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Combining ability analysis and estimation of heterosis for resistance to head blight caused by *Fusarium graminearum* in spring wheat

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Abstract

Fusarium graminearum Schwabe, the causative agent of Fusarium head blight (FHB), is an economically important pathogen of wheat. Improvement of the FHB resistance by developing new varieties requires sound knowledge on the inheritance of resistance. A half diallel cross using seven spring wheat genotypes was carried out to estimate inheritance for disease index (DI), disease incidence (DIC), disease severity (DSV), Fusarium damage kernels (FDK) and incidence-severity-kernels (ISK). Analysis of variance for studied traits indicated highly significant differences among the genotypes. In all traits, significant general combining ability (GCA) revealed meaningful contributions of additive type of gene action in governing the traits. Specific combining ability (SCA) effects were significant only in DIC and FDK. Ratio of GCA to SCA indicated the preponderance of additive gene effects in determining the inheritance of all traits. High broad sense heritability was measured for all characters, allowing for considerable progress by selection.

Keywords: FHB, diallel, GCA, SCA, heterosis.

Abbreviations: DI_Disease index; DIC_Disease incidence; DSV_Disease severity; FDK_Fusarium damaged kernels; HB_Fusarium head blight; GCA_General combining ability; ISK_Incidence-Severity-Kernels; SCA_Specific combining ability.

Introduction

Fusarium head blight (FHB) is economically one of the most important fungal diseases of wheat throughout the world (Steiner et al., 2008). The Fusarium head blight (FHB) complex has been associated with at least 17 Fusarium Spp (Browne and cooke, 2004). The main causative agents of FHB are mainly Fusarium graminearum and Fusarium culmorum in Iran (Zamanizadeh and Khorsandi, 1995). Also, it is an important disease of wheat in different areas of Iran, such as Mazandaran, Gorgan, Gonbad and Moghan regions (Moosavi et al., 2007). Infection with fungi of Fusarium genus results in severe reduction in crop yield and quality. The most serious threat associated with FHB is the accumulation of mycotoxins in the harvested grain (Bai and Shaner, 2004). These compounds can function as inhibitors of protein synthesis, which exhibits deleterious effects on animal production and human health (Bai and Shaner, 2004; Berek et al., 2001). Various cultivated practices and application of Fungicide at anthesis have been proposed to eliminate sources of primary inoculum or decrease spread after fungal infection. But the measures are of only limited efficacy to control the disease and costly treatment. The application of fungicide might also pollute the environment. Genetic resistance offers the greatest potential for reducing FHB (Ma et al., 2009). The expression of resistance to FHB in wheat is complex (Kolb et al., 2001), and there is no complete resistance to FHB in wheat, although sources of partial resistance have been identified through extensive surveys of germplasm (Browne et al., 2005; Mc Kendry et

al., 2004). Resistance to FHB is separated into five categories: Type I, resistance to initial infection; Type II, resistance to spread of infection; Type III, resistance to kernel infection; Type IV, tolerance; and Type V, resistance to the deoxynivalenol (DON) mycotoxin (Schroeder and Christensen, 1963; Wang and Miller, 1998; Mesterhazy, 1995). Variation of FHB resistance has been documented in wheat and its relatives (Bai and Shaner, 1994; Mesterhazy, 1995, 1997; Chen et al., 1997; Rudd, 1997; Buerstmayr et al., 2000). However, the limited information on the genetics and inheritance of the disease resistance and the complex evaluation procedures, have slowed down progress in resistance breeding (Devkota et al., 1999). Inheritance of FHB resistance involves many loci on different chromosomes (Buerstmayr, 2008). Heritability estimates for FHB resistance are sparse and contradictory, depending on used genetic materials and methods. Snijders (1990a) reported broad-sense heritability of FHB resistance in F₂ single plant populations varied from 0.05 to 0.89. Heritability estimates by Saur and Trottet (1992) and Singh et al (1995) were in the range of 0.66 to 0.93 but were derived from single environments. Yu et al (2008) reports narrow sense heritability of resistance in 139 F₆ recombinant inbred lines were developed from a cross between Wangshuibai and FHB-susceptible cultivar, Wheaton, were low for Type I resistance (0.37 to 0.4) but moderately high for Type II resistance (0.45 to 0.61) and Type III resistance (0.44 to 0.67). Narrow sense heritability estimates by Malla et al (2009) was moderate (0.4 to 0.64). Results of studies on combining ability of FHB response indicated that the variation among the crosses was primarily

Table 1. Genotype, origin, pedigree and reaction to Fusarium head blight (FHB) of wheat genotypes used as parent for diallel crossing scheme

Genotype	enotype Origin			Pedigree	FHB-reaction				
Frontana	na Brazil		H	Fronteira/Mentan	Moderately resistant				
Sumai3		China		Funo/Taiwanxiaomai		Funo/Taiwanxiaomai		Resistant	
Wangshuibai		China				Resistant			
Morvarid		Mexico		Milan/Shanghai		Resistant			
Tajan	CIMMYT,Mexico		E	Bow "S"/Nkt"S	Moderately resistant				
Falat	CIM	CIMMYT,Mexico		Kvz/Buho''s''//Kal/Bb=seri82		susceptible			
Golestan	CIM	IMYT,Mexico				susceptible			
T able 2. Analysis o	f variance (1	nean squares valu	es) for different	traits in wheat					
S.O.V	Df	DIC	DSV	FDK	DI	ISK			
Genotypes	27	1815.94**	821.72**	4.97**	302.61**	627.48^{**}			

208.22*

56.1

* Significant at the 0.05 level of probability, ** significant at the 0.01 level of probability and ns= non-significant.

473.36^{ns}

111.93

due to the general combining ability (GCA) and thus most of the variation is attributed to additive effects (Snijders, 1990b; Miedaner et al., 1993; Jiang., 1998; Buerstmayr et al., 1999; Devkota et al., 1999; Hall et al., 2001; Mardi et al., 2004; Malla et al., 2009). Improvement of FHB resistance by developing new varieties would benefit from knowledge on combining ability effects in potential crossing partners. In this study, seven spring wheat genotypes were analyzed in a half diallel crossing design in order to achieve: (1) a better understanding of FHB resistance in the parental genotypes, (2) estimation of general (GCA) and specific (SCA) combining ability for FHB resistance to design an efficient plan for improvement of the existing materials, (3) identifying the most promising combinations for the selection of improved breeding lines and (4) estimation of heterosis and heterobeltiosis among F1 hybrids to investigate the performance and relationship of F1 hybrids and parents and to select suitable parents and population for designing an effective wheat breeding program.

2

54

Replications

Error

Materials and method

Plant material

Seven spring wheat genotypes with different levels of FHB resistance (Table 1) were crossed in a diallel manner without reciprocals. The resulting 21 F_1 progenies along with seven parental genotypes were used in this study. The wheat lines and crosses were evaluated at experimental field of Gorgran agricultural research in 2009 using a randomized complete-block design with three replications.

Inoculation and disease assessment

To prepare inoculums, fungal isolate was collected from field trap nursery and cultured on potato dextrose agar medium. About 5gr straw powder were added to 125ml of distilled water into 250mL flask. Mixtures were autoclaved at 120°C and 1 atmosphere for 30 minutes two times during 48 hours. Then, each flask was inoculated with an agar plug from a clean *F. graminearum* isolate under laminar flow hood. The flasks were swirled gently at 120 rpm at 25°C for 96 hours. The number of conidiospores per mL was determined by counting spores using a hemacytometer and adjusted to the desired spore concentration (10⁵ conidia spores/mL) with distilled water. At the beginning of anthesis and two days later (at full flowering) each plot was inoculated with the conidial suspension by spraying of inoculums on each plot using a manual atomizer. Inoculated plots were misted using

mist irrigation system for 30 min after each inoculation to favor development of the disease.

144.43*

28.29

5.39^{ns}

31.09

Disease assessment

0.64^{ns}

0.28

Most studies indicate that visual assessment of FHB disease symptoms gives a good indication of FHB-associated yield loss (Arseniuk et al., 1993: Doohan et al., 1999; Mentewab et al., 2000). Other researcher have found strong relationships between visual FHB score and the fungal DNA content of grain (Doohan et al., 1999) or mycotoxin content of grain (Mesterhazy, 2002). In this study, our observation is on the basis of visual assessment. Disease incidence (DIC) (type I resistance) and disease severity (DSV) (type II resistance) were recorded 21 days after the first conidial suspension application in the field and Fusarium damaged kernels (FDK) (type III resistance) recorded after harvesting spikes when mature. Disease rating for each entry was averaged across 30 heads. Disease incidence was measured as the percentage of number of spikes infected across total spikes. Disease severity was measured as the percentage of infected spikelet(s) within the spike. The field disease severity was recorded based on 0-5 scale (0= no disease, 1= to 20%, 2= to 40%, 3= to 60%, 4= to 80% and 5= more than 80% disease severity) (Wan et al., 1997). Fusarium damaged kernel (FDK) was measured as percentage of infected kernels within the spike. The Disease index (Brown, 2007) and Incidenceseverity- kernels (ISK) index (Gilbert and Woods, 2006) were calculated according to the following formulas: $DI = [(incidence \times severity)/100]$

ISK= (0.3*incidence) + (0.4*severity) + (0.4*FDK)

Statistical and genetic analyses

All data were tested for normality using the kolmogorovsmirnov test in SPSS software. All data except FDK and DI were normal, so they were transformed using square root to adjust them to a normal distribution. Analysis of variance for each genotype was calculated using the general linear model (GLM) procedure of the SAS/STAT software (SAS Institue Inc., 2002& 2003). Diallel analysis based on Griffing's method II, model 1 (Griffing, 1956), where one set of crosses (F_1 and parents) was included [P(P+1)/2 entries], was used to estimate GCA and SCA. Diallel analysis carried out by D₂ statistical package. The percent increase or decrease of F_1 hybrids over mid parent as well as better parent was calculated to estimate possible heterotic effects for above mentioned parameters (Fonseca and Patterson, 1968).

Table 3. Mean performance and statistical significance for different traits in wheat parents and crosses.

Genotypes	DIC	DSV	FDK	DI	ISK
Morvarid	73.33 ^{efghi}	37.5 ^{efgh}	1.56 ^{hi}	5.24 ^{defgh}	34.18 ^{fghij}
Tajan	96.67 ^{ab}	47.33 ^{cde}	2.43 ^{efgh}	6.73 ^{bc}	45.41 ^{cd}
Falat	100^{a}	72.67 ^a	4.89 ^a	8.52 ^a	61.3 ^a
Wangshuibai	34.43 ^{lm}	21.63 ^{jkl}	1.39 ^{hi}	2.71 ^k	17.4 ^{mno}
Golestan	95.53 ^{abc}	72.83 ^a	4.28^{ab}	8.34 ^a	57.78 ^{ab}
Sumai3	26.63 ^m	22^{jkl}	0.78^{i}	2.39 ^k	14.65 ^{no}
Frontana	65.57 ^{fghij}	27.93 ^{hijk}	1.25 ⁱ	4.27 ^{ghi}	28.47 ^{ijkl}
Frontana*Sumai3	26.67 ^m	20^{kl}	0.8^{i}	2.3 ^k	14.06 ^{no}
Frontana*Golestan	78.9 ^{cdefg}	32.07 ^{fghijk}	1.65 ^{ghi}	5.15 ^{defgh}	34.18 ^{fghij}
Frontana*Wangshuibai	34.43 ^{lm}	24.9^{ijkl}	0.92 ⁱ	2.87 ^{jk}	17.98 ^{mno}
Frontana*Falat	76.67 ^{defgh}	40.9^{defg}	3.07 ^{cde}	5.58 ^{cdef}	39.09 ^{defg}
Frontana*Tajan	80 ^{bcdef}	36.13 ^{efghi}	1.91 ^{efghi}	5.36 ^{defg}	36.231 ^{efghi}
Frontana*Morvarid	50 ^{jkl}	32 ^{fghijk}	0.95 ⁱ	3.98 ^{hij}	24.8 ^{klm}
Sumai3*Golestan	$61.1^{\rm hijk}$	30.9 ^{ghijk}	1.71 ^{fghi}	4.34 ^{fghi}	28.61 ^{ijkl}
Sumai3*Wangshuibai	25.533 ^m	14.73^{1}	0.88^{i}	2.26 ^k	12.2°
Sumai3*Falat	71.1 ^{efghi}	30.2 ^{ghijk}	1.22 ⁱ	4.61 ^{efgh}	30.8 ^{ghijk}
Sumai3*Tajan	52.2 ^{jk}	21.53 ^{jkl}	0.81 ⁱ	3.29 ^{ijk}	22.19 ^{klmn}
Sumai3*Morvarid	47.8 ^{kl}	22.8^{jkl}	0.95 ⁱ	3.34 ^{ijk}	21.35 ^{lmn}
Golestan*Wangshuibai	84.43 ^{abcde}	50.47 ^{cde}	2.42 ^{efgh}	6.23 ^{cd}	41.43 ^{def}
Golestan*Falat	96.67 ^{ab}	69.03 ^{ab}	4.98 ^a	8.16 ^a	59.57 ^{ab}
Golestan*Tajan	97.77 ^a	57.63 ^{bc}	3.77 ^{bcd}	7.48 ^{ab}	52.43 ^{bc}
Golestan*Morvarid	92.23 ^{abcd}	50.47 ^{cd}	2.84 ^{def}	6.81 ^{bc}	46.08 ^{cd}
Wangshuibai*Falat	62.23 ^{ghijk}	32.77 ^{fghij}	1.94 ^{efghi}	4.51 ^{efghi}	29.93 ^{hijkl}
Wangshuibai*Tajan	52.23 ^{jk}	30.67 ^{ghijk}	1.59 ^{hi}	3.99 ^{hij}	25.71 ^{jklm}
Wangshuibai* Morvarid	57.8 ^{ijk}	33.5^{efgh}	1.21 ⁱ	4.39 ^{fghi}	27.8 ^{ijkl}
Falat*Tajan	100^{a}	66.9 ^{ab}	4.16 ^{abc}	8.17^{a}	56.82 ^{ab}
Falat* Morvarid	91.13 ^{abcd}	43.43 ^{def}	2.79^{defg}	6.27 ^{bcd}	43.47 ^{de}
Tajan* Morvarid	86.67 ^{abcde}	37.9 ^{efgh}	$1.48^{\rm hi}$	5.72 ^{cde}	38.12 ^{defgh}

Means with the at least one same letter don't have significant differences.

Table 4. Mean squares of	general/	specific com	bining	abilities and	1 their ratio
- abie in filean be all ob of	Serier and	opeenie eom	· · · · · · · · · · · · · · · · · · ·	aominios am	a chiefi i cacio

S.O.V	Mean square								
	DIC	DSV	FDK	DI	ISK				
GCA	2507.48*	1072.439*	6.527*	15.384*	886.037*				
SCA	61.84 ^{ns}	45.755 [*]	0.273^{*}	0.293 ^{ns}	15.767 ^{ns}				
Error	37.3	18.699	0.096	0.187	9.43				
$\frac{2GCA}{2GCA + SCA}$	0.99	0.98	0.97	0.99	0.99				
$h_{b,s}^2$	0.94	0.93	0.94	0.94	0.95				
h^2_{ns}	0.9	0.83	0.83	0.91	0.92				

GCA= General combining ability, SCA= Specific combining ability, * significant at the 0.05 level of probability, ** significant at the 0.01 level of probability and ns= non-significant, h_{bs}^2 = broad sense heritability, h_{ns}^2 = narrow sense heritability

$$Ht (\%) = \frac{F_1 - MP}{MP} \times 100$$
$$Hbt (\%) = \frac{F_1 - BP}{BP} \times 100$$

Where Ht is Heterosis, Hbt is Heterobeltiosis, MP is Mid Parent value and BP is Better Parent Value. The t test was manifested to determine whether F_1 hybrid means were statistically different from mid parent and better parent means as follows (Wynne *et al.*, 1970).

$$tij = F_1 ij - MP \sqrt{\frac{3}{8} EMS}$$
$$tij = F_1 ij - BP \sqrt{\frac{1}{2} EMS}$$

Where F_1 ij is the mean of the ijth F_1 cross, MP ij is the mid parent for ijth cross, BP ij is the better parent values for ijth cross and EMS is error mean square

Results and discussion

The populations originating from seven parent diallel crosses were evaluated in the field in 2009. Uniform infection with FHB depends on a number of factors, apart from resistance, such as time, type and amount of infection and in environmental variation (parry et al., 1995). Since FHB resistance is non-specific and horizontal (Van Eeuwijk et al., 1995), the inoculation was carried out using a highly aggressive Fusarium isolate at anthesis, which is the most susceptible developmental stage for Fusarium ear infection (pough et al., 1933). In order to account for ear to ear variation in flowering time within each plot, repeated inoculations were applied. Optimal humidity was provided using a mist-irrigation system. Combining ability analysis using Griffing's method estimates the average additive and dominance effects of all the genes involved in expression of the trait via GCA and SCA based on progeny performance (Dobholkar, 1992). The analysis of variance for DIC, DSV, DI and ISK manifested highly significant differences between parents and F1 crosses (Table 2). The mean performance of

	Frontana	Sumai3	Golestan	Wangshuibai	Falat	Tajan	Morvarid
				DIC			
Frontana	-7.79**	-10.67 ^{ns}	1.063 ^{ns}	-8.22^{ns}	-0.69^{ns}	6.6 ^{ns}	-13.41**
Sumai3		-23.36**	-1.17 ^{ns}	-1.55 ^{ns}	9.31*	-5.63 ^{ns}	-0.037 ^{ns}
Golestan			17.14^{**}	16.85**	-5.62 ^{ns}	-0.56 ^{ns}	3.9 ^{ns}
Wangshuibai				-18.04**	-4.87^{ns}	-10.91*	4.64 ^{ns}
Falat					16.65**	2.16 ^{ns}	3.28 ^{ns}
Tajan						12.7**	2.77 ^{ns}
Morvarid							2.708 ^{ns}
				DSV			
Frontana	-7.308**	2.572 ^{ns}	-12.913**	2.802 ^{ns}	-3.683 ^{ns}	0.787 ^{ns}	2.246^{ns}
Sumai3		-13.719**	-7.669*	-0.954 ^{ns}	-7.972^{*}	-7.402^{*}	-0.543 ^{ns}
Golestan			13.833**	3.128 ^{ns}	3.309 ^{ns}	1.146 ^{ns}	-0.428^{ns}
Wangshuibai				-9.049**	-10.076**	-2.939 ^{ns}	5.487 ^{ns}
Falat					13.437**	10.809^{**}	-7.065*
Tajan						4.199^{**}	-3.361 ^{ns}
Morvarid							-1.393 ^{ns}
				FDK			
Frontana	-0.684**	-0.056 ^{ns}	-0.75 ^{ns}	-0.884 ^{ns}	0.595 ^{ns}	-0.119 ^{ns}	0.011 ^{ns}
Sumai3		-1.496**	0.291 ^{ns}	0.177 ^{ns}	-0.909 ^{ns}	-0.9 ^{ns}	-0.114 ^{ns}
Golestan			1.348^{**}	0.046^{ns}	-0.344 ^{ns}	-0.052^{ns}	-0.149 ^{ns}
Wangshuibai				-0.525***	-0.172^{ns}	-0.119 ^{ns}	-0.132 ^{ns}
Falat					1.447^{**}	0.337 ^{ns}	0.049^{ns}
Tajan						0.423^{*}	-0.246^{ns}
Morvarid							-0.513*
				DI			
Frontana	-0.781**	-0.236 ^{ns}	-0.728^{*}	-0.195 ^{ns}	-0.242^{ns}	0.3 ^{ns}	-0.347 ^{ns}
Sumai3		-1.745**	-0.56 ^{ns}	0.176 ^{ns}	-0.235 ^{ns}	-0.776^{*}	-0.017 ^{ns}
Golestan			1.538^{**}	0.797^{*}	0.008^{ns}	0.087^{ns}	0.133 ^{ns}
Wangshuibai				-1.229**	-0.85^{*}	-0.61 ^{ns}	0.499^{ns}
Falat					1.483**	0.826^{*}	-0.344 ^{ns}
Tajan						0.726^{**}	-0.134 ^{ns}
Morvarid							0.009^{ns}
				ISK			
Frontana	-5.731**	-1.638 ^{ns}	-5.888*	-1.2^{ns}	-1.474 ^{ns}	2.331 ^{ns}	-3.288 ^{ns}
Sumai3		-12.93**	-4.262^{ns}	0.222^{ns}	-2.566 ^{ns}	-4.515^{ns}	0.465^{ns}
Golestan			11.442^{**}	5.072^{*}	1.832 ^{ns}	1.354 ^{ns}	0.824 ^{ns}
Wangshuibai				9.445**	-6.921**	-4.473 ^{ns}	3.429 ^{ns}
Falat					11.934**	5.254^{*}	-2.28 ^{ns}
Tajan						5.273**	-0.968 ^{ns}
Morvarid							-0.543 ^{ns}

Table 5. General combining ability effects (diagonal values) and specific combining ability effects (above diagonal) for studied characters

* significant at the 0.05 level of probability, ** significant at the 0.01 level of probability and ns= non-significant

parents and F1 crosses regarding above mentioned traits is presented in Table 3. Sumai3 parents showed the lowest amount of all traits between parents except for DSV, which the lowest DSV belong to Wangshuibai. Between crosses, the lowest amount of all recorded traits was observed in Sumai3 × Wangshuibai, except for FDK where Frontana × Sumai3 showed the lowest FDK. As shown in Table 4, all traits showed significant GCA mean squares, but significant SCA mean squares existed in two traits (DSV and FDK). Significant GCA mean squares indicated that additive gene action was important and studied genotypes varied in their contribution to resistance when used as parents in hybrid combinations. This is in agreement with reports of Malla et al (2009). Significant SCA mean squares highlighted the importance of non-additive (dominance and/or epistatic) gene action expressed in hybrid combinations that performed better or worse than the mean of their parents (Sprague and Tatum, 1942). Also, GCA effect was more than SCA effects which indicated the importance of additive genetic components in controlling FHB resistance in studied wheat genotypes. Baker ratio for traits (Baker, 1978) has indicated in Table 4. The high Baker ratio for all traits further

emphasized the importance of additive gene effects. Same results recorded by Bai et al. (2000), Hall and Sanford (2003), Mardi et al. (2004) and Malla et al. (2009). This implies that the parent had a high influence on the performance of progenies in determining response to the disease. High narrow and broad sense heritabilities were recorded (Table 4) for all traits. Heritability in broad sense estimates the genetic proportion (additive + dominance + interaction) of the total phenotypic variation, while heritability in narrow sense estimates only the additive portion. Their relative magnitude explicates the proportion of additive variation within genetic variation. Thus, here greater portion of heritable variation was of additive nature. This is in good agreement with published reports (Buerstmayr et al., 2000; Jiang et al., 2006; Bai et al., 2000; Saur and Trottet., 1992; Waldron et al., 1999). To select most resistant genotypes, those with less value of all the studied traits are desirable. Thus negative values of GCA, SCA and heterosis are useful. The mean DIC, DSV, FDK, DI and ISK and general combining ability effects (GCA) of parental genotypes showed that the genotypes with lowest DIC, DSV and DI and highest negative GCA values were 'Sumai3',

Crosses	DIC		DSV		FDK		DI		ISK	
	%MP	%BP	%MP	%BP	%MP	%BP	%MP	%BP	%MP	%BP
Frontana*Sumai3	-42.17**	0^{ns}	-19.89 ^{ns}	-9.09 ^{ns}	-21.02 ^{ns}	2.54 ^{ns}	-31.04 ^{ns}	-3.94 ^{ns}	-34.79**	-4 ^{ns}
Frontana*Golestan	-2.07ns	20.34 ^{ns}	-36.35**	14.8 ^{ns}	-40.27**	32.36 ^{ns}	-18.4 ^{ns}	20.52 ^{ns}	-20.74**	20.04 ^{ns}
Frontana*Wangshuibai	-31.11*	2.06 ^{ns}	0.47 ^{ns}	15.1 ^{ns}	-30.11 ^{ns}	-26 ^{ns}	-17.69 ^{ns}	6.1 ^{ns}	-21.61 ^{ns}	3.32 ^{ns}
Frontana*Falat	-7.38 ^{ns}	16.95 ^{ns}	-18.69*	46.42^{*}	0 ^{ns}	145.76**	-12.75 ^{ns}	30.68 ^{ns}	-12.92 ^{ns}	37.28**
Frontana*Tajan	-1.37 ^{ns}	22.03 ^{ns}	-3.99 ^{ns}	29.36 ^{ns}	3.85 ^{ns}	53.1 ^{ns}	-2.49 ^{ns}	25.63 ^{ns}	-1.93 ^{ns}	27.24^{*}
Frontana* Morvarid	-28**	-23.72*	-55.5 ^{ns}	14.56 ^{ns}	-32.06 ^{ns}	-23.55 ^{ns}	-16.22 ^{ns}	-6.69 ^{ns}	-20.85*	-12.91 ^{ns}
Sumai3*Golestan	1.16×10^{-14ns}	129.17**	-34.83**	40.45 ^{ns}	-32.35*	119.17*	-19.16 ^{ns}	81.45 ^{ns}	-21*	95.34**
Sumai3*Wangshuibai	-16.36 ^{ns}	-4.17 ^{ns}	-32.47 ^{ns}	-31.9 ^{ns}	-18.82 ^{ns}	13.01 ^{ns}	-11.5 ^{ns}	-5.68 ^{ns}	-23.84 ^{ns}	-16.67 ^{ns}
Sumai3*Falat	12.28 ^{ns}	166.67**	-36.2**	37.27 ^{ns}	-56.9**	56.25 ^{ns}	-15.44 ^{ns}	92.95 ^{ns}	-18.9*	110.28**
Sumai3*Tajan	-15.32 ^{ns}	95.83**	-37.88**	-2.12 ^{ns}	-49.79*	3.2 ^{ns}	-27.92 ^{ns}	37.52 ^{ns}	-26.11*	51.49*
Sumai3* Morvarid	-4.44 ^{ns}	79.16**	-23.36 ^{ns}	3.64 ^{ns}	-18.85 ^{ns}	21.57 ^{ns}	-12.55 ^{ns}	39.56 ^{ns}	-12.54 ^{ns}	45.79 ^{ns}
Golestan*Wangshuibai	29.91**	145.16**	-1.83 ^{ns}	114.32**	-14.78 ^{ns}	73.48*	12.75 ^{ns}	130.2 ^{ns}	10.21 ^{ns}	138.04**
Golestan*Falat	-1.14 ^{ns}	1.16 ^{ns}	-5.11 ^{ns}	-5 ^{ns}	8.78 ^{ns}	16.44 ^{ns}	-3.18 ^{ns}	-2.15 ^{ns}	0.04 ^{ns}	3.1 ^{ns}
Golestan*Tajan	1.73 ^{ns}	2.33 ^{ns}	-4.08 ^{ns}	21.76 ^{ns}	12.29 ^{ns}	55.03 ^{ns}	-0.73 ^{ns}	11.14 ^{ns}	1.62 ^{ns}	15.45 ^{ns}
Golestan* Morvarid	9.21 ^{ns}	25.76^{*}	-8.52 ^{ns}	34.58*	-2.68 ^{ns}	82.24**	0.23 ^{ns}	29.9 ^{ns}	0.22 ^{ns}	34.81**
Wangshuibai*Falat	-7.44 ^{ns}	80.65**	-30.51**	51.46*	-38.15**	39.28 ^{ns}	-19.57 ^{ns}	66.85 ^{ns}	-23.95**	71.96**
Wangshuibai*Tajan	-20.34*	51.61*	-11.07 ^{ns}	41.76 ^{ns}	-16.6 ^{ns}	14.4 ^{ns}	-15.5 ^{ns}	47.38 ^{ns}	-18.13 ^{ns}	47.75*
Wangshuibai* Morvarid	7.22 ^{ns}	67.74**	13.3 ^{ns}	54.85 [*]	-17.77 ^{ns}	-12.88 ^{ns}	10.38 ^{ns}	62.09 ^{ns}	7.78 ^{ns}	59.74**
Falat*Tajan	1.69 ^{ns}	3.45 ^{ns}	11.5 ^{ns}	41.34**	13.76 ^{ns}	71.18**	7.11 ^{ns}	21.34 ^{ns}	6.49 ^{ns}	25.12**
Falat* Morvarid	5.12 ^{ns}	24.24^{*}	-21.15*	15.82 ^{ns}	-13.23 ^{ns}	79.25**	-8.83 ^{ns}	19.7 ^{ns}	-8.95 ^{ns}	27.17^{*}
Tajan* Morvarid	1.96 ^{ns}	18.18 ^{ns}	-10.65 ^{ns}	1.07 ^{ns}	-25.86 ^{ns}	-5.19 ^{ns}	-4.41 ^{ns}	9.2 ^{ns}	-4.21 ^{ns}	11.52 ^{ns}

Table 6. Estimation of percent heterosis (Ht%) and heterobeltiosis (Hbt%) for different parameters

* Significant at the 0.05 level of probability, ** significant at the 0.01 level of probability and ns= non-significant

'Frontana' and 'Wangshuibai', the genotypes with lowest FDK were 'Frontana', 'Sumai3', 'Wangshuibai' and 'Morvarid' and the genotypes with lowest ISK and negative GCA values were 'Frontana' and 'Sumai3' (Table 5). The best SCA combination to reduce symptoms of disease and increasing resistance belongs to hybrids between Frontana and Morvarid, Golestan and Frontana, Falat and Wangshuibai and Falat and Wangshuibai for DIC, DSV, DI and ISK, respectively (Table 5). The estimates of F1 heterosis over mid and better parent(s) for all five traits are presented in Table 6. On the basis of heterotic studies for DIC, Negative heterosis over mid parent was observed from 12 crosses and negative heterosis over better parent was observed from 2 crosses out of 21 crosses. Frontana × Sumai3 showed highest negative value for heterosis (- 42.17) and Frontana × Morvarid showed highest negative value for heterobeltiosis (-23.7). Heterotic studies for DSV revealed, Negative heterosis over mid parent was observed from 18 crosses and negative heterosis over better parent was observed from 4 crosses out of 21 crosses. Frontana × Golestan showed highest negative value for heterosis (- 36.35) and Sumai3 × Wangshuibai showed highest negative value for heterobeltiosis (- 31.9). In case of

heterotic effects for FDK, Sumai3 × Falat contributed highest negative value for mid-parent heterosis (-56.9) and Sumai $3 \times$ Wangshuibai showed highest negative value for heterobeltisosis (-26). In case of heterotic effects for DI, Frontana × Sumai3 contributed highest negative value for mid-parent heterosis (-31.04) and Frontana × Morvarid showed highest negative value for heterobeltiosis (-6.69). The estimate of heterotic effects for ISK showed that among crosses Frontana × Sumai3 had maximum negative value (-34.79) for mid-parent heterosis and Sumai3 × Wangshuibai showed highest negative value for heterobeltiosis (-16.67). In attention to results of mean performance, the best hybrid was Sumai3×Wangshuibai. Therefore presumably, there have been QTL combinations in two variety- Sumai3 and Wangshuibai. Additive variance has estimated more than dominant variance in all traits. Therefore, selection is the effective breeding method for FHB resistance. High negative GCA value in Sumai3 for all studied traits indicating that this genotype carrying resistant additive genes and so have potential for obtaining superior lineages in selection programs for FHB resistance. Crosses with these parents because of additive nature inheriting resistance consistently and through selection program can accumulate resistant in

one genotype. Heritability of all traits is high. Therefore early generation selection would be effective.

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