

Identification of resistant sources against spot blotch and stripe rust of barley

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Article history

Received: 16 Apr., 2019

Revised: 11 Dec., 2019

Accepted: 05 Jan., 2020

Citation

Kumar V, PS Shekhawat, SR Vishwakarma, SC Bharadwaj, S Kumar, AS Kharub and GP Singh 2020. Identification of resistant sources against spot blotch and stripe rust of barley. *Journal of Cereal Research* 12(1):50-54. <http://doi.org/10.25174/2582-2675/2020/88973>.

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Abstract

Stripe rust and spot blotch are major biotic constraints in yield maximization of barley. Stripe rust, caused by fungus, *Puccinia striiformis* f. sp. *hordei*, is wide spread in northern hills and in the states of Punjab, Haryana and Rajasthan. Spot blotch (*Bipolaris sorokiniana*) is one of the major diseases in north eastern Indo-Gangetic plains. The resistant sources for stripe rust are available but the genetic resources for spot blotch are indeed meagre. Therefore, present investigation was aimed to identify combined resistant sources for stripe rust and spot blotch in barley. The experiments for stripe rust were conducted at Durgapura and Karnal during 2015-16 to 2017-18. While, spot blotch evaluation was carried out for two years (2015-16 and 2016-17) at Faizabad and Karnal centres. The indigenous genotypes, DWRB127, DWRB128, DWRB136, DWRB137, DWRB143, RD2786 and Dolma showed resistance for stripe rust. Based upon stripe rust and spot blotch reactions four genotypes DWRB136, Notch-2, Orosus and Bella Union were found promising. Similarly, the cross combination viz., Lbiran/Una80//Lignee640/3/Bbsc/4/Chamico and P.sto/3/Libran/Una80//Lignee640/4/Bllu/5/ Petunia1 were also considered promising for barley stripe rust and spot blotch. Therefore, these identified genotypes can be incorporated in future barley breeding programmes for stripe rust and spot blotch resistance.

Keywords: Barley, resistant sources, stripe rust, spot blotch

1. Introduction

Barley is one of the oldest crops presumably domesticated nearly ten thousand years ago and further moved from its origin in the 'Fertile Crescent' (Middle East) to the rest of the world (Baik and Ullrich, 2008; Kumar *et al.*, 2018). The uses of the crop are very wide from food and feed to malting and brewing purposes. Genetically, barley is hardy in nature, requires low-input and a good option under rainfed, salinity, alkalinity and other adverse conditions. This adaptability to harsh environments and unique malting properties favour its cultivation primarily in Rajasthan, Uttar Pradesh, Madhya Pradesh, Bihar,

Haryana, Punjab, Jammu and Kashmir, Himachal Pradesh and Uttarakhand. Unlike abiotic stresses, various biotic stresses in barley, cause marked grain yield reduction and significant losses to grain quality (Line, 2002; Kuldeep *et al.*, 2008). Stripe rust and spot blotch are two major fungal foliar diseases in barley and occur in the major barley growing areas. Stripe rust of barley is caused by the pathogen *Puccinia striiformis* f. sp. *hordei* (Psh) and considered as *formae speciales* of wheat stripe rust pathogen *Puccinia striiformis* f. sp. *tritici* and host ranges are almost similar of these separate forms (Wellings, 2011; Derevnina *et al.*, 2015).

Similarly, spot blotch is an economically important disease and a major constraint in production and productivity enhancement in barley. Barley spot blotch is caused by ascomycetous hemi-biotrophic filamentous fungus *Cochliobolus sativus* (Ito and Kurib.) Drechs. ex Dastur [anamorph: *Bipolaris sorokiniana* (Sacc.) Shoem.] (Wang *et al.*, 2017). The north eastern *Indo-Gangetic* plains and the parts of eastern Uttar Pradesh, Bihar and west Bengal are highly prone for foliar blight incidences due to the warm and humid climatic conditions. The disease also affects barley in the north western plains (Haryana, Punjab and Rajasthan) during later stages of crop due to risen temperature and other favourable weather parameters (Singh *et al.*, 2014). The fungus penetrates in to the cuticle and cell wall followed by the hyphae development, which leads to the death of epidermal and mesophyll layers (Kumar *et al.*, 2002). The sesquiterpenoid toxins (helminthosporol) are produced by the fungus, which are harmful to plant cells and can cause severe damage.

Both the diseases namely stripe rust and spot blotch are devastating and can cause marked yield reductions (up to 60%) in barley (Kuldeep *et al.*, 2008). Both the diseases may be managed partially by use of fungicides. However, use of chemicals is costly and the resource poor small and marginal farmers can not afford costly spray schedules and increasing awareness regarding their deleterious effects on soil, water, environmental and human health restricts their use. On the other hand, development and deployment of resistant varieties is a cost effective, sustainable, practically feasible, farmer and eco-friendly alternative for the management of these diseases. Identification of resistance sources and their characterization is pre-requisite for any breeding programme aimed to develop resistance varieties. Though, the genetic resources for barley stripe rust are available but the resistant sources for spot blotch are indeed meagre. Therefore, the present investigation was aimed to identify promising genetic resources for combined stripe rust and spot blotch resistance from indigenous and exotic gene pool.

2. Materials and methods

A set of 60 indigenous and exotic barley genotypes including internationally designated gene sources was evaluated to identify effective resistant sources for barley stripe rust and spot blotch. The internationally designated sources were Trumpf (*rpsTr1*, *rpsTr2*), Emir (*rpsEm1*,

rpsEm2), Hiproly (*rpsHi1*, *rpsHi2*), Bigo (*rps1.b* (*yr*)), Abed Binder12 (*rps2* (*yr2*)), I5 (*rps3* (*yr3*), *rpsI5*) and Astrix (*Rps4* (*Yr4*), *rpsAst*). The evaluation for barley stripe rust was conducted at ICAR-Indian Institute of Wheat and Barley Research (ICAR-IIWBR), Karnal and Rajasthan Agricultural Research Institute, Durgapura for adult plant resistance (APR) during 2015-16 to 2017-18. The seedling resistance test (SRT) was conducted at ICAR-IIWBR, RS, Shimla and spot blotch evaluation at Narendra Deva University of Agricultural and Technology, Faizabad (natural hot spot) during 2015-16 to 2016-17. Each genotype was grown in the paired rows of 2.5 meter length with row to row spacing of 25 cm and all the recommended agronomic package of practices were followed to raise the good crop. The genotypes were inoculated with the mixture of four races of barley stripe rust pathogen *viz.*, 57 (0S0), 24 (0S0-1), M (1S0) and G (4S0) to create epiphytotic conditions at Karnal and Durgapura centres. The spreader lines were injected and artificially inoculated at 21 days seedling stage (Zadoks GS 20) and extra irrigation was applied for maintaining congenial micro-climate for stripe rust (Zadoks *et al.*, 1974). The modified Cobb's scale (Peterson *et al.*, 1948) based on per cent infected host tissue and infection types (ITs) was used for disease data recording as (Mishra *et al.*, 2005)- R (resistant): necrotic areas with or without minute uredia; MR (moderately resistant): small uredia surrounded by necrotic areas; MS (moderately susceptible): medium uredia with no necrosis but chlorotic areas may be present; S (susceptible): large uredia with no necrosis and little or no chlorosis. In seedling resistance test (SRT)- infection types (ITs) (0, 0;, 1 and 2) were considered as resistant (R), 2 and 2+ (Moderately resistant-MR); 3 and 3 (Moderately susceptible-MS) and 3+ and 33+ (Susceptible-S).

The spot blotch observations were recorded thrice at flowering (Zadok GS 55), early milk (Zadok GS 73) and soft dough (Zadok GS 85) growth stages for disease severity. The spot blotch was recorded as per cent infected area with spot blotch on the flag leaf and penultimate (flag-1) leaf using double digit scale (00-99) (Prasad *et al.*, 2013; Singh *et al.*, 2014). In this double digit score, first digit displayed flag leaf per cent area covered by the spot blotch and the second digit denoted the flag-1 leaf disease severity, respectively. The reactions were grouped as no disease (00, immune), resistant-R (01-24, lesions absent

or small without chlorosis), moderately resistant-MR (25-46, lesions small but with small chlorosis), moderately susceptible-MS (47-57, large lesions with more chlorosis but little or no coalescence) and susceptible-S (58-78, large lesions and coalescence with chlorosis) and highly susceptible-HS (>78, large lesions, extensive chlorosis and coalescence), respectively.

3. Results and discussion

In total, 60 genotypes were selected from exotic gene pool (ICARDA), indigenous varieties, genetic stocks and advance breeding materials and were considered for stripe rust and spot blotch studies. Among the test genotypes, 50 were of exotic origin and rest 10 genotypes, DWRB127, DWRB128, DWRB136, DWRB137, DWRB143, RD2552, RD2786, Dolma, RD2035 and Lakhan were from Indian gene pool. The results for seedling resistance test (SRT), adult plant resistance (APR) and spot blotch for international designated sources are presented in the Table 1. The genotypes *viz.*, Trumpf (*rpsTr1*, *rpsTr2*), Emir (*rpsEm1*, *rpsEm2*) and Astrix (*Rps4* (*Yr4*), *rpsAst*) showed resistant reactions at adult plant stage for stripe rust (Table 1). However, in SRT analysis only genotype Trumpf was found resistant to all races of rust races pathogen. Other designated sources, Hiporly (40S), Bigo (40S) and I5 (30S) exhibited susceptibility for stripe rust at both seedling and adult plant stages (Table 1). However, the genotype Abed Binder12 was found moderately susceptible (10MS) but showed susceptible response for all the barley Psh races *viz.*, 57, 24, M and G. The internationally designated sources were also evaluated for spot blotch and the genotypes Emir (35) and Bigo (46) were categorized as

Table 1. Response of designated sources for stripe rust and spot blotch in barley

Genotype	Genes	APR (HS)	Seedling resistance				Spot blotch
			24	57	G	M	
Trumpf	<i>rpsTr1</i> , <i>rpsTr2</i>	0	0;	0;	0;	0;	78
Emir	<i>rpsEm1</i> , <i>rpsEm2</i>	5MR	3+	3+	3+	3+	35
Hiporly	<i>rpsHi1</i> , <i>rpsHi2</i>	40S	3	3	3+	3+	67
Bigo	<i>rps1.b</i> (<i>yr</i>)	40S	3+	3+	3+	3+	46
Abed Binder 12	<i>rps2</i> (<i>yr2</i>)	10MS	3+	3+	3+	33+	57
I5	<i>rps3</i> (<i>yr3</i>), <i>rpsI5</i>	30S	3+	3+	3+	3+	67
Astrix	<i>Rps4</i> (<i>Yr4</i>), <i>rpsAst</i>	10MR	3+	3	3+	3	68

moderately resistant on the double digit scale. Verma *et al.*, (2018) revealed the genotypes Trumpf and Astrix as effective sources for stripe rust but here we found only the genotype Trumpf (*rpsTr1*, *rpsTr2*) promising against Indian races of barley yellow rust pathogen.

In addition to the designated sources, Indian and exotic genotypes were also evaluated for stripe rust and spot blotch. Among indigenous materials, the genotypes *viz.* DWRB127, DWRB128, DWRB136, DWRB137, DWRB143, RD2552, RD2786 and Dolma exhibited the resistant reactions for stripe rust. Out of these genotypes, the genotypes, DWRB127, DWRB137, DWRB143, RD2552 and RD2786 also confirmed seedling resistance for all the Psh races. The hulless genotype Dolma was resistant for the races 57 and G but showed susceptibility to the races 24 and M. Similarly, the two-rowed barley genotype DWRB136 was found resistant for Psh races 24, 57 and G and showed susceptibility for the race M (Table 2). Kumar *et al.*, (2015) also reported that the genotype DWRB143 possessed both seedling and adult plant resistance for barley stripe rust. For further confirmation of data, field reactions of susceptible checks, RD2035 and Lakhan were recorded, where both the check varieties showed stripe rust reactions of 80S and confirmed susceptibility. Both the released varieties were also found susceptible in SRT to all the Psh races.

Among 49 exotic genotypes, C9430, Orosus, Aloe/Geranio//Mja, Lbiran/Una80//Lignee640/3/Bbsc/4/Chamico, Bella Union, Canela/Cheri and San cristobal were found resistant at adult plant stage (Table 2).

In seedling resistance test, the genotypes, C9430, Orosus and Canela/Cheri confirmed R or MR reactions against different Psh races. The genotypes, Notch-2, Moronera Inia and P.sto/3/Libran/Una80//Lignee640/4/Bllu/5/Petunia1 showed moderate resistance under field conditions. The genotype Robust/Ibta Maltera depicted susceptible reaction (10S) for yellow rust at adult plant stage. Here, the genotypes Notch-2 and Moronera Inia exhibited MR-R reactions for Psh races 24, 57 and G but showed susceptibility to race M.

Identification of genotypes with multiple disease resistance is one of the main objectives in breeding programmes. In the present study, the genotypes having spot blotch resistance in addition to stripe rust resistance were

Table 2. Reactions of barley genotypes for stripe rust and spot blotch

Genotype	YR (HS)	Seedling resistance				Spot blotch
		24	57	G	M	
Notch-2	10MR	2-	2-	0;	3	36
C 9430	0	2	2	0;	2-	46
Moronera Inia	5MR	0;	0;	0;	3+	46
Orosus	0	2-	2	0;	2	25
Aloe/Geranio// Mja	0	3+	3	3+	3	46
Lbiran/Una80// Lignee640/3/ Bbsc/4/Chamico	0	3+	33+	3+	3+	24
P.sto/3/Lbiran/ Una80// Lignee640/4/ Bllu/5/Petunia1	TMR	3+	0;	0;	3+	25
Bella union	0	0;	0;	0;	3+	36
Robust/Ibta Maltera	10S	3+	3	3+	3+	25
Canela/Cheri	0	;	0;	0;	;-	46
San cristobal	0	3+	3+	3+	3+	46
DWRB128	0	3+	0;	0;	3+	46
DWRB136	0	0;	0;	0;	3+	35
DWRB143	0	;	0;	0;	0;	45
Dolma	0	3	0;	0;	3+	46
Susceptible checks						
RD2035	80S	3+	3+	3+	3+	78
Lakhan	80S	3+	3+	3+	3+	67

identified. The cross Lbiran/Una80//Lignee640/3/ Bbsc/4/Chamico showed spot blotch score of 24 at Faizabad for consecutive two years and could be regarded as promising source for spot blotch resistance in barley. Similarly, the genotypes, Orosus, P.sto/3/Libran/Una80// Lignee640/4/Bllu/5/Petunia1 and Robust/Ibta Maltera also showed moderate resistance (25) for spot blotch. Based on response to both stripe rust and spot blotch, the genotypes, DWRB136, Notch-2, Orosus, Bella Union, Lbiran/Una80//Lignee640/3/Bbsc/4/Chamico and P.sto/3/Libran/Una80//Lignee640/4/Bllu/5/Petunia1 were found promising under Indian conditions.

4. Acknowledgements

Authors sincerely acknowledge use of exotic materials procured from International Centre for Agricultural

Research in the Dry Areas (ICARDA) for research purposes during the course of study.

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