

COMBINING BEHAVIOUR OF EXOTIC X LOCAL WHEATS FOR DURABLE RESISTANCE TO STRIPE RUST

By

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(J-18-M-600)

**Thesis submitted to Faculty of Post Graduate Studies
in partial fulfillment of the requirements
for the degree of**

**MASTER OF SCIENCE IN AGRICULTURE
GENETICS AND PLANT BREEDING**



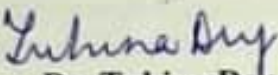
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Main Campus, Chatha, Jammu 180009**

2021

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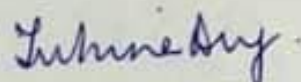

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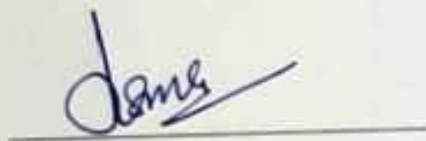
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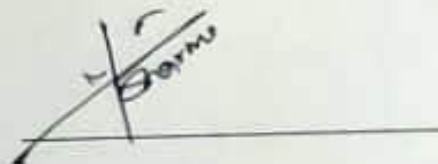
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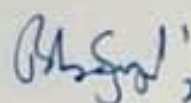


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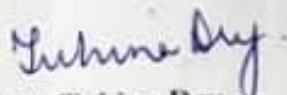
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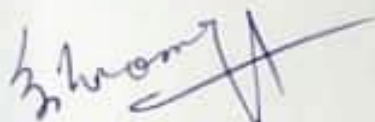
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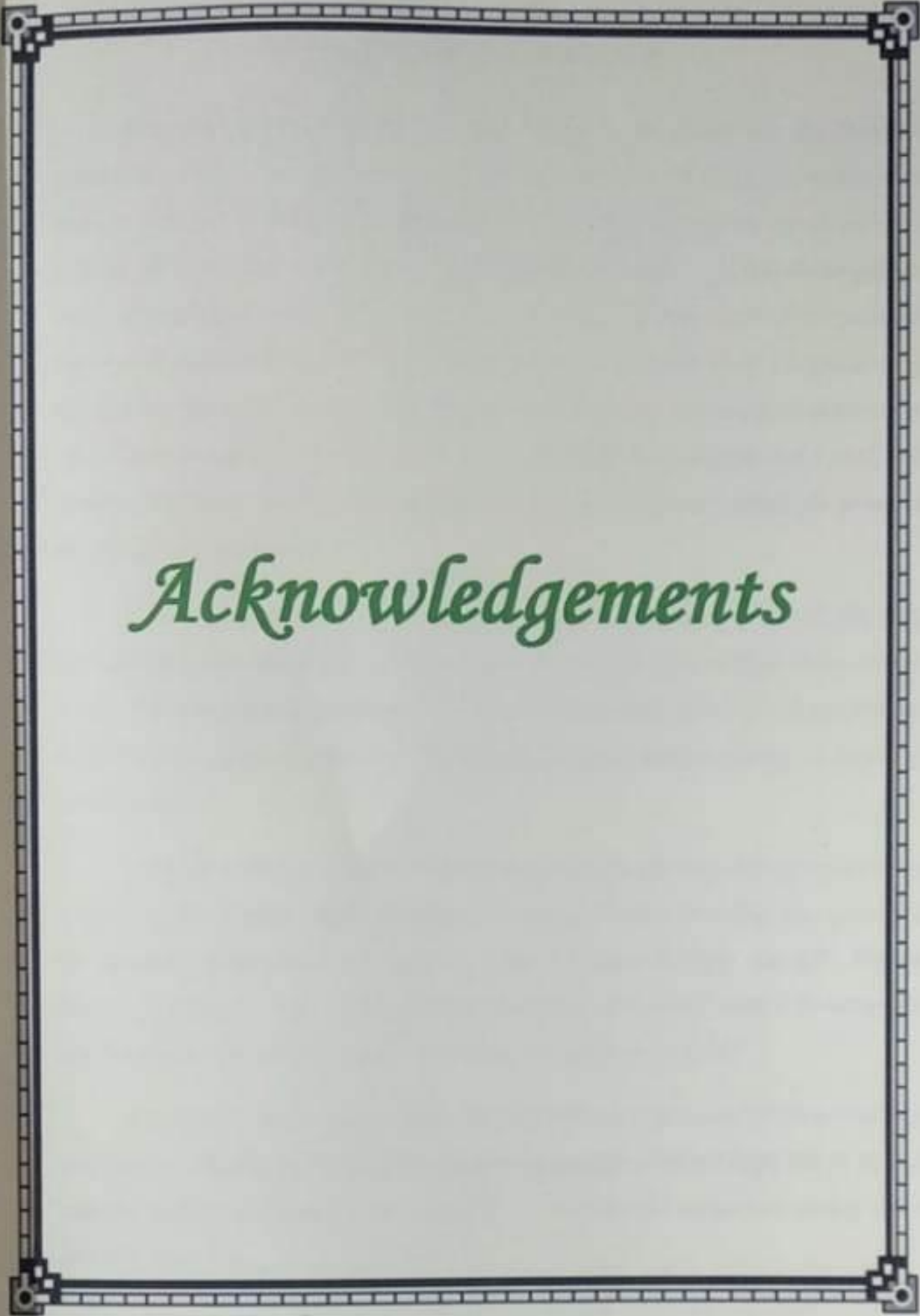
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ABSTRACT

Title of Thesis/Dissertation : **Combining behaviour of exotic x local wheats for durable resistance to stripe rust.**
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Abstract

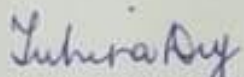
Stripe rust is an important biotic stress effecting wheat and the development of varieties with durable resistance is a viable alternative. The present investigation entitled "**Combining behaviour of exotic x local wheats for durable resistance to stripe rust**" targeted the development of F₁s involving eight resistant lines obtained from a diverse exotic core germplasm collection and three adapted varieties in line x tester design. A set as thirty-five genotypes including eleven parents and twenty-four F₁s were evaluated in randomized block design during *Rabi* 2019. Observations on yield related traits *viz.*, number of tillers per plant, flag leaf area, spike length, number of spikelets per spike, chlorophyll content of flag leaf, 1000 grain weight and grain yield per plant and stripe rust score as per Modified Cobb Scale was recorded on five randomly selected plants.

Analysis of variance revealed that mean sum of square due to genotypes, parents, parents vs hybrid were highly significant for all the traits indicating the existence of sufficient genetic variability in the material under study. GCA effects of parents revealed that the genotype SUNLINE with highly significant *gca* effect in desired direction for spike length, chlorophyll content of flag leaf, 1000 grain weight and grain yield per plant. The other parents that showed significant positive GCA effect for grain yield per plant were SUNTOP, DANPHE, HAR-421, RSP 561 and WB-2.

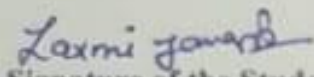
The cross BOTH X RSP-561, MAJENTA X WB-2 and ENKOY X JAUW-584 showed significant *sca* effect with disease score of 20MS, 10MR and 20S, respectively and positive but non-significant heterobeltiosis. Four F₁s showed significant positive heterobeltiosis for grain yield per plant *viz.*, SUNTOP X JAUW-584, SUNLINE X JAUW-584, DANPHE X JAUW-584 and HAR-421 X JAUW-584.

MAJENTA X WB-2 with significant positive *sca* effect for yield and component traits along with 10MR stripe rust score and positive heterobeltiosis may lead to potential APR breeding lines. The presence of non-additive gene action governing all traits indicates that selection of superior individual plants should be delayed till F₄ or F₅ generations.

Keywords: Wheat, Stripe rust, GCA, SCA



Signature of Major Advisor



Signature of the Student

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Chapter-I

Introduction

Wheat (*Triticum aestivum* L.) is the staple diet of the majority of people in India and a vital component towards food security. India is the second largest producer of wheat in the world after China. During 2019-20, India produced 107.18 million tonnes of wheat with an area of 30.55 million hectare whereas in Jammu and Kashmir, the total production was 504 thousand tonnes in 288 thousand hectare (Anonymous 2019). Wheat attracts substantial research attention in the face of challenge of feeding a predictable global population of 9.8 billion by 2050 amidst climate change (Godfray *et al.*, 2010). There is an anticipated thirty per cent reduction in South Asia's wheat yield in the next decade with the existing cultivars and practices due to the vagaries of climate change (CGIAR, 2017). Climate changes lead to abiotic stresses like drought and floods, increased and variable rainfall that makes the micro and macro climate conducive for development of diseases like stripe rust, fusarium head blight, powdery mildew, black point and Karnal bunt.

The damage by stripe rust is manifests in the form of decreased yield related grain quality and forage value with distinguishing symptoms in the forming yellow pustules (urediniospores) appearing mostly on the leaves and under severe conditions, on the leaf sheaths, spikes, glumes and awns(McIntosh 1995).

Stripe rustis caused due to *Puccinia striiformis* f.sp. *Tritici* (*Pst*) and the presence of genetic resistance in wheat towards *Puccinia striiformis* f.sp. *Tritici* (*Pst*) was resolved for the first time by Biffen in 1905. The presence of naturally occurring resistance in wheat germplasm which can express at the seedling or adult plant stage (Bariana and McIntosh, 1995) lead to the development of resistant varieties for race specific or broad spectrum multiple race resistance.

Presently, almost 83 genes conferring stripe rust resistance to *P. striiformis* f. sp. *tritici* (*Pst*) have been catalogued, a majority of these genes belong to the seedling

resistance while some resistance genes express only at the post seedling stages and are referred to as adult plant resistance (APR) genes (Li, *et al.*, 2020).

Durable resistance is a mechanism conferring resistance to a cultivar for a long period of time during its widespread cultivation within environments that harbor favourable conditions for disease spread. This type of resistance is mainly associated with minor genes, which are also known as slow rusting genes (Zaman *et al.*, 2017) imparted due to adult plant stripe rust resistance genes like *Yr18*, *Yr29*, and *Yr46* (Herrera-Foessel *et al.*, 2011).

Hybridization is the mechanism to overcome yield barriers and improve varieties with other desirable traits using specified mating design. Combining ability analysis helps in the selection of desirable parents together with information regarding the nature and magnitude of controlling quantitative traits (Masood *et al.*, 2014). A systematic breeding program is based on the selection of parents with desirable traits having good general combining ability (GCA) and crosses with specific combining ability (SCA) effects for yield and its component traits (Gowda *et al.*, 2012). Line x tester technique developed by Kempthorne (1957) measures the performance of parents and different cross combinations and the nature and magnitude of gene effects in expression of quantitative traits.

Keeping in view the importance of stripe rust of wheat grown in North Western Plan Zone (NWPZ) and durable rust resistance holding promise for prolonged effectiveness, the present study was undertaken with the following objectives:

- To develop crosses from adult plant resistance (APR) introgressed exotic wheat x local wheat varieties.
- To study the combining ability for disease resistance and yield traits in wheat.

Chapter-II

Review of Literature

CHAPTER-II

REVIEW OF LITERATURE

Wheat breeding program globally focus on developing genetically superior, high yielding, disease resistant cultivars with desired quality.

Wheat crop subjected to several biotic and abiotic stresses and stripe rust is one of the most severe biotic stresses which threaten its yield. Especially in North Western Plain Zones of India with conducive cool climate that flourishes the crop as well as the pathogen. It thus becomes relevant to develop wheat varieties having enhanced durable resistance against stripe rust in addition to having other desirable agronomic / yield traits.

The literature pertaining to different aspects of morphological, physiological and genetics of stripe rust resistance with special reference to durable resistance in wheat have been reviewed and are presented as under:

- 2.1 Stripe rust in wheat
- 2.2 Durable resistance against stripe rust in wheat
- 2.3 Combining ability studies in wheat for yield and stripe rust resistance

2.1 Stripe rust in wheat

Stripe rust in wheat was first reported in 1777 in Europe (Singh *et al.*, 2002) also known as yellow rust is caused by *Puccinia striiformis f. sp. Tritici*. (Ye *et al.*, 2019), causing yield loss up to 10-70 percent (Begum *et al.*, 2014).

McDonald *et al.* (2004) reported that the basis of stripe rust resistance in wheat variety PBW 343 is due to gene *Yr27* (from Selkirk) located on chromosome 2B. The large scale cultivation of PBW 343 facilitated the selection of virulence for *Yr9* and *Yr27* to the new pathotype “78S84” of stripe rust pathogen which probably, originated in Eastern Africa or Western Europe and migrated to South Asia and India (Prashar *et al.*, 2007).

Kumar and Pal (2006) studied the inheritance of stripe rust resistance against pathotype 46S119 in wheat genotype PBW 343 and newly registered resistance sources namely FLW 3, WBM 1587 and WBM 1591. They reported that cultivar WBM 1587 and WBM 1591 carry diverse resistance gene useful in breeding program in Indian sub continent.

Afzal *et al.* (2007) assessed yield losses due to stripe rust in wheat varieties viz., Bakhtawar, Inquilab 91, Wafaq 2001 at Islamabad and recorded that Inquilab-91 was most resistant followed by Wafiq-2001 and Bakhatwar with yield loss of 5.77, 6.63 and 14.9 per cent, respectively.

Luo *et al.* (2008) studied the allelic relationship of stripe rust resistance genes on wheat chromosome 2BS and reported that genes *Yr27*, *Yr31*, *YrSp*, *YrV23*, and *YrCN19* on chromosome 2BS confer resistance to *Puccinia striiformis* f. sp. *tritici* races CYR31, CYR32, SY11-4, and SY11-14 in the greenhouse and concluded that the gene *Yr41* was effective against all races tested. The resistance array for *YrSp* can be complemented with that of *Yr27*, *Yr31*, or *YrV23*.

Nazari and Welling (2008) studied genetic analysis of seedling stripe rust resistance in the Australian wheat cultivar 'Batavia by crossing Batavia with Avocet S. Parental cultivars, F₁'s and genetic populations were scored for seedling resistance to pathotypes 110 E143 A+ and 134 E16 A+. The 16 F₁s tested against Pst pt. 110 E143 A+ and 134 E16 A+, were the two gene (*YrBat1* and *YrBat2*) combination would remain effective to other Australian Pst.

Bux *et al.* (2012) stressed the importance of stripe rust caused by *Puccinia striiformis* f. sp. *tritici* as an important disease of wheat causing considerable yield losses in wheat growing areas worldwide. Wheat germplasm consisting of twenty Chinese cultivars, ninety five synthetic hexaploids and eighty five advanced breeding lines were evaluated under field conditions at two hot spot locations (Pirsabak and Islamabad) in Pakistan during 2007-08 and 2008-09 wheat growing seasons. Seedling test revealed that synthetic hexaploids have seedling resistance with presence of stripe rust resistance genes *Yr3*, *Yr5*, *Yr10*, *Yr15*, *YrSP* and *YrCV* while advanced lines and Chinese cultivars showed

adult plant resistance under field conditions. Most of the genotypes were susceptible at seedling stage.

Khan *et al.* (2012) studied Australian wheat cultivar Cook for the stripe rust resistance under glasshouse and field conditions against the most virulent race 46S119 and reported that stripe rust resistance in cultivar Cook is conditioned by one hypersensitive and one non-hypersensitive gene *Yr18*.

Chen *et al.* (2013) studied the suppression of stripe rust in interspecific crosses of wheat comprising of eight amphidiploid wheat lines developed and evaluated in the seedling stage for resistance to five pathotypes of stripe rust. Resistance in one or both parents was frequently suppressed in synthetic hexaploid lines, indicating the presence of suppressor genes in both *Ae. tauschii* and *T. carthlicum*. Results further revealed that suppression of stripe rust resistance commonly occurs in the synthetic.

Mukhtar *et al.* (2015) studied molecular characterization of thirty nine wheat genotype for stripe rust resistance and identification of candidate line for stripe rust breeding in Kashmir under both field and green house conditions. They reported that the single, double and triple gene based resistance was detected in nine, twenty and eight entries respectively and all four gene based resistance was detected in one cultivar (HPW-42). Waqar *et al.* (2018) reported that yellow or stripe rust (produced by *Puccinia striiformis*), is a globally significant disease of wheat causing 50 – 100 per cent damage due to infected plants with shriveled grain. They emphasised that durable resistance genes must be identified in the land races and incorporated in modern cultivars as high temperature adult plant resistance (HTAP) resistance is effective against all races when plants grow old and temperature increases.

2.2 Durable resistance against stripe rust in wheat

The concept of horizontal, or race nonspecific, resistance was generally used in breeding stem rust resistance in wheat (Borlaug, 1972) and leaf rust resistance (Caldwell, 1968). Johnson, (1988) designated the concept of durable resistance to leaf and stripe rusts of several cultivars based on slow rusting genes having additive effects. APR is expressed at the adult plant stage where in resistance is conferred by multiple additive

genes possessing quantitative inheritance not subjected to the “boom and bust cycle” of disease epidemics. These APR is considered more durable than all stage resistance (ASR) or seedling resistance or race-specific resistance governed by a major gene providing hypersensitive response (HR).

Milus and Line (1986) showed that non-race specific high temperature adult plant in the winter wheat “Gaines”, “Nugaines”, and “Luke” is quantitatively inherited and that the high temperature adult plant resistance in these cultivars is partially recessive with no maternal inheritance and additive gene action among loci.

Johnson and Lupton (1987) studied breeding for disease resistance and suggested that genetic control of resistance to stripe rust wheat is complex and possibly consist of some component which is race specific and an indefinite number of non race specific genes.

Singh and Rajaram (1994) studied the genetics of adult plant resistance in ten spring bread wheat variety against stripe rust and found that resistance in Penjamo 62, Lerma Rojo, Nacozari 76 and Tesia 79 and Wheaton was due to *Yr18* only while resistance in Tonichi 81 was based on additive interaction involving *Yr18* and two additional partially effective genes. The resistance assigned as *Yr18* complex was durable.

Bariana and McIntosh (1995) evaluated genetics of adult plant resistance in Australian wheat by crossing two stripe rust susceptible cultivars namely Avocet 'R' and Avocet 'S' with cultivars Bersee, Flinders, Harrier. King and M2435. Genetic analysis based on F₂ and F₃ populations indicated that APR genes in cultivar Harrier, Flinders and M2435 were inherited monogenically whereas King possessed two genes for resistance while high level of resistance in cultivar Barsee was controlled by four genes.

Chen and Line (1995) studied the genetics of stripe rust resistance in wheat cultivars Stephans and Druchamp and reported that these wheats possessed both durable, high temperature adult plant (HTAP) resistance and race specific seedling resistance to stripe rust. Two out of three HTAP resistance genes showed partially recessive inheritance.

Ma and Singh (1996) founded that *Yr 18* gene confer slow rusting resistance in adult plants and protected grain yield in the range of 36-58 per cent.

Torabi and Nazari (1998) studied seedling and adult plant resistance in twenty five advanced promising and commercial bread wheat cultivars in Iran against five stripe rust pathotype namely 14E176A+, 134E142A+, 6E210A+, 4E128k and 64EI46A. Two cultivars M70-4 and MV 17 were found to be resistant to all the five pathotypes (which included *Yr9* virulence) at seedling stage and also showed good adult plant resistance.

Boukhatem *et al.* (2002) detected two quantitative trait loci (QTLs) for yellow rust resistance in a population at the adult plant stage derived from the cross of Camp Remy and Michigan Amber. Partial scanning of the genome enabled the identification of two QTLs located on chromosome 2B and 2A that accounted for 46 to 15 per cent of the total phenotypic variance, respectively. They also reported that Camp Remy might possess a specific seedling stage resistance gene *Yr7* on chromosome 2B.

Kaur and Singh (2004) reported that two wheat genotypes A206 and VL404 showed seedling resistance and adult plant resistance to the races namely 46S103 and 46S119 whereas seven genotypes namely CIM 5, CIM 7, CIM 53, CPAN 1922, Dove, Emu and Pari 73 showed seedling resistance and adult plant resistance against race 46S103 and adult plant resistance to race 46S119. There were another nine genotypes viz; BW 11, Chilero, CIM 25, CIM 42, Flinders, Romany, Potam 70 and Torim 73 with only adult plant resistance to race 46S103.

Navabi *et al.* (2004) studied inheritance of adult-plant resistance to stripe rust in spring wheat genotypes and concluded that additive gene effects were more important than non additive in inheritance of adult plant resistance to stripe rust.

Khanna *et al.* (2005) reported that a stripe rust resistance gene in line CSP44 is allelic to *Yr18* in RL6058 and revealed that the presence of the new stripe rust resistance gene in CSP44 in addition to *Yr18*, may also confer long lasting resistance durable resistance. The evaluation of F₁, F₂, F₃ generations and F₆ SSD families from the cross of CSP44 with susceptible wheat cultivar WL711 indicated that the resistance in CSP44 is based on two genes showing additive effect.

Uauy *et al.* (2005) reported that the high-temperature adult-plant (HTAP) stripe rust resistance proved to be more durable than seedling resistance due to its non-race-specific nature. The characterization of new HTAP resistance gene derived from *Triticum turgidum* ssp. *dicoccoides* accession FA15-3 from Israel (Avivi 1978) was designated as Yr36 (McIntosh *et al.* 2005). Lines carrying this gene were susceptible to almost all the stripe rust pathogen races at the seedling stage but showed adult-plant resistance to the prevalent races in California when tested at high diurnal temperatures.

Kaur *et al.* (2008) concluded that the long lasting resistance of cultivar Tonichi to leaf and stripe rust in the Indian subcontinent may be due to interactive action of the leaf rust and stripe rust resistance genes carried by the cultivar. These type of gene combinations may be a good alternative for durable resistance as it behaves like horizontal resistance thus avoiding the evolution of new races of pathogen.

Lagudah (2011) catalogued over 150 resistant genes that confer resistance to either leaf, stripe or stem rust in wheat and reported that few of the genes from the 'slow rusting' adult plant resistant (APR) class confer partial resistance in a race non specific manner to one or multiple rusts. The cloning of two of these genes, *Lr34/Yr18*, a dual APR for leaf and stripe rust, and *Yr36* a stripe rust APR gene showed that they differ from other classes of plant resistant genes.

Kumar *et al.* (2014) studied the postulation of resistance genes *Yr2*, *Yr9* and *Yr18* singly or in combination with other genes. *Yr2* gene was postulated in nine varieties namely GW173, HUW234, HW741, K8027, K9107, Lok-1, Raj3077, Raj3065 and VL616. In GW173 and K9107, *Yr2* was characterized in combination with *Yr18* in six varieties namely GW173, K9006, K9107, NIAW34, VL738 and WH542 where it occurred in combination with other genes in the four varieties.

2.3 Combining ability studies in wheat for yield and stripe rust resistance

Wagoire *et al.* (1998) investigated the inheritance of adult field resistance to stripe rust in a complete diallel set of crosses in eight bread wheat cultivars and reported that additive, dominance and epistatic effects control the genes for rust resistance with the former being more important.

Faiz *et al.* (2006) studied two lines and two testers in L x T mating design with four genotypes and their F₁s used to estimate heterosis and combining ability effects on yield and yield influencing traits viz., plant height, number of productive tillers per plant, number of spikelets per spike, number of filled grains per spike, sterility percentage and grain yield. Significant differences were observed in lines, testers and F₁s.

Akbar *et al.* (2009) studied combining ability, variance and gene effect in wheat using line x tester mating design for five traits viz., grain yield per plant, tiller per plant, spike length, spikelet per spike and 1000 grain weight. The result revealed lines Faisalabad-85 and Faisalabad -83 as good general combiners while tester PBW 65/ROER / 3 / PB6 // MIRLOW / BUC and PBW 502 was good general combiner for all traits. GCA and SCA variances revealed predominantly non-additive gene action for the traits.

Cifci and Yagdi (2010) evaluated combining ability of bread wheat in F₁ and F₂ generations using five breeding lines by crossing with three testers in line x tester mating design. Plant height, spike length, number of spikelets per spike, grain per spike, 1000 grain weight revealed that non-additive gene effect play role in both F₁ and F₂.

Nour *et al.* (2011) used line x tester analysis for studying combining ability variance and effect for yield and its contributing traits in bread wheat. They crossed eighteen wheat genotypes with three local wheat cultivars in line x tester design. The result revealed that non additive gene effect were larger than additive effect and the maximum contribution to total variance of grain yield per plant and other traits was made by female lines. Some hybrids were good combiners for specific combining ability effects for all characters including grain yield per plant.

Punia *et al.* (2011) crossed the twelve lines and four testers in L x T mating fashion and evaluated 48 crosses with their parents under normal and late sown seasons at Udaipur. Lines Kalyan Sona, DWR 195, C 306 and K 9708 were found to be good combiners for different heat tolerant parameters along with grain yield. Combinations of Raj 3077 x Kailash under normal (E₁) and late sown (E₂), C 306 x PBN 51 (E₁) and C

306 x HD 2189 (E₂) were observed to be superior for grain yield also exhibited high *sca* effects.

Yadav *et al.* (2011) studied combining ability for grain yield and other related characters by crossing between twelve lines and three testers in a completely Randomized Block Design (RBD) with three replications. They concluded that line HD 2687 was good general combiner for all characters. The parents involved in these crosses were average x average general combiners and/or poor x average combiners. Desirable specific combining ability of the crosses involving such parents was mainly due to complementation of the genes and hence these crosses can be exploited for grain yield by using biparental mating system.

Singh *et al.* (2012) reported that line x tester mating design is the most powerful design among various mating designs available, to assess the combining ability of genotypes. Seven genotypes of wheat were mated with three testers in a line x tester fashion with results show that comparing *sca* were more justifiable than those of *gca*. For the improvement of grain yield along with related traits, CPAN 3004, V 22 and K 8504 as male and Lok-1 and WH 147 as female parent appeared to be good for use in intensive hybridization program.

Srivastava *et al.* (2012) conducted an experiment to assess the combining ability of 12 lines and 4 testers, with 48 F₁'s using line x tester analysis. The experiment revealed that variance due to *sca* was found higher than that of *gca* for all the characters, indicating greater importance of non-additive gene action and thus suggested heterosis breeding to be useful.

Lohithaswa *et al.* (2013) conducted an experiment using line x tester analysis for the estimation of gene action, combining ability for yield and yield attributing traits, quality and rust resistance over environments in wheat. The general and specific combining ability variance ratio revealed the preponderance of additive gene action for all the traits except number of seeds per spike. Significant *gca* effect for grain yield and its component traits was exhibited by the lines Vijay and DK-1001 and testers DWR-1006 and Raj1555.

Fellahi *et al.* (2013) evaluated genetic variability among parents and hybrids derived using five genotypes, Acsad901, Acsad899, Acsad1135, Acsad1069 and Ain Abid used as lines and four genotypes Mahon Demias, Rmada, HD1220, Wifak as testers. The tester and the interaction of line x tester contributed more to the variation for the expression of different traits. There was preponderance of non-additive type of gene action indicating that selection of superior plants should be postponed to later generations.

Singh and Kumar (2014) analysed the gene action for yield and yield contributing traits in fifteen parental wheat genotypes and thirty six F₁ hybrids. Highly significant differences among the genotypes for all the characters were observed with both additive and non-additive gene effects being important for the different characters studied.

Aslam *et al.* (2014) evaluated combining ability effect of wheat genotype by crossing three elite lines with three testers in randomized block design and concluded that both additive and non-additive gene action controlled the expression of the traits so selection should be practiced either for hybrid breeding or pure line selection in succeeding generations.

Barot *et al.* (2014) studied heterosis and combining ability for yield and its component traits in wheat by crossing four lines with eight testers in line x tester mating design. Both additive and non-additive gene action were found to control the expression of traits. The line GW 11 and tester, GW 322 were good general combiners for grain yield per plant, harvest index and protein content. The magnitude of general combining ability variance was higher than specific combining ability variance for all the traits, which indicate the preponderance additive gene action in the inheritance of these traits.

Abro *et al.* (2016) conducted an experiment to estimate the combining ability effects of wheat genotypes for some quantitative traits. They were crossed 2 lines with 3 testers. Variances due to F₁ hybrids, lines, testers and line x tester were significant for grain yield for almost all characters and these attributes were controlled by both additive and non-additive inheritance. These parents and cross combinations may be used for varietal improvement through selection in segregating generations to increase yield.

Afridi *et al.* (2017) studied combining ability of yellow rust resistance, yield and yield related traits using Griffing's combining ability analysis in wheat cultivars. They crossed genotype Pirsabak-85, Khyber-87, Saleem-2000, Pirsabak-04, Pirsabak-05 and Shahkar-13 in 6×6 half diallele fashion and reported significant differences among F_1 and F_2 populations and their parents for most of the traits. Variance due to GCA were less than variance due to SCA and ratios due to $\sigma^2\text{GCA}/\sigma^2\text{SCA}$ were also less than unity reflecting predominance of non-additive gene effect for yellow rust resistance in both F_1 and F_2 generations.

Jatav *et al.* (2017) studied combining ability for grain yield and its different components by crossing 7 lines with 3 testers in line x tester mating design in a randomized block design with two replications under stressed and non-stressed environments. They reported that both additive and non-additive components were prevalent for the control of grain yield and its components under both stressed and non-stressed environments except spike length. Most of the good specific combinations for various traits involved parents with high x low or low x low or low x high GCA effects. They further concluded that these parents may be used for varietal improvement through the simple recurrent selection.

Rajput (2018) studied combining ability and heterosis for grain yield and its component through line x tester analysis. Genetic analysis revealed that GCA and SCA variances were significant for all characters which indicated that all the traits were controlled by both additive and non-additive components. These parents involved may yield superior transgressive recombinant which may be exploited either through pedigree selection or progeny selection or mass selection.

Serpoush *et al.* (2018) studied the inheritance of resistance to stripe rust race 198E154+ in wheat cv. Morvarid. They concluded that there were significant differences between the generations for two traits (Infection type and latent period) with high broad sense heritability, additive, dominance and epistasis gene actions having a significant role in control of these traits. The narrow-sense heritability was average for infection type and low for latent period. Information of these analyses is useful as breeding methods of wheat rust resistance selection.

Chapter-III

Material and Methods

CHAPTER-III

MATERIAL AND METHODS

The present investigation entitled “**Combining behavior of exotic x local wheats for durable resistance to stripe rust**” was carried out at the Research Farm, Division of Plant Breeding and Genetics, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Main Campus, Chatha, Jammu during *Rabi* 2018-20.

3.1 Experimental material

The experimental material comprised of eleven genotypes (eight stripe rust resistant germplasm obtained from diverse eco-geographic regions and three adapted commercial varieties of wheat) available in the Division of Plant Breeding & Genetics.

Details about the source of these genotypes are provided in Table 3.1.

3.2 Experimental Methods

3.2.1 Experiment No. 1

The eleven genotypes were evaluated for disease and yield related traits in a randomized block design with five replications. Recommended agronomic practices were followed to raise a healthy crop during *Rabi* 2018-19.

3.2.2 Experiment No. 2: (Development of F₁s)

The eight lines BOTH, MAJENTA, SUNLINE, SUNTOP, DANPHE, ENKOY, FH-11-6-24, HAR -421 were crossed with three adapted commercial varieties RSP-561, WB-2, JAUW-584 in line x tester design during *Rabi* 2018-19 to obtain F₁s.

3.2.3 Experiment No. 3

The F₁ along with parents were sown in a Randomized block design (RBD) during *Rabi* 2019-20. Data on disease reaction against stripe rust and related physiological traits were recorded on five randomly selected plants.

3.2.4. Recording of observation

Data on disease reaction to stripe rust and yield related traits were recorded on five randomly selected plants.

Table 3.1: List of genotypes

Sr. No.	Name of parents	Source	Disease score (2018-19) Chatha	
LINES				
1	BOTH	Australian yellow rust resistant germplasm	TR	
2	MAJENTA	Australian yellow rust resistant germplasm	40MS	
3	SUNLINE	Australian yellow rust resistant germplasm	10R	
4	SUNTOP	Australian yellow rust resistant germplasm	10R	
5	DANPHE	African yellow rust resistant germplasm	20MS	
6	ENKOY	African yellow rust resistant germplasm	10MS	
7	FH-11-6-24	African yellow rust resistant germplasm	20MR	
8	HAR-421	African yellow rust resistant germplasm	10S	
TESTERS				
	Name of parents	Pedigree	Source	Disease score (2018-19) chatha
9	RSP-561	HD 2637/ <i>Ae.crassa</i> /HD 2687	Division of Plant Breeding & Genetics	60S
10	JAUW-584	PDW 233/ <i>Ae. crassa</i> /PBW 343	Division of Plant Breeding & Genetics	20S
11	WB-2	<i>T. dicoccom</i> C/9309/ <i>Ae. crassa</i> (409)/3/Milan/S87230//BAV92/4/2 Milan/S87320//BAV92	IIWBR, Karnal	40MS

3.2.4.1 Number of tillers per plant:

The number of fertile tillers per plant at maturity was counted and averaged.

3.2.4.2 Flag leaf area (cm²) was measured as per the protocol of Muller 1991.

When the leaves were fully turgid at booting stage in the morning hours, the mother shoot leaves was collected and maximum length and width was recorded and then multiplied with 0.74 to get flag leaf area in cm².

$$\text{Flag leaf area} = \text{Flag leaf length} \times \text{Flag leaf width} \times 0.74$$

3.2.4.3 Spike length (cm):

The spike length was measured in centimeters from the base of the first fertile spikelet to the tip of the spike excluding awns.

3.2.4.4 Number of spikelets per spike:

Number of spikelets per spike was recorded from randomly selected spike.

3.2.4.5 Chlorophyll content of flag leaf:

Chlorophyll content was measured using chlorophyll meter/SPAD-502 (Soil Plant Analysis Development (SPAD) Section, Minolta Camera Co, Osaka, Japan). Three readings were taken along the middle section of the flag leaf, and mean used for analysis and values were expressed as SPAD unit which corresponds to the amount of chlorophyll present in the sample leaf. The chlorophyll content was recorded at 15 days after anthesis. SPAD measurement area was 2 x 3 mm (Minolta, 1989).

3.2.4.6 1000 grain weight (g):

One thousand grains from each genotype / F₁ was counted and weighed in grams on electrical balance.

3.2.4.7 Grain yield per plant (g):

The grain yield per plant was measured at 12.5 per cent seed moisture.

3.2.5. Statistical Analysis1

The treatment means for all the traits recorded as per the procedure mentioned above for each replication were subjected statistical data analyzed using the software windostat version 8.1. The mean values of parental lines and F₁s have been appended as in Appendix-A. The statistical methods are as adopted in the present study.

3.2.5.1 Analysis of variance and mean performance of parents and F₁s

3.2.5.2 Combining ability analysis

3.2.5.3 Studies on gene action

3.2.5.4 Estimation of heterosis in exotic x local wheats

3.2.5.5 Disease reaction of the parents and F₁s

3.2.5.1 Analysis of variance and mean performance of parents and F₁s

The mean values of five randomly selected plants were calculated over the single replication of a particular genotype. This mean value was taken as representative value for a particular genotype for a particular trait.

The data collected on five plants in each treatment in each replication were subjected to the analysis of variance for 35 entries with five replications. The test of variation among genotypes was analyzed by the usual statistical procedure following model of Panse and Sukhatme (1985).

$$Y_{ij} = \mu + \beta_i + \tau_j + \Sigma_{ij}$$

Where,

- Y_{ij} = Yield of j^{th} genotype in i^{th} replication
 μ = general mean effect
 β_i = effect of the i^{th} entry ($i = 1, 2, \dots, v$)
 τ_j = effect of the j^{th} replication ($j = 1, 2, \dots, v$)
 Σ_{ij} = Experimental error (uncontrolled variation) due to j^{th} genotype in i^{th} replication.

The partitioning of degrees of freedom from the different sources of variation is given below.

Analysis of variance (ANOVA)

Sources of variation		d. f.	MSS	Expectation of MSS	Cal. 'F'
[A]	Replications	(r-1)	Mr		Mr/Me
[B]	Genotypes	(g-1)	Mg	$\sigma_e^2 + r\sigma_g^2$	Mg/Me
	(1) Parents	(p-1)	Mp		Mp/Me
	(a) Females	(f-1)	Mf	$\sigma_e^2 + r\sigma_{fm}^2 + rm\sigma_f^2$	Mf/Mfm
	(b) Males	(m-1)	Mm	$\sigma_e^2 + r\sigma_{fm}^2 + rm\sigma_m^2$	Mm/Mfm
	(c) Females vs. Males	1	Mfm	$\sigma_e^2 + r\sigma_{fm}^2$	Mfm/Me
	(2) Hybrids	(h-1)	Mh		Mh/Me
	(3) Parents vs. Hybrids	1	Mph		Mph/Me
[C]	Error	(g-1) (r-1)	Me	σ_e^2	-
Total :		(rg-1)	Mt		-

Where,

r	=	Number of replication,
g	=	Number of genotype,
p	=	Number of parent,
f	=	Number of female,
m	=	Number of male, and
h	=	Number of hybrid.

Standard Error:

Expressed as the mean difference between sample estimates of mean and the population parameter μ i.e. it is the measure of uncontrolled variation present in a sample. The Standard error of a variable mean was calculated by dividing the estimate of Standard deviation by the root of the number of the observations in the sample. Mathematically

$$\text{Standard error} = \frac{\text{Standard deviation}}{\sqrt{N}}$$

where,

N = Total number of observations

Critical Difference (C.D.):

In order to ascertain whether the difference between two treatments was significant, Critical Difference (C. D.) was calculated as,

$$CD = S.E(d) \times \text{table } t_{0.05} \text{ at error d.f.}$$

3.2.5.2 Combining ability analysis

The variation among the hybrids was partitioned further into sources attributable to general and specific combining ability components in accordance with the procedure suggested by Kempthorne (1957) and modified by Arunachalam (1974).

The analysis of variances for the combining ability was based on the following statistical model.

Statistical model

The statistical model used to study the general and specific combining ability was:

$$Y_{ijk} = m + g_i + g_j + s_{ij} + r_k + e_{ijk}$$

Where,

- i = Number of female parent (1, 2....f)
j = Number of male parent (1, 2....m)
k = Number of replication (1, 2....r).

The term,

- Y_{ijk} = Value of the hybrid involving i^{th} female and j^{th} male parent in k^{th} replication,
m = General mean of all hybrids,
 g_i = GCA effect of i^{th} female parent,
 g_j = GCA effect of j^{th} male parent,
 s_{ij} = SCA effect of the progeny of $(i \times j)^{\text{th}}$ cross,
 r_k = Effect of k^{th} replication, and
 e_{ijk} = Uncontrolled variation associated with ijk^{th} observation.

The analysis of variance (ANOVA) table for combining ability is given as under

Analysis of variance for combining ability

Sources of variation	d.f.	MSS
Replications	(r-1)	-
Hybrids (h)	(h-1)	M_h
Lines (L)	(l-1)	M_l
Testers (T)	(t-1)	M_t
$L \times T$	(l-1) (t-1)	M_{lt}
Error	(r-1) (h-1)	M_e

Where,

- l = Number of line,
- t = Number of tester,
- h = Number of hybrid,
- r = Number of replication,

Estimation of *gca* and *sca* effects

The general combining ability (*gca*) and specific combining ability (*sca*) effects were calculated using following relationships.

$$\begin{aligned} g_i &= Y_{i.} - Y_{..} \\ g_j &= Y_{.j} - Y_{..} \\ s_{ij} &= Y_{ij} - Y_{i.} - Y_{.j} + Y_{..} \end{aligned}$$

Where,

g_i , g_j and s_{ij} has the same meaning mentioned under the statistical model for combining ability analysis.

- $Y_{i.}$ = The mean performance of i^{th} female parent with all male parents in hybrid combinations,
- $Y_{.j}$ = The mean performance of j^{th} male parent with all female parents in hybrid combinations,
- Y_{ij} = The mean performance of hybrid from j^{th} male parent and i^{th} female parent
- $Y_{..}$ = The overall mean performance of hybrids all male and female parents in hybrid combination
- G_i = General combining effect of line (female)
- G_j = General combining effect of tester (male)
- S_{ij} = Specific combining effect of ij^{th} crosses

3.2.5.3. Studies on gene action

Gene action is the ratio of *gca* variance and *sca* variance. Mainly two types of gene action, additive gene action and non-additive gene action. When the ratio of *gca* and *sca* variance is more than one, that indicates additive gene action and wherever the ratio is less than one; the gene action is non-additive.

$$\text{Gene action} = \frac{\text{Var. } gca}{\text{Var. } sca}$$

3.2.5.4 Estimation of heterosis in exotic x local wheats

The overall mean values of each character for each parent and hybrid were utilized and heterobeltiosis was estimated as difference between the mean of the F_1 and that of the parent with greater expression for each of the characters in each hybrid combination.

Heterobeltiosis (Better parent heterosis)

Heterobeltiosis was calculated using the method given by Fonesca and Patterson (1968). It was measured as the proportion of deviation of F_1 value from the better parent, expressed in percentage.

$$\text{Heterobeltiosis(\%)} = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

Where,

F_1 = Mean performance of F_1

BP = Mean value of the better parent

The significance of heterosis was tested in both the situations by calculating the critical difference (C.D) at 5% and 1% levels error degrees of freedom.

$$\text{S.E (d) for BP} = \sqrt{2 \text{ MSe} / r}$$

$$\text{C.D. for BP} = \text{S.E (d)} \times t \text{ value at error d. f.}$$

Where,

MSe = Error Mean Square

r = Number of replications.

Test of significance of heterosis by using 't' test.

$$t = \frac{F_1 - BP}{\text{S.E. of heterosis over BP}}$$

Test of significance was evaluated by calculated 't' values were compared with tabulated 't' values at error degree of freedom.

3.2.5.5 Disease reaction of the parents and hybrids

The stripe rust severity as percent infection and field response scale (Infection type) was recorded as per modified Cobb's scale (Peterson *et al.*, 1948) as shown in a Fig. a and Fig. b, respectively. The data on disease severity and host reaction was combined to calculate the coefficient of infection (CI) by multiplying the severity value of 0.2, 0.4, 0.8, 1.0 for host response ratings R, MR, MS, S respectively is given in Table 3.2. (Pathan & Park., 2006).

Table 3.2: Host response to stripe rust in field

Reaction	Description	Observation	R. value
Resistant	Visible chlorosis/necrosis, no uredina are present	R	0.2
Moderately-Resistant	Small uredina surrounded by chlorotic or necrotic areas	MR	0.4
Moderately-Susceptible	Uredina medium sized with no necrotic margins but possibly some distinct chlorosis	MS	0.8
Susceptible	Large necrosis with no necrosis or very little necrosis	S	1.0

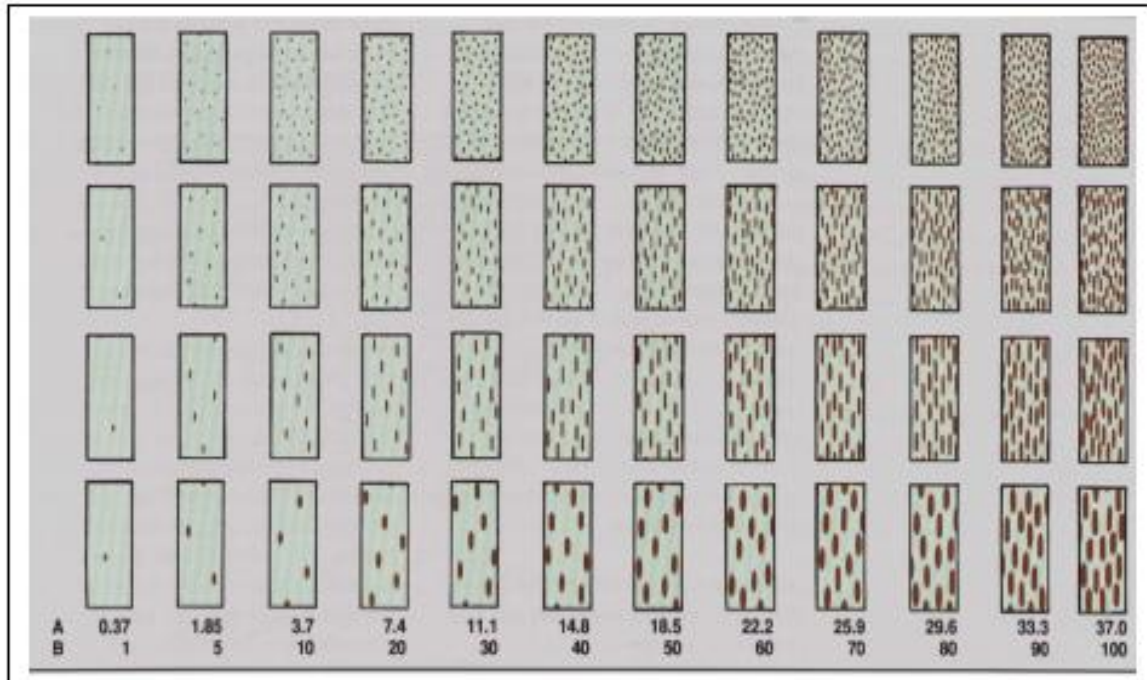


Figure 3A: The Modified Cobb's scale A: refers to the actual percentage occupied by rust uredinia A; and B: pertains to rust severities of the modified Cobb's scale after Peterson *et al.*, 1948 (Source: Knott, 1989).

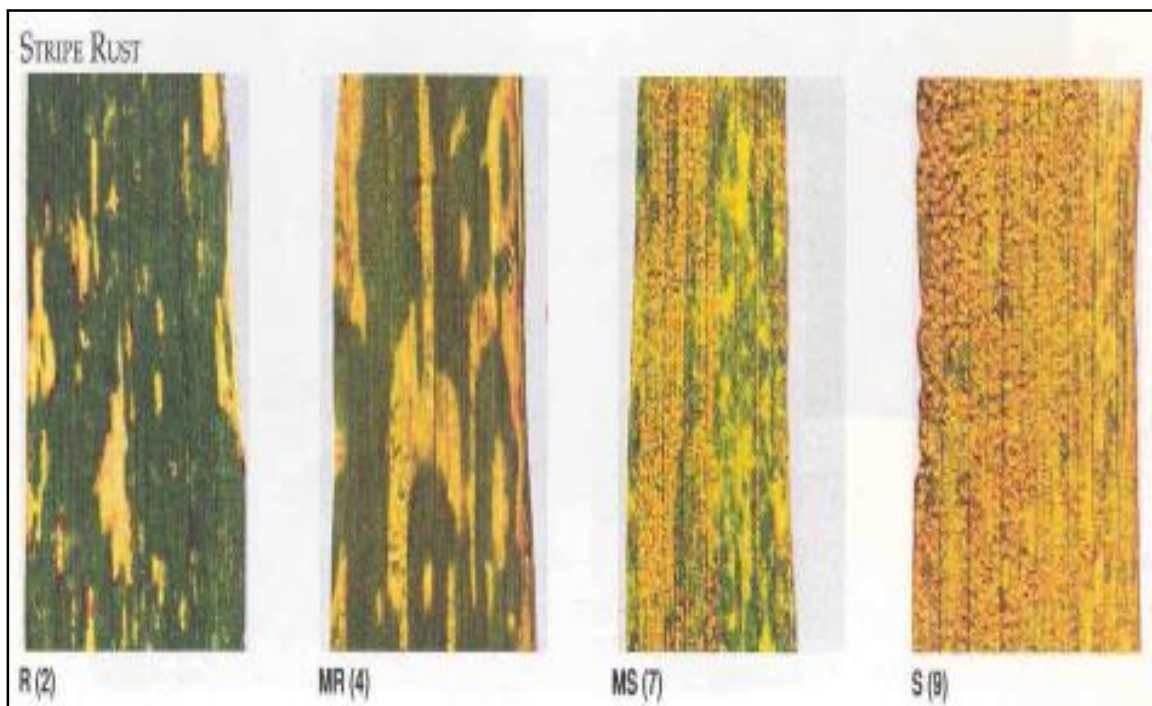


Figure 3B: The Modified Cobb's scale (Source: McIntosh *et al.*, 1995)

Chapter-IV

Results

The present study entitled “**Combining behaviour of exotic x local wheats for durable resistance to stripe rust**” was carried out with an idea to develop breeding material in wheat with enhanced stripe rust resistance. The material for the study involved eleven wheat genotypes which included eight resistant and three adapted cultivars. The eight stripe rust resistant lines were BOTH, MAJENTA, SUNLINE, SUNTOP, DANPHE, ENKOY, FH-11-6-24, HAR-421 obtained from the minicore collection of resistant germplasm from Australia, Africa. The three testers were RSP-561, JAUW-584, WB-2 which are commercial varieties suitable for timely sown irrigated condition of Jammu. The parental material was sown during *Rabi* 2018 for evaluation of disease and yield related traits and twenty four F₁s were generated using eight lines x three testers in LXT design. The F₁s were evaluated in randomized block design with five replications during *Rabi* 2019. The results obtained have been tabulated and discussed under following sub-heads:

- 4.1 Analysis of variance and mean performance of parents and F₁s
- 4.2 Studies on combining behaviour of exotic x local wheats
 - 4.2.1 Analysis of variance for combining ability
 - 4.2.2 Estimates of general and specific combining ability effects
- 4.3 Studies on gene action
- 4.4 Estimation of heterosis in exotic x local wheat crosses
- 4.5 Disease score of the parents and F₁s

4.1 Analysis of variance and mean performance of parents and F₁s

Analysis of variance is a mathematical process of partitioning the total sum of squares into different sources of variation. It is a summary of how much of the total variability among individual responses can be explained by the treatment means and how much remains as unexplained variation among the responses for a given treatment.

The analysis of variance for parents and F₁s was carried out to test the difference among parents and their F₁s for seven quantitative traits presented in Table 4.1. Analysis of variance revealed that mean sum of square due to genotype, parents and parents vs F₁s were highly significant for all the traits indicating the existence of genetic variability in the parental material used. The mean sum of squares due to lines was highly significant for all the traits except for number of tillers per plant and 1000 grain weight. Comparisons of mean square due to line vs tester was significant for all the traits except number of spikelets per plant. Mean square due to testers was significant for spike length and grain yield per plant. This indicated that existence of considerable amount of variability in line and tester except for the traits mentioned.

The mean performance of the eleven parents and twenty four F₁s for seven quantitative traits which include disease related physiological traits viz., flag leaf area and chlorophyll content and yield related traits viz., no. of tillers per plant, spike length, no. of spikelets per spike, 1000 grain weight and grain yield per plant have been presented as Appendix-A.

4.1.1 No. of tillers per plant

Maximum number of seven tillers per plant was recorded in the line HAR-421 and tester RSP-561 (10). MAJENTA x JAUW-584 recorded maximum of thirteen tillers per plant exceeding both the parents with 5.8 and 9.4 tillers respectively. The range for this traits in the F₁s varied from 6.8 to 13.60.

4.1.2 Flag leaf area (cm²)

Maximum flag leaf area was recorded in line MAJENTA (69.89) and minimum in FH-11-6-24 (39.68). Among the F₁s, MAJENTA X JAUW-584 recorded maximum flag leaf area of 64.51. The range of flag leaf area in the F₁s varied from the F₁s 47.92 to 64.51. The genotype MAJENTA appears to be a donor for flag leaf area.

4.1.3 Spike length (cm)

The range of spike length in the parents varied from 7.82 cm to 11.98 cm while that in the F₁s from 7.94 to 15.06 cm. Maximum spike length was recorded in the genotype SUNTOP (11.98 cm) whereas the F₁s SUNTOP X WB-2 had maximum spike length measuring 15.06. The

Table 4.1: Analysis of variance (mean square) of parents and F₁s for disease related and yield component traits in bread wheat

Source of variation	d.f.	No. of tillers per plant	Flag leaf area (cm ²)	Spike length (cm)	No. of spikelets per spike	Chlorophyll content of flag leaf	1000 grain weight (g)	Grain yield per plant (g)
Replication	4	2.1	51.2	1.23*	2.02	12.81	5.41	0.33
Genotype	34	27.00**	259.54**	20.64**	27.35**	71.40**	31.53**	24.37**
Parents	10	17.64**	525.63**	6.89**	12.81**	20.38**	23.28**	31.49**
Parents (Line)	7	3.02	700.89**	8.05**	17.92**	16.28*	5.68	34.88**
Parents(Tester)	2	1.26	12.34	4.91**	1.06	0.85	0.6	15.18**
Line vs. Tester	1	152.72**	325.37*	2.75**	0.51	88.14**	191.80**	40.36**
Parents vs. hybrids	1	294.88**	896.80**	367.82**	603.20**	186.88**	405.45**	76.95**
Hybrids	23	19.43	116.13*	11.52**	8.64**	88.56**	18.86	18.99**
Line effect	7	34.27	173.41	23.65*	20.55**	223.14**	26.58	30.68
Tester effect	2	11.6	36.24	5.89	4.25	0.044	26.66	20.29
Line * Tester effect	14	13.13**	98.91	6.26**	3.31*	33.93**	13.88**	12.95*
Error	136	2.67	64.16	0.37	1.81	6.71	3.4	1.08

* $P \leq 0.05$, ** $P \leq 0.01$

range of spike length in the F_1 s was in a higher range of 12 to 15cm far exceeding their respective parents.

4.1.4 Number of spikelets per spike

Among the lines, the maximum number of spikelets per spike was recorded in the line MAJENTA (22.2) while minimum in BOTH (16.4). Among the testers, the maximum number of spikelets per spike was recorded in WB-2 (19) followed by 18.20 in RSP-561 and JAUW-584. Among the F_1 s, the F_1 s MAJENTA X RSP-561 recorded maximum 25 spikeletes per spike and the range for this trait in the F_1 s was 19.60 to 25.

4.1.5 Chlorophyll content of flag leaf

The range for chlorophyll content in the genotype varied from 36.54 - 42.86. The genotype JAUW-584 had the maximum chlorophyll content of 42.86. The range of chlorophyll content in F_1 s was between 29.72 to 47.14 maximum observed in BOTH x WB-2.

4.1.6 1000 Grain weight (g)

Relatively narrow range of thousand grain weight was recorded in the resistant lines (34.23 to 37.27). The testers being the commercial varieties had higher thousand grain weight being maximum in WB-2 (40.0g). None of the F_1 s exceed WB-2 with respect to test weight indicating per se yield inferiority of F_1 s. The best F_1 s with respect to thousand grain weight was SUNLINE X RSP-561 (36.55g).

4.1.7 Grain yield per plant (g)

Maximum grain yield per plant was recorded line in FH-11-6-24 (13.16g) and tester, by WB-2 (13.14) while that in F_1 s combination in MAJENTA X WB-2 (14.45g). Per se yield superiority was not recorded in any of the F_1 s involving FH-11-6-24, although four F_1 s viz., MAJENTA X WB-2 (14.45), SUNLINE X WB-2 (13.60), SUNTOP X WB-2 (13.17) and HAR-421 X WB-2 (13.23) exceeded WB-2 for grain yield per plant.

4.2 Studies on combining behaviour of exotic x local wheats.

Combining ability is the ability of a strain to produce superior progeny upon hybridization with other strains (Singh 2009). The concept of combining ability in terms of genetic variation was first given by Sprague and Tatum (1942). They defined the term general

combining ability (GCA) as an average performance of a line in F_1 s combinations and specific combining ability (SCA) as the combinations which do relatively better or worse than that would be expected on the basis of the average performance of the lines involved.

According to Griffing (1956), general combining ability (GCA) is related to additive as well as additive $\times$ additive interaction, whereas specific combining ability (SCA) is related to the dominance variance and all the three types of interactions (additive $\times$ additive, additive $\times$ dominance and dominance $\times$ dominance).

4.2.1 Analysis of variance for combining ability

The analysis of variance segmentation of the total genetic variance into general combining ability indicates additive type of gene action and specific combining ability as a measure of non-additive gene action was carried out for seven traits and presented in Table 4.2. Mean square due to F_1 s and line $\times$ tester were significant for all the traits under study while that due to line was significant for spike length, number of spikelets per spike and chlorophyll content of flag leaf.

The magnitude of specific combining ability variance was higher than general combining ability variance for the all trait indicating that non-additive gene effect is greater than additive effect. The ratio ($\sigma^2_{gca} / \sigma^2_{sca}$) variance was less than unity for all the traits indicating that non-additive components play relatively more pronounced role in the inheritance of all the traits.

4.2.2 Estimates of General and specific combining ability effects

The estimates of GCA effects of the parents for all the traits have been presented in Table 4.3 and the suitable combiners based on general combining ability effects have been summarized in Table 4.4. The estimates of specific combining ability effects of the twenty four F_1 s have been presented in Table 4.5.

4.2.2.1 No. of tillers per plant

Among the lines BOTH and MAJENTA recorded significantly high *gca* effect in desirable direction for number of tillers per plant. Estimate of *gca* effect ranged from -2.34

Table 4.2: Analysis of variance (mean square) for combining ability and estimates of components of variance for different traits in bread wheat

Source of variation	d.f.	No. of tillers per plant	Flag leaf area (cm ²)	Spike length (cm)	Number of spikelets per spike	Chlorophyll content of flag leaf	1000 grain weight (g)	Grain yield per plant (g)
Replication	4	2.39	81.35	1.01*	1.76	19.76	9.90*	0.82
Crosses	23	19.43**	116.13*	11.52**	8.64**	88.56**	18.86**	18.99**
Line	7	34.27	173.41	23.65*	20.55**	223.14**	26.58	30.68
Tester	2	11.6	36.24	5.89	4.25	0.04	26.66	20.29
Line × Tester	14	13.13**	98.91	6.26**	3.31*	33.93**	13.88**	12.95**
Error	92	3.33	59.02	0.39	1.8	8.62	3.59	1.12
σ² line		1.4	4.96	1.15	1.14	12.61	0.84	1.18
σ² tester		-0.03	-1.56	-0.01	0.02	-0.84	0.31	0.18
σ² gca		0.08	0.23	0.07	0.07	0.75	0.06	0.08
σ² sca		1.95	7.97	1.17	0.3	5.06	2.05	2.36
σ² gca/ σ² sca		0.04	0.02	0.05	0.23	0.75	0.02	0.03

* P ≤ 0.05, ** P ≤ 0.01

Table 4.3: General combining ability (*gca*) effects of lines and testers for disease related and yield component traits in bread wheat

Sr. No.	Parents	No. of tillers per plant	Flag leaf area (cm ²)	Spike length (cm)	No. of spikelets per spike	Chlorophyll content of flag leaf	1000 grain weight (g)	Grain yield per plant (g)
1	BOTH	1.33**	-2.28	-2.55**	-2.24**	6.58**	-1.32**	-2.27**
2	MAJENTA	1.86**	3.12	-0.42*	1.49**	2.84**	-1.51**	-2.28**
3	SUNLINE	0.86	-1.52	1.15**	0.09	1.91*	2.39**	1.08**
4	SUNTOP	0.79	1.78	1.25**	-0.51	-2.63**	1.24*	0.83**
5	DANPHE	-0.81	-2.23	-0.36*	-0.44	-3.59**	-0.48	0.78**
6	ENKOY	-1.81**	6.43**	0.36*	0.09	-4.75**	-0.76	0.41
7	FH-11-6-24	0.13	-2.96	1.01**	0.16	0.89	0.53	0.38
8	HAR-421	-2.34**	-2.33	-0.44**	1.36**	-1.51*	-0.1	1.07**
9	RSP-561	0.56	-0.5	0.39**	0.34	0.01	0.34	0.36*
10	JAUW-584	-0.04	1.1	-0.01	-0.03	-0.04	-0.93**	-0.82**
11	WB-2	-0.52	-0.6	-0.38**	-0.31	0.03	0.59*	0.46**

* $P \leq 0.05$, ** $P \leq 0.01$

Table 4.4: GCA effects of parents for contributing traits in bread wheat

Sr. No	Parents	Traits						
		No. of tillers per plant	Flag leaf area (cm ²)	Spike length (cm)	No. of spikelets per spike	Chlorophyll content of flag leaf	1000 grain weight (g)	Grain yield per plant (g)
1	BOTH	G	A	P	P	G	P	P
2	MAJENTA	G	A	P	G	G	P	P
3	SUNLINE	A	A	G	A	G	G	G
4	SUNTOP	A	A	G	A	P	G	G
5	DANPHE	A	A	P	A	P	A	G
6	ENKOY	P	G	G	A	P	A	A
7	FH-11-6-24	A	A	G	A	A	A	A
8	HAR-421	P	A	P	G	P	A	G
9	RSP-561	A	A	G	A	A	A	G
10	JAUW-584	A	A	P	A	A	P	P
11	WB-2	A	A	P	A	A	G	G

G = Good general combiner (significant and desirable for particular trait)

A = Average general combiner (non-significant negative and positive)

P = Poor general combiner (significant and negative for particular trait)

Table 4.5: Specific combining ability (*sca*) effect of F₁s for disease related and yield component traits in bread wheat

Sr. No.	Parents	No. of tillers per plant	Flag leaf area (cm²)	Spike length (cm)	No. of spikelets per spike	Chlorophyll content of flag leaf	1000 grain weight (g)	Grain yield per plant (g)
1	BOTH X RSP-561	-2.83**	-3.37	1.31**	-0.01	1.32	1.96*	2.53**
2	BOTH X JAUW-584	1.17	7.77*	1.28**	-0.43	-3.46**	-1.33	-1.58**
3	BOTH X WB-2	1.65*	-4.4	-2.59**	0.44	2.14	-0.63	-0.95*
4	MAJENTA X RSP-561	-2.36**	-4.21	-1.09**	0.86	-0.83	-1.97*	-2.41**
5	MAJENTA X JAUW-584	2.24**	5.09	-0.35	-0.77	-0.33	-1.5	-1.25**
6	MAJENTA X WB-2	0.12	-0.89	1.44**	-0.09	1.16	3.47**	3.66**
7	SUNLINE X RSP-561	0.84	5.11	-0.25	-0.34	3.01*	0.44	0.21
8	SUNLINE X JAUW -584	-0.36	-5.46	0.24	0.03	-1.24	-0.59	-0.32
9	SUNLINE X WB-2	-0.48	0.35	0.01	0.31	-1.77	0.15	0.1
10	SUNTOP X RSP-561	1.91*	-0.01	-0.05	-1.54*	-2.26	-0.58	-0.35
11	SUNTOP X JAUW-584	-1.49	2.21	-0.68*	1.03	1.82	-0.08	0.43
12	SUNTOP X WB-2	-0.42	-2.2	0.73*	0.51	0.44	0.66	-0.08
13	DANPHE X RSP-561	1.71*	2.13	0.75**	0.79	0.48	0.73	0.44
14	DANPHE X JAUW-584	-1.49	-0.82	-0.35	0.37	0.12	0.44	0.01
15	DANPHE X WB-2	-0.22	-1.3	-0.4	-1.16	-0.6	-1.17	-0.45
16	ENKOY X RSP-561	0.31	-2	-0.13	-0.34	-3.66**	-1.09	0.14
17	ENKOY X JAUW-584	-0.49	-1.39	-0.53	0.03	2.72*	2.40**	1.03*
18	ENKOY X WB -2	0.18	3.39	0.66*	0.31	0.94	-1.31	-1.17*
19	FH-11-6-24 X RSP-561	0.38	1.66	-0.41	-0.01	0.17	0.01	-0.07
20	FH-11-6-24 X JAUW-584	0.57	-2.54	-0.26	-0.43	3.00*	-0.11	0.91
21	FH-11-6-24 X WB-2	-0.95	0.87	0.67*	0.44	-3.17*	0.12	-0.84
22	HAR-421 X RSP-561	0.04	0.68	-0.12	0.59	1.78	0.52	-0.49
23	HAR-421 X JAUW-584	-0.16	-4.85	0.65*	0.17	-2.64*	0.78	0.75
24	HAR-421 X WB-2	0.12	4.17	-0.53	-0.76	0.86	-1.3	-0.26

*** P ≤ 0.05, ** P ≤ 0.**

(HAR-421) to 1.86 (MAJENTA) and out of eleven parent two had significant *gca* effect in desirable direction.

Estimation of specific combining ability effects for this trait ranged from -2.83 in (BOTH X RSP-561) to 2.24 (MAJENTA X JAUW-584). Out of 24 F₁s, four F₁ viz., MAJENTA X JAUW-584 (2.24), BOTH X WB-2 (1.65), SUNTOP X RSP-561 (1.91) and DANPHE X RSP-561 (1.71) showed significant positive specific combining ability effects for number of tillers per plant.

4.2.2.2 Flag leaf area (cm²)

Among the lines, ENKOY showed significant *gca* effect for flag leaf area in desirable direction (6.43). The GCA of parents ranged from -2.96 to 6.43 for flag leaf area. The Specific combining ability of F₁s ranged from -5.46 to 7.77 for flag leaf area.

4.2.2.3 Spike length (cm)

The *gca* effect for spike length ranged from -2.55 in (BOTH) to 1.25 in (SUNTOP). Among the lines SUNLINE (1.15), SUNTOP (1.25) and FH-11-6-24 (1.01) showed highly significant positive general combining ability effects and thus are good combiners for spike length.

The *sca* effects ranged from -2.59 in BOTH X WB-2 to 1.44 in MAJENTA X WB-2. Significant and desirable *sca* effects was recorded in eight F₁'s viz. BOTH X RSP-561 (1.31), BOTH X JAUW-584 (1.28), MAJENTA X WB-2 (1.44), SUNTOP X WB-2 (0.73), DANPHE X RSP-561 (0.75), ENKOY X WB -2 (0.66), FH-11-6-24 x WB-2 (0.67) and HAR-421 X JAUW-584 (0.65) for this trait.

4.2.2.4. Number of spikelets per spike

For the trait, spikelets per spike the *gca* effects of lines varied from -2.24 in BOTH to 1.49 in MAJENTA. Among the lines MAJENTA (1.49) and HAR-421 (1.36) recorded significant *gca* effects and contributed maximum favourable genes. The *sca* effects for number of spikelets per spike ranged between -1.54 (SUNTOP X RSP-561) to 1.03 (SUNTOP X JAUW-584). None of the F₁s recorded significant positive *sca* effects in desirable direction.

4.2.2.5 Chlorophyll content of flag leaf

The line BOTH and MAJENTA exhibited highly significant *gca* effect in a desirable direction. The *gca* effect for this trait ranged between –0.51 in SUNTOP to 6.58 in BOTH. None of the tester showed significant GCA for chlorophyll content.

Results revealed that *sca* effect for chlorophyll content ranged between –3.66 (ENKOY X RSP-561) to 3.01 (SUNLINE X RSP-561). The combination SUNLINE X RSP-561 (3.01) produced the highest significant *sca* effect followed by FH-11-6-24 X JAUW-584 (3.00) and ENKOY X JAUW-584 (2.72).

4.2.2.6 1000 grain weight (g)

Among the lines positive significant *gca* effects was exhibited by SUNLINE (2.39). and SUNTOP (1.92). WB-2 (0.59) among tester recorded significant *gca* effect in desirable direction for 1000 grain weight. Among eleven parents, three parents exhibited (two lines and one tester) significant *gca* effect in desirable direction.

The F_1 s that exhibited highly significant *sca* effect in desirable direction are MAJENTA X WB-2, ENKOY X JAUW-584 and BOTH X RSP-561. The range of *sca* effect for this trait ranged from -1.97 in MAJENTA X RSP-561 to 3.47 in MAJENTA X WB-2.

4.2.2.7 Grain yield per plant (g)

Highly significant positive *gca* effects was observed in SUNLINE (1.08), SUNTOP (0.83), DANPHE (0.78) and HAR-421 (1.07), RSP-561 (0.56) and WB-2 (0.46) indicating these genotype to be good general combiner for grain yield per plant.

The extent of *sca* effects for grain yield was high in MAJENTA X WB-2 (3.66) followed by BOTH X RSP-561 (2.53) and ENKOY X JAUW-584 (1.03). Out of 24 F_1 s obtained three F_1 s showed significantly high *sca* effects for grain yield per plant. These have further been classified based on degree of disease incidence.

4.3 Studies on gene action

The GCA and SCA variance, their ratio along with gene action and heritability estimates

Table 4.7: Contribution of lines, testers and lines x testers interaction for F₁s variation.

Traits	Contribution of lines (per cent)	Contribution of testers (per cent)	Contribution of lines x testers (per cent)
No. of tillers per plant	53.68	5.19	41.13
Flag leaf area (cm²)	45.44	2.71	51.84
Spike length (cm)	62.46	4.45	33.10
No. of spikelets per spike	72.37	4.28	23.35
Chlorophyll content of flag leaf	76.68	0	23.32
1000 grain weight (g)	42.90	12.29	44.81
Grain yield per plant (g)	49.17	9.29	41.54

4.4.1 No. of tillers per plant

Positive heterosis for number of tillers is desirable because number of fertile tillers directly affects the grain yield. The magnitude of heterobeltiosis for number of tillers ranged from -25.53 to 44.68 per cent. Positive and significant heterobeltiosis was recorded in F₁s BOTH X WB-2, MAJENTA X JAUW-584, SUNTOP X RSP-561 and BOTH X JAUW-584, highest being in MAJENTA x JAUW-584 (44.68%).

4.4.2 Flag leaf area (cm²)

Heterobeltiosis for flag leaf area ranged from -25.80 to 34.82 cm² while positive and significant heterobeltiosis was exhibited by two F₁s viz., ENKOY X RSP-561, and SUNLINE X RSP-561. Positive and highly significant heterobeltiosis was exhibited by two F₁s viz., ENKOY X JAUW-584, ENKOY X WB -2.

4.4.3 Spike length (cm)

Heterobeltiosis for spike length ranged from -22.31 to 39.38 per cent. The positive and highly significant heterobeltiosis was exhibited by twenty out of twenty four F₁. These include viz., BOTH X RSP-561, MAJENTA X RSP-561, MAJENTA X WB-2, SUNLINE X RSP-561, SUNLINE X JAUW-584, SUNLINE X WB-2, SUNTOP X RSP-561, SUNTOP X JAUW-584,

Table 4.8: Heterobeltiosis for grain yield and its contributing traits in Exotic x local F₁s in bread wheat

Sr.No.	F ₁ s	No. of tillers per plant	Flag leaf area(cm ²)	Spike length (cm)	No. of spikelets per spike	Chlorophyll content of flag leaf	1000 grain weight (g)	Grain yield per plant (g)
1	BOTH X RSP-561	-14.00	-24.04**	25.50**	12.09**	8.89*	-12.63**	-1.1
2	BOTH X JAUW-584	27.66*	-4.33	2.87	7.69	-3.22	-25.12**	-26.59**
3	BOTH X WB-2	33.33**	-25.80**	-22.31**	6.32	10.87**	-19.93**	-30.06**
4	MAJENTA X RSP-561	-4.00	-23.28**	15.54**	12.61**	-4.52	-23.13**	-39.99**
5	MAJENTA X JAUW-584	44.68**	-7.69	7.09*	3.6	-5.27	-26.04**	-37.88**
6	MAJENTA X WB-2	22.22	-18.68*	32.02**	5.41	-0.47	-10.18**	4.96
7	SUNLINE X RSP-561	18.00	26.57*	34.73**	23.08**	2.43	-7.05*	7.06
8	SUNLINE X JAUW -584	6.38	9.72	25.34**	23.08**	-9.57*	-13.94**	19.83**
9	SUNLINE X WB-2	4.44	11.21	30.16**	17.89**	-9.58*	-8.71**	3.5
10	SUNTOP X RSP-561	28.00**	-6.22	25.54**	13.19**	-20.93**	-12.57**	0.64
11	SUNTOP X JAUW-584	-6.38	0.11	17.03**	25.27**	-13.02**	-15.54**	24.88**
12	SUNTOP X WB-2	4.44	-10.03	25.71**	15.79**	-15.11**	-10.31**	0.21
13	DANPHE X RSP-561	10	18.54	36.92**	26.37**	-16.70**	-13.62**	6.49
14	DANPHE X JAUW-584	-23.40*	18.45	7.60*	21.98**	-19.23**	-18.55**	20.17**
15	DANPHE X WB-2	-11.11	6.28	18.46**	7.37	-19.83**	-19.19**	-2.98
16	ENKOY X RSP-561	-14	28.37*	34.87**	23.08**	-29.31**	-18.99**	1.26
17	ENKOY X JAUW-584	-23.40*	34.82**	12.16**	23.08**	-15.87**	-14.35**	0.56
18	ENKOY X WB -2	-17.78	34.07**	35.06**	17.89**	-18.93**	-20.25**	-11.26*
19	FH-11-6-24 X RSP-561	6	15.94	39.38**	25.27**	-6.76	-12.95**	-3.97
20	FH-11-6-24 X JAUW-584	8.51	13.02	19.93**	20.88**	-2.05	-17.41**	-5.5
21	FH-11-6-24 X WB-2	-8.89	9.28	42.47**	18.95**	-15.30**	-13.43**	-9.16
22	HAR-421 X RSP-561	-22.00*	0.82	32.27**	24.24**	-8.66*	-13.18**	1.43
23	HAR-421 X JAUW-584	-25.53*	-6.67	15.37**	20.20**	-20.81**	-16.75**	13.67*
24	HAR-421 X WB-2	-24.44*	7.25	18.40**	14.14**	-11.47**	-18.55	0.68

* P ≤ 0.05, ** P ≤ 0.01

SUNTOP X WB-2, DANPHE X RSP-561, DANPHE X WB-2, ENKOY X RSP-561, ENKOY X JAUW-584, ENKOY X WB-2, FH-11-6-24 X RSP-561, FH-11-6-24 X JAUW-584, FH-11-6-24 X WB-2, HAR-421 X RSP-561, HAR-421 X JAUW-584 and HAR-421 X WB-2 while positive and significant heterobeltiosis was exhibited by two F_1 s viz., MAJENTA X JAUW-584 and DANPHE X JAUW-584.

4.4.4 Number of spikelets per spike

Heterobeltiosis for spikelets per spike ranged from 3.60 to 26.37. The positive and highly significant heterobeltiosis was exhibited by nineteen F_1 s viz., BOTH X RSP-561, MAJENTA X RSP-561, SUNLINE X RSP-561, SUNLINE X JAUW-584, SUNLINE X WB-2, SUNTOP X RSP-561, SUNTOP X JAUW-584, SUNTOP X WB-2, DANPHE X RSP-561, DANPHE X JAUW-584, ENKOY X RSP-561, ENKOY X JAUW-584, ENKOY X WB-2, FH-11-6-24 X RSP-561, FH-11-6-24 X JAUW-584, FH-11-6-24 X WB-2, HAR-421 X RSP-561, HAR-421 X JAUW-584 and HAR-421 X WB-2.

4.4.5 Chlorophyll content of flag leaf

Chlorophyll content is more related to disease development and heterosis for this trait is an indicator of healthy plant free from disease. Heterobeltiosis for chlorophyll content ranged from -29.31 to 10.87. BOTH X WB-2 exhibited positive and highly significant heterobeltiosis for chlorophyll content while BOTH X RSP-561 exhibited positive and significant heterobeltiosis. Further, BOTH is a good general combiner for chlorophyll content.

4.4.6 Grain yield per plant (g)

Positive heterosis is desirable for grain yield per plant. Heterobeltiosis for grain yield per plant ranged from -39.99 to 24.8 per cent. Three F_1 s exhibited positive and highly significant heterobeltiosis viz., SUNLINE X JAUW-584, SUNTOP X JAUW-584, DANPHE X JAUW-584, while one F_1 s viz., HAR-421 X JAUW-584 exhibited positive and significant heterobeltiosis for grain yield per plant. JAUW-584 appears to be a contribute to high heterosis of all the F_1 for grain yield per plant but this can't be correlated to its *gca*.

4.5 Disease score of the parents and F₁s:

Results pertaining to the disease score of the parents and F₁s in terms of adult plant reaction to stripe rust under field conditions have been presented in the Table 4.9. Adult plant reaction of the lines (the source of resistance) ranged from TR to 40MS. The testers which are the high yielding adapted varieties showed the disease score ranging from 20S in WB-2 to 40MS in JAUW-584 and 60S in RSP-561. F₁s showed the disease score ranging from 10MR to 60S. There were three F₁s that showed 10MR reaction while six showed 20MS reaction, four showed 20S reaction, one F₁ showed 40MS reaction, six F₁s showed 40S reaction and four F₁s showed 60S reaction.

The F₁s MAJENTA X WB-2, DANPHE X RSP-561 and HAR-421 X WB-2 were moderately resistant with 10MR type of reaction to stripe rust while BOTH X RSP-561, SUNLINE X RSP-561, SUNLINE X JAUW-584, SUNLINE X WB-2, DANPHE X WB-2, HAR-421 X RSP-561 showed 20MS type of reaction. The three F₁s with 10MR can be considered potential lines for use in later generations provided they throw high yielding segregants.

Table 4.11 depicted the moderately resistant F₁s with their grain yield per plant (the ultimate trait of interest). It is pertinent to note that out of the twenty four F₁s, three F₁s show moderate resistance and significantly high grain yield (MAJENTA X WB-2, DANPHE X RSP-561 and HAR-421 X WB-2). The best identified F₁s was MAJENTA X WB-2 with grain yield 14.45g and showing 10MR type of disease reaction. The F₁ DANPHE X RSP-561 and HAR-421 X WB-2 produced 13.52 and 13.23 grain yield respectively and both the F₁s show 10MR type of disease reaction.

Table 4.9: Disease score of parents and F₁s in the adult plant stage

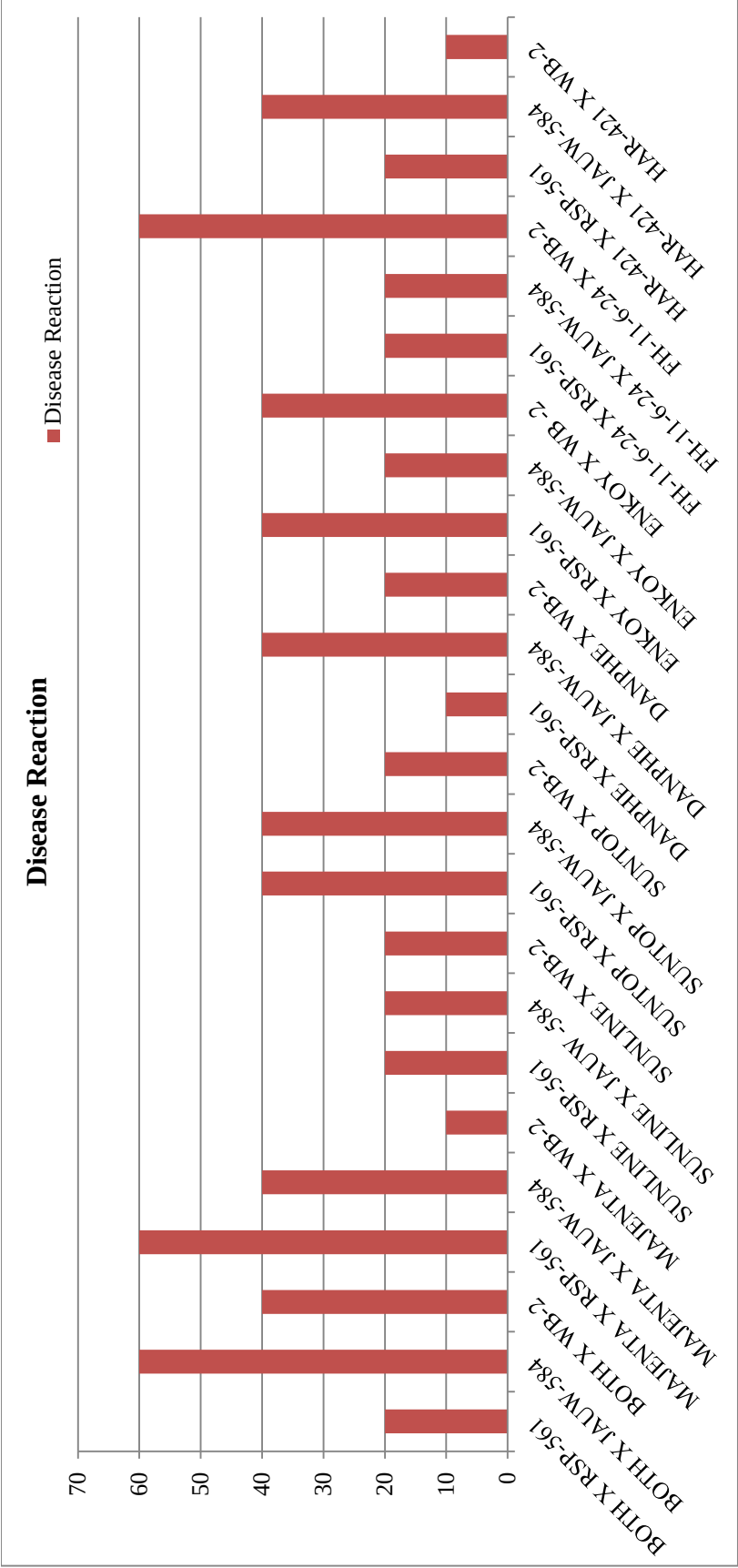
LINE	TESTER	DESEASE SCORE	F ₁ s	DESEASE SCORE
BOTH (TR)	RSP-561	60S	BOTH x RSP-561	20MS
	JAUW-584	40MS	BOTH x JAUW-584	60S
	WB-2	20S	BOTH x WB-2	40S
MAJENTA (40MS)	RSP-561	60S	MAJENTA x RSP-561	60S
	JAUW-584	40MS	MAJENTA x JAUW-584	40S
	WB-2	20S	MAJENTA x WB-2	10MR
SUNLINE (10R)	RSP-561	60S	SUNLINE x RSP-561	20MS
	JAUW-584	40MS	SUNLINE x JAUW-584	20MS
	WB-2	20S	SUNLINE x WB-2	20MS
SUNTOP (10R)	RSP-561	60S	SUNTOP x RSP-561	40S
	JAUW-584	40MS	SUNTOP x JAUW-584	40S
	WB-2	20S	SUNTOP x WB-2	20S
DANPHE (20MS)	RSP-561	60S	DANPHE x RSP-561	10MR
	JAUW-584	40MS	DANPHE x JAUW-584	40MS
	WB-2	20S	DANPHE x WB-2	20MS
ENKOY (10MS)	RSP-561	60S	ENKOY x RSP-561	40S
	JAUW-584	40MS	ENKOY x JAUW-584	20S
	WB-2	20S	ENKOY x WB-2	40S
FH-11-6-24 (20MR)	RSP-561	60S	FH-11-6-24 x RSP-561	20S
	JAUW-584	40MS	FH-11-6-24 x JAUW-584	20S
	WB-2	20S	FH-11-6-24 x WB-2	60S
HAR-421 (10S)	RSP-561	60S	HAR-421 x RSP-561	20MS
	JAUW-584	40MS	HAR-421 x JAUW-584	40S
	WB-2	20S	HAR-421 x WB-2	10MR

Table 4.10: Summary table of grain yield and disease score in the exotic x local crosses in bread wheat

Sr. No.	F₁s	Grain yield per plant (g)	Disease score
1	BOTH X RSP-561	12.58	20 MS
2	BOTH X JAUW-584	7.29	60 S
3	BOTH X WB-2	9.19	40 S
4	MAJENTA X RSP-561	7.64	60 S
5	MAJENTA X JAUW-584	7.61	40 S
6	MAJENTA X WB-2	14.45	10 MR
7	SUNLINE X RSP-561	13.86	20 MS
8	SUNLINE X JAUW -584	12.12	20 MS
9	SUNLINE X WB-2	13.60	20 MS
10	SUNTOP X RSP-561	12.81	40 S
11	SUNTOP X JAUW-584	12.41	40 S
12	SUNTOP X WB-2	13.17	20 S
13	DANPHE X RSP-561	13.52	10 MR
14	DANPHE X JAUW-584	11.94	40 MS
15	DANPHE X WB-2	12.75	20 MS
16	ENKOY X RSP-561	12.88	40 S
17	ENKOY X JAUW-584	12.58	20 S
18	ENKOY X WB -2	11.66	40 S
19	FH-11-6-24 X RSP-561	12.64	20 S
20	FH-11-6-24 X JAUW-584	12.44	20 S
21	FH-11-6-24 X WB-2	11.95	60 S
22	HAR-421 X RSP-561	12.91	20 MS
23	HAR-421 X JAUW-584	12.97	40 S
24	HAR-421 X WB-2	13.23	10 MR

Table 4.11: Prominent F₁s identified on the basis of *per se* grain yield per plant and disease score

Sr. No.	F₁s	Grain yield per plant (g)	Disease
1	MAJENTA X WB-2	14.45	10MR
2	DANPHE X RSP-561	13.52	10MR
3	HAR-421 X WB-2	13.23	10MR
4	SUNLINE X RSP-561	13.86	20MS
5	SUNLINE X WB-2	13.60	20MS
6	HAR-421 X RSP-561	12.91	20MS
7	BOTH X RSP-561	12.58	20MS
8	SUNLINE X JAUW-584	12.12	20MS



10 MR	: Moderately resistance
20 MS	: Moderately susceptible
20 S	: Susceptible
40 MS	: Moderately susceptible
40 S	: Susceptible
60 S	: Susceptible

Fig. 4.1: Disease response and susceptibility response of F₁s in bread wheat

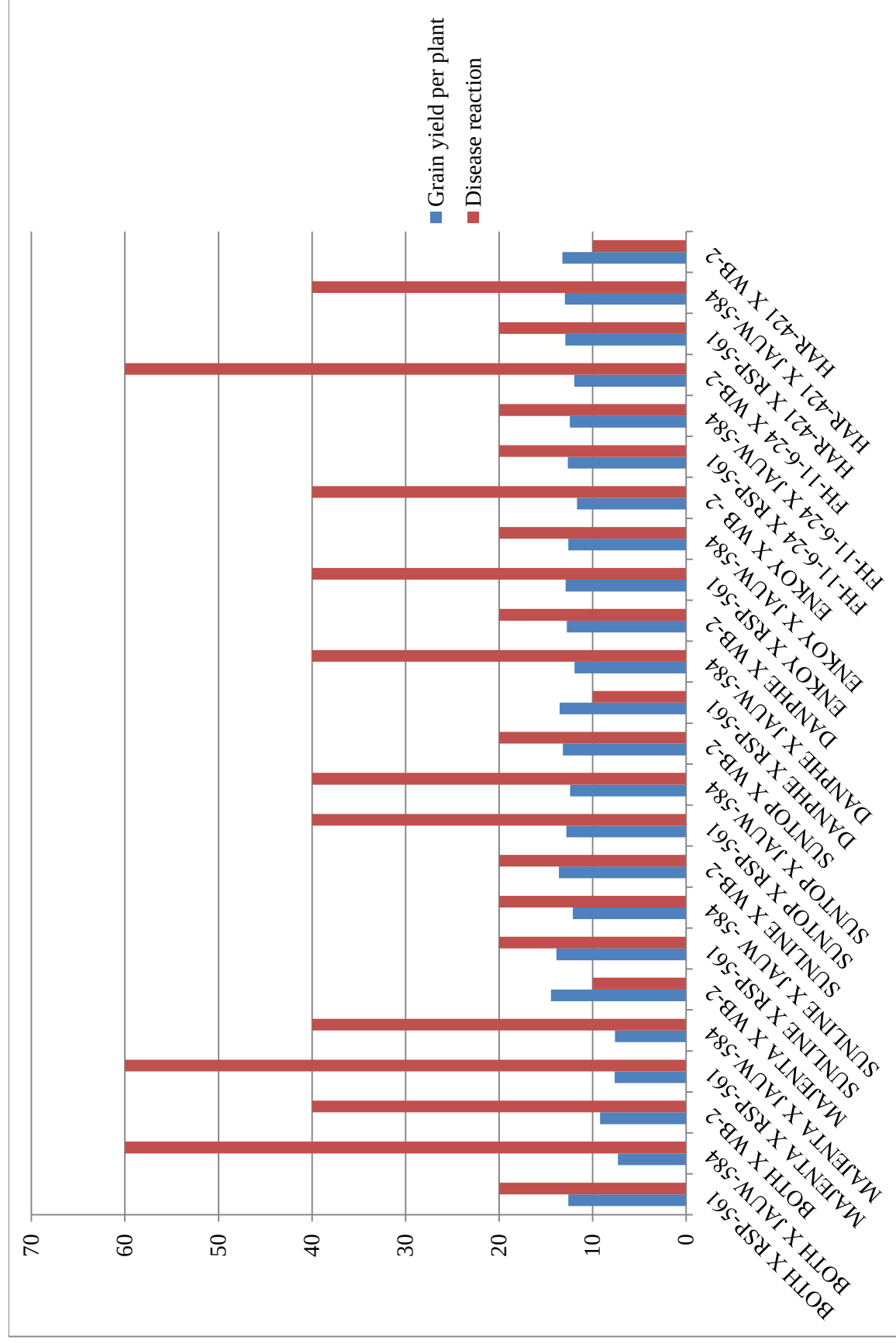


Fig 4.2: Disease response vis-a-vis grain yield per plant of F₁s in bread wheat

Chapter-V

Discussion

The long term objective of most plant breeding program is to increase yield potential of a crop which is intensely associated with resistance to biotic and abiotic stresses. One of the key strategies of resistance breeding in wheat is hybridization methods between suitable parents and subsequent selection of desirable offspring showing transgressive segregation for traits determining yield and disease resistance.

The present investigation directed toward the isolation of best combiners for grain yield associated traits and to identify F₁s with superior specific combining ability through combining ability analysis of exotic x local wheat.

Results of the present investigation are discussed in the light of available literature and possible explanations for the trends obtained are discussed

- 5.1 Analysis of variance and mean performance of parents and F₁s
- 5.2 Studies on combining behaviour and gene action of exotic x local wheats
- 5.3 Heterosis studies in exotic x local wheats
- 5.4 Durable rust resistance in parents and F₁s

5.1 Analysis of variance and Mean performance of parents and F₁s

The analysis of variance for the of thirty five genotypes including parents, parents vs hybrids and line vs tester effect for all seven traits were significantly different revealing the presence of sufficient genetic variability among genotypes and F₁s for majority of the traits studied. Significant variation due to line and hybrids was observed for all the traits except number of tillers per plant and 1000 grain weight (Barot *et al.*, 2014) whereas line vs tester showed significant variance for all traits except for number of spikelets per spike (Tabassum *et al.*, 2017). The variances due to testers were significant for spike length and grain yield per plant being due to the eight lines being the sources of stripe rust resistance perform distinctly with respect to yield.

The study of mean performance of the parents for seven traits revealed that none of the parents show consistent high performance for all the traits under study which further reflects that correlation between yield (the ultimate character) and its contributing traits is variable across genotype. Mean performance of hybrids were higher than their parents for number of tillers per plant, flag leaf area, spike length, number of spikelets per spike and grain yield per plant, with the exception of chlorophyll content of flag leaf and 1000 grain weight. The lower mean of the crosses for chlorophyll content of flag leaf may be due to overall poor disease score of the crosses as compared to the parents. Negative correlation between chlorophyll content and disease severity due to stripe rust has been reported by Mishra *et al.*, 2015. None of the F₁s showed consistent high mean performance for all character. F₁s with superior *per se* performance for two or more traits was recorded in MAJENTA X JAUW-584, SUNLINE X RSP-561, BOTH X WB-2, SUNLINE X WB-2 and SUNTOP X RSP-561 While MAJENTA X WB-2 found best *per se* performance for grain yield per plant. No common trend for the parents involved in the crosses could be deciphered because each resistant line besides showing variable degree of resistance shows variability for other traits under study. WB-2 recorded the best performance as a tester in most of the cases as it is a recently release high yielding variety.

5.2 Studies on combining behaviour and gene action of exotic x local wheats

With the advancement in biometrical genetics, several biometrical tools are available which permits analysis and selection of promising parents and F₁s for further exploitation.

Combining ability is an index of how well a line performs in producing crosses which experience high heterosis. Combining behavior as measured through line x tester analysis is useful for estimating the genetic worth of relatively small number of parents with great precision. It also elucidates the nature of gene action involved in the inheritance of traits as the relative amount GCA and SCA effects play important role in planning appropriate and sound breeding programme. Thus, the present investigation was directed towards estimation of general and specific combining ability of parents and hybrids respectively and to ascertain the type of gene action governing grain yield per

plant and its component traits. Thus, potential stripe rust resistant high yielding lines can be identified for use in hybridization and further combinations with high *sca* and disease resistance can be advanced to isolate useful segregants.

The analysis of variance due to mean square and variance estimates for combining ability reveal that mean square due to F_1 s and line x tester were significant for number of tillers per plant, 1000 grain weight and grain yield per plant. The results are in agreement with the findings of Raj and Kandalkar, 2013 and Kapoor et al., 2011.

Mean square observed due to line was significant for spike length, number of spikelets per spike and chlorophyll content of flag leaf.

Perusal of the *gca* effect of parents reveal that none of the parents were good general combiner for all the traits however the line SUNLINE is the best general combiner for grain yield. The genotype SUNLINE was identified as a good general combiner for most of the traits including disease related traits viz., chlorophyll content of flag leaf and flag leaf area. High yielding variety like WB-2 and RSP-561 along with resistant lines SUNTOP, DANPHE, and HAR-421 show significant *gca* effect in desirable direction for grain yield per plant. These resistant lines are novel exotic material and can be termed as resistant general combiners in stripe rust breeding program.

The magnitude of *sca* effect is important in selecting cross combinations with high probability of generating transgressive segregants. Among F_1 s, MAJENTA X WB-2 and BOTH X RSP-561 was found as good specific combiner for spike length, 1000 grain weight and grain yield per plant. SUNLINE X RSP-561, FH-11-6-24 X JAUW-584 and ENKOY X JAUW-584 were found good specific combiner for chlorophyll content of flag leaf which is expected to through resistant segregants. SCA indicate that none of the cross combination were superior for all the traits. On the basis of *sca* effect and *per se* performance of the F_1 s indicated that the crosses were not exactly same with order of ranking. This indicated that the choice of best cross combination on the basis of high *sca* effect could not necessarily be which has high *per se* performance because it was a realized value while *sca* effect was an estimate which should be given performance for

the isolation of superior cross combination thus high *sca* would necessarily reflect high performance of the F1.

GCA effect of the parents and *sca* effect of their crosses indicated that the crosses between two good general combiners did not necessarily yield the best specific combination for different traits. This may be due to the lack of complementation of the parental gene. Similar results have been shown by Reddy *et al.*, 2013 in okra.

In the present study the proportion of variance components were calculated in order to obtain an estimate of relative importance of additive and non-additive type of gene action. The variance due to GCA was lower than variance due to SCA for all characters indicating the importance of non-additive gene action in governing these traits. Similar results have been shown by Hamada *et al.*, 2002 and Mohammad *et al.*, 2009.

The presence of non-additive type of gene action for number of tillers per plant, flag leaf area, spike length, number of spikelets per spike, chlorophyll content of flag leaf, 1000 grain weight and grain yield per plant was confirmed by the ratio of σ^2 GCA to σ^2 SCA as less than unity for all characters, indicating the presence of non-additive gene action. The results are in confirmation with reported by Nour *et al.*, 2011 and Fellahi *et al.*, 2013. Zeeshan, 2013 reported that non additive gene action as mean component of genetic variance.

The information on nature of gene action for yield and yield component traits in different population is imperative for planning effective breeding program. Kamaluddin *et al.* (2007) proposed the intermating between F₁s followed by the selection as a useful strategy for obtaining desirable segregants in crosses from general x poor GCA parents.

5.3 Heterosis studies in exotic x local wheats

Exploitation of heterosis is considered to be one of the outstanding achievements in plant breeding. Although not traditionally exploited for the development of hybrids in wheat, high heterotic F₁s are expected to throw transgressive segregants. Heterosis calculated as deviation of the mean of F₁s, over better parent mean is termed as heterobeltiosis (Fonesca and Patterson, 1968). Among the traits under study, positive

heterosis for traits viz., flag leaf area and chlorophyll content is desirable as it is intermittently related to disease development. Heterotic F_1 s for flag leaf area and chlorophyll content would contribute toward healthy leaves and hence healthy plant. The other traits viz., number of tillers per plant, spike length, number of spikelets per spike, thousand grain weight and grain yield per plant are contributing toward yield hence positive heterosis is desirable.

Highly significant positive heterosis for grain yield /plant is exhibited by three crosses viz., SUNTOP X JAUW-584 (24.88), DANPHE X JAUW-584 (20.17) and SUNLINE X JAUW-584 (19.83). None of these showed significant heterosis for its component traits as well. Further the F_1 HAR-421 X JAUW-584 (13.67) exhibit significant positive heterosis for grain yield per plant. BOTH X RSP-561 exhibited positive significant heterosis for chlorophyll content of flag leaf. None of the F_1 s exhibited positive significant heterosis for 1000 grain weight over better parent while all the F_1 s for negatively significant for the same. SUNLINE and SUNTOP was good general combiner for most of the traits.

5.4 Durable rust resistance in parents and F_1 s

In India, stripe rust has gained importance in recent past particularly in North-Western Plain Zone as well as Northern Hills Zone due to favorable environment conditions (low temperature and high humidity) and the vulnerability of available varieties to prevalent races of pathogen. Breeding for adult plant resistance with stacking of different resistant genes in F_1 or in pyramids lines in proposed strategy for durable resistance provides moderate degree of resistance against the plethora of races. Identification of sources of resistance from diverse geographical / genetic background, if good combiner for important traits can result in crosses with high *sca* and thus better transgressive segregants.

A major emphasis of the present investigation was directed toward developing stripe rust resistant breeding material utilizing exotic resistant sources for APR. Disease score of the lines (the source of resistance) range from TR to 40MS. The testers which are the high yielding adapted varieties showed the disease score ranging from 20S in

WB-2 to 40MS in JAUW-584 and 60S in RSP-561. F₁s showed the disease severity ranging from 10MR to 60S. The emergence of F₁s with R (Infection type) while those having parents with S (Infection type) predict resistance being governed by recessive gene as also shown by Biffin, 1905.

Three F₁s (MAJENTA X WB-2, DANPHE X RSP-561, HAR-421 X WB-2) can be considered as potential APR breeding lines with 10MR reaction. Breeding for stripe rust resistance in wheat through use of APR have been reported by Bariana and McIntosh (1995), Khanna *et al.* (2005).

A list of moderately resistant F₁ with high *per se* grain yield, high *sca* has been presented in Table 5.1.

Table 5.1: Prominent F₁s identified on the basis of *per se* grain yield per plant, *sca* effect for traits, heterobeltiosis and disease score

Sr. No.	F ₁ s	<i>per se</i> grain yield per plant (g)	Significant positive <i>sca</i> for traits	Hetero beltiosis	Disease score
1	MAJENTA X WB-2	14.45	Spike length, 1000 grain weight, grain yield per plant	4.96	10MR
2	DANPHE X RSP-561	13.52	No. of tillers per plant, spike length	6.49	10MR
3	HAR-421 X WB-2	13.23	-	0.68	10MR

Chapter-VI

Summary and Conclusions

CHAPTER-IV

SUMMARY AND CONCLUSIONS

The present investigation entitled “**Combining behaviour of exotic x local wheats for durable resistance to stripe rust**” was carried out during *Rabi* 2018-20 at Research Farm Division of PBG, SKUAST, Jammu.

The salient findings of the present study are summarized as follow:

1. Genotypes including parents, parents vs hybrids and line vs tester showed significant differences for all seven traits under study revealing the presence of sufficient genetic variability. Variances due to line and hybrids were significant for all the traits except number of tillers per plant and 1000 grain weight. Variance due to line vs testers was significant for all traits except number of spikelets per spike. Variance due to tester was significant for spike length and grain yield per plant.
2. Mean performance of parents were lower than their F_1 s for number of tillers per plant, flag leaf area, spike length, number of spikelets per spike and grain yield per plant, with the exception of chlorophyll content of flag leaf and 1000 grain weight.
3. The estimates of GCA effects of parents revealed the genotype SUNLINE with high significant *gca* effect in desired direction for spike length, chlorophyll content of flag leaf, 1000 grain weight and grain yield per plant. SUNTOP, DANPHE, HAR-421, RSP-561 and WB-2 showed significant *gca* effect in desired direction for grain yield per plant.

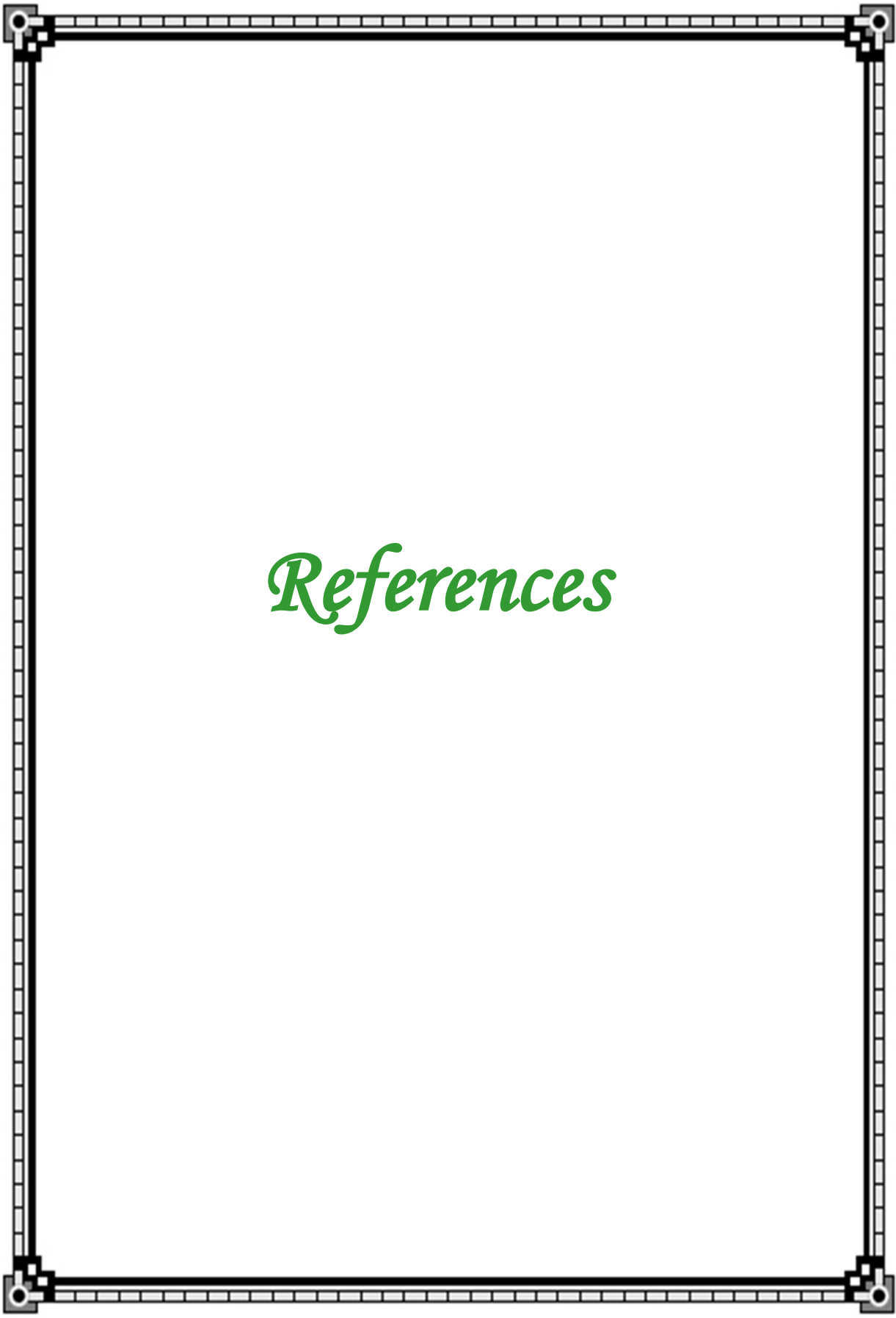
Lines identified on the basis of good *gca* effect of grain yield per plant, *per se* grain yield and disease resistance reaction are:

Sr.No.	Lines	GCA effect of grain yield per plant (g)	<i>per se</i> grain yield per plant (g)	Disease score
1	SUNLINE	1.08**	7.27	10R
2	SUNTOP	0.83**	9.01	10R
3	DANPHE	0.78**	6.29	20MS
4	HAR-421	1.07**	11.41	10S
5	RSP-561	0.36**	12.65	60S
6	WB-2	0.46**	13.14	20S

4. Among crosses, BOTH X RSP-561 and MAJENTA X WB-2 were found as good specific combiner for spike length, 1000 grain weight and grain yield per plant. ENKOY X JAUW-584 was a good specific combiner effect for chlorophyll content of flag leaf, 1000 grain weight and grain yield per plant.
5. Significant heterobeltiotic crosses occurred most frequently for spike length followed by number of spikelets per spike, grain yield per plant and flag leaf area. Four F₁s showed significant positive heterobeltiosis for grain yield per plant viz., SUNTOP X JAUW-584, SUNLINE X JAUW-584, DANPHE X JAUW-584 and HAR-421 X JAUW-584.
6. Disease score of the heterobeltiotic crosses for grain yield range from 20MS to 40S and thus are not the potential candidates possessing APR.
7. Suitable parents with high GCA effects and crosses with high SCA effects would be suitable strategy for yield enhancement *vis a vis* stripe rust resistance.

F₁ identified on the basis of good *sca* effect, *per se* grain yield per plant, high heterosis for yield and disease resistance reaction is MAJENTA X WB-2 with the following features-

F ₁	SCA effect for grain yield per plant (g)	<i>per se</i> grain yield per plant (g)	Heterobeltiosis	Disease score
MAJENTA X WB-2	3.66**	14.45	4.96	10MR



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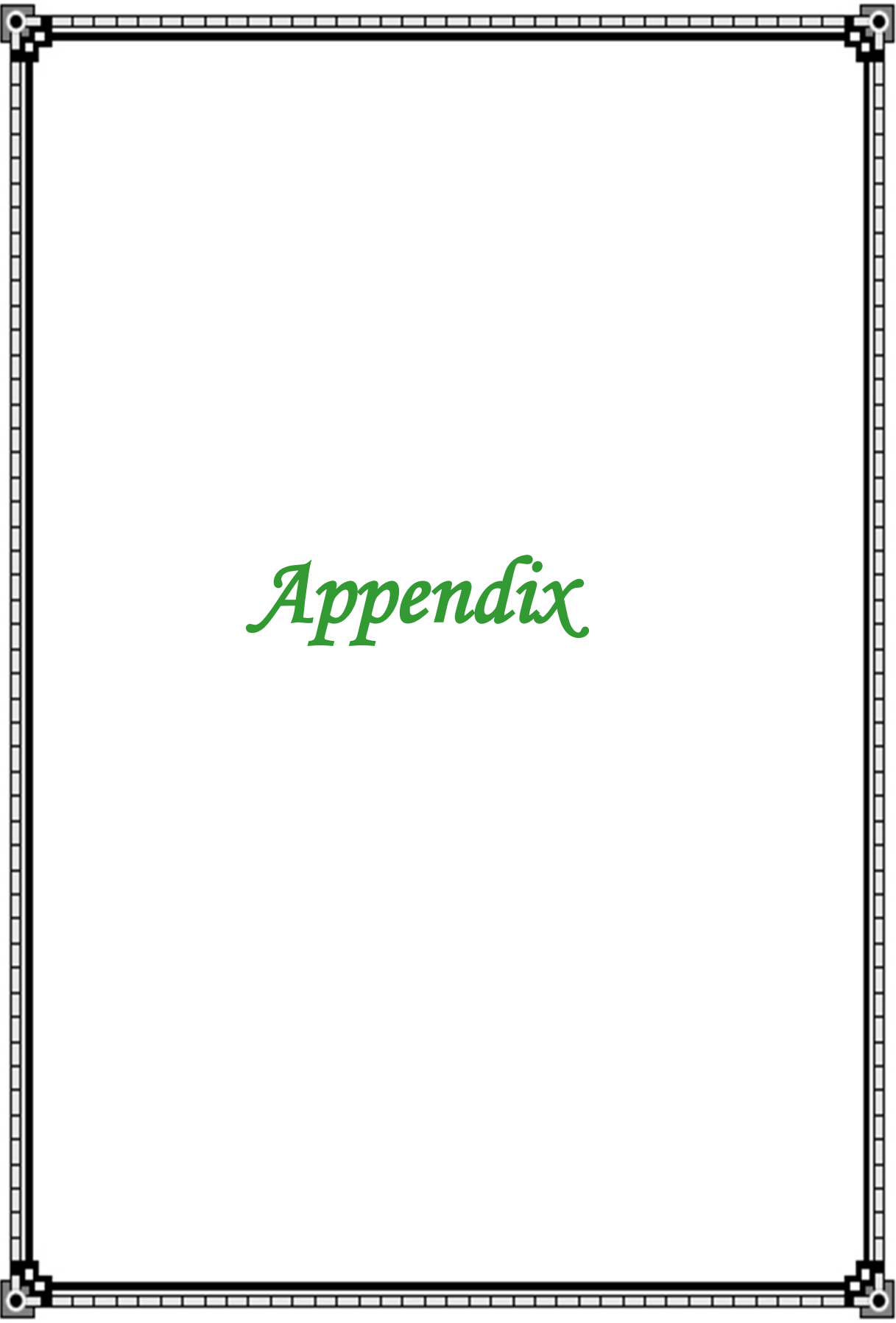
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Appendix

Appendix A: Mean performance of line, tester and F₁s for disease related & yield component traits in bread wheat

Sr. No.	Parents/hybrids	Number of tillers per plant	Flag leaf area(cm ²)	Spike length	Number of spikelets per spike	Chlorophyll content of flag leaf	1000 grain weight(g)	Grain yield per plant(g)
Parents:								
1	BOTH	5.40	64.58	7.82	16.40	42.52	34.23	8.19
2	MAJENTA	5.80	69.89	10.68	22.20	40.18	36.13	12.25
3	SUNLINE	5.40	41.16	10.94	18.00	37.64	34.37	7.27
4	SUNTOP	5.20	60.22	11.98	16.80	36.54	34.61	9.01
5	DANPHE	4.80	40.87	10.40	17.40	40.26	35.40	6.29
6	ENKOY	5.40	45.49	10.44	18.00	39.82	35.79	12.51
7	FH-11-6-24	6.80	39.68	10.36	17.40	40.10	37.27	13.16
8	HAR-421	7.00	52.62	8.96	19.80	39.56	36.32	11.41
9	RSP-561	10.00	46.06	10.04	18.20	42.04	39.32	12.65
10	JAUW-584	9.40	44.95	11.84	18.20	42.86	39.80	9.94
11	WB-2	9.00	48.05	10.22	19.00	42.36	40.00	13.14
Parental Mean:		6.75	50.32	10.33	18.31	40.35	36.66	10.53
Hybrids:								
12	BOTH X RSP-561	8.60	49.06	12.60	20.40	46.30	34.36	12.58
13	BOTH X JAUW-584	12.00	61.78	12.18	19.60	41.48	29.80	7.29
14	BOTH X WB-2	12.00	47.92	7.94	20.20	47.14	32.43	9.19
15	MAJENTA X RSP-561	9.60	53.62	12.34	25.00	40.14	30.23	7.64
16	MAJENTA X JAUW-584	13.60	64.51	12.68	23.00	40.60	29.43	7.61
17	MAJENTA X WB-2	11.00	56.83	14.10	23.40	42.16	35.93	14.45
18	SUNLINE X RSP-561	11.80	58.30	14.74	22.40	43.06	36.55	13.86
19	SUNLINE X JAUW -584	10.00	49.32	14.84	22.40	38.76	34.25	12.12
20	SUNLINE X WB-2	9.40	53.44	14.24	22.40	38.30	36.52	13.60

Contd...

Sr. No.	Parents/hybrids	Number of tillers per plant	Flag leaf area(cm ²)	Spike length	Number of spikelets per spike	Chlorophyll content of flag leaf	1000 grain weight(g)	Grain yield per plant(g)
21	SUNTOP X RSP-561	12.80	56.48	15.04	20.60	33.24	34.38	12.81
22	SUNTOP X JAUW-584	8.80	60.29	14.02	22.80	37.28	33.61	12.41
23	SUNTOP X WB-2	9.40	54.18	15.06	22.00	35.96	35.88	13.17
24	DANPHE X RSP-561	11.00	54.60	14.24	23.00	35.02	33.97	13.52
25	DANPHE X JAUW-584	7.20	53.24	12.74	22.20	34.62	32.41	11.94
26	DANPHE X WB-2	8.00	51.07	12.32	20.40	33.96	32.33	12.75
27	ENKOY X RSP-561	8.60	59.13	14.08	22.40	29.72	31.86	12.88
28	ENKOY X JAUW-584	7.20	61.33	13.28	22.40	36.06	34.09	12.58
29	ENKOY X WB -2	7.40	64.42	14.10	22.40	34.34	31.90	11.66
30	FH-11-6-24 X RSP-561	10.60	53.40	14.44	22.80	39.20	34.23	12.64
31	FH-11-6-24 X JAUW-584	10.20	50.80	14.20	22.00	41.98	32.87	12.44
32	FH-11-6-24 X WB-2	8.20	52.51	14.76	22.60	35.88	34.63	11.95
33	HAR-421 X RSP-561	7.80	53.05	13.28	24.60	38.40	34.14	12.91
34	HAR-421 X JAUW-584	7.00	49.11	13.66	23.80	33.94	33.13	12.97
35	HAR-421 X WB-2	6.80	56.43	12.10	22.60	37.50	32.58	13.23
Hybrid Mean		9.54	55.20	13.46	22.31	38.13	33.40	12.01
General Mean		8.66	53.67	12.48	21.05	38.83	34.42	11.54
S.Em±		0.73	3.58	0.27	0.60	1.16	0.83	0.4649
CD at 5 %		2.03	9.93	0.76	1.67	3.21	2.29	1.2888
CV %		18.89	14.93	4.9	6.39	6.68	5.37	9.03



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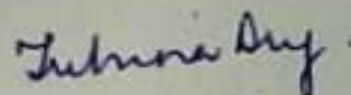
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CERTIFICATE-IV

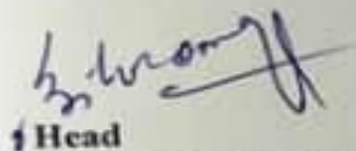
Certified that the necessary corrections as suggested by the external examiner and the advisory committee have been duly incorporated in the thesis entitled "**Combining behaviour of exotic x local wheats for durable resistance to stripe rust**" submitted by **Ms. Laxmi Jangir**, Registration number **J-18-M-600**.



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