2023).

However, these heritability estimates are specific to the environments and experimental conditions under which the trials were conducted and should therefore be interpreted with caution, as they do not directly predict

Fig. 4: Sequential field images showing phenological progression and early maturity of wheat genotype WW-103 from 10 to 27 May.

selection response across diverse environments. High heritability alone does not guarantee effective selection, particularly under cold-prone environments where G x E interactions may significantly influence trait expression. Consequently, heritability was interpreted in conjunction with genetic advance as a percentage of mean (GAM) to better assess the expected response to selection. Traits such as SL; GAM = 35.5%, SNS; 25.4%, GPS; 13.6%, and YPP; 71.2% exhibited relatively high GAM values, indicating a greater scope for improvement through selection and suggesting a substantial contribution of additive genetic variance. Therefore, indirect selection for these component traits may be more effective and reliable than direct selection for grain yield alone across variable environments (Kumar et al., 2014).

3.3 Principal Component Analysis (PCA) and Phenotypic Correlation

Correlation analysis provided deeper insight into the inter-relationship among agronomic traits, which is crucial for indirect selection in breeding (Ajayi, 2020). Biplots for PCA showing the phenotypic correlations among different traits and correlation matrices for the pooled dataset are provided in Figure 5&6. A total of eight eigenvalues, representing the principal components, were obtained, each contributing differently to the overall variance. Among these, the first, second and third PC, with an eigenvalue greater than 1 were considered significant and selected. The first three PCs of these biplots explained 82.37 % of the total variability (Table 6). Correlation analysis revealed varying levels of association among yield and yield-related traits. DTF exhibited a highly significant and strong positive correlation with DTM (r = 0.86*), consistent with previous findings (Al-Ashkar *et al.*, 2020; Wu *et al.*, 2022). A significant positive correlation was recorded between 1000 GW and SL (r = 0.54*). YPP showed significant positive correlations with SL (r = 0.61), GPS (r = 0.49), and SNS (r = 0.60*). GPS exhibited strong positive and highly significant correlations with SL (r = 0.78) and SNS (r = 0.70*). The strongest positive association among all traits was observed between SL and SNS (r = 0.86*). Significant positive correlations between YPP and spike-related traits such as SL, GPS and SNS, reconfirming earlier reports that spike architecture traits significantly influence grain yield in wheat (Ai *et al.*, 2024; Ji *et al.*, 2025).

In contrast, several significant negative relationships were also detected. PH showed a significant negative correlation with YPP (r = –0.55*), which aligns with the widely accepted preference for semi-dwarf wheat genotypes in terms of the yield perspective as these are responsive to agricultural inputs, like fertilizer, irrigation, etc. (Borojevic and Borojevic, 2005). Taller plants are likely to lodge and need more energy to transport photosynthates to the grains in wheat (Rashid *et al.*, 2025). DTF was negatively correlated with YPP (r = –0.48 *), SL (r = –0.52), and SNS (r = –0.61*). Similarly, DTM displayed

Table 5: Pooled genetic variability of 20 wheat genotypes with two checks evaluated across five environments for days to flowering (DTF), days to maturity (DTM), plant height (PH), spike length (SL), spikelet number per spike (SNS), grains per spike (GPS), grain yield (YPP), and thousand-grain weight (1000GW).

S. No.	Traits	Range			Variance			Coefficient of variance		Selection parameters		
		Mean	Min	Max	EV	GV	PV	GCV	PCV	H^2 (%)	GA (5%)	GA as (%) of mean
1	DTF	189.13	171.71	207.05	4.58	70.27	74.85	4.53	4.61	93.88	16.77	8.87
2	DTM	243.97	224.73	258.60	1.15	36.54	37.69	2.47	2.52	96.95	12.28	5.04
3	PH	118.84	106.96	137.31	4.13	34.74	38.87	5.05	5.34	89.37	11.49	9.66
4	SL	11.83	8.44	16.93	0.90	4.90	5.80	12.41	16.58	84.48	4.20	35.5
5	SNS	19.70	15.83	26.44	1.11	6.82	7.93	8.90	12.53	86.00	5.01	25.4
6	GPS	47.72	40.77	54.76	0.63	10.44	11.07	6.96	8.70	94.31	6.48	13.6
7	YPP	3.89	3.21	4.69	0.70	2.34	3.04	3.61	4.81	76.97	2.77	71.2
8	1000GW	46.54	40.39	52.79	0.15	5.56	5.71	5.05	5.86	97.37	4.80	10.32

EV = Environment variance; GV= Genotypic variance; PV= Phenotypic variance; GCV= Genotypic coefficient of variance; PCV=Phenotypic coefficient of variance; H^2= Heritability; GA= Genetic advance

Table 6: Pooled principal component analysis (PCA) of 20 wheat genotypes along with two checks evaluated across five environments for days to flowering (DTF), days to maturity (DTM), plant height (PH), spike length (SL), spikelet number per spike (SNS), grains per spike (GPS), grain yield (YPP), and thousand-grain weight (1000GW).

Source	PC-1	PC-2	PC-3	PC-4	PC-5	PC-6	PC-7	PC-8
Eigen Value	4.31	1.23	1.04	0.75	0.39	0.14	0.08	0.05
Percentage of Variance	53.93	15.39	13.05	9.42	4.87	1.70	1.04	0.60
Cumulative Variance	53.93	69.32	82.37	91.79	96.66	98.36	99.40	100.00

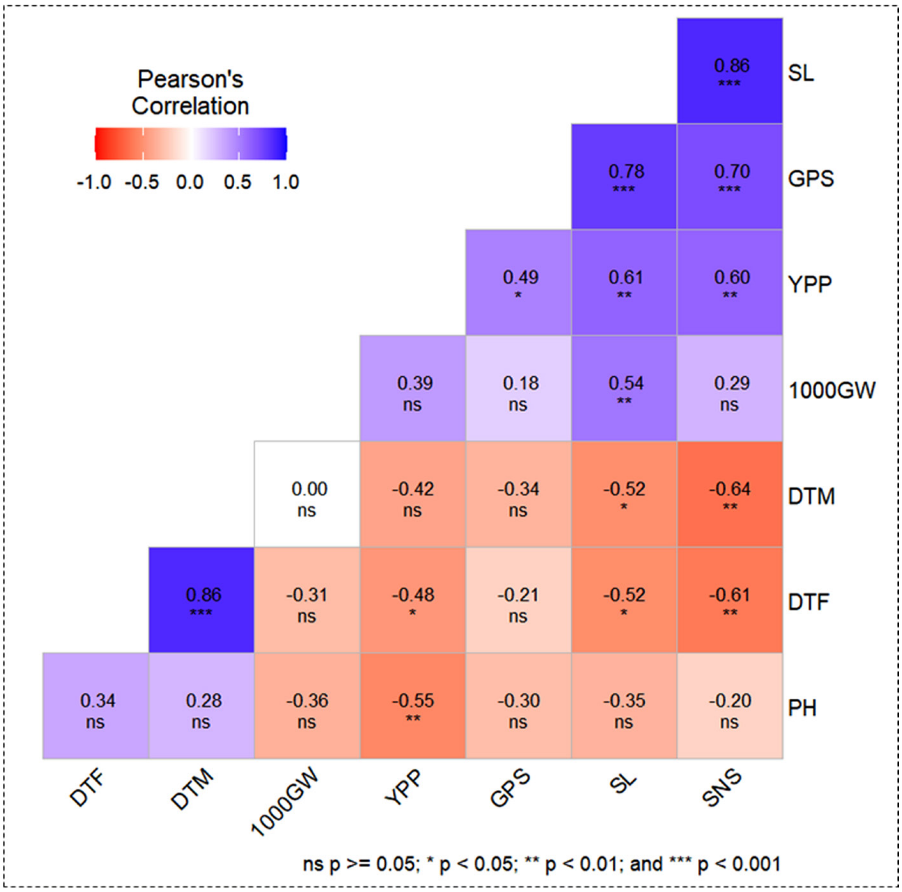

Fig. 5: Pooled Pearson correlation plot of 20 wheat genotypes along with two checks evaluated across five environments for days to flowering (DTF), days to maturity (DTM), plant height (PH), spike length (SL), spikelet number per spike (SNS), grains per spike (GPS), grain yield (YPP), and thousand-grain weight (1000GW).

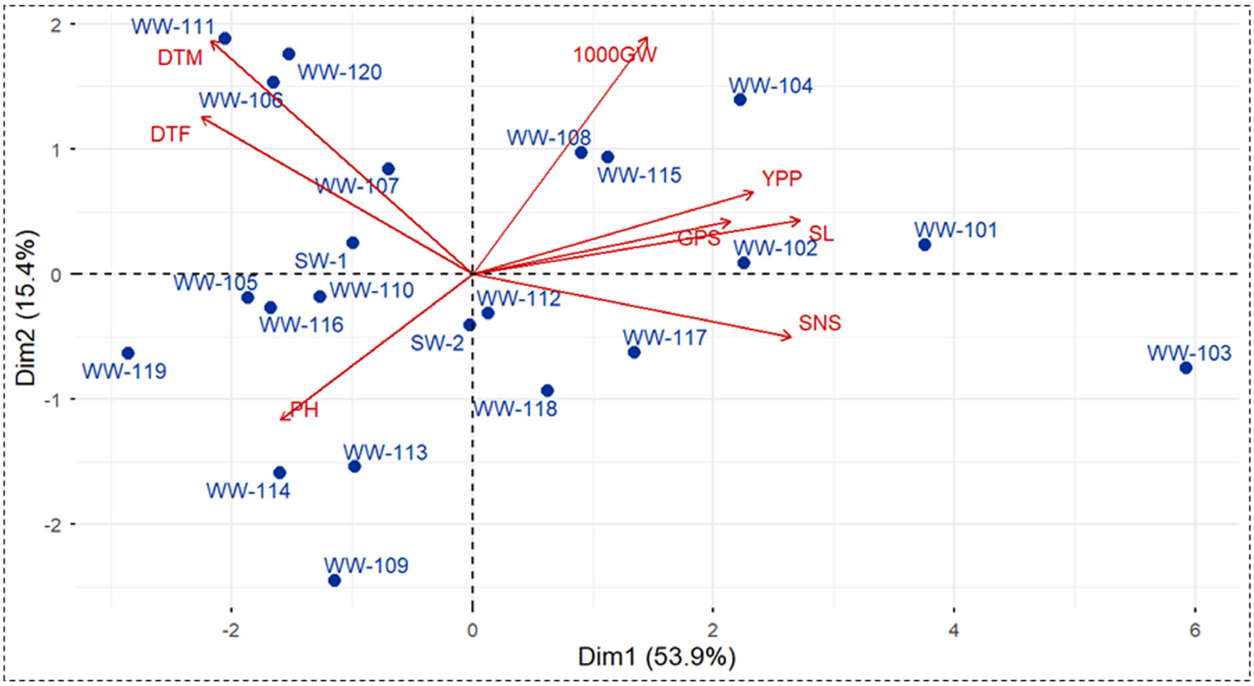

Fig. 6: Pooled Principal component analysis biplot of 20 wheat genotypes along with two checks evaluated across five environments for days to flowering (DTF), days to maturity (DTM), plant height (PH), spike length (SL), spikelet number per spike (SNS), grains per spike (GPS), grain yield (YPP), and thousand-grain weight (1000GW).

significant negative correlations with SL (r = –0.52) and SNS (r = –0.64**). These negative associations suggest that earliness does not necessarily compromise yield potential, supporting earlier research indicating that early flowering or maturity can coexist with moderate to high yield in favourable conditions (Ehlers *et al.,* 2020; Singh *et al.,* 2020; Geneti *et al.,* 2022, Omrani *et al.,* 2025). Such trait associations provide breeders a strategic advantage, enabling simultaneous improvement of multiple traits that influence yield. In crop improvement efforts, such positive correlations between yield and related traits are beneficial, as this allows for the simultaneous enhancement of interconnected traits.

Overall, the proposed three varieties, WW-101, WW-102 and WW-103 demonstrated strong adaptability and reliable performance under the cold-temperate conditions of the Kashmir Valley. Their combined advantages of timely phenology, favourable yield attributes and consistent expression across seasons position them valuable candidates for strengthening local wheat improvement efforts and supporting a timely and efficient RWCS.

Conclusion and Future Directions

The multi-season evaluation of 20 wheat genotypes under cold-temperate conditions of the Kashmir Valley revealed substantial variability in phenological and yield-related traits. Early maturity emerged as a critical factor for enabling timely rice–wheat rotation. Among these, WW-103 consistently combined the earliest maturity with the highest yield, outperforming regional checks, and stands out as the strongest candidate for varietal release. Alongside WW-101 and WW-102, these genotypes demonstrated stable performance across five seasons, confirming their adaptability to low-temperature stress and potential to strengthen rice–wheat cropping system adoption. Their deployment can significantly enhance productivity and regional food security. Future efforts should focus on genomic characterization, marker-assisted breeding, and farmer-participatory trials to accelerate adoption and maximize impact.

Statements and declarations

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Author contributions

Reyazul Rouf Mir: Writing - original draft, investigations, interpretation of results; Mukesh Rathore, Nikita Aggarwal: Data compilation, formal analysis and software; Farkhandah Jan, Safoora Shafi, Mohd. Tahir: Review and editing; Mohd. Ashraf Bhat, Mohd. Anwar Khan, Parvaze Ahmad Sofi, Asif Bashir Shikari: Provided all technical assistance. All the authors read and approved the final manuscript.

Conflicts of Interests

The authors declare that they have no conflicts of interest.

Ethical approval

The article doesn't contain any study involving ethical approval.

Declaration on the use of Generative AI or AI-assisted technologies

The authors declare that no generative AI or AI-assisted technologies were used in the preparation of this manuscript. All text, data interpretation, and analysis were conducted entirely by the authors.

References

1. Aggarwal N, M Rathore, M Shakeel, MA Khan & RR Mir. 2025. First Report of *Bipolaris sorokiniana* Causing Spot Blotch on Wheat (*Triticum aestivum*) from the Kashmir Valley of Western Himalayas, India. *Plant disease*, **109**(10): 2206.https://doi.org/10.1094/PDIS-03-25-0697-PDN

2. Ahmad A and RK Gupta. 2023. Genetic variability, heritability and genetic advance for yield and yield associated traits in bread wheat (*Triticum aestivum* L.). *Annals of Agricultural and Crop Sciences*, **8**(1): 1125.

3. Ai G, C He, S Bi, Z Zhou, A Liu, X Hu, W Yan. 2024. Dissecting the molecular basis of spike traits by integrating gene regulatory networks and genetic

variation in wheat. *Plant Communications*, 5(5). DOI: 10.1016/j.xplc.2024.100879

4. Ajayi AT. 2020. Genetic variability, character association and yield potentials of twenty-five accessions of cowpea (*Vigna unguiculata* L. Walp). *Journal of Pure and Applied Agriculture*, **5**(2).

5. Akbarzai DK, V Singh, S Yashveer, S Nimbal, M Kumar, MS Dalal, S Devi. 2023. Evaluation of genetic diversity of wheat (*Triticum aestivum*) lines under terminal heat stress in the Hisar environment. *Science Letters*, **11**(2): 59-66.

6. Al-Ashkar I, M Alotaibi, Y Refay, A Ghazy, A Zakri, A Al-Doss. 2020. Selection criteria for high-yielding and early-flowering bread wheat hybrids under heat stress. *Plos one*, **15**(8): e0236351.https://doi.org/10.1371/journal.pone.0236351

7. CGIAR Research Program on Wheat. 2025. https://www.cgiar.org/research/program-platform/wheat/

8. Chang CYY, K Bräutigam, NP Hüner, and I Ensminger. 2021. Champions of winter survival: cold acclimation and molecular regulation of cold hardiness in evergreen conifers. *New Phytologist*, **229**(2): 675-691. https://doi.org/10.1111/nph.16904

9. Chevuturi A, AP Dimri, and RJ Thayyen. 2018. Climate change over Leh (Ladakh), India. *Theoretical and Applied Climatology*, **131**(1): 531-545.https://doi.org/10.1007/s00704-016-1989-1

10. Crossa J. 1990. Statistical analyses of multilocation trials. *Advances in agronomy*, *44*, 55-85.

11. Dar SB, RH Kanth, W Raja, SA Bangroo and SA Mir. 2018. Performance of wheat in relation to sowing dates and nitrogen levels under rainfed conditions of Kashmir. *International Journalof Current Microbiology Applied Science*, **7**(4): 2600-2608.

12. Dar SB, RH Kanth, W Raja, SA Bangroo, Z Rashid, ZA Dar and SH Wani. 2020. Performance of wheat variety Shalimar Wheat-2 under rainfed conditions of temperate Kashmir as influenced by sowing dates and nitrogen levels. *Journal of Cereal Research*, **12**(2): 129-136.10.25174/2582-2675/2020/100138

13. Discover India. 2025. Wheat production in India: State-wise breakdown for 2024–25. Agriculture, India Maps. https://www.discoverindia.gov.in/agriculture/wheat-production-india

14. Ganaie SA, MJA Parry and MS Bhat. 2017. Cropping land use shift and food deficit–a disaster in making in Jammu and Kashmir, India. *AGU International Journal of Professional Studies & Research*, **5**, 134-44.

15. Gaur SC. 2019. Genetic improvement through variability, heritability and genetic advance for grain yield and its contributing traits in wheat (*Triticum aestivum* L.). *International Journalof Pure Applied Bioscience*, **7**(1): 368-373.

16. Geneti GS, SA Kebede, and TB Mekonnen. 2022. Genetic variability and association of traits in bread wheat (*Triticum aestivum* L.) genotypes in Gechi district, South WestEthiopia. *Advances in Agriculture*, **2022**(1):7132424. https://doi.org/10.1155/2022/7132424

17. Gull R, MA Bhat, TA Sheikh, FJ Wani, SA Mir and MA Bhat. 2024. Performance of Wheat (*Triticum aestivum* L.) as Affected by Different Densities of Ranunculus spp. under Temperate Conditions of Kashmir Valley, India. *Journal of Scientific Research and Reports*, **30**(12): 81-88.https://doi.org/10.9734/jsrr/2024/v30i122652

18. Hassan MA, C Xiang, M Farooq, N Muhammad, Z Yan, X Hui and L Jincai. 2021. Cold stress in wheat: plant acclimation responses and management strategies. *Frontiers in plant science*, **12**, 676884.https://doi.org/10.3389/fpls.2021.676884

19. Jan F, M Parthiban, S Jan, AK Pradhan, S Kumar, S Shafi, M Bashir, D Sharma, N Qureshi, MK Vishwakarma, S Kaur, J Kaur, PK Bhati, S Kaur, MA Khan, RK Varshney and Mir RR. 2025a. Integrated Genome-wide Association Study (GWAS) and Metabolomics Identify Genetic and Metabolic Drivers of Stripe Rust Resistance in Wheat from the Western Himalayas. *Functional and Integrative Genomics*. https://doi.org/10.1007/s10142-025-01799-4.

20. Jan F, M Rathore, DK Saini, A Singh, N Qureshi, N Aggarwal, M Bashir, M Shakeel, V Gupta, S Kumar, RK Varshney and RR Mir. 2025b. Wheat's War Against Stripe Rust: Integrating Host Immunity, Genomics and Breeding for Durable Resistance. *The*

Plant Genome, 2025; e70174. https://doi.org/10.1002/tpg2.70174

21. Jan S, S Kumar, M Yousuf, S Shafi, R Majid, MA Khan and RR Mir. 2023. Do diverse wheat genotypes unleash their biochemical arsenal differentially to conquer cold stress? A comprehensive study in the Western Himalayas. *Physiologia plantarum*, **175**(6), e14069.https://doi.org/10.1111/ppl.14069

22. Kour M, KN Singh, M Singh, NP Thakur, D Kachroo. 2010. Phenophase prediction model for wheat (*Triticum aestivum*) growth using agro meteorological indices sown under different environments in temperate region of Kashmir. *Journal of Agrometeorology*, **12**(1): 33-36.

23. Littell RC, GA Milliken, WW Stroup and RD Wolfinger. 1996. SAS system for mixed models. *SAS Institute Cary, NC.*

24. Liu J, Q He, G Zhou, Y Song, Y Guan, X Xiao, R Wang. 2023. Effects of sowing date variation on winter wheat yield: conclusions for suitable sowing dates for high and stable yield. *Agronomy*, **13**(4): 991. **https://doi.org/10.3390/agronomy13040991** Ji Z, Liu X, Yan F, Wu S, Du Y. 2025. The Genetic Basis of Wheat Spike Architecture. *Agriculture*, **15**(15): 1575. **https://doi.org/10.3390/agriculture15151575**

25. Mahdi SS, A Gagnon, J Ruckhsana, OA Wani, A Bhat, FA Bahar and RA Bhat. 2025. Optimising the resilience of winter wheat to a changing climate in North Kashmir, India. *Current Science*,https://researchonline.ljmu.ac.uk/id/eprint/26901

26. Mullualem D, A Tsega, T Mengie, D Fentie, Z Kassa, A Fassil and T Astatkie. 2024. Genotype-by-environment interaction and stability analysis of grain yield of bread wheat (*Triticum aestivum* L.) genotypes using AMMI and GGE biplot analyses. *Heliyon*, **10**(12). 10.1016/j.heliyon.2024.e32918 External Link

27. Pradhan GP and PV Prasad. 2015. Evaluation of wheat chromosome translocation lines for high temperature stress tolerance at grain filling stage. *PLoS One*, **10**(2): e0116620. https://doi.org/10.1371/journal.pone.0116620

28. Pant K, D Pandey, B Bastola, M Subedi, R Acharya, N Gautam and R Basnet. 2023. Wheat Varietal Development for the Mid and High Hill region of Nepal. In *Proceedings of 32nd National Winter Crop Workshop, January.*

29. Qammer NA, FA Shaheen, SA Wani and FJ Wani. 2022. Technical, Economic and Allocative Efficiencies of Wheat (*Triticum aestivum*) Growing Farmers in Intermediate Zones of J and K. *Current Agriculture Research Journal*, **10**(2).http://dx.doi.org/10.12944/CARJ.10.2.09

30. Rana V, D Basandrai, VK Sood and A Rana. 2023. Studies on genetic variability in bread wheat (Triticum aestivum L.) under multiple environments in Northern western Himalayas. *Himachal Journal of Agricultural Research*, 155-162. http://hjar.org/index.php/hjar/article/view/172479

31. Rana V. 2024. Identification of promising and stable genotypes of wheat (*Triticum aestivum* L.) for grain yield under varied climatic conditions of north-western Himalayas using joint regression analysis. *Journal of Cereal Research*, **15**(2).

32. Rashid A, FA Sheikh, A Kumar, SH Wani, RR Mir, MA Wani and S Mishra. 2025. Genetic variability for yield and yield attributing traits in Advance wheat breeding lines evaluated under Temperate Ecology. *Agriculture Association of Textile Chemical and Critical Reviews*, **13**(2): 108-112.

33. Salaria S, RS Rana, T Sharma, G Chauhan, SK Sandal, V Kalia and Priyanka. 2024. Optimizing Sowing Windows for Wheat (*Triticum aestivum* L.) in the Sub-temperate Climate of the North-western Himalayas of India. *International Journal of Plant & Soil Science*, **36**(9): 911-918.

34. Sharma A, V Rana, D Basandrai, S Kumar, N Kumar, A Mohapatra and A Sharma. 2025. Genetic variability and correlation studies based on diverse wheat panel for grain yield and related attributes under north-western Himalayan conditions. *Vegetos*, 1-12.https://doi.org/10.1007/s42535-025-01400-0

35. Shi W, C Hao, Y Zhang, J Cheng, Z Zhang, J Liu and J Guo. 2017. A combined association mapping and linkage analysis of kernel number per spike in common wheat (*Triticum aestivum* L.). *Frontiers*

in plant science, **8**: 1412.https://doi.org/10.3389/fpls.2017.01412

36. Singh KP, V Singh, G Sharma, MP Chauhan, T Singh and RDS Yadav. 2020. Correlation and Path Coefficient Analysis in Wheat (*Triticum aestivum* L.). *International Journal of Current Microbiology and Applied Science*, **9**(11): 1570-1581.

37. Singh C, A Gupta, P Kumar, R Sendhil, K Gopalareddy, V Gupta and GP Singh. 2020. multi-environment analysis of grain yield in a diverse set of bread wheat genotypes. *Journal of Cereal Research*, **12**(1): 29-39.

38. Singh C, S Yadav, V Khare, V Gupta, UR Kamble, OP Gupta and R Tiwari. 2024. Unraveling the secrets of early-maturity and short-duration bread wheat in unpredictable environments. *Plants*, **13**(20), 2855.

39. Kumar V, P Sharma, H Kumar and G Gupta. 2014. Studies of variability and association of yield with some agromophological characters in bread wheat (Triticum aestivum L.). *Indian Journal Agriculture Research,* **48**(6) 429-436. doi:10.5958/0976-058X.2014.01326.2

40. World Health Organization. 2023. The State of Food Security and Nutrition in the World2023: Urbanization, agrifood systems transformation and healthy diets across the rural–urban continuum (Vol. 2023). *Food & Agriculture Org*https://coilink.org/20.500.12592/31zct0h

41. Yanagi M. 2024. Climate change impacts on wheat production: Reviewing challenges and adaptation strategies. *Advances in Resources Research*, **4**(1): 89-107. https://doi.org/10.50908/arr.4.1_89

42. Yousaf MI, K Hussain, H Hussain, AG Ghani, M Arshad, M Mumtaz and RA Hameed. 2018. Characterization of indigenous and exotic maize hybrids for grain yield and quality traits under heat stress. International journal of agricultural and biology, **20**(2):333-337. DOI: 10.17957/IJAB/15.0493

43. Yue H, HG Gauch, J Wei, J Xie, S Chen, H Peng and Jiang X. 2022. Genotype by environment interaction analysis for grain yield and yield components of summer maize hybrids across the huanghuaihai region in China. *Agriculture*, **12**(5): 602. https://doi.org/10.3390/agriculture12050602