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Original Article

Characterization of wheat-*Thinopyrum bessarabicum* genetic stock for stripe rust and Karnal bunt resistance

Caracterização do estoque genético de trigo-*Thinopyrum bessarabicum* para resistência de ferrugem e Karnal bunt

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Abstract

Utilization of modern breeding techniques for developing high yielding and uniform plant types ultimately narrowing the genetic makeup of most crops. Narrowed genetic makeup of these crops has made them vulnerable towards disease and insect epidemics. For sustainable crop production, genetic variability of these crops must be broadened against various biotic and abiotic stresses. One of the ways to widen genetic configuration of these crops is to identify novel additional sources of durable resistance. In this regard crops wild relatives are providing valuable sources of allelic diversity towards various biotic, abiotic stress tolerance and quality components. For incorporating novel variability from wild relative's wide hybridization technique has become a promising breeding method. For this purpose, wheat-*Th. bessarabicum* amphiploid, addition and translocation lines have been screened in field and screen house conditions to get novel sources of yellow rust and Karnal bunt resistant. Stripe rust screening under field conditions has revealed addition lines 4JJ and 6JJ as resistant to moderately resistant while addition lines 3JJ, 5JJ, 7JJ and translocation lines Tr-3, Tr-6 as moderately resistant wheat-*Thinopyrum-bessarabicum* genetic stock. Karnal bunt screening depicted addition lines 5JJ and 4JJ as highly resistant genetic stock. These genetic stocks may be used to introgression novel stripe rust and Karnal bunt resistance from the tertiary gene pool into susceptible wheat backgrounds.

Keywords: wheat (*Thinopyrum bessarabicum*) addition and translocation lines, yellow rust, Karnal bunt, biotic stress resistance.

Resumo

A utilização de técnicas modernas de melhoramento para o desenvolvimento de tipos de plantas uniformes e de alto rendimento, em última análise, estreitando a composição genética da maioria das culturas. A composição genética restrita dessas plantações tornou-as vulneráveis a doenças e epidemias de insetos. Para uma produção agrícola sustentável, a variabilidade genética dessas culturas deve ser ampliada contra vários estresses bióticos e abióticos. Uma das maneiras de ampliar a configuração genética dessas culturas é identificar novas fontes adicionais de resistência durável. A esse respeito, os parentes selvagens das culturas estão fornecendo fontes valiosas de diversidade alélica para vários componentes de qualidade e tolerância ao estresse abiótico e biótico. Para incorporar a nova variabilidade da ampla técnica de hibridização de parente selvagem tornou-se um método de reprodução promissor. Para esse efeito, trigo-*Th*. As linhas anfiploides, de adição e translocação de *bessarabicum* foram selecionadas em condições de campo e de casa de tela para obter novas fontes de ferrugem amarela e resistência ao bunt de Karnal. A triagem de ferrugem em faixas em condições de campo revelou as linhas de adição 4JJ e 6JJ como resistentes a moderadamente resistentes, enquanto as linhas de adição 3JJ, 5JJ, 7JJ e as linhas de translocação Tr-3, Tr-6 como estoque genético de trigo-*Thinopyrum bessarabicum* moderadamente resistente. A triagem Karnal bunt descreveu as linhas de adição 5JJ e 4JJ como estoque genético altamente resistente. Esses estoques genéticos podem ser usados para introgressão da nova ferrugem e resistência ao bunt de Karnal do pool genético terciário em origens de trigo suscetíveis.

Palavras-chave: linha de adição e translocação de trigo (*Thinopyrum bessarabicum*), ferrugem amarela, Bunt Karnal, resistência ao estresse biótico.

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1. Introduction

World's diet constitutes about 93 percent of the plants. Among these plants, cereals contribute two-thirds of all food. Wheat, maize and rice constitute about 80 percent of total global cereal production (Getachew and Biruk, 2018). Wheat (*Triticum aestivum* L.) is the world's leading cereal grain used as staple food by more than one third of the world's population (FAO, 2018) . It is a leading source of calories as well as protein consumption for both humans and livestock (Narang et al., 2020). Modern day agriculture is facing severe challenges from biotic and abiotic stresses, threating its food security and sustainable development (Jinya et al., 2020). Among various kinds of biotic stresses, fungi are the most devastating one causing the majority of plant diseases (Robert-Seilaniantz et al., 2011). Wheat crop is hosted by variety of fungal pathogens which causes infection at different developmental stages; among them the important ones are stripe rust and karnal bunt. (Bishnoi et al., 2020). Most important wheat foliar disease yellow rust (stripe rust) is caused by a fungus known as *Puccinia striiformis* f. sp. tritici. Almost all the continents except Antarctica host this disease (Ali et al., 2017). Wheat grain loss of about 30 to 100% due to this fungus imposing global threat to wheat production (Chen, 2005). Various reports have revealed that this disease had the ability to destroy the entire wheat crops under favorable conditions (Mengesha, 2020). In Pakistan, losses due to this disease are not estimated (Shakoor et al., 2015), but at global level yield loss of at least 5.5 million tons per year is caused by yellow rust disease (Marcelo et al., 2020). *Puccinia striiformis* f. sp. destroys the plants respiratory system by causing necrosis, stunting plant growth and by reducing grain yield (Line, 2002; Chen, 2005). Defending measures against the destruction of this pathogen are of primary concern for world food security (Chakravarty, 2011). Diverse disease control strategies like use of chemicals and agronomic practices are proven profitable to lessen the losses (Foster et al., 2017), but it has been reported that recurrent use of the same chemical fungicide for several years under extensive wheat production area might favor the development of resistant pathogens ultimately necessitating the use of alternate fungicide (Getachew and Biruk, 2018). So, in this situation host genetic resistance is the most practicable method to control stripe rust alternatively. Crops genetic resistance exploitation is economical, and bears no health and environmental hazards and proving resistant for a longer period of time ensuring crop sustainability (Hovmøller et al., 2017; Farrokhi et al., 2011). Stripe rust resistance of two types, all-stage resistance (also called race specific) and adult-plant resistance (also called race nonspecific) have been identified. Among these two types, adult plant resistance (Apr) has been found to be effective against all races conferring durable resistance. (Chen, 2013). On the contrary, race specific resistance becomes ineffective within three to five years (Line and Qayoum, 1992). Strategy of pyramiding these major (race specific) and minor (race non-specific) genes (Singh et al., 2004) could result in sustainable resistance. *Tilletia Indica* Mitra causing karnal bunt disease of wheat reported first time from Karnal, Haryana, India in 1931 (Mitra 1931). Bonde et al. (1997) and Rush et al. (2005) have also reported the prevalence of this disease in other countries. Karnal Bunt infection does not cover the entire wheat ear, rather it restricts its infection to a few kernels within a spike and to a part of the grain and rarely the whole grain, thereby, the disease has also been given the name partial bunt (Pandey et al., 2019). The fungus infests the ovaries in the emerging wheat heads resulting in partially or completely filled powdery masses of teliospores emitting a foul smell of trimethylamine (Shakoor et al., 2015). Wheat grains infected with KB are of low quality as they port an unacceptable odor, color, and taste and at as low as 1% infection the grains/flour become unpalatable (Kashyap et al., 2018). Most devastating effect of Karnal bunt (KB) is to quarantine regulations that may restrict the free global trade of wheat besides the loss of grain yield and quality as well (Bishnoi et al., 2020; Sukhwinder et al., 2007). Cultural practices and chemical treatments have been futile due to soil-borne and an airborne sporidial stage (Carris et al., 2006; Garrett and Bowden, 2002, Kumar et al., 2014). The morphological barriers as well as the physiological traits manifests the genetic resistance against KB fungus in wheat and Durum. For example, the higher degree of resistance expressed by triticale and durum wheat in comparison to bread wheat is attributed to the morphological defense barriers like pubescence rather than it being physiological (Warham, 1988). The morphological traits like leaf sheath, flag leaf base, glumes and rachis with higher number of stomata and glumes and rachis with low hair count and compact arrangement of spikelets are relevant to the resistant lines (Bishnoi et al., 2020). The Gogoi et al. (2002) elaborated that relatively more resistant durum wheat and triticale have lower glume opening and low ear emergence period. Thus, the best approach to protect the crop from yellow rust and Karnal bunt pathogens is to breed for genetic resistance. (McIntosh et al., 2018). Due to limited genetic diversity within cultivated crops (Reif et al., 2005), cytogeneticists, breeders and farmers are sorting out additional and novel sources of resistance from primary, secondary, and tertiary gene pools of wheat (Feuillet et al., 2008, Milus et al.., 2015). Wheat wild relatives from tertiary gene pool are providing valuable sources of genetic diversity having a variety of R genes for rust and Karnal bunt resistance that could enable more sustainable disease control (Kerber and Dyck, 1990; Narang et al., 2020). Genes from over 52 allien species including *T. umbellulatum, T. comosum, Thinopyrum intermedium, Th. elongatum, Th. ponticum* and *Secale cereale* have been introgressed (McIntosh et al., 1995) into wheat to exploit natural variation of alien species for wheat improvement (Wulff and Moscou, 2014).

In this regard, characterization of various wheat-allien genetic stocks for identification of such novel resistances is paramount. Keeping in view the importance of Yellow rust and Karnal bunt diseases, Present study was carried out to screen wheat-*Th. bessarabicum* genetic stocks possessing resistance against stripe rust and Karnal bunt to enhance cultivar improvement by using these wheat-allien genetic stocks in breeding programs in Pakistan.

2. Materials and Methods

2.1. Field evaluation for stripe rust resistance

Wheat-*Th. bessarabicum* genetic stocks along with Chinese Spring wheat variety, and standard check variety Morocco (Table 1) were screened for adult plant resistance in field conditions of NARC Islamabad during wheat growing cycles (2012-2015). The material was raised in Randomize Complete Block design (RCBD) with three replications. Each plot consisted of one row of 2.5 m length spaced at 30 cm between rows and 15 cm between plants. Every fifth row was seeded with Morocco check cultivar. Other recommended cultural practices for wheat production were followed during the growing seasons. All the genetic stock was inoculated thrice by Uredio-spore suspension to create stripe rust epidemic after 6 weeks of planting. The data were analyzed by using modified Cobb scale (Mengesha, 2020).

2.2. Disease scoring for adult plant resistance

Data was taken at flag leaf stage for disease severity and infection after every 10-days interval. The data was recorded by using modified Cobb scale (Mengesha, 2020) as percent (%) of the rust infection on the plants surface. Field response referring to the type of infection was recorded according to the Table 2. The data was recorded for disease severity first time when the susceptible check (Morocco) had reached up to 100% disease infection (Table 2).

Table 1. Pdigree of wheat-*Th. bessarabicum* genetic stocks.

Genetic Stock	Pedigree
Tr-1	6BS.6BL-6J (CS/Th.bess//CSph/3/4*Prinia
Tr-2	1DS.1JS
Tr-3	3JS.3BL, (CS/Th.bess//CSph/3/3*Prinia
Tr-4	1AS.1AL-1JL
Tr-5	7DS.7DL-4J, (CS/Th.bess//CSph/3/4*Prinia
Tr-6	6JS.7DL, (CS/Th.bess//CSph/3/4*Prinia
Tr-7	5JS.5DS.5DL
Amphiploid	CS/*Thinopyrum bessarabicum*
1JJ	CS+1JJ (2n = 6x= 42+2= AABBDD+1JJ)
2JJ	CS+2 JJ (2n = 6x= 42+2= AABBDD+2JJ)
3JJ	CS+3 JJ (2n = 6x= 42+2= AABBDD+3JJ)
4JJ	CS+4 JJ (2n = 6x= 42+2= AABBDD+4JJ)
5JJ	CS+5JJ (2n = 6x= 42+2= AABBDD+5JJ)
6JJ	CS+6JJ (2n = 6x= 42+2= AABBDD+6JJ)
7JJ	CS+7JJ (2n = 6x= 42+2= AABBDD+7JJ)
3JJ42	CS+Tr 3J(2n = 6x= 42 = AABBDD+Tr3J)
3JJ44	CS+Tr 3JJ(2n = 6x= 42+2= AABBDD+Tr3JJ)
CS/bess// Pav	CS/Th. bess//Pavon (7x = 49 =42+7 = AABBDDJ)
CS/bess// Gen	CS/Th. bess//Genaro (7x = 49 =42+7 = AABBDDJ)
CS, Genaro 81, Morroco	Wheat cultivars

2.3. Karnal bunt

2.3.1. Inoculation technique and disease scoring

For Karnal bunt screening, 1 ml tiller^{-1} sporodial suspension taken from Crop disease research institute (CDRI) of NARC Islamabad was injected by using a hypodermal syringe at booting stage (Stages 48-49) (Zadoks et al., 1974) for two consecutive wheat growing cycles in NARC fields, i.e., 2013- 2015. Tagging of injected tillers was done. Susceptibility category was evaluated for all genetic stocks inoculated on the basis of CI Table 3, following the susceptibility category given by Aujla et al. (1989).

3. Results

3.1. Stripe Rust and Karnal bunt

Wheat-*Thinopyrum bessarabicum* addition and translocation lines along with Chines Spring variety, Chines Spring wheat-*Thinopyrum bessarabicum* amphiploid and check cultivar Morocco were screened for stripe rust resistance. Yellow rust disease surveillance was done by using modified Cobb scale (Mengesha, 2020). Data for rust resistance evaluation is represented in Table 4. Average Coefficient of infection (ACI) for these genetic stocks is calculated from CI (Coefficient of infection) values of each genetic stock shown in the Table 4. Wheat-*Thinopyrum bessarabicum* addition line 4JJ (2.0) and 6JJ (2.33) distinguished as resistant material toward stripe rust fungal pathogen (Table 4). Addition line 3JJ (9.3), 5JJ (13.3), 7JJ (6.67), Tr-3 (10.0) and Tr-6 (11) were ranked as moderately resistant (Table 4). Translocation lines Tr-4 (16.0), Tr-5 (26.67) comes under moderately susceptible category while addition line 1JJ (34.0), translocation lines Tr-1 (38.0), Tr-2 (32.0), Tr-7 (42.0), Tr-8 and Tr-9 (34.0) behaved as susceptible and wheat cultivar used in developing these addition and translocation lines CS and amphiploid were late.

3.2. Karnal bunt

Percent incidence caused by *Tilletia indica* showed variety of susceptibility categories in all wheat-*Th. bessarabicum* genetic stocks (Table 5). Wheat-*Thinopyrum bessarabicum* addition line 4JJ, 5JJ and amphiploid delineated highly resistant attitude, addition line 2JJ, 3JJ, 7JJ, translocation line Tr-1. Tr-3, Tr-5, Tr-7, Tr-42, Tr-44, and two BC1s self-fertile lines were ranked as resistant (Table 6). 6JJ addition line comes under moderately susceptible category while addition line 1JJ, translocation lines Tr-2, Tr-4, Tr-6, and wheat cultivars used in developing these addition and translocation lines Genaro-81 showed response as susceptible (Table 6).

Table 2. Rust reaction, infection type for field response and response value.

Reaction	Infection type	Field response	Response value
No disease	0	No visible infection	0
Resistant	R	Necrotic areas with or without minute uredia	0.2
Moderately resistant	MR	Small uredia present surrounded by necrotic area	0.4
Moderately resistant	MRMS	Small uredia present surrounded by necrotic areas as well as medium	0.6
moderately susceptible	MS	uredia with no necrosis but possible some distinct chlorosis	
Moderately susceptible		Medium uredia with no necrosis but possible some distinct chlorosis	0.8
Moderately susceptible-susceptible	MSS	Medium uredia with no necrosis but possible some distinct chlorosis as well as large uredia with little or chlorosis present	0.9
Susceptible	S	Large uredia and little or no chlorosis present	1

(Mengesha, 2020).

Table 3. Standardization of vulnerability category based on CI value.

Co-efficient of Infection (CI)	Susceptibility Category
0	Highly resistant (HR)
0.1 – 5.0	Resistant (R)
5.1-10.0	Moderately Susceptible (MS)
10.1- 20.0	Susceptible (S)
20.0 and above	Highly Susceptible (HS)

(Aujla et al., 1989).

4. Discussion

Wheat is the largest cereals crop of the world. Despite its importance as cereal crop, its yield and productions are prone to various biotic and abiotic factors among which wheat rust diseases are the most important. One of the most important objectives of wheat breeding programs in all wheat growing regions of the world is to develop durable tolerance against yellow rust in wheat cultivars (Akfirat et al., 2010). Durable resistance can be obtained by pyramiding various ASR and APR genes into one variety (Klarquist et al., 2016). Due to swift breakdown of commercially deployed resistance genes, characterization of diverse and novel sources of resistance is constantly needed to replace the defeated genes. Wheat wild relatives are a potential source of novel rust resistance genes for developing new and diverse resistant germplasm (Kerber and Dyck, 1990). In present study, wheat-*Th. bessarabicum* addition line 4JJ and 6JJ exhibited resistance attitude towards yellow rust (Table 4). As these lines were not immune to yellow rust indicating the presence of minor genes which are desirable for durable resistance. Two novel QTLs for adult plant resistance have already been identified on group 4A and 6B chromosomes of wheat (Klarquist et al., 2016). Other addition lines 3JJ, 5JJ, 7JJ, and translocation lines Tr-3 (3JS.3BL), Tr-6 (6JS.7DL) were ranked as moderately resistant. Several QTLs for stripe rust resistance have been shown in group 3, 5 and 7 of wheat (Rosewarne, et al., 2013). It can be concluded that chromosome 3J, 5J, 4J, 6J and 7J of *Th. bessarabicum* may possess some of the adult plant resistance (APR) genes loci which have provided adult plant resistance against stripe rust in 3JJ, 5JJ, 4JJ, 6JJ and 7JJ additions and translocation lines in CS background. Data for CS and amphiploid could not be taken due to late maturity of these materials. Karnal bunt or partial bunt, caused by *T. indica* (syn. *Neovossia indica* [Mitra] Mundkur) also occurs endemically in (Punjab) Pakistan (Sajjad et al., 2018). For screening the germplasm, boot inoculation technique is one of the useful methodologies that allow the maximum ratio of successful infection (Beniwal et al., 2001). There is scarceness of resistance in the commercial cultivars against Karnal bunt in the country (Raza et al., 2019) and across the border (Bishnoi et al., 2020). Due to lack of resistance in commercial cultivars (Shakoor et al., 2015) wheat *Th. bessarabicum* genetic stock has been evaluated by boot inoculation technique. Results showed that amphiploid and addition lines 4JJ, 5JJ are immune to the KB while addition line 2JJ, 3JJ, 7JJ, translocation line Tr-1, Tr-3, Tr-5, Tr-7, Tr-42, Tr-44, and two BC1s self-fertile lines were ranked as resistant (Table 6). KB resistance in wheat is polygenic (Brar et al., 2018; Gupta et al., 2019). This polygenic resistant attitude was partly based on the fact that six wheat chromosomes (1D, 2A, 3B, 3D, 5D, 7A) were attributed to influence the reaction against the pathogen (Gill et al., 1993; Singh et al., 1994). . In 2019, Gupta et al. also reported novel QTLs on chromosomes 1DL, 2DL, 4AL, 5AS, 6BL, 6BS, 7BS, and 7DL. Nine other QTLs were also detected on chromosomes 3B, 4A, 4B, 5A, 5B, and 7A (Brar et al., 2018; Singh et al., 2007). It is probable that there are numeral genes that affect resistance against KB, because diverse mechanisms could operate for shielding the plant against the pathogen and each of them may be controlled by different genes (kumar et al., 2019; Gurjar et al., 2019;

Table 4. Response of wheat-*Thinopyrum bessarabicum* genetic stocks to yellow rust infections during 2012 -2015.

Serial No	Genotypes	2012-13	2013-14	2014-15	CI	CI	CI	ACI
					2012-13	2013-14	2014-15	
1	1JJ	50MRMS	60MRMS	60MRMS	30	36	36	34
2	2JJ	30MRMS	20MR	20MRMS	18	8	12	12.23
3	3JJ	20MR	20MRMS	20MR	8	12	8	9.3
4	4JJ	5RMR	10RMR	5RMR	1.5	3	1.5	2
5	5JJ	25MR	30MR	30MRMS	10	12	18	13.3
6	6JJ	5RMR	10MR	5RMR	1.5	4	1.5	2.33
7	7JJ	10MR	20MR	20MR	4	8	8	6.67
8	Tr-1	60MRMS	70MRMS	60MRMS	36	42	36	38
9	Tr-2	50MRMS	60MRMS	50MRMS	30	36	30	32
10	Tr-3	20RMR	30MR	30MR	6	12	12	10
11	Tr-4	40RMR	50MR	40MR	12	20	16	16
12	Tr-5	40MRMS	50MRMS	40MRMS	26	30	24	26.67
13	Tr-6	30RMR	30MR	20MRMS	9	12	12	11
14	Tr-7	60MRMS	80MRMS	70MRMS	36	48	42	42
15	CS	Late	20MR	TMR	0	8	0	8
16	Amphiploid	Late	0	0	0	0	0	0
19	Morocco	100S	100S	100S				

Table 5. Susceptibility category of each wheat-*Thinopyrum bessarabicum* genetic stock, based on coefficient of infection when inoculated with mixture of isolates.

Genotypes	Total Grains	Infested Grains	% infection	0	1	2	3	4	5	Gross Total	CI
1JJ	166	15	26.819	151	2	5	3	4	11	17.25	10.392
2JJ	82	4	14.880	78	2	2	0	0	0	1	1.220
3JJ	148	6	11.578	142	3	1	1	0	1	2.5	1.689
4JJ	169	0	0.000	169	0	0	0	0	0	0	0.000
5JJ	135	0	0.000	135	0	0	0	0	0	0	0.000
6JJ	210	18	25.768	192	1	4	4	5	4	11	5.238
7JJ	137	10	21.347	127	0	1	5	3	1	6	4.380
Tr-1	178	14	23.865	164	8	1	3	2	0	5.25	2.949
Tr-2	165	26	47.152	139	1	2	9	10	4	16.75	10.152
Tr-3	82	7	25.478	75	0	5	2	0	0	2.25	2.744
Tr-4	171	26	0.000	145	5	2	4	5	10	17.5	10.234
Tr-5	170	7	12.352	163	0	2	5	0	0	3	1.765
Tr-6	198	29	44.118	169	0	6	4	6	13	21	10.606
Tr-7	177	6	9.996	171	6	0	0	0	0	1.5	0.847
GEN 81	195	31	0.000	164	0	5	7	5	14	22.5	11.538
CS/Bs/P	117	1	2.500	116	0	1	4	0	0	2.25	1.923
CS/Bs/G	86	3	9.838	83	3	5	0	0	0	2	2.326
3JJ42	183	8	13.192	175	0	4	5	0	0	3.5	1.913
3JJ44	166	7	12.370	159	0	3	4	0	0	2.75	1.657
CS	126	27	64.264	99	1	3	8	7	8	18.25	14.484
Amphiploid	85	0	0.000	85	0	0	0	0	0	0	0.000

Table 6. Resistance /susceptibility category of wheat-*Thinopyrum bessarabicum* genetic stock.

CI Value/ Category	Genetic stock
0(HR)	4JJ, 5JJ, amphiploid
0.1-5 (R)	2JJ, 3JJ, 7JJ, Tr-1. Tr-3, Tr-5, Tr-7, Tr-42, Tr-44, BC1s self-fertile lines
5.1-10 (MS)	6JJ
10.1-20 (S)	1JJ, Tr-2, Tr-4, Tr-6, Genaro
>20.1(HS)	Morocco (Check cultivar)

Emebiri et al., 2019). This defense mechanism possesses phenotypic barriers (wax, cell wall, stomatal aperture or lenticles) and chemicals comprise of a diverse array of secondary metabolites (phenolics, sulphur compounds, saponins, cyanogenic glycosides, and glucosinolates) have been synthesized by plant, many of which are deterrent to fungal activity (Osbourn, 1996). Resistance due to secondary metabolite has also been observed in Rice blast disease against different strains of *Magnaporthe oryzae* (Singh et al., 2020). Broad-spectrum resistance has also been observed due to resistance (R) and defense-regulator(DR) genes to the blast disease of rice (Li et al., 2019). In the light of these studies, it can be demonstrated that amphiploid and addition lines 4JJ and 5JJ might possess genes encode various plant defense mechanisms including some of above-mentioned physical barriers and or chemical barriers scattered on 4J and 5J homoeologous chromosomes from *Thinopyrum bessarabicum* which confer immunity against KB. This result is in accordance with the finding that QTLs for KB resistance are present on 5D (Begum and Mathur, 1989) and on 4B (Sukhwinder-Singh et al., 2003; Emebiri et al., 2019) chromosomes of wheat. Resistance against KB has also been found in the screening of wheat and rye addition lines on 4R, 5R and long arm of 7R chromosomes (Sidhu et al., 2001). Other addition line 2JJ, 3JJ, 7JJ, translocation line Tr-1 (6BS.6BL-6J), Tr-3 (3JS.3BL), Tr-5 (7DS.7DL-4J), Tr-7 (5JS-5DS.5DL), Tr-42 (2n=6X=41+Tr3J), Tr-44 (2n=6X=42+Tr3JJ), and two BC1s self-fertile lines ((2n=7X=42+7J) also possess resistance gene(s) distributed on different homoeologous *Th. bessarabicum* chromosomes/ chromosomal arms, as QTLs for KB resistance are also present on 2A, 3B, 3D, 5D, 7A (Begum and Mathur, 1989; Emebiri et al., 2019) and 4B chromosomes of wheat (Sukhwinder-Singh et al., 2003). Homoeology of *Thinopyrum bessarabicum* chromosomes with wheat have already been explained in another study carried out by William and Mujeeb-Kazi (1995). These highly resistant addition and translocation lines of wheat-*Th. bessarabicum* identified in the present screening stands as a preferred candidate for KB resistance as an added positive attribute from tertiary gene pool.

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