

Original Research Article

Combining ability analysis for morpho-physiological traits and grain yield under heat stress in durum wheat (*Triticum durum* Desf.)

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Abstract

Combining ability analysis for morpho-physiological and grain yield traits was performed using ten selected parents in half diallel to develop forty-five crosses were tested under during Rabi 2016-17. Across the environments mean squares due to $GCA \times E$ and $SCA \times E$ were significant for grain filling period, flag leaf length, flag leaf width flag leaf area, peduncle length, total number of tillers plant⁻¹, number of productive tillers plant⁻¹, spike length, number of spikelet's spike⁻¹, spike weight productive tillers⁻¹, grain weight spike⁻¹, biological yield plant⁻¹, economic yield plant⁻¹, harvest index, protein content, proline content, heat injury ind,ex and leaf canopy temperature. In addition to the above traits the , mean square due to $GCA \times E$ was also significant for days to 50 % flowering, days to maturity, and test weight revealed the influence of the environment on GCA. The σ^2 sca was considerably higher than their corresponding σ^2 GCA for all the characters in all the three environments except for plant height in E_1 and E_3 , which indicated preponderance of non-additive gene action in the inheritance of these traits except for plant height in E_1 and E_3 . The estimates of general combining ability effects indicated that parents NIDW-295 and HI 8498 were good general combiners for grain yield plant⁻¹ and most of components along with heat tolerance characters. The SCA effects for grain yield plant⁻¹ were significantly positive for 16 crosses in the pool. Crosses PDW-233 \times PDW-314, HI-8737 \times HI-8498, PDW-274 \times PDW-291, NIDW-295 \times PDW-274 and Raj-1555 \times PDW-274 in pooled had maximum SCA. All these crosses were also having significant SCA effects for one or more components and heat tolerant characters indicate their genetic worth for these characters in respective environments.

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Keywords: Combining ability, grain yield, half diallel, wheat (*Triticum durum* Desf.)

Introduction

Wheat is the second most important staple food crop of the world after rice. It is a self-pollinated crop of the *Poaceae* family and is one of the leading cereals of many countries of the world including India. It is the most important food crop of India and accounts for 20% of human

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consumption of calories and is an important source of protein, vitamins and minerals. Wheat has relatively high content of niacin and thiamine which are principally concerned in providing the special protein called 'Gluten'. Globally, *aestivum* wheat is most important species which covers 90 per cent of the area. Next popular wheat being durum wheat which covers about 9 percent of the total area while *T. diccoum* and *T. monococcum* cover less than the 1 per cent of the total area (Giraldo et al. 2019).

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Durum wheat mostly grown in the temperate environmental conditions. However, it is predominantly consumed in tropical and subtropical regions of the world. In subtropical regions it is cultivated in winter season but exposed to high temperature stress at the end of the season *i.e.* at grain filling stage, resulting shriveled and thin grains. Heat stress is one of the major limiting factors for growth and productivity in wheat crop particularly in warmer region. The optimum temperature for wheat crop has been reported between 18⁰C to 24⁰C with minimum and maximum growth temperature of 3⁰ to 4⁰C and 30⁰ to 32⁰C respectively. While for anthesis and grain filling, optimum temperature range is 12-22⁰C (Sabella et al. 2020).

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Breeding genotypes for heat tolerance has become an integral component of wheat improvement. To achieve this goal, growing of breeding lines over time and space has become an integral part of any plant breeding programme. The task of breeder is to screen out genotypes planted at different interval and to those genotypes which are suitable for wider range of planting. Information on phenotypic stability is useful for the selection of crop varieties as well as for breeding programs. Some genotypes may perform well in certain environment, but, fail in several others. Genotype-environment interaction is extremely important in the development and evolution of plant varieties because they reduce the genotypic-stability values under diverse environments. Progress from selection is also reduced due to a large effect of genotypes and environment interaction as shown by Comstock and Moll (1963).

The diallel analysis studies developed by Hayman (1954) and Jinks (1955), provides a fairly reliable mechanism to properly understand the nature of gene action involved in the development of complex genetic characters of economic value. This technique employed to determine the pattern of gene action for yield potential. The diallel cross designs are frequently used in plant breeding research to obtain information about genetic properties of parental lines or estimates of general combining ability (GCA), specific combining ability (SCA) and heritability (El Maghraby et al. 2005).

The concept of combining ability as a measure of gene action refers to the capacity or ability of a genotype to transmit superior performance to its crosses. The value of an inbred line depends on its ability to produce superior hybrids in combination with other inbreds. Combining ability analysis helps in the evaluation of inbreds in terms of their genetic value and in the selection of suitable parents for hybridization. Genetic analysis of some economic characters show different pattern of inheritance. Therefore, it is necessary to study the genetic architecture of wheat genotypes in relation to the environment for which they have to be developed. Wheat production can be enhanced through the development of new cultivars having wider genetic base.

Materials and Methods

Ten wheat genotypes were selected as parents on the basis of their diverse geographical origin, morpho-physiological characters viz., earliness, high yield potential, heat tolerance, wide variation and their adaptability for different agro-climatic zones of India. These genotypes were crossed in diallel fashion (excluding reciprocals) to develop forty five crosses during *Rabi* 2015-16. The experimental trials were conducted at three different locations viz., the Instructional Research Farm, Rajasthan College of Agriculture, Udaipur, College of Technology and Agriculture Engineering, Udaipur and Agriculture Research Sub-Station, Vallabhnagar during *Rabi* 2016-17. All necessary facilities for cultivation of successful crop including field preparation, inputs, irrigation facilities and labourers were provided from the AICRP on wheat and barley, Rajasthan Collage of Agriculture, Udaipur. The Udaipur is situated at zone IVa under Arawali Hills area of southern Rajasthan. Soil of this region is clay loam having good porosity, fertility and water holding capacity. It is sufficient with organic matters which are essential for plant growth and symbiotic organisms. These ten parents along with forty five crosses and two checks were evaluated by single row in three replications with randomized block design sown in row length of 3.0 meters with spacing 22.5×10 cm during *Rabi* 2016-17 at three different locations. The experiments were conducted under irrigated conditions. Recommended crop production practices were followed to raise the successful healthy crop. The observations were recorded on five randomly selected competitive plants in each replication for twenty one characters viz., plant height (cm), flag leaf length (cm), flag leaf width (cm), flag leaf area (cm²), peduncle length (cm), total number of tillers plant⁻¹, total number of productive tillers plant⁻¹, spike length (cm), spikelet's spike⁻¹,

grains spike⁻¹, spike weight productive tiller⁻¹ (g), grain weight spike⁻¹ (g), biological yield plant⁻¹ (g), economic yield plant⁻¹ (g), harvest index (%), test weight (g), protein content (%), proline content (µg/100 mg fresh leaf tissue), chlorophyll content estimation (mg/g), chlorophyll stability index, heat injury (%), remaining characters viz., days to 50% heading, days to maturity, grain filling period and leaf canopy temperature (°c) which were recorded on plot basis. The combining ability analysis was carried out using the method suggested by Singh (1973 and 1979), which is an extension of Griffing's method II, model I (1956) to estimate the interactions of general and specific combining ability effects with environments, besides determining the significance of general and specific combining ability variance.

Results and Discussion

Combining ability which is a tool to discriminate good as well as poor combiners and selecting appropriate parental material for breeding programme. At the same time it also gives the information about the nature of gene effects involved in the inheritance of various traits. The resulting total genetic variance is partitioned into the variance due to general combining ability and specific combining ability. This helps the breeder in knowing the relative proportion of additive and non-additive genetic variance involved in the inheritance of various characters as well as deciding the appropriate breeding method for effective exploitation of available genetic variation. The presence of non-additive genetic variance is the primary justification for initiating the hybrid breeding programme (Cockerham, 1961). In self-pollinated crop, recombination breeding has been extensively used to develop the variability reservoirs for exploitation in breeding programme. Combining ability analysis was carried out in the present study to obtain information on selection of better parents and cross combinations for their further use in hybrid breeding programme. They are discussed in the subsequent paragraphs.

The analysis of variance for combining ability, using diallel mating design in respect of ten parents and forty five crosses for all the twenty five characters in individual environments are presented in Table 1 and over the environment presented in Table 2. The analysis of variance in each environment (Griffings, 1956 method II model I) revealed that mean squares due to general combining ability (GCA) was significant for all the characters in all the three environments except days to 50 % heading in E₃, days to maturity in E₂, grain filling period E₁ and E₃, plant height in E₁, E₂ and E₃, flag leaf area in E₃. Likewise, mean squares due to specific combining

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ability (SCA) was significant for all the characters in all the three environments except days to 50 % heading in E₃ environments, days to maturity in E₂ and E₃, plant height in E₁ and E₃ environments and canopy leaf temperature in E₃ environments. Significantly mean square due GCA and SCA for the concern characters suggested difference between parents for GCA and between hybrids for SCA. Jain and Sastry, 2012 and Adel and Ali, 2013 also observed significant difference in their study in wheat. The σ^2_{sca} was considerably higher than their corresponding σ^2_{gca} for all the characters in all the three environments except for plant height in E₁ and E₃ (Table-1), which indicated preponderance of non-additive gene action in the inheritance of these traits except for plant height in E₁ and E₃. Preponderance of non-additive variance in the expression of different traits in wheat have also been reported Desale and Mehta, 2013; Hammad *et al.* 2013.

In pooled analysis (Singh, 1976 & 1979, method II model I), mean square due to environment, GCA and SCA significant for all the characters except plant height SCA revealed difference between parents for GCA and difference between crosses for SCA. Similarly, mean square due to GCA × E and SCA × E were significant for grain filling period, flag leaf length, flag leaf width, flag leaf area, peduncle length, total number of tillers plant⁻¹, number of productive tillers plant⁻¹, spike length, number of spikelets spike⁻¹, spike weight productive tillers⁻¹, grain weight spike⁻¹, biological yield plant⁻¹, economic yield plant⁻¹, harvest index, protein content, proline content, heat injury index and canopy temperature depression. In addition to above traits, mean square due to GCA × E was also significant for days to 50 % heading, days to maturity and test weight revealed influence of environment on GCA. Significant GCA × environments and SCA × environments interaction for one or more characters were also observed by Joshi *et al.* (2002); Singh and Yadav, 2011 (Table 2). The σ^2_{gca} was higher than their respective σ^2_{sca} for all the characters except plant height, flag leaf length, flag leaf width, flag leaf area, peduncle length, number of productive tillers plant⁻¹, spike length, number of spikelets spike⁻¹, number of grain spike⁻¹, spike weight productive tillers⁻¹, grain weight spike⁻¹, biological yield plant⁻¹, protein content, chlorophyll content, chlorophyll stability index and heat injury index indicated that additive type of gene action played role in the expression of all these traits. While, $\sigma^2_{gca} \times E$ was higher than their respective $\sigma^2_{sca} \times E$ for all the characters. Similar finding have been reported by Sharma *et al.* 2003 and Singh and Yadav, 2011. The estimate of general combining

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ability effects of the parents and specific combining ability effects of the crosses for different characters for individual and pooled environments are presented in Table S1 to S14.

In the present study an overall approach of GCA effects indicated that parents NIDW-295, HI-8498 and PDW-274 were found best for grain yield as well as other attributing, heat tolerance characters in all environments and pool. The estimates of gca effects revealed that the parent PDW-274 had the significant and desirable effects for flag leaf length, flag leaf area, spike length, spikelet's spike⁻¹, spike weight productive tillers⁻¹, grain weight spike⁻¹, grains spike⁻¹, economical yield plant⁻¹, biological yield plant⁻¹ and proline content where, as RAJ-1555 represented that flag leaf length, flag leaf area, spike length, spikelet's spike⁻¹, spike weight productive tillers⁻¹, grain weight spike⁻¹, economic yield plant⁻¹ and harvest index had good gca effects. Similar study were recorded Ribadia *et al.*(2007), Gami *et al.*(2010), Lohithaswa *et al.* (2013) reported that Raj 1555 and Jairaj were significantly superior general combiners for seed yield and its components Saini *et al.* (2006).General combining ability (GCA) components were higher for spikelet's/spike, spike length, plant height and days to heading, but for grain yield, spike number, proline content chlorophyll stability index and protein content specific combining ability (SCA) components were higher Singh *et al.* (1983). Significant positive GCA effects for length of main spike, spikelet's spike⁻¹, biological yield plant⁻¹ and economic yield plant⁻¹Ribadia *et al.* (2007).

Among the parents, genotype NIDW-295 and HI-8498, PDW-274 and PDW-314 exhibited superior mean and good gca effects for various traits and hence, should be exploited more in cross to develop genotypes having good yield and desirable characters. The similar trends for combining ability in wheat were also reported by Singh *et al.* (2007), Abdel *et al.* (2009) and Brahim & Mohamed (2014). General combining ability and specific combining ability variances were highly significant for all the characters in the present study similar finding in wheat have also reported by Gami *et al.* (2010).The mean performance showed significant association with specific combining ability effects indicating that selection of the cross combinations on the basis of heterotic response may be reliable. In the present study the parents (high × low or low × low general combiners) were involved in the high expression of sca effects in the superior crosses. Sixteen crosses recorded significant sca effects in all three environments, for grain yield and related traits the cross HI-8737 × HI-8498,PDW-274 × PDW-291, NIDW-295 ×PDW-274 and Raj-1555 × PDW-291 exhibited significant sca effects in the desired direction for economical

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yield and heat tolerance traits. These findings are in conformity with the findings of Lohithaswa *et al.* (2013).

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In the present study the estimates of general combining ability effects indicated that parents NIDW-295, and HI 8498 were good general combiners for grain yield plant⁻¹ and most of components along with heat tolerance characters. The SCA effects for grain yield plant⁻¹ were significantly positive for 16 crosses in pool. The 14, 17, and 13 crosses in E₁, E₂ and E₃ respectively had significant positive SCA. Crosses PDW-233 × PDW-314, HI-8737 × HI-8498, PDW-274 × PDW-291, NIDW-295 × PDW-274 and Raj-1555 × PDW-274 pools had maximum SCA. All these crosses were also having significant SCA effects for one or more components and heat tolerant characters indicate their genetic worth for these characters in respective environments.

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Table 1 Combining ability mean square for different characters

SN	Characters	Env	Source			Var Model I		
			GCA [9]	SCA [45]	Error [108]	GCA	SCA	Error
1	Days to 50% heading	1	13.72*	11.62**	5.95	1.94	84.95	5.95
		2	23.33**	10.88**	5.02	4.58	87.90	5.02
		3	3.47	3.62	3.26	0.05	5.35	3.26
2	Days to maturity	1	13.33*	12.98**	5.41	1.98	113.62	5.41
		2	6.22	4.58	3.93	0.57	9.88	3.93
		3	8.67*	4.13	3.37	1.33	11.42	3.37
3	Grain Filling periods	1	0.9	1.18**	0.56	0.09	9.35	0.56
		2	4.59**	2.18**	0.71	0.97	22.03	0.71
		3	0.93	1.28**	0.65	0.07	9.34	0.65
4	Plant height (cm)	1	27.78	16.7	18.88	2.22	-32.81	18.88
		2	24.21	29**	13.05	2.79	239.36	13.05
		3	17.91	8.9	12.68	1.31	-56.61	12.68
5	Flag Leaf Length (cm)	1	16.24**	12.21**	1.00	3.81	168.22	1.00
		2	17.67**	8.75**	1.45	4.06	109.48	1.45
		3	5.78**	2.9**	1.37	1.10	22.95	1.37
6	Flag leaf width (cm)	1	0.04**	0.03**	0.00	0.01	0.45	0.00
		2	0.07**	0.05**	0.01	0.02	0.63	0.01
		3	0.03*	0.02*	0.02	0.00	0.14	0.02
7	Flag Leaf area (cm ²)	1	78.93**	61.09**	1.20	19.43	898.23	1.20
		2	61.42**	44.8**	2.86	14.64	629.10	2.86
		3	20.08	28.28**	15.86	1.05	186.31	15.86
8	Penduncle length (cm)	1	3.24*	3.63**	1.56	0.42	31.10	1.56
		2	8.63**	4.96**	1.46	1.79	52.52	1.46
		3	6.85**	5.91**	1.33	1.38	68.77	1.33
9	Total No. of tillers plant ⁻¹	1	23.45**	33.26**	1.48	5.49	476.70	1.48
		2	39.55**	28.66**	1.01	9.63	414.72	1.01
		3	19.27**	24.13**	1.68	4.40	336.78	1.68
10	No. of prod. Tillers plant ⁻¹	1	24.86**	31.8**	1.50	5.84	454.50	1.50
		2	35.28**	24.22**	1.15	8.53	345.92	1.15
		3	23.32**	17.31**	1.61	5.43	235.47	1.61
11	Spike length (cm)	1	2.47**	0.72**	0.07	0.60	9.74	0.07
		2	3.13**	0.65**	0.10	0.76	8.27	0.10
		3	1.44**	0.46**	0.05	0.35	6.16	0.05
12	No. of Spiklets spike ⁻¹	1	7.76**	3**	0.51	1.81	37.40	0.51
		2	2.27**	1.64**	0.70	0.39	14.09	0.70
		3	2.27**	1.64**	0.70	0.39	14.09	0.70
13	No. of grain spike ⁻¹	1	258.17**	103.2**	7.65	62.63	1433.28	7.65
		2	281.4**	92.96**	12.22	67.29	1211.19	12.22
		3	281.4**	92.96**	12.22	67.29	1211.18	12.22
14	Spike weight productive tiller ⁻¹ (g)	1	1.57**	0.62**	0.02	0.39	8.99	0.02
		2	1.1**	0.47**	0.05	0.26	6.30	0.05
		3	1.3**	0.46**	0.07	0.31	5.77	0.07
15	Grain weight spike ⁻¹ (gm)	1	0.95**	0.4**	0.01	0.23	5.85	0.01
		2	0.41**	0.51**	0.07	0.08	6.63	0.07
		3	1.21**	0.46**	0.07	0.29	5.91	0.07
16	Biological yield Plant ⁻¹ (g)	1	1240.08**	1246.86**	50.52	297.39	17945.20	50.52
		2	932.66**	1362.78**	79.56	213.28	19248.20	79.56
		3	501.82**	887.43**	36.66	116.29	12761.50	36.66
17	Economic yield	1	142.62**	186.78**	7.65	33.74	2687.02	7.65

SN	Characters	Env	Source			Var Model I		
			GCA [9]	SCA [45]	Error [108]	GCA	SCA	Error
	Plant ⁻¹ (g)	2	109.78**	174.41**	3.52	26.56	2563.39	3.52
		3	39.74**	81.25**	2.89	9.21	1175.48	2.89
18	Harvest index (%)	1	27.53**	19.74**	5.74	5.45	210.07	5.74
		2	30.81**	40.48**	6.58	6.06	508.47	6.58
		3	18.3**	32.77**	4.47	3.46	424.50	4.47
19	Test weight (g)	1	64.59**	50.24**	3.98	15.15	693.84	3.98
		2	59.93**	50.18**	11.30	12.16	583.26	11.30
		3	59.93**	50.18**	11.30	12.16	583.26	11.30
20	Protein Content (%)	1	0.62**	0.3**	0.07	0.14	3.42	0.07
		2	0.62**	0.22**	0.07	0.14	2.23	0.07
		3	0.41**	0.28**	0.05	0.09	3.40	0.05
21	Proline Content (µg)	1	10.24**	7.95**	0.25	2.50	115.38	0.25
		2	12.6**	10.71**	0.17	3.11	158.01	0.17
		3	17.28**	7.15**	0.40	4.22	101.27	0.40
22	Chlorophyll content (mg)	1	0.1**	0.08**	0.01	0.02	1.18	0.01
		2	0.1**	0.08**	0.00	0.02	1.20	0.00
		3	0.1**	0.08**	0.01	0.02	1.19	0.01
23	Chlorophyll Stability Index	1	2.71**	3.12**	0.25	0.62	43.04	0.25
		2	2.59**	2.97**	0.18	0.60	41.96	0.18
		3	2.71**	3.12**	0.19	0.63	43.97	0.19
24	Heat Injury Index (%)	1	80.79**	35.07**	1.51	19.82	503.46	1.51
		2	80.84**	34.73**	1.49	19.84	498.64	1.49
		3	37.38**	28.28**	1.82	8.89	396.79	1.82
25	Leaf Canopy Temperature (°C)	1	3.77**	0.59**	0.24	0.88	5.24	0.24
		2	0.46*	1.21**	0.22	0.06	14.73	0.22
		3	6.92**	0.81	1.16	1.44	-5.16	1.16

*,** Significant at 5 and 1 percent respectively (Model I)

Table 2 Combining ability mean square and EMS over the environments for different characters

SN Characters	Source						Variance Model I				
	Env	GCA	SCA	GCA x E	SCA x E	Pool Error	GCA	SCA	GCA x E	SCA x E	Error
	[2]	[9]	[45]	[18]	[90]	[324]					
1 Days to 50% heading	923.36**	21.93**	15.85**	9.3*	5.13	4.75	33.40	4.30	166.57	6.82	4.75
2 Days to maturity	1204.47**	11.76**	11.31**	8.23*	5.19	4.23	43.65	1.88	106.24	6.00	4.23
3 Grain Filling periods	288.32**	3.56**	2.47**	1.43**	1.08**	0.64	10.46	0.73	27.49	1.18	0.64
4 Plant height (cm)	227.81**	42.49**	20.39	13.70	17.11	14.87	7.74	6.91	82.86	-1.75	14.87
5 Flag Leaf Length (cm)	8.24**	27.97**	11.1**	5.86**	6.38**	1.27	0.25	6.67	147.36	6.88	1.27
6 Flag leaf width (cm)	0.08**	0.1**	0.05**	0.03**	0.03**	0.01	0.00	0.02	0.61	0.03	0.01
7 Flag Leaf area (cm ²)	258.06**	109.43**	67.48**	25.5**	33.34**	6.64	9.14	25.70	912.64	28.28	6.64
8 Peduncle length (cm)	13.72**	5.25**	4.69**	6.73**	4.91**	1.45	0.45	0.95	48.68	7.93	1.45
9 Total No. of tillers plant ⁻¹	322.12**	43.88**	49.53**	19.2**	18.27**	1.39	11.66	10.62	722.04	26.71	1.39
10 No. of prod. Tillers plant ⁻¹	278.79**	42.56**	41.29**	20.45**	16.02**	1.42	10.09	10.28	598.02	28.54	1.42
11 Spike length (cm)	0.79**	6.52**	0.99**	0.26**	0.43**	0.08	0.03	1.61	13.66	0.28	0.08
12 No.of Spiklets spike ⁻¹	10.51**	6.29**	4.6**	3**	0.84*	0.64	0.36	1.41	59.47	3.54	0.64
13 No.of grain spike ⁻¹	14.54	814.24**	275.61**	3.36	6.76	10.69	0.14	200.89	3973.76	-11.00	10.69
14 Spike weight productive tiller ⁻¹ (g)	0.78**	2.34**	0.48**	0.81**	0.53**	0.05	0.03	0.57	6.51	1.15	0.05
15 Grain weight spike ⁻¹ (g)	1.58**	1.44**	0.57**	0.57**	0.4**	0.05	0.06	0.35	7.75	0.77	0.05
16 Biological yield Plant ⁻¹ (g)	7187.66**	1803.58**	2528.53**	435.49**	484.27**	55.58	259.35	437437.00	37094.30	569.86	55.58
17 Economic yield Plant ⁻¹ (g)	2309.98**	218.74**	354.65**	36.7**	43.9**	4.69	83.83	53.51	5249.50	48.02	4.69
18 harvest index (%)	161.12**	16.62**	49.42**	30.01**	21.79**	5.60	5.66	2.76	657.28	36.61	5.60
19 Test weight (g)	309.58**	175.57**	117.66**	4.44	16.47**	8.86	10.94	41.68	1632.04	-6.63	8.86
20 Protein Content (%)	0.13	0.72**	0.46**	0.46**	0.17**	0.07	0.00	0.16	5.88	0.59	0.07
21 Proline Content (µg)	415.42**	10.92**	11.68**	14.6**	7.06**	0.27	15.10	2.66	171.07	21.49	0.27
22 Chlorophyll content (mg)	0.53**	0.3**	0.25**	0.00	0.00	0.01	0.02	0.07	3.73	-0.01	0.01
23 Chlorophyll Stability Index	24.83**	8.01**	9.21**	0.00	0.00	0.21	0.90	1.95	135.12	-0.31	0.21
24 Heat Injury Index (%)	105.83**	76.75**	55.87**	61.13**	21.1**	1.61	3.79	18.79	814.01	89.28	1.61
25 Canopy Temperature Depression (°C)	86.04**	5.22**	0.88**	2.96**	0.86**	0.54	3.11	1.17	5.09	3.64	0.54

*,** Significant at 5 and 1 percent respectively (Model I)

Table 3 GCA and SCA effects for Days to 50% flowering, and Days to maturity

SN	Genotype	Days to 50% heading				Days to maturity			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	HI-8737	-0.95	-1.36*	0.56	-0.58	-0.73	1.08*	0.93	0.43
2	NIDW-295	-1.34*	-1.74**	0.83	-0.75*	-0.89	1.24*	1.77**	0.71*
3	HI-8498	0.38	-0.02	-0.53	-0.06	0.66	-0.28	-0.29	0.03
4	HI-8663	-0.03	-0.44	-0.28	-0.25	-0.14	-0.42	-0.59	-0.39
5	WH-896	0.11	-0.30	-0.86	-0.35	0.05	-0.95	-1.01*	-0.64
6	RAJ-1555	-1.70*	-1.63**	-0.19	-1.18*	-2.12**	-0.64	-0.59	-1.12*
7	PDW-274	0.63	0.23	0.61	0.49	0.36	0.30	0.29	0.32
8	PDW-233	0.13	1.39*	0.03	0.52	0.33	0.19	0.35	0.29
9	PDW-314	1.77**	2.23**	0.11	1.37**	1.69**	-0.01	-0.18	0.50
10	PDW-291	0.99	1.64**	-0.28	0.79*	0.80	-0.51	-0.68	-0.13
11	HI-8737×NIDW-295	-1.84	-1.47	-1.81	-1.71	-2.11	-2.39	-1.95	-2.15
12	HI-8737×HI-8498	0.44	0.81	-0.79	0.15	1.00	-0.53	-0.57	-0.03
13	HI-8737×HI-8663	3.52	3.89	-0.37	2.35*	3.81	-0.39	-0.26	1.05
14	HI-8737×WH-896	0.38	0.75	1.21	0.78	3.28	3.81*	3.82*	3.64**
15	HI-8737×RAJ-1555	0.19	0.09	1.88	0.72	0.44	1.83	1.74	1.34
16	HI-8737×PDW-274	-0.81	-0.44	1.08	-0.06	-0.03	1.56	1.52	1.02
17	HI-8737×PDW-233	0.02	-1.28	1.66	0.14	-0.33	1.00	0.80	0.49
18	HI-8737×PDW-314	1.72	1.22	0.58	1.17	1.31	-0.14	-0.01	0.39
19	HI-8737×PDW-291	3.49	2.81	0.96	2.42*	3.19	0.36	0.49	1.35
20	NIDW-295×HI-8498	0.49	0.86	1.27	0.88	-0.17	0.64	-0.07	0.14
21	NIDW-295×HI-8663	2.91	3.28	0.69	2.29	2.64	0.44	-0.09	1.00
22	NIDW-295×WH-896	1.44	1.81	1.94	1.73	0.11	0.64	-0.01	0.25

SN	Genotype	Days to 50% heading				Days to maturity			
		E1	E2	E3	Pool	E1	E2	E3	Pool
23	NIDW-295×RAJ-1555	1.58	1.47	1.94	1.66	1.28	1.67	0.91	1.28
24	NIDW-295×PDW-274	2.24	2.61	3.80*	2.89*	3.14	4.72*	4.02*	3.96**
25	NIDW-295×PDW-233	1.74	0.45	1.05	1.08	2.83	2.17	1.30	2.10
26	NIDW-295×PDW-314	0.44	-0.05	1.63	0.67	0.81	2.03	1.49	1.44
27	NIDW-295×PDW-291	3.22	2.53	1.02	2.26	4.03	1.86	1.32	2.40*
28	HI-8498×HI-8663	3.86	4.22*	0.05	2.71*	4.08	0.31	0.30	1.56
29	HI-8498×WH-896	1.72	2.09	1.63	1.81	2.22	2.17	2.05	2.14
30	HI-8498×RAJ-1555	-1.81	-1.91	1.96	-0.59	-1.61	2.19	1.96	0.85
31	HI-8498×PDW-272	-0.48	-0.11	-1.17	-0.59	-1.08	-1.75	-1.93	-1.59
32	HI-8498×PDW-233	1.36	0.06	-0.59	0.27	-0.06	-1.97	-2.32	-1.45
33	HI-8498×PDW-314	4.05	3.56	-0.01	2.53*	3.92	-0.11	-0.12	1.23
34	HI-8498×PDW-291	4.83*	4.14*	1.05	3.34**	3.81	0.06	0.05	1.30
35	HI-8663×WH-896	-2.87	-2.50	1.38	-1.33	-2.97	1.31	1.35	-0.11
36	HI-8663×RAJ-1555	-1.39	-1.50	0.71	-0.73	-1.47	0.67	0.60	-0.07
37	HI-8663×PDW-274	-3.73	-3.36	0.24	-2.28	-4.61*	-0.61	-0.62	-1.95
38	HI-8663×PDW-233	1.44	0.14	-1.17	0.14	1.08	-1.50	-1.68	-0.70
39	HI-8663×PDW-314	0.80	0.31	-0.92	0.06	1.06	-0.64	-0.48	-0.02
40	HI-8663×PDW-291	-5.76*	-6.44**	-0.87	-4.36**	-6.06**	-1.14	-0.98	-2.73*
41	WH-896×RAJ-1555	1.47	1.36	-2.37	0.15	2.33	-1.47	-1.65	-0.26
42	WH-896×PDW-274	1.80	2.17	-2.17	0.60	3.19	-0.75	-0.87	0.52
43	WH-896×PDW-233	4.30	3.00	-2.59	1.57	5.22*	-1.64	-1.93	0.55
44	WH-896×PDW-314	4.33	3.84	-2.01	2.05	4.53*	-1.78	-1.73	0.34
45	WH-896×PDW-291	-0.56	-1.25	-2.29	-1.36	-0.92	-2.61	-2.57	-2.03

SN	Genotype	Days to 50% heading				Days to maturity			
		E1	E2	E3	Pool	E1	E2	E3	Pool
46	RAJ-1555×PDW-274	2.94	2.84	-2.84	0.98	4.03	-1.72	-1.95	0.12
47	RAJ-1555×PDW-233	-1.56	2.34	-0.92	-0.05	-0.94	-0.28	-0.68	-0.63
48	RAJ-1555×PDW-314	2.13	1.17	-1.34	0.65	1.03	-2.42	-2.48	-1.29
49	RAJ-1555×PDW-291	3.24	2.09	-2.29	1.02	1.25	-4.25*	-4.32*	-2.44*
50	PDW-274×PDW-233	2.44	1.14	1.60	1.73	0.58	-0.22	-0.57	-0.07
51	PDW-274×PDW-314	2.47	1.97	-0.48	1.32	1.56	-1.36	-1.37	-0.39
52	PDW-274×PDW-291	3.24	2.56	0.58	2.13	3.44	0.81	0.80	1.68
53	PDW-233×PDW-314	-1.70	2.14	0.10	0.18	-2.42	-0.58	-0.76	-1.25
54	PDW-233×PDW-291	-3.92	2.06	0.49	-0.46	-4.53*	-0.08	-0.26	-1.62
55	PDW-314×PDW-291	-4.23	-1.44	-1.59	-2.42*	-4.22	-1.56	-1.40	-2.39*
	Standard error								
	Gi	0.67	0.61	0.49	0.34	0.64	0.54	0.50	0.33
	Gi-Gj	1.00	0.92	0.74	0.51	0.95	0.81	0.75	0.48
	Sii	2.01	1.85	1.49	1.04	1.92	1.64	1.51	0.98
	Sij	2.25	2.06	1.66	1.16	2.14	1.83	1.69	1.09
	Sij-ik	3.30	3.03	2.45	1.70	3.15	2.68	2.48	1.61
	Sij-Skl	3.15	2.89	2.33	1.62	3.00	2.56	2.37	1.53

*, ** Significant at 5 per cent and 1 per cent respectively

Table 4 GCA and SCA effects for Grain Filling periods, and Plant height (cm)

SN	Genotype	Grain Filling periods				Plant height (cm)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	HI-8737	0.22	0.44	0.16	0.27*	-0.85	-0.64	0.34	-0.39
2	NIDW-295	0.44*	0.47*	0.60**	0.51**	-0.88	-0.99	-1.76	-1.21*
3	HI-8498	0.28	-0.00	0.21	0.16	-0.93	-0.18	-1.55	-0.88
4	HI-8663	-0.11	-1.08**	-0.18	-0.46*	2.42*	-1.58	0.05	0.30
5	WH-896	-0.06	-0.75**	-0.12	-0.31*	0.79	1.51	0.94	1.08
6	RAJ-1555	-0.42*	-0.58*	-0.26	-0.42*	1.01	1.76	0.82	1.20
7	PDW-274	-0.28	0.17	-0.18	-0.10	0.68	1.42	2.22*	1.44*
8	PDW-233	0.19	0.06	0.18	0.14	1.30	-0.00	0.16	0.49
9	PDW-314	-0.08	0.42	-0.15	0.06	-0.65	1.09	-1.13	-0.23
10	PDW-291	-0.19	0.86**	-0.26	0.14	-2.90*	-2.38*	-0.08	-1.78*
11	HI-8737×NIDW-295	-0.27	-0.01	-0.43	-0.24	-1.74	0.73	-3.49	-1.50
12	HI-8737×HI-8498	0.56	0.13	0.62	0.44	3.64	7.49*	1.04	4.06
13	HI-8737×HI-8663	0.28	2.88**	0.34	1.17**	2.36	-3.04	3.56	0.96
14	HI-8737×WH-896	2.89**	1.21	2.95**	2.35**	3.43	-2.68	-0.09	0.22
15	HI-8737×RAJ-1555	0.26	0.71	0.09	0.35	1.69	0.62	-0.98	0.44
16	HI-8737×PDW-274	0.78	0.30	0.68	0.59	-4.63	-1.51	0.46	-1.89
17	HI-8737×PDW-233	-0.36	1.74*	-0.35	0.35	-2.08	-4.86	-0.85	-2.60
18	HI-8737×PDW-314	-0.41	-0.29	-0.35	-0.35	-4.12	0.44	-1.45	-1.71
19	HI-8737×PDW-291	-0.30	-1.40	-0.24	-0.65	-2.02	2.95	3.36	1.43
20	NIDW-295× HI-8498	-0.66	-1.90*	-0.82	-1.13**	-3.67	-2.35	4.30	-0.57
21	NIDW-295× HI-8663	-0.27	-1.15	-0.43	-0.62	2.38	-7.22*	-1.04	-1.96
22	NIDW-295× WH-896	-1.33	-1.48	-1.49*	-1.43**	3.82	-0.31	0.95	1.48

SN	Genotype	Grain Filling periods				Plant height (cm)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
23	NIDW-295×RAJ-1555	-0.30	-0.65	-0.68	-0.54	-1.08	-0.88	-0.28	-0.75
24	NIDW-295×PDW-274	0.89	1.27	0.57	0.91*	2.46	-1.88	-1.99	-0.47
25	NIDW-295×PDW-233	1.09	1.38	0.87	1.11*	-5.95	7.52*	-3.07	-0.50
26	NIDW-295×PDW-314	0.37	1.69*	0.20	0.75	-6.14	-3.53	-3.81	-4.49*
27	NIDW-295×PDW-291	0.81	2.91**	0.65	1.46**	-2.06	-0.22	-1.00	-1.09
28	HI-8498×HI-8663	0.23	-0.34	0.29	0.06	-0.65	6.28	-3.04	0.86
29	HI-8498×WH-896	0.51	0.33	0.57	0.47	-1.85	-13.93**	-3.75	-6.51**
30	HI-8498×RAJ-1555	0.20	0.16	0.04	0.13	3.92	5.95	-6.08	1.26
31	HI-8498×PDW-272	-0.61	-0.26	-0.71	-0.53	-0.61	-1.03	-3.27	-1.64
32	HI-8498×PDW-233	-1.41*	0.19	-1.41	-0.88*	-0.09	-1.91	4.95	0.99
33	HI-8498×PDW-314	-0.13	1.83*	-0.07	0.54	5.19	4.12	-1.19	2.71
34	HI-8498×PDW-291	-1.02	0.71	-0.96	-0.42	0.12	9.89**	5.12	5.04*
35	HI-8663×WH-896	-0.11	1.41	-0.05	0.42	-1.74	2.66	3.14	1.35
36	HI-8663×RAJ-1555	-0.08	1.24	-0.24	0.31	0.69	7.46*	0.08	2.74
37	HI-8663×PDW-274	-0.88	1.49	-0.99	-0.13	-1.01	-2.83	1.16	-0.90
38	HI-8663×PDW-233	-0.36	0.60	-0.35	-0.03	-3.07	0.19	1.11	-0.59
39	HI-8663×PDW-314	0.26	-0.76	0.32	-0.06	-0.12	0.96	-1.09	-0.09
40	HI-8663×PDW-291	-0.30	-2.87**	-0.24	-1.14**	3.44	-5.41	-5.58	-2.52
41	WH-896×RAJ-1555	0.87	-1.09	0.70	0.16	1.59	-5.41	3.03	-0.26
42	WH-896×PDW-274	1.39*	0.49	1.29	1.06*	-2.81	-0.71	1.84	-0.56
43	WH-896×PDW-233	0.92	-1.06	0.93	0.26	-0.42	4.57	-2.38	0.59
44	WH-896×PDW-314	0.20	1.58*	0.26	0.68	3.14	8.24*	2.41	4.60*
45	WH-896×PDW-291	-0.36	1.13	-0.30	0.16	-0.72	-1.32	1.82	-0.07

SN	Genotype	Grain Filling periods				Plant height (cm)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
46	RAJ-1555×PDW-274	1.09	0.99	0.76	0.95*	-4.59	5.15	1.34	0.63
47	RAJ-1555×PDW-233	0.62	-0.23	0.40	0.26	7.15	-10.91**	-0.90	-1.55
48	RAJ-1555×PDW-314	-1.11	1.74*	-1.27	-0.21	-13.99**	-7.16*	4.23	-5.64**
49	RAJ-1555×PDW-291	-1.99**	0.96	-2.16**	-1.06*	-0.13	4.86	1.07	1.93
50	PDW-274×PDW-233	-1.86**	0.35	-2.02**	-1.17**	0.90	2.62	-0.86	0.89
51	PDW-274×PDW-314	-0.91	-0.67	-1.02	-0.87*	5.37	-1.21	4.60	2.92
52	PDW-274×PDW-291	0.20	0.21	0.09	0.17	6.60	4.85	-3.56	2.63
53	PDW-233×PDW-314	-0.72	0.44	-0.71	-0.33	6.30	4.06	1.45	3.94
54	PDW-233×PDW-291	-0.61	-0.34	-0.60	-0.52	-1.43	-3.30	-2.44	-2.39
55	PDW-314×PDW-291	0.01	-0.37	0.07	-0.10	-1.54	-8.83**	1.09	-3.09
	Standard error								
	Gi	0.20	0.23	0.22	0.13	1.19	0.99	0.98	0.61
	Gi-Gj	0.30	0.34	0.33	0.19	1.77	1.47	1.45	0.91
	Sii	0.62	0.70	0.67	0.38	3.59	2.98	2.94	1.84
	Sij	0.69	0.78	0.74	0.43	4.00	3.33	3.28	2.05
	Sij-ik	1.01	1.14	1.09	0.63	5.88	4.89	4.82	3.01
	Sij-Skl	0.96	1.09	1.04	0.60	5.61	4.66	4.60	2.87

*, ** Significant at 5 per cent and 1 per cent respectively

Table 5 GCA and SCA effects for Flag Leaf Length (cm), and Flag leaf width (cm)

SN	Genotype	Flag Leaf Length (cm)				Flag leaf width (cm)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	HI-8737	-1.84**	-1.87**	-0.75*	-1.49*	-0.05**	-0.05*	0.02	-0.03
2	NIDW-295	-1.50**	-1.32**	-1.13**	-1.32*	-0.08**	-0.15**	-0.03	-0.09*
3	HI-8498	-0.03	-1.14**	-0.44	-0.54*	0.07**	0.12**	0.01	0.06**
4	HI-8663	0.13	-0.08	0.63	0.23	-0.01	0.01	0.03	0.01
5	WH-896	0.12	0.96**	-0.48	0.20	-0.06**	-0.05*	-0.06	-0.06*
6	RAJ-1555	1.72**	-0.45	-0.04	0.41*	0.11**	0.11**	-0.01	0.07**
7	PDW-274	-1.11**	0.43	0.14	-0.18	0.01	0.03	0.09**	0.04**
8	PDW-233	0.72**	0.36	0.98**	0.69**	0.00	-0.01	0.07	0.02
9	PDW-314	1.19**	1.10**	0.79*	1.03**	-0.01	-0.01	-0.04	-0.02
10	PDW-291	0.60*	2.01**	0.29	0.97**	0.02	0.01	-0.07	-0.01
11	HI-8737×NIDW-295	2.72**	-0.58	0.91	1.02	-0.04	-0.05	0.06	-0.01
12	HI-8737×HI-8498	-4.45**	-1.93	-0.55	-2.31**	-0.09	-0.51**	0.22	-0.12*
13	HI-8737×HI-8663	-5.38**	-2.05	1.02	-2.14**	-0.10	0.10	0.13	0.04
14	HI-8737×WH-896	5.10**	4.71**	-0.74	3.02**	-0.06	-0.00	0.19	0.05
15	HI-8737×RAJ-1555	-8.23**	-7.54**	5.05**	-3.57**	-0.13*	-0.39**	0.28*	-0.08
16	HI-8737×PDW-274	2.03*	-0.84	-0.87	0.11	0.07	-0.14	-0.13	-0.07
17	HI-8737×PDW-233	0.70	-2.24*	0.60	-0.31	0.18**	-0.01	0.20	0.12*
18	HI-8737×PDW-314	-1.94*	0.75	-0.83	-0.67	-0.02	0.23**	-0.06	0.05
19	HI-8737×PDW-291	1.52	2.06	-2.32*	0.42	-0.14*	0.08	-0.20	-0.09
20	NIDW-295×HI-8498	-3.56**	-4.84**	-0.24	-2.88**	-0.36**	-0.02	-0.13	-0.17**
21	NIDW-295×HI-8663	-2.05*	-0.25	2.09	-0.07	-0.08	-0.17*	0.28*	0.01
22	NIDW-295×WH-896	2.45**	1.86	-0.36	1.32*	0.17**	0.06	0.11	0.11*

SN	Genotype	Flag Leaf Length (cm)				Flag leaf width (cm)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
23	NIDW-295×RAJ-1555	-1.58	0.60	-0.44	-0.47	-0.10	0.25**	-0.00	0.05
24	NIDW-295×PDW-274	2.89**	0.66	0.24	1.26*	0.10	-0.01	-0.04	0.01
25	NIDW-295×PDW-233	-0.61	0.48	-0.92	-0.35	-0.09	0.18*	-0.09	0.00
26	NIDW-295×PDW-314	-3.11**	-3.88**	-2.91**	-3.30**	-0.08	0.02	-0.04	-0.04
27	NIDW-295×PDW-291	-0.32	-0.66	-0.47	-0.49	0.29**	-0.01	-0.12	0.05
28	HI-8498×HI-8663	4.81**	3.71**	0.24	2.92**	0.07	0.17*	0.01	0.09
29	HI-8498×WH-896	-1.05	0.63	-2.60*	-1.00	0.32**	0.15*	0.00	0.16**
30	HI-8498×RAJ-1555	0.16	1.73	-0.47	0.47	0.14*	0.03	-0.18	-0.00
31	HI-8498×PDW-272	-2.11*	-1.21	-0.45	-1.26*	0.05	0.23**	-0.02	0.09
32	HI-8498×PDW-233	1.19	2.54*	1.00	1.58**	-0.14*	0.15	0.07	0.03
33	HI-8498×PDW-314	1.32	2.09	1.53	1.65**	-0.03	-0.02	-0.19	-0.08
34	HI-8498×PDW-291	-1.99*	-3.78**	0.46	-1.77**	-0.16*	-0.00	-0.19	-0.12*
35	HI-8663×WH-896	-0.69	-0.27	2.14*	0.39	-0.10	-0.19*	-0.09	-0.13*
36	HI-8663×RAJ-1555	-2.17*	2.55*	1.27	0.55	0.09	0.08	-0.17	-0.00
37	HI-8663×PDW-274	-0.95	-0.37	0.08	-0.41	0.03	-0.01	0.13	0.05
38	HI-8663×PDW-233	0.62	1.28	-0.40	0.50	-0.26**	-0.37**	-0.15	-0.26**
39	HI-8663×PDW-314	-0.65	-0.07	-1.27	-0.66	-0.05	-0.18*	-0.04	-0.09
40	HI-8663×PDW-291	2.05*	0.48	-2.80*	-0.09	-0.18**	-0.21**	-0.08	-0.16**
41	WH-896×RAJ-1555	-1.57	-0.66	-0.82	-1.01	-0.12	-0.06	-0.18	-0.12*
42	WH-896×PDW-274	0.66	-1.52	-0.37	-0.41	-0.12	-0.01	0.02	-0.04
43	WH-896×PDW-233	-1.97*	-2.33*	-0.87	-1.72**	-0.08	-0.02	0.14	0.01
44	WH-896×PDW-314	0.96	0.07	0.17	0.40	0.10	-0.09	-0.20	-0.06
45	WH-896×PDW-291	2.85**	1.02	-0.96	0.97	-0.03	0.07	-0.16	-0.04

SN	Genotype	Flag Leaf Length (cm)				Flag leaf width (cm)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
46	RAJ-1555×PDW-274	-0.24	1.69	0.98	0.81	-0.00	-0.02	0.07	0.02
47	RAJ-1555×PDW-233	-2.17*	0.93	0.65	-0.19	0.01	0.06	0.13	0.07
48	RAJ-1555×PDW-314	4.06**	5.34**	0.67	3.36**	0.32**	0.12	0.07	0.17**
49	RAJ-1555×PDW-291	-0.54	3.58**	-0.93	0.70	0.19**	0.25**	0.23	0.22**
50	PDW-274×PDW-233	5.47**	2.71*	1.28	3.15**	0.11	0.34**	-0.04	0.14**
51	PDW-274×PDW-314	1.46	-0.35	0.90	0.67	0.22**	0.08	0.03	0.11*
52	PDW-274×PDW-291	1.42	-0.90	-1.41	-0.30	0.13*	0.29**	0.06	0.16**
53	PDW-233×PDW-314	2.61**	0.67	0.80	1.36*	0.05	-0.11	0.02	-0.01
54	PDW-233×PDW-291	2.26*	0.52	-1.90	0.29	0.30**	0.07	0.15	0.17**
55	PDW-314×PDW-291	5.19**	5.90**	2.58*	4.56**	0.21**	0.38**	0.09	0.23**
	Standard error								
	Gi	0.27	0.33	0.32	0.18	0.02	0.02	0.03	0.02
	Gi-Gj	0.41	0.49	0.48	0.27	0.03	0.03	0.05	0.02
	Sii	0.83	0.99	0.97	0.54	0.06	0.07	0.10	0.05
	Sij	0.92	1.11	1.08	0.60	0.06	0.08	0.12	0.05
	Sij-ik	1.35	1.63	1.58	0.88	0.09	0.11	0.17	0.07
	Sij-Skl	1.29	1.55	1.51	0.84	0.09	0.11	0.16	0.07

*, ** Significant at 5 per cent and 1 per cent respectively

Table 6 GCA and SCA effects for Flag Leaf area (cm²)

SN	Genotype	Flag Leaf area (cm ²)			
		E1	E2	E3	Pool
1	HI-8737	-3.64**	-3.01**	-0.52	-2.39*
2	NIDW-295	-3.71**	-4.70**	-1.88	-3.43*
3	HI-8498	1.09**	0.80	-0.51	0.46
4	HI-8663	0.45	0.13	-0.06	0.17
5	WH-896	-1.24**	0.19	-1.73	-0.92*
6	RAJ-1555	4.70**	0.80	0.53	2.01**
7	PDW-274	-1.34**	1.07*	2.24*	0.66
8	PDW-233	0.52	0.39	1.61	0.84*
9	PDW-314	1.63**	0.97*	0.36	0.98*
10	PDW-291	1.54**	3.37**	-0.05	1.62**
11	HI-8737×NIDW-295	3.32**	-0.97	1.61	1.32
12	HI-8737×HI-8498	-9.22**	-10.20**	2.72	-5.57**
13	HI-8737×HI-8663	-8.62**	-1.85	5.16	-1.77
14	HI-8737×WH-896	6.18**	6.06**	1.74	4.66**
15	HI-8737×RAJ-1555	-15.23**	-14.35**	12.19**	-5.80**
16	HI-8737×PDW-274	3.87**	-3.57*	-3.91	-1.20
17	HI-8737×PDW-233	4.50**	-3.40*	8.18*	3.09*
18	HI-8737×PDW-314	-3.56**	4.87**	-2.06	-0.25
19	HI-8737×PDW-291	-0.76	3.27*	-8.19*	-1.89
20	NIDW-295×HI-8498	-11.76**	-5.79**	-4.05	-7.20**
21	NIDW-295×HI-8663	-4.54**	-4.55**	9.85**	0.25
22	NIDW-295×WH-896	6.82**	3.99*	2.75	4.52**

SN	Genotype	Flag Leaf area (cm ²)			
		E1	E2	E3	Pool
23	NIDW-295×RAJ-1555	-2.47*	5.59**	1.79	1.64
24	NIDW-295×PDW-274	5.76**	0.94	-2.28	1.47
25	NIDW-295×PDW-233	-3.69**	2.05	-2.39	-1.34
26	NIDW-295×PDW-314	-7.02**	-5.58**	-3.77	-5.46**
27	NIDW-295×PDW-291	5.63**	-1.34	-3.79	0.17
28	HI-8498×HI-8663	9.76**	11.87**	2.36	8.00**
29	HI-8498×WH-896	6.35**	3.41*	-2.19	2.52
30	HI-8498×RAJ-1555	1.63	2.94	-3.31	0.42
31	HI-8498×PDW-272	-3.79**	-1.12	-2.52	-2.48
32	HI-8498×PDW-233	-0.43	6.86**	3.56	3.33*
33	HI-8498×PDW-314	1.25	2.52	-3.17	0.20
34	HI-8498×PDW-291	-6.13**	-6.72**	-2.73	-5.19**
35	HI-8663×WH-896	-2.98**	-3.48*	3.58	-0.96
36	HI-8663×RAJ-1555	-5.34**	5.38**	-3.58	-1.18
37	HI-8663×PDW-274	-1.69	-0.75	1.89	-0.18
38	HI-8663×PDW-233	-4.08**	-4.96**	-15.11**	-8.05**
39	HI-8663×PDW-314	-2.59*	-3.11*	-0.46	-2.05
40	HI-8663×PDW-291	-1.56	-2.41	-5.40	-3.12*
41	WH-896×RAJ-1555	-4.57**	-3.75*	-4.97	-4.43**
42	WH-896×PDW-274	-1.09	-1.97	-1.39	-1.48
43	WH-896×PDW-233	-7.37**	-3.20*	3.71	-2.29
44	WH-896×PDW-314	3.29**	-1.11	-4.56	-0.80
45	WH-896×PDW-291	3.27**	2.31	-6.38	-0.27

SN	Genotype	Flag Leaf area (cm ²)			
		E1	E2	E3	Pool
46	RAJ-1555×PDW-274	-0.75	2.76	3.33	1.78
47	RAJ-1555×PDW-233	-0.91	2.78	2.58	1.48
48	RAJ-1555×PDW-314	13.44**	3.78*	1.75	6.32**
49	RAJ-1555×PDW-291	4.04**	10.28**	4.95	6.42**
50	PDW-274×PDW-233	10.82**	10.16**	2.95	7.98**
51	PDW-274×PDW-314	7.74**	2.15	2.49	4.13**
52	PDW-274×PDW-291	2.71**	4.57**	2.92	3.40*
53	PDW-233×PDW-314	4.75**	-1.05	0.43	1.38
54	PDW-233×PDW-291	9.63**	1.52	0.74	3.96**
55	PDW-314×PDW-291	12.04**	16.75**	6.13	11.64**
	Standard error				
	Gi	0.30	0.46	1.09	0.41
	Gi-Gj	0.45	0.69	1.63	0.61
	Sii	0.91	1.40	3.29	1.23
	Sij	1.01	1.56	3.67	1.37
	Sij-ik	1.49	2.29	5.39	2.01
	Sij-Skl	1.42	2.18	5.14	1.92

*, ** Significant at 5 per cent and 1 per cent respectively

Table 7 GCA and SCA effects for Peduncle length (cm), and total no. of tillers plant⁻¹

SN	Genotype	Peduncle length (cm)				Total no. of tillers plant ⁻¹			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	HI-8737	-0.61	0.94**	1.10**	0.48*	0.89**	1.19**	-2.25**	-0.05
2	NIDW-295	-0.68	-0.68*	-1.26**	-0.87*	-1.01**	-0.33	0.09	-0.42*
3	HI-8498	0.64	0.26	0.00	0.30	-2.10**	-3.06**	-1.45**	-2.20*
4	HI-8663	0.92**	0.22	-0.79*	0.12	-0.62	-1.12**	-0.81*	-0.85*
5	WH-896	0.05	-0.71*	-0.11	-0.26	1.96**	0.81**	-0.17	0.87**
6	RAJ-1555	-0.09	0.63	-0.06	0.16	0.91**	0.51	0.83*	0.75**
7	PDW-274	-0.49	1.56**	-0.55	0.17	1.21**	3.25**	-0.30	1.39**
8	PDW-233	0.26	-0.94**	0.14	-0.18	1.21**	1.46**	1.19**	1.29**
9	PDW-314	0.13	-0.56	1.09**	0.22	-1.64**	-1.70**	1.81**	-0.51*
10	PDW-291	-0.13	-0.72*	0.43	-0.14	-0.81*	-1.02**	1.06**	-0.26
11	HI-8737×NIDW-295	3.08**	3.13**	-0.32	1.96**	-0.00	-1.14	-1.90	-1.02
12	HI-8737×HI-8498	-1.33	1.56	0.44	0.23	4.19**	4.12**	-4.44**	1.29*
13	HI-8737×HI-8663	0.69	-2.10	3.10**	0.56	6.71**	4.10**	4.78**	5.20**
14	HI-8737×WH-896	1.76	1.19	0.36	1.10	-4.77**	-5.23**	-2.65*	-4.21**
15	HI-8737×RAJ-1555	-1.11	-2.87*	0.19	-1.26	5.18**	5.77**	-0.97	3.32**
16	HI-8737×PDW-274	2.79*	-0.30	0.73	1.07	-8.42**	-10.30**	-3.51**	-7.41**
17	HI-8737×PDW-233	-3.85**	3.39**	0.84	0.13	-2.52*	-3.11**	-2.69*	-2.77**
18	HI-8737×PDW-314	-3.42**	2.38*	-0.49	-0.51	-3.87**	-4.12**	1.38	-2.20**
19	HI-8737×PDW-291	-0.86	-2.53*	-2.15*	-1.85**	4.10**	-0.13	5.13**	3.03**
20	NIDW-295×HI-8498	-1.43	0.01	-3.29**	-1.57*	-2.61*	2.40*	-7.03**	-2.41**
21	NIDW-295×HI-8663	-3.72**	3.82**	-1.27	-0.39	-6.88**	-3.78**	-2.01	-4.22**
22	NIDW-295×WH-896	-1.49	0.81	2.19*	0.50	-6.67**	-0.27	1.02	-1.97**

SN	Genotype	Peduncle length (cm)				Total no. of tillers plant ⁻¹			
		E1	E2	E3	Pool	E1	E2	E3	Pool
23	NIDW-295×RAJ-1555	-0.24	-1.75	-1.73	-1.24	1.47	-4.51**	3.02*	-0.00
24	NIDW-295×PDW-274	1.66	-0.12	-3.91**	-0.79	8.51**	7.95**	-2.51*	4.65**
25	NIDW-295×PDW-233	-0.78	-0.39	0.60	-0.19	0.34	-4.23**	-4.34**	-2.75**
26	NIDW-295×PDW-314	-2.26	-3.97**	3.55**	-0.89	1.24	-0.16	-4.96**	-1.30*
27	NIDW-295×PDW-291	0.68	-1.15	-2.36*	-0.94	-1.95	-2.40*	2.46*	-0.63
28	HI-8498×HI-8663	-2.89*	1.31	3.36**	0.60	-1.00	4.92**	4.86**	2.92**
29	HI-8498×WH-896	-0.76	-2.49*	-5.71**	-2.99**	6.42**	1.72	1.56	3.23**
30	HI-8498×RAJ-1555	-0.23	2.84*	-3.40**	-0.26	-10.43**	-6.88**	0.56	-5.58**
31	HI-8498×PDW-272	1.85	-0.85	-0.71	0.09	5.77**	-0.95	-1.97	0.95
32	HI-8498×PDW-233	-0.48	-0.76	0.90	-0.11	4.17**	0.94	-3.80**	0.44
33	HI-8498×PDW-314	2.03	0.96	0.48	1.16	-5.65**	-4.56**	-6.09**	-5.43**
34	HI-8498×PDW-291	1.99	-1.35	1.18	0.61	11.76**	11.39**	-2.67*	6.83**
35	HI-8663×WH-896	0.08	0.97	-0.09	0.32	3.05**	4.52**	-1.76	1.94**
36	HI-8663×RAJ-1555	-1.60	0.58	2.63*	0.53	-3.37**	-2.92**	3.25**	-1.02
37	HI-8663×PDW-274	0.23	-2.32*	-1.99	-1.36*	1.70	-3.83**	-4.43**	-2.19**
38	HI-8663×PDW-233	0.49	-0.09	-4.04**	-1.21	5.60**	3.34**	-4.45**	1.49*
39	HI-8663×PDW-314	-0.42	1.13	-3.62**	-0.97	-1.15	-1.88*	-5.07**	-2.70**
40	HI-8663×PDW-291	0.83	0.55	-0.20	0.39	-1.11	0.55	-4.98**	-1.85**
41	WH-896×RAJ-1555	1.73	0.54	2.25*	1.51*	3.56**	6.22**	-10.39**	-0.20
42	WH-896×PDW-274	-1.46	-0.89	-0.63	-0.99	5.07**	7.45**	-3.26**	3.09**
43	WH-896×PDW-233	-0.13	-0.80	-0.71	-0.55	-6.91**	-10.26**	-3.75**	-6.97**
44	WH-896×PDW-314	1.06	-4.41**	-1.77	-1.71**	-1.98	-3.60**	-2.71*	-2.76**
45	WH-896×PDW-291	1.21	-0.62	0.62	0.41	-5.91**	-3.54**	-2.62*	-4.03**

SN	Genotype	Peduncle length (cm)				Total no. of tillers plant ⁻¹			
		E1	E2	E3	Pool	E1	E2	E3	Pool
46	RAJ-1555×PDW-274	-0.75	-1.42	-3.15**	-1.77**	-2.01	-3.01**	1.48	-1.18
47	RAJ-1555×PDW-233	0.41	-0.66	-2.83**	-1.03	1.53	2.87**	0.58	1.66**
48	RAJ-1555×PDW-314	0.09	0.69	-0.69	0.03	-0.23	0.34	-0.70	-0.20
49	RAJ-1555×PDW-291	0.95	1.58	-0.40	0.71	3.39**	-1.82	3.27**	1.62*
50	PDW-274×PDW-233	1.23	2.51*	1.29	1.67*	5.35**	5.67**	3.38**	4.80**
51	PDW-274×PDW-314	-2.31*	1.69	-0.67	-0.43	0.36	-1.24	0.43	-0.15
52	PDW-274×PDW-291	1.61	-2.45*	2.83**	0.66	10.56**	10.19**	6.62**	9.12**
53	PDW-233×PDW-314	1.31	-2.45*	1.82	0.23	4.15**	6.80**	3.60**	4.85**
54	PDW-233×PDW-291	-1.76	-2.69*	0.07	-1.46*	-7.42**	-7.03**	-1.65	-5.37**
55	PDW-314×PDW-291	-0.96	-1.23	-1.28	-1.16	-1.43	-2.04*	0.15	-1.11
	Standard error								
	Gi	0.34	0.33	0.32	0.19	0.33	0.28	0.36	0.19
	Gi-Gj	0.51	0.49	0.47	0.28	0.50	0.41	0.53	0.28
	Sii	1.03	1.00	0.95	0.57	1.01	0.83	1.07	0.56
	Sij	1.15	1.11	1.06	0.64	1.12	0.93	1.19	0.63
	Sij-ik	1.69	1.63	1.56	0.94	1.65	1.36	1.76	0.92
	Sij-Skl	1.61	1.56	1.49	0.90	1.57	1.30	1.67	0.88

*, ** Significant at 5 per cent and 1 per cent respectively

Table 8GCA and SCA effects for no. of prod. tillers plant⁻¹ and spike length (cm)

SN	Genotype	No. of prod. Tillers/plant				Spike length (cm)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	HI-8737	1.12**	1.17**	-2.53**	-0.08	-0.02	-0.04	-0.13*	-0.06
2	NIDW-295	-1.68**	-0.30	-0.53	-0.84*	-0.05	0.26**	0.14*	0.12**
3	HI-8498	-2.16**	-2.88**	-1.28**	-2.11*	-0.27**	-0.40**	-0.41**	-0.36*
4	HI-8663	-0.54	-1.07**	-0.80*	-0.80*	1.09**	1.08**	0.63**	0.93**
5	WH-896	1.74**	0.24	0.18	0.72**	-0.38**	-0.49**	-0.33**	-0.40*
6	RAJ-1555	0.95**	0.93**	0.89*	0.92**	-0.20**	-0.42**	-0.21**	-0.28*
7	PDW-274	1.30**	3.13**	-0.58	1.28**	-0.05	0.07	-0.11	-0.03
8	PDW-233	1.30**	1.26**	1.37**	1.31**	0.48**	0.55**	0.54**	0.52**
9	PDW-314	-1.33**	-1.48**	1.84**	-0.32	-0.24**	-0.19*	-0.15*	-0.19*
10	PDW-291	-0.71*	-1.01**	1.46**	-0.09	-0.35**	-0.42**	0.03	-0.25*
11	HI-8737×NIDW-295	0.04	-0.04	-1.32	-0.44	0.51*	-0.30	-0.11	0.03
12	HI-8737×HI-8498	4.43**	4.09**	-3.03*	1.83**	-0.63*	-0.36	-0.06	-0.35*
13	HI-8737×HI-8663	4.73**	3.92**	4.18**	4.28**	1.44**	0.94**	1.60**	1.33**
14	HI-8737×WH-896	-3.48**	-4.86**	-3.50**	-3.94**	0.11	0.09	0.13	0.11
15	HI-8737×RAJ-1555	5.63**	5.85**	-0.65	3.61**	-0.76**	-0.60*	-0.43*	-0.60**
16	HI-8737×PDW-274	-8.14**	-9.35**	-1.88	-6.46**	0.26	0.16	0.53*	0.32*
17	HI-8737×PDW-233	-2.14	-3.08**	-2.59**	-2.60**	-0.84**	-0.67*	-0.04	-0.52**
18	HI-8737×PDW-314	-3.89**	-4.57**	0.39	-2.69**	0.07	0.32	0.32	0.23
19	HI-8737×PDW-291	5.07**	0.13	3.69**	2.96**	-0.71**	-0.11	-1.54**	-0.79**
20	NIDW-295×HI-8498	-3.77**	2.97**	-6.40**	-2.40**	0.28	0.26	-0.53*	0.00
21	NIDW-295×HI-8663	-5.53**	-3.12**	-1.76	-3.47**	0.76**	0.95**	1.05**	0.92**
22	NIDW-295×WH-896	-5.46**	-0.23	1.05	-1.55*	-0.01	0.16	-0.45*	-0.10

SN	Genotype	No. of prod. Tillers/plant				Spike length (cm)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
23	NIDW-295×RAJ-1555	2.96*	-4.28**	2.24	0.31	-0.11	-0.79**	-0.60**	-0.50**
24	NIDW-295×PDW-274	7.75**	7.32**	-3.62**	3.81**	0.35	0.21	-0.20	0.12
25	NIDW-295×PDW-233	-0.04	-5.31**	-4.03**	-3.12**	-0.01	1.28**	-0.03	0.41**
26	NIDW-295×PDW-314	1.21	0.63	-3.48**	-0.55	-0.66**	0.13	-0.54**	-0.36*
27	NIDW-295×PDW-291	-2.19	-2.10*	1.78	-0.84	-0.85**	-1.09**	0.60**	-0.45**
28	HI-8498×HI-8663	-1.58	4.67**	4.91**	2.67**	1.22**	1.10**	-0.98**	0.45**
29	HI-8498×WH-896	6.77**	1.99*	1.85	3.54**	0.59*	0.74*	0.50*	0.61**
30	HI-8498×RAJ-1555	-9.30**	-6.56**	0.09	-5.26**	0.56*	-0.73*	-0.62**	-0.26
31	HI-8498×PDW-272	5.12**	-1.06	-3.58**	0.16	-1.00**	0.16	-0.65**	-0.50**
32	HI-8498×PDW-233	4.54**	0.41	-3.00*	0.65	0.85**	-0.27	-0.09	0.16
33	HI-8498×PDW-314	-4.84**	-4.25**	-5.03**	-4.70**	0.55*	0.39	0.96**	0.63**
34	HI-8498×PDW-291	11.57**	9.88**	-2.48*	6.33**	-1.30**	-1.10**	0.75**	-0.55**
35	HI-8663×WH-896	3.21**	5.11**	-0.30	2.67**	-1.13**	-0.76*	-0.33	-0.74**
36	HI-8663×RAJ-1555	-2.72*	-2.74**	2.36*	-1.04	0.21	0.18	0.97**	0.45**
37	HI-8663×PDW-274	2.31*	-4.01**	-3.50**	-1.74**	0.02	0.09	-0.79**	-0.23
38	HI-8663×PDW-233	5.56**	2.66**	-3.36**	1.62*	-0.61*	-0.45	-0.46*	-0.51**
39	HI-8663×PDW-314	-1.28	-2.20*	-5.50**	-2.99**	-1.63**	-1.76**	0.03	-1.12**
40	HI-8663×PDW-291	-0.89	0.77	-4.40**	-1.51*	0.48	0.77*	-1.23**	0.01
41	WH-896×RAJ-1555	4.45**	5.58**	-9.08**	0.32	-0.35	0.26	-0.00	-0.03
42	WH-896×PDW-274	4.75**	6.04**	-1.43	3.12**	1.62**	1.77**	-0.13	1.09**
43	WH-896×PDW-233	-7.50**	-10.02**	-2.78*	-6.76**	0.18	0.37	1.22**	0.59**
44	WH-896×PDW-314	-3.35**	-4.01**	-1.76	-3.04**	0.47	-0.46	-0.14	-0.04
45	WH-896×PDW-291	-5.59**	-2.88**	-1.70	-3.39**	0.58*	-0.23	-0.47*	-0.04

SN	Genotype	No. of prod. Tillers/plant				Spike length (cm)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
46	RAJ-1555×PDW-274	-3.87**	-2.78**	1.24	-1.80**	-0.69**	-0.30	-0.10	-0.36*
47	RAJ-1555×PDW-233	2.82*	2.93**	0.92	2.22**	0.99**	1.42**	-0.46*	0.65**
48	RAJ-1555×PDW-314	-0.36	0.91	0.33	0.29	0.44	1.26**	-0.21	0.49**
49	RAJ-1555×PDW-291	3.27**	-1.86	4.69**	2.03**	0.61*	-0.20	-0.50*	-0.03
50	PDW-274×PDW-233	5.59**	5.13**	2.48*	4.40**	0.40	-0.37	-0.25	-0.07
51	PDW-274×PDW-314	0.65	-0.10	2.31	0.95	0.95**	-0.04	0.03	0.31*
52	PDW-274×PDW-291	10.65**	8.04**	4.90**	7.86**	0.69**	0.50	0.19	0.46**
53	PDW-233×PDW-314	4.07**	6.14**	1.98	4.06**	0.56*	0.48	-0.75**	0.10
54	PDW-233×PDW-291	-8.26**	-6.16**	-0.60	-5.01**	0.99**	0.97**	0.67**	0.88**
55	PDW-314×PDW-291	-1.22	-1.72	1.13	-0.61	0.98**	0.86**	0.43*	0.75**
	Standard error								
	Gi	0.34	0.29	0.35	0.19	0.07	0.09	0.06	0.04
	Gi-Gj	0.50	0.44	0.52	0.28	0.11	0.13	0.09	0.06
	Sii	1.01	0.89	1.05	0.57	0.22	0.26	0.19	0.13
	Sij	1.13	0.99	1.17	0.63	0.25	0.30	0.21	0.15
	Sij-ik	1.66	1.46	1.72	0.93	0.36	0.43	0.30	0.21
	Sij-Skl	1.58	1.39	1.64	0.89	0.35	0.41	0.29	0.20

Table 9 GCA and SCA effects for no.of spiklets spike⁻¹

SN	Genotype	No.of Spiklets spike ⁻¹			
		E1	E2	E3	Pool
1	HI-8737	-0.67**	0.42	0.42	0.06
2	NIDW-295	-0.87**	-0.84**	-0.84**	-0.85*
3	HI-8498	-0.70**	0.47*	0.47*	0.08
4	HI-8663	1.57**	0.17	0.17	0.64**
5	WH-896	0.30	0.20	0.20	0.23
6	RAJ-1555	-0.32	-0.43	-0.43	-0.39*
7	PDW-274	1.13**	-0.21	-0.21	0.24
8	PDW-233	0.13	0.36	0.36	0.29*
9	PDW-314	-0.37	0.20	0.20	0.01
10	PDW-291	-0.21	-0.35	-0.35	-0.30*
11	HI-8737×NIDW-295	2.05**	1.08	1.08	1.40**
12	HI-8737×HI-8498	-0.06	-0.37	-0.37	-0.26
13	HI-8737×HI-8663	1.57*	0.47	0.47	0.84
14	HI-8737×WH-896	0.88	-1.54*	-1.54*	-0.73
15	HI-8737×RAJ-1555	-2.17**	0.04	0.04	-0.70
16	HI-8737×PDW-274	0.05	1.02	1.02	0.70
17	HI-8737×PDW-233	-0.95	0.23	0.23	-0.17
18	HI-8737×PDW-314	-0.45	-1.16	-1.16	-0.92*
19	HI-8737×PDW-291	-0.61	1.32	1.32	0.68
20	NIDW-295× HI-8498	0.07	1.34	1.34	0.92*
21	NIDW-295× HI-8663	-0.19	0.00	0.00	-0.06
22	NIDW-295× WH-896	-0.92	0.25	0.25	-0.14

SN	Genotype	No. of Spiklets spike ⁻¹			
		E1	E2	E3	Pool
23	NIDW-295×RAJ-1555	-0.31	-0.53	-0.53	-0.46
24	NIDW-295×PDW-274	2.24**	-0.60	-0.60	0.35
25	NIDW-295×PDW-233	-0.76	-1.04	-1.04	-0.95*
26	NIDW-295×PDW-314	-0.26	1.54*	1.54*	0.94*
27	NIDW-295×PDW-291	-2.42**	-1.18	-1.18	-1.59**
28	HI-8498×HI-8663	1.63*	-0.31	-0.31	0.34
29	HI-8498×WH-896	0.91	-0.13	-0.13	0.22
30	HI-8498×RAJ-1555	-0.48	0.77	0.77	0.35
31	HI-8498×PDW-272	-3.93**	-2.09**	-2.09**	-2.70**
32	HI-8498×PDW-233	-0.93	0.25	0.25	-0.15
33	HI-8498×PDW-314	-0.43	-2.27**	-2.27**	-1.66**
34	HI-8498×PDW-291	3.41**	2.24**	2.24**	2.63**
35	HI-8663×WH-896	-1.36*	2.03*	2.03*	0.90*
36	HI-8663×RAJ-1555	-0.74	-0.33	-0.33	-0.47
37	HI-8663×PDW-274	-0.19	0.05	0.05	-0.03
38	HI-8663×PDW-233	0.81	0.15	0.15	0.37
39	HI-8663×PDW-314	-0.69	-2.04**	-2.04**	-1.59**
40	HI-8663×PDW-291	1.05	1.12	1.12	1.10*
41	WH-896×RAJ-1555	0.53	0.58	0.58	0.56
42	WH-896×PDW-274	3.08**	0.28	0.28	1.21**
43	WH-896×PDW-233	4.08**	2.07**	2.07**	2.74**
44	WH-896×PDW-314	0.58	0.65	0.65	0.63
45	WH-896×PDW-291	0.42	2.09**	2.09**	1.53**

SN	Genotype	No.of Spiklets spike ⁻¹			
		E1	E2	E3	Pool
46	RAJ-1555×PDW-274	1.69*	0.89	0.89	1.16**
47	RAJ-1555×PDW-233	2.69**	0.14	0.14	0.99*
48	RAJ-1555×PDW-314	-0.81	-0.24	-0.24	-0.43
49	RAJ-1555×PDW-291	1.04	-0.27	-0.27	0.16
50	PDW-274×PDW-233	-0.76	-1.24	-1.24	-1.08*
51	PDW-274×PDW-314	1.74**	0.56	0.56	0.96*
52	PDW-274×PDW-291	-0.42	-1.34	-1.34	-1.03*
53	PDW-233×PDW-314	0.74	-0.37	-0.37	-0.00
54	PDW-233×PDW-291	-1.42*	-0.63	-0.63	-0.89*
55	PDW-314×PDW-291	1.08	0.73	0.73	0.85*
Standard error					
	Gi	0.20	0.23	0.23	0.13
	Gi-Gj	0.29	0.34	0.34	0.19
	Sii	0.59	0.69	0.69	0.38
	Sij	0.66	0.77	0.77	0.43
	Sij-ik	0.96	1.14	1.14	0.62
	Sij-Skl	0.92	1.08	1.08	0.60

*, ** Significant at 5 per cent and 1 per cent respectively

Table10 GCA and SCA effects for no.of grain spike⁻¹, and spike weight productive tiller⁻¹ (g)

SN	Genotype	No.of grain spike ⁻¹				Spike weight productive tiller ⁻¹ (g)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	HI-8737	-1.31	-0.91	-0.91	-1.04*	0.16**	0.17**	0.50**	0.28**
2	NIDW-295	-0.85	-1.45	-1.45	-1.25*	-0.04	0.13*	-0.00	0.03
3	HI-8498	-5.08**	-6.97**	-6.97**	-6.34*	-0.41**	-0.09	-0.11	-0.20*
4	HI-8663	8.32**	8.78**	8.78**	8.63**	0.63**	0.29**	0.09	0.34**
5	WH-896	-4.22**	-4.04**	-4.04**	-4.10*	-0.16**	-0.35**	-0.55**	-0.35*
6	RAJ-1555	-4.65**	-3.92**	-3.92**	-4.16*	-0.24**	-0.05	-0.25**	-0.18*
7	PDW-274	0.30	-0.04	-0.04	0.08	0.28**	0.61**	-0.13	0.25**
8	PDW-233	5.67**	6.09**	6.09**	5.95**	0.45**	-0.32**	0.53**	0.22**
9	PDW-314	4.29**	3.54**	3.54**	3.79**	-0.31**	-0.10	0.10	-0.11*
10	PDW-291	-2.46**	-1.09	-1.09	-1.55*	-0.36**	-0.29**	-0.17*	-0.27*
11	HI-8737×NIDW-295	11.14**	6.78*	6.78*	8.23**	0.90**	-0.32	0.29	0.29*
12	HI-8737×HI-8498	-5.63*	-3.00	-3.00	-3.88*	-0.74**	-0.04	0.97**	0.06
13	HI-8737×HI-8663	8.67**	10.60**	10.60**	9.96**	-0.32*	-0.29	1.84**	0.41**
14	HI-8737×WH-896	-6.53*	-9.46**	-9.46**	-8.48**	-0.71**	0.10	-0.24	-0.28*
15	HI-8737×RAJ-1555	-7.63**	-7.35*	-7.35*	-7.44**	-0.42**	-0.39	0.51*	-0.10
16	HI-8737×PDW-274	-11.55**	-10.25**	-10.25**	-10.68**	-0.47**	-0.90**	-0.56*	-0.64**
17	HI-8737×PDW-233	-4.39	-5.02	-5.02	-4.81**	-0.45**	-0.02	-0.39	-0.29*
18	HI-8737×PDW-314	-7.00**	-6.57*	-6.57*	-6.71**	0.38**	0.13	-0.31	0.07
19	HI-8737×PDW-291	-6.25*	-7.21*	-7.21*	-6.89**	-0.55**	0.19	-1.35**	-0.57**
20	NIDW-295× HI-8498	8.91**	-9.37**	-9.37**	-3.27	-0.01	0.08	-0.53*	-0.15
21	NIDW-295× HI-8663	8.87**	4.20	4.20	5.76**	0.37**	0.25	-0.15	0.16
22	NIDW-295× WH-896	-0.95	-1.24	-1.24	-1.14	0.36**	-0.56**	0.18	-0.01

SN	Genotype	No. of grain spike ⁻¹				Spike weight productive tiller ⁻¹ (g)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
23	NIDW-295×RAJ-1555	3.48	3.49	3.49	3.49*	-0.03	0.15	0.25	0.12
24	NIDW-295×PDW-274	1.54	2.39	2.39	2.10	-0.10	0.20	0.28	0.13
25	NIDW-295×PDW-233	-13.51**	-4.11	-4.11	-7.24**	-0.06	-0.03	-0.54*	-0.21
26	NIDW-295×PDW-314	-7.46**	-4.76	-4.76	-5.66**	-0.39**	-0.17	0.16	-0.14
27	NIDW-295×PDW-291	-15.37**	-12.87**	-12.87**	-13.70**	-1.44**	1.08**	0.69**	0.11
28	HI-8498×HI-8663	17.74**	19.74**	19.74**	19.08**	1.28**	0.82**	0.47	0.86**
29	HI-8498×WH-896	5.28*	3.81	3.81	4.30*	0.14	0.38	0.92**	0.48**
30	HI-8498×RAJ-1555	-3.29	2.97	2.97	0.89	-0.02	0.14	0.41	0.18
31	HI-8498×PDW-272	-17.23**	-17.02**	-17.02**	-17.09**	-0.93**	1.71**	-0.93**	-0.05
32	HI-8498×PDW-233	5.39*	6.14	6.14	5.89**	0.30*	0.08	-0.27	0.04
33	HI-8498×PDW-314	16.78**	15.93**	15.93**	16.22**	1.40**	-0.79**	-0.08	0.18
34	HI-8498×PDW-291	-1.47	-1.51	-1.51	-1.50	-0.36**	-0.43*	-0.10	-0.29*
35	HI-8663×WH-896	-8.12**	-6.96*	-6.96*	-7.35**	-0.61**	-0.07	-0.08	-0.25*
36	HI-8663×RAJ-1555	-12.69**	-12.62**	-12.62**	-12.64**	-0.11	0.66**	-0.26	0.09
37	HI-8663×PDW-274	2.36	2.93	2.93	2.74	0.40**	0.19	-0.11	0.16
38	HI-8663×PDW-233	-13.02**	-11.44**	-11.44**	-11.97**	-1.01**	0.24	0.11	-0.22
39	HI-8663×PDW-314	-6.63*	-12.95**	-12.95**	-10.84**	-0.19	-1.11**	0.41	-0.30*
40	HI-8663×PDW-291	2.12	8.86**	8.86**	6.62**	0.38**	-1.03**	-0.94**	-0.53**
41	WH-896×RAJ-1555	4.85	-1.94	-1.94	0.32	0.33*	-0.83**	-0.04	-0.18
42	WH-896×PDW-274	20.57**	21.91**	21.91**	21.46**	2.05**	-0.32	0.89**	0.87**
43	WH-896×PDW-233	4.52	7.13*	7.13*	6.26**	-0.26	-0.34	1.15**	0.19
44	WH-896×PDW-314	7.91**	8.50**	8.50**	8.30**	-0.48**	1.34**	0.08	0.31**
45	WH-896×PDW-291	7.66**	7.06*	7.06*	7.26**	0.81**	0.26	-0.61*	0.15

SN	Genotype	No. of grain spike ⁻¹				Spike weight productive tiller ⁻¹ (g)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
46	RAJ-1555×PDW-274	5.33*	6.12	6.12	5.86**	-0.10	0.59**	-0.76**	-0.09
47	RAJ-1555×PDW-233	11.95**	8.12*	8.12*	9.40**	0.85**	-0.44*	-0.76**	-0.11
48	RAJ-1555×PDW-314	-3.66	-1.72	-1.72	-2.37	-0.96**	0.14	-0.10	-0.30**
49	RAJ-1555×PDW-291	1.09	-2.52	-2.52	-1.31	0.60**	0.53**	0.62*	0.58**
50	PDW-274×PDW-233	-9.99**	-13.82**	-13.82**	-12.55**	-1.59**	-0.32	0.26	-0.55**
51	PDW-274×PDW-314	11.40**	5.34	5.34	7.36**	1.18**	0.54**	0.48	0.73**
52	PDW-274×PDW-291	8.15**	7.54*	7.54*	7.74**	0.34*	-1.34**	0.44	-0.19
53	PDW-233×PDW-314	1.02	1.17	1.17	1.12	-0.12	1.39**	0.29	0.52**
54	PDW-233×PDW-291	12.77**	6.60*	6.60*	8.66**	0.61**	-0.42*	0.57*	0.25*
55	PDW-314×PDW-291	-4.51	-4.47	-4.47	-4.48*	-0.94**	0.31	0.92**	0.10
	Standard error								
	Gi	0.76	0.96	0.96	0.52	0.04	0.06	0.07	0.03
	Gi-Gj	1.13	1.43	1.43	0.77	0.06	0.09	0.11	0.05
	Sii	2.28	2.89	2.89	1.56	0.12	0.18	0.22	0.10
	Sij	2.55	3.22	3.22	1.74	0.14	0.20	0.25	0.12
	Sij-ik	3.74	4.73	4.73	2.56	0.20	0.30	0.36	0.17
	Sij-Skl	3.57	4.51	4.51	2.44	0.19	0.28	0.34	0.16

*, ** Significant at 5 per cent and 1 per cent respectively

Table 11 GCA and SCA effects for Grain weight spike⁻¹ (g)

SN	Genotype	Grain weight spike ⁻¹ (g)			
		E1	E2	E3	Pool
1	HI-8737	0.11**	-0.00	0.43**	0.18**
2	NIDW-295	-0.03	-0.07	0.00	-0.03
3	HI-8498	-0.34**	-0.08	-0.11	-0.18*
4	HI-8663	0.49**	0.40**	0.10	0.33**
5	WH-896	-0.12**	-0.01	-0.55**	-0.23*
6	RAJ-1555	-0.17**	0.07	-0.24**	-0.12*
7	PDW-274	0.19**	-0.01	-0.13	0.02
8	PDW-233	0.37**	-0.15*	0.54**	0.25**
9	PDW-314	-0.24**	0.15*	0.10	0.00
10	PDW-291	-0.26**	-0.30**	-0.16*	-0.24*
11	HI-8737×NIDW-295	0.82**	-0.63**	0.35	0.18
12	HI-8737×HI-8498	-0.65**	0.48*	1.04**	0.29*
13	HI-8737×HI-8663	-0.45**	-1.32**	1.90**	0.04
14	HI-8737×WH-896	-0.57**	-0.05	-0.18	-0.27*
15	HI-8737×RAJ-1555	-0.12	0.04	0.57*	0.16
16	HI-8737×PDW-274	-0.21	-0.22	-0.50*	-0.31*
17	HI-8737×PDW-233	-0.12	0.60*	-0.33	0.05
18	HI-8737×PDW-314	0.26*	0.19	-0.24	0.07
19	HI-8737×PDW-291	-0.46**	-0.45	-1.29**	-0.73**
20	NIDW-295×HI-8498	0.01	-0.16	-0.53*	-0.23
21	NIDW-295×HI-8663	0.30**	0.45	-0.16	0.20
22	NIDW-295×WH-896	0.31**	0.03	0.17	0.17

SN	Genotype	Grain weight spike ⁻¹ (g)			
		E1	E2	E3	Pool
23	NIDW-295×RAJ-1555	-0.14	-0.08	0.24	0.00
24	NIDW-295×PDW-274	0.03	0.14	0.27	0.15
25	NIDW-295×PDW-233	0.11	0.73**	-0.54*	0.10
26	NIDW-295×PDW-314	-0.43**	-0.69**	0.15	-0.32**
27	NIDW-295×PDW-291	-1.14**	-0.72**	0.69**	-0.39**
28	HI-8498×HI-8663	0.82**	1.21**	0.47	0.83**
29	HI-8498×WH-896	0.35**	0.01	0.91**	0.43**
30	HI-8498×RAJ-1555	0.07	-0.23	0.40	0.08
31	HI-8498×PDW-272	-0.76**	-0.71**	-0.94**	-0.80**
32	HI-8498×PDW-233	0.36**	0.91**	-0.27	0.33**
33	HI-8498×PDW-314	1.24**	0.43	-0.08	0.53**
34	HI-8498×PDW-291	-0.55**	-0.20	-0.10	-0.29*
35	HI-8663×WH-896	-0.64**	-0.53*	-0.08	-0.42**
36	HI-8663×RAJ-1555	0.13	0.14	-0.27	-0.00
37	HI-8663×PDW-274	0.41**	0.59*	-0.12	0.30*
38	HI-8663×PDW-233	-0.71**	-0.06	0.10	-0.22
39	HI-8663×PDW-314	-0.07	-1.16**	0.40	-0.28*
40	HI-8663×PDW-291	0.46**	0.87**	-0.95**	0.13
41	WH-896×RAJ-1555	0.33**	1.87**	-0.05	0.72**
42	WH-896×PDW-274	1.51**	0.13	0.88**	0.84**
43	WH-896×PDW-233	-0.30**	-0.37	1.15**	0.16
44	WH-896×PDW-314	-0.02	0.24	0.07	0.10
45	WH-896×PDW-291	0.59**	0.66**	-0.62*	0.21

SN	Genotype	Grain weight spike ⁻¹ (g)			
		E1	E2	E3	Pool
46	RAJ-1555×PDW-274	-0.01	-0.15	-0.76**	-0.31*
47	RAJ-1555×PDW-233	0.47**	-0.88**	-0.76**	-0.39**
48	RAJ-1555×PDW-314	-1.11**	-0.37	-0.10	-0.53**
49	RAJ-1555×PDW-291	0.50**	1.27**	0.61*	0.79**
50	PDW-274×PDW-233	-1.38**	0.07	0.25	-0.35**
51	PDW-274×PDW-314	0.94**	0.69**	0.48	0.70**
52	PDW-274×PDW-291	0.13	-0.27	0.44	0.10
53	PDW-233×PDW-314	-0.23*	-0.99**	0.28	-0.31*
54	PDW-233×PDW-291	0.54**	-0.33	0.56*	0.26*
55	PDW-314×PDW-291	-0.44**	-0.00	0.91**	0.16
	Standard error				
	Gi	0.03	0.07	0.07	0.04
	Gi-Gj	0.05	0.11	0.11	0.05
	Sii	0.10	0.21	0.22	0.11
	Sij	0.11	0.24	0.25	0.12
	Sij-ik	0.16	0.35	0.36	0.18
	Sij-Skl	0.15	0.33	0.34	0.17

*, ** Significant at 5 per cent and 1 per cent respectively

Table 12 GCA and SCA effects for biological yield plant⁻¹ (g), and economic yield plant⁻¹ (g)

SN	Genotype	Biological yield plant ⁻¹ (g)				Economic yield plant ⁻¹ (g)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	HI-8737	-9.53**	-5.45*	-2.89	-5.96*	0.77	-0.50	-2.19**	-0.64
2	NIDW-295	13.14**	13.27**	2.35	9.59**	2.38**	3.34**	1.05*	2.26**
3	HI-8498	1.92	4.02	7.46**	4.47**	5.10**	6.56**	0.91	4.19**
4	HI-8663	0.29	0.87	1.75	0.97	-1.81*	-0.24	0.68	-0.46
5	WH-896	-1.18	-1.47	2.56	-0.03	-1.35	-1.22*	0.28	-0.76*
6	RAJ-1555	-2.55	-3.39	-9.35**	-5.10*	-1.50	-3.18**	-1.43**	-2.04*
7	PDW-274	11.66**	12.92**	0.47	8.35**	3.68**	0.85	2.51**	2.35**
8	PDW-233	12.07**	-4.96*	10.96**	6.03**	2.32**	-0.10	1.71**	1.31**
9	PDW-314	-17.36**	0.66	-7.25**	-7.98*	-5.89**	-2.41**	-0.17	-2.82*
10	PDW-291	-8.47**	-16.47**	-6.07**	-10.34*	-3.71**	-3.11**	-3.35**	-3.39*
11	HI-8737×NIDW-295	14.21*	5.97	-2.33	5.95	14.17**	11.32**	7.16**	10.88**
12	HI-8737×HI-8498	11.19	20.18*	55.73**	29.03**	20.15**	17.68**	11.41**	16.41**
13	HI-8737×HI-8663	24.06**	36.80**	20.97**	27.28**	3.49	-4.07*	8.36**	2.59*
14	HI-8737×WH-896	17.09*	17.49*	21.33**	18.64**	9.67**	14.63**	2.39	8.90**
15	HI-8737×RAJ-1555	-45.63**	-39.44**	-24.73**	-36.60**	-17.27**	-7.41**	-4.61**	-9.76**
16	HI-8737×PDW-274	-39.13**	-38.43**	-23.64**	-33.73**	-14.81**	-13.00**	-15.65**	-14.49**
17	HI-8737×PDW-233	-43.02**	-45.02**	-37.44**	-41.83**	-16.22**	-13.17**	-17.82**	-15.74**
18	HI-8737×PDW-314	33.25**	18.92*	13.67*	21.95**	19.28**	20.84**	0.96	13.69**
19	HI-8737×PDW-291	-38.82**	-28.00**	-13.38*	-26.73**	-22.99**	-22.81**	-10.56**	-18.79**
20	NIDW-295× HI-8498	55.71**	50.20**	13.95*	39.95**	14.05**	16.59**	-0.39	10.08**
21	NIDW-295× HI-8663	-8.91	-10.95	-24.31**	-14.72**	-10.44**	-10.71**	-13.46**	-11.54**
22	NIDW-295× WH-896	-42.22**	-48.77**	-12.26*	-34.41**	-9.50**	-13.56**	-0.33	-7.80**

SN	Genotype	Biological yield plant ⁻¹ (g)				Economic yield plant ⁻¹ (g)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
23	NIDW-295×RAJ-1555	1.44	-7.35	64.48**	19.52**	-7.55**	-8.76**	11.94**	-1.46
24	NIDW-295×PDW-274	53.37**	45.94**	24.34**	41.21**	17.06**	24.20**	2.27	14.51**
25	NIDW-295×PDW-233	-18.93**	11.52	-6.50	-4.64	-1.59	-0.17	-1.18	-0.98
26	NIDW-295×PDW-314	28.24**	1.61	26.90**	18.92**	7.63**	4.69**	3.00	5.11**
27	NIDW-295×PDW-291	9.55	6.61	-4.53	3.88	3.83	5.25**	-3.95*	1.71
28	HI-8498×HI-8663	22.31**	25.01**	-14.95**	10.79**	-2.57	0.75	-1.86	-1.23
29	HI-8498×WH-896	-43.72**	-44.83**	-20.45**	-36.33**	-5.83*	0.05	-2.38	-2.72*
30	HI-8498×RAJ-1555	-51.35**	-38.15**	-9.42	-32.97**	-14.36**	-16.75**	-5.54**	-12.22**
31	HI-8498×PDW-272	-14.80*	-26.86**	-14.60*	-18.75**	-13.71**	-19.24**	-11.34**	-14.77**
32	HI-8498×PDW-233	-0.94	16.35*	21.02**	12.14**	-0.62	5.02**	5.05**	3.15**
33	HI-8498×PDW-314	-21.72**	-41.96**	-8.66	-24.11**	-9.34**	-13.19**	-3.37*	-8.63**
34	HI-8498×PDW-291	24.17**	14.57	29.02**	22.58**	14.28**	12.91**	4.60**	10.60**
35	HI-8663×WH-896	12.39	8.07	15.68**	12.05**	-2.97	-1.14	-1.80	-1.97
36	HI-8663×RAJ-1555	-45.38**	-46.69**	-20.40**	-37.49**	-12.72**	-13.50**	-10.69**	-12.30**
37	HI-8663×PDW-274	-12.00	-29.44**	18.08**	-7.79	2.30	4.64**	9.32**	5.42**
38	HI-8663×PDW-233	-54.27**	-40.11**	-31.50**	-41.96**	-21.41**	-16.98**	-14.47**	-17.62**
39	HI-8663×PDW-314	-33.47**	-43.71**	-28.24**	-35.14**	-4.63	-11.22**	2.55	-4.44**
40	HI-8663×PDW-291	-4.99	-22.12**	-28.11**	-18.41**	-2.21	-0.34	2.74	0.06
41	WH-896×RAJ-1555	34.51**	34.02**	-8.21	20.11**	5.04	0.02	2.85	2.64*
42	WH-896×PDW-274	18.31**	17.70*	-16.23**	6.59	0.54	-4.22*	-10.09**	-4.59**
43	WH-896×PDW-233	28.31**	38.62**	18.98**	28.64**	2.40	-2.27	2.33	0.82
44	WH-896×PDW-314	13.30*	4.92	-4.25	4.66	-0.46	-10.84**	0.60	-3.57**
45	WH-896×PDW-291	-29.30**	-25.24**	30.17**	-8.12*	-18.10**	-2.79	5.26**	-5.21**

SN	Genotype	Biological yield plant ⁻¹ (g)				Economic yield plant ⁻¹ (g)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
46	RAJ-1555×PDW-274	24.78**	13.44	12.15*	16.79**	6.20*	-5.78**	3.66*	1.36
47	RAJ-1555×PDW-233	33.64**	-16.12	-67.01**	-16.49**	1.43	-7.65**	-17.29**	-7.84**
48	RAJ-1555×PDW-314	-31.56**	6.29	-12.71*	-12.66**	-7.28**	7.32**	-7.95**	-2.64*
49	RAJ-1555×PDW-291	25.88**	52.13**	1.39	26.47**	21.84**	13.01**	6.88**	13.91**
50	PDW-274×PDW-233	11.02	-25.66**	47.40**	10.92**	8.73**	7.16**	11.14**	9.01**
51	PDW-274×PDW-314	-9.48	82.24**	-16.38**	18.79**	0.10	7.17**	-1.43	1.95
52	PDW-274×PDW-291	61.26**	67.37**	12.51*	47.04**	23.79**	14.15**	10.20**	16.05**
53	PDW-233×PDW-314	55.88**	43.07**	51.01**	49.99**	21.76**	16.96**	17.10**	18.61**
54	PDW-233×PDW-291	27.38**	-24.74**	36.23**	12.96**	9.07**	-9.13**	-1.41	-0.49
55	PDW-314×PDW-291	-13.48*	-19.18*	-31.65**	-21.44**	-16.80**	-13.75**	-15.30**	-15.28**
Standard error									
	Gi	1.95	2.44	1.66	1.18	0.76	0.51	0.47	0.34
	Gi-Gj	2.90	3.64	2.47	1.76	1.13	0.77	0.69	0.51
	Sii	5.87	7.37	5.00	3.55	2.28	1.55	1.40	1.03
	Sij	6.55	8.22	5.58	3.96	2.55	1.73	1.57	1.15
	Sij-ik	9.62	12.08	8.20	5.83	3.74	2.54	2.30	1.69
	Sij-Skl	9.18	11.52	7.82	5.56	3.57	2.42	2.19	1.61

*, ** Significant at 5 per cent and 1 per cent respectively

Table 13 GCA and SCA effects for harvest index (%), and test weight (g)

SN	Genotype	Harvest Index (%)				Test weight (g)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	HI-8737	2.39**	0.39	-1.21*	0.52	0.69	1.11	1.11	0.97*
2	NIDW-295	-1.56*	-1.65*	0.65	-0.85*	1.29*	0.90	0.90	1.03*
3	HI-8498	2.83**	2.89**	-1.17*	1.52**	0.13	1.13	1.13	0.80
4	HI-8663	-1.29	-0.64	0.19	-0.58	-1.33*	-2.08*	-2.08*	-1.83*
5	WH-896	-0.35	-0.14	-0.52	-0.34	-2.28**	-1.95*	-1.95*	-2.06*
6	RAJ-1555	0.13	-1.06	1.24*	0.10	-3.40**	-2.09*	-2.09*	-2.53*
7	PDW-274	-0.35	-1.94**	1.64**	-0.22	-2.10**	-1.57	-1.57	-1.75*
8	PDW-233	-1.39*	1.33	-1.45*	-0.50	4.47**	5.13**	5.13**	4.91**
9	PDW-314	0.34	-1.07	1.66**	0.31	1.56**	-0.62	-0.62	0.11
10	PDW-291	-0.74	1.90**	-1.03	0.04	0.96	0.05	0.05	0.35
11	HI-8737×NIDW-295	4.52*	5.89*	8.28**	6.23**	-6.16**	-16.90**	-16.90**	-13.32**
12	HI-8737×HI-8498	8.72**	5.71*	-2.86	3.86**	6.60**	10.59**	10.59**	9.26**
13	HI-8737×HI-8663	-3.15	-9.17**	0.87	-3.82**	6.36**	7.65*	7.65*	7.22**
14	HI-8737×WH-896	1.39	4.31	-2.91	0.93	-4.49*	-5.13	-5.13	-4.92**
15	HI-8737×RAJ-1555	0.82	5.83*	3.25	3.30*	8.43**	9.72**	9.72**	9.29**
16	HI-8737×PDW-274	0.71	-0.34	-7.79**	-2.47	-0.07	2.98	2.98	1.96
17	HI-8737×PDW-233	0.12	4.00	-6.80**	-0.89	-3.34	1.26	1.26	-0.27
18	HI-8737×PDW-314	3.70	7.28**	-2.91	2.69*	0.93	6.19*	6.19*	4.43**
19	HI-8737×PDW-291	-4.84*	-10.64**	-6.56**	-7.34**	-0.73	4.22	4.22	2.57
20	NIDW-295×HI-8498	-3.64	-0.91	-3.94*	-2.83*	-2.01	1.69	1.69	0.46
21	NIDW-295×HI-8663	-4.15	-3.95	-6.26**	-4.79**	5.26**	3.66	3.66	4.19**
22	NIDW-295×WH-896	3.99	2.71	2.01	2.90*	-0.65	5.48	5.48	3.44*

SN	Genotype	Harvest Index (%)				Test weight (g)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
23	NIDW-295×RAJ-1555	-5.11*	-3.99	-5.93**	-5.01**	-3.19	3.63	3.63	1.36
24	NIDW-295×PDW-274	-0.87	3.82	-4.64*	-0.57	5.72**	-3.82	-3.82	-0.64
25	NIDW-295×PDW-233	3.10	-2.74	-0.23	0.04	-7.45**	1.42	1.42	-1.54
26	NIDW-295×PDW-314	-1.74	1.90	-4.94*	-1.59	5.16**	-2.28	-2.28	0.20
27	NIDW-295×PDW-291	0.59	1.57	-3.25	-0.37	-0.54	3.06	3.06	1.86
28	HI-8498×HI-8663	-6.25**	-4.89*	1.58	-3.19*	-5.18**	4.70	4.70	1.40
29	HI-8498×WH-896	8.44**	14.31**	2.87	8.54**	-11.74**	-4.73	-4.73	-7.07**
30	HI-8498×RAJ-1555	4.08	-2.27	-2.75	-0.31	3.39	-14.17**	-14.17**	-8.32**
31	HI-8498×PDW-272	-5.31*	-7.27**	-5.76**	-6.12**	6.88**	1.73	1.73	3.45*
32	HI-8498×PDW-233	-0.76	-1.51	-0.83	-1.04	1.52	-1.62	-1.62	-0.57
33	HI-8498×PDW-314	-0.41	1.24	-0.67	0.05	5.32**	4.38	4.38	4.69**
34	HI-8498×PDW-291	2.44	4.34	-3.12	1.22	-1.07	-0.49	-0.49	-0.68
35	HI-8663×WH-896	-4.38*	-3.22	-5.03*	-4.21**	1.03	-2.16	-2.16	-1.10
36	HI-8663×RAJ-1555	2.17	1.95	-4.17*	-0.02	-4.45*	-1.65	-1.65	-2.58
37	HI-8663×PDW-274	3.77	9.62**	1.71	5.03**	15.35**	10.55**	10.55**	12.15**
38	HI-8663×PDW-233	-1.56	-2.34	-4.84*	-2.91*	-4.22*	-0.78	-0.78	-1.93
39	HI-8663×PDW-314	6.38**	2.14	12.03**	6.85**	6.99**	-2.24	-2.24	0.83
40	HI-8663×PDW-291	-0.05	6.22**	11.17**	5.78**	1.69	-0.77	-0.77	0.05
41	WH-896×RAJ-1555	-4.79*	-7.49**	4.44*	-2.61*	-2.50	1.60	1.60	0.23
42	WH-896×PDW-274	-3.65	-6.76**	-4.43*	-4.94**	-2.70	-3.65	-3.65	-3.33*
43	WH-896×PDW-233	-3.93	-10.04**	-2.08	-5.35**	-6.07**	7.36*	7.36*	2.88
44	WH-896×PDW-314	-3.74	-9.41**	1.31	-3.95**	-3.17	-17.58**	-17.58**	-12.77**
45	WH-896×PDW-291	-5.66*	4.85*	-2.73	-1.18	3.14	-2.50	-2.50	-0.62

SN	Genotype	Harvest Index (%)				Test weight (g)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
46	RAJ-1555×PDW-274	-2.01	-6.89**	-0.39	-3.10*	-18.28**	-2.84	-2.84	-7.99**
47	RAJ-1555×PDW-233	-5.37*	3.33	5.48**	1.15	-3.95*	-10.13**	-10.13**	-8.07**
48	RAJ-1555×PDW-314	3.66	1.59	-3.28	0.66	-6.25**	-1.29	-1.29	-2.94
49	RAJ-1555×PDW-291	6.49**	-4.22	5.03*	2.43	1.36	0.70	0.70	0.92
50	PDW-274×PDW-233	2.30	10.26**	-2.54	3.34**	1.35	-4.69	-4.69	-2.68
51	PDW-274×PDW-314	2.42	-9.05**	4.52*	-0.70	0.05	7.21*	7.21*	4.82**
52	PDW-274×PDW-291	0.66	-5.82*	4.18*	-0.33	-13.74**	-12.53**	-12.53**	-12.94**
53	PDW-233×PDW-314	0.42	-0.87	-0.07	-0.17	2.69	-0.65	-0.65	0.46
54	PDW-233×PDW-291	-0.18	-0.08	-7.31**	-2.52*	2.39	2.23	2.23	2.28
55	PDW-314×PDW-291	-8.88**	-6.95**	-5.91**	-7.25**	-2.70	1.43	1.43	0.05
Standard error									
	Gi	0.66	0.70	0.58	0.37	0.55	0.92	0.92	0.47
	Gi-Gj	0.98	1.05	0.86	0.56	0.81	1.37	1.37	0.70
	Sii	1.98	2.12	1.75	1.13	1.65	2.78	2.78	1.42
	Sij	2.21	2.36	1.95	1.26	1.84	3.10	3.10	1.58
	Sij-ik	3.24	3.47	2.86	1.85	2.70	4.55	4.55	2.33
	Sij-Skl	3.09	3.31	2.73	1.76	2.58	4.34	4.34	2.22

*, ** Significant at 5 per cent and 1 per cent respectively

Table 14 GCA and SCA effects for protein content (%), and proline content (μg)

SN	Genotype	Protein Content (%)				Proline Content (μg)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	HI-8737	-0.12	0.55**	-0.17**	0.09*	1.03**	-0.48**	1.05**	0.53**
2	NIDW-295	-0.12	-0.11	-0.15*	-0.12*	-0.40**	0.52**	-1.11**	-0.33*
3	HI-8498	0.03	-0.01	0.08	0.03	-1.33**	1.33**	-1.84**	-0.62*
4	HI-8663	-0.05	0.03	0.01	-0.00	-1.43**	0.67**	-0.92**	-0.56*
5	WH-896	-0.34**	-0.23**	-0.22**	-0.26*	0.45**	0.25*	0.66**	0.45**
6	RAJ-1555	-0.30**	0.08	-0.24**	-0.15*	1.39**	-0.31**	2.09**	1.06**
7	PDW-274	0.14	0.04	0.20**	0.13**	0.63**	-1.51**	0.87**	-0.00
8	PDW-233	0.20**	-0.18*	0.11	0.04	0.07	-0.98**	0.30	-0.20*
9	PDW-314	0.31**	0.04	0.27**	0.21**	-0.19	-1.01**	-0.28	-0.49*
10	PDW-291	0.25**	-0.23**	0.12	0.05	-0.22	1.53**	-0.81**	0.16*
11	HI-8737×NIDW-295	0.56*	-0.79**	0.75**	0.17	-2.57**	2.20**	-2.97**	-1.12**
12	HI-8737×HI-8498	0.76**	-0.14	0.84**	0.49**	-1.41**	1.53**	-2.36**	-0.75**
13	HI-8737×HI-8663	-0.38	0.29	-0.24	-0.11	1.69**	0.05	2.54**	1.43**
14	HI-8737×WH-896	-0.19	0.33	0.10	0.08	-1.87**	0.81*	3.42**	0.79**
15	HI-8737×RAJ-1555	0.03	0.43	-0.01	0.15	-0.71	0.86*	-0.86	-0.24
16	HI-8737×PDW-274	0.34	0.44	-0.15	0.21	2.23**	-3.57**	1.05	-0.10
17	HI-8737×PDW-233	0.81**	0.36	0.22	0.47**	2.64**	-4.28**	2.10**	0.15
18	HI-8737×PDW-314	-0.51*	1.12**	0.04	0.22	3.46**	-4.01**	2.37**	0.60*
19	HI-8737×PDW-291	-0.86**	-0.41	-0.59**	-0.62**	-0.85	3.33**	-0.68	0.60*
20	NIDW-295×HI-8498	-0.91**	-0.12	-0.93**	-0.66**	2.03**	2.96**	2.17**	2.39**
21	NIDW-295×HI-8663	-0.44	0.11	-0.39	-0.24	2.34**	3.39**	1.39*	2.37**
22	NIDW-295×WH-896	0.13	0.61*	0.07	0.27	0.55	0.82*	0.47	0.61*

SN	Genotype	Protein Content (%)				Proline Content (µg)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
23	NIDW-295× RAJ-1555	0.45	0.47	0.32	0.41**	0.04	1.26**	-0.79	0.17
24	NIDW-295× PDW-274	-0.54*	0.30	-0.52*	-0.25	1.22*	2.57**	0.23	1.34**
25	NIDW-295× PDW-233	-0.09	-0.45	-0.09	-0.21	-3.92**	-3.81**	-3.56**	-3.76**
26	NIDW-295× PDW-314	0.09	-0.16	0.17	0.03	-1.67**	-3.91**	-1.56**	-2.38**
27	NIDW-295× PDW-291	0.27	0.16	0.51*	0.31*	-2.83**	-6.46**	-0.99	-3.43**
28	HI-8498×HI-8663	-0.19	-0.46	-0.14	-0.26	-3.15**	1.93**	-1.36*	-0.86**
29	HI-8498×WH-896	-0.09	-0.39	-0.17	-0.21	-4.90**	0.17	-2.55**	-2.43**
30	HI-8498×RAJ-1555	0.23	0.01	0.04	0.09	-5.57**	0.26	-4.55**	-3.29**
31	HI-8498×PDW-272	-0.59*	-0.61*	0.08	-0.37**	0.65	-2.48**	-1.27*	-1.03**
32	HI-8498×PDW-233	-0.33	0.22	-0.20	-0.10	1.37**	-2.67**	0.45	-0.29
33	HI-8498×PDW-314	0.09	0.44	0.09	0.21	1.27**	-3.30**	0.22	-0.60*
34	HI-8498×PDW-291	0.01	-0.29	0.15	-0.05	0.75	3.73**	1.11	1.86**
35	HI-8663×WH-896	0.19	-0.30	0.32	0.07	0.62	4.96**	-1.38*	1.40**
36	HI-8663×RAJ-1555	0.98**	-0.71**	0.93**	0.40**	-0.47	5.29**	-3.35**	0.49
37	HI-8663×PDW-274	0.33	0.60*	0.29	0.41**	-6.16**	0.57	-2.72**	-2.77**
38	HI-8663×PDW-233	0.45	0.62*	-0.18	0.30*	-5.55**	-0.76*	-2.35**	-2.89**
39	HI-8663×PDW-314	0.89**	0.63*	0.96**	0.83**	-4.78**	-0.55	-2.14**	-2.49**
40	HI-8663×PDW-291	-0.66**	-0.21	-0.49*	-0.45**	2.25**	-6.77**	-0.48	-1.67**
41	WH-896×RAJ-1555	0.83**	0.29	0.42*	0.51**	-1.50**	-4.42**	-3.60**	-3.17**
42	WH-896×PDW-274	0.12	0.05	0.01	0.06	-0.58	-3.02**	-2.48**	-2.03**
43	WH-896×PDW-233	-0.37	-0.11	-0.25	-0.24	0.68	4.86**	-0.66	1.63**

SN	Genotype	Protein Content (%)				Proline Content (µg)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
44	WH-896×PDW-314	-0.41	-0.57*	-0.40	-0.46**	0.64	2.69**	-0.69	0.88**
45	WH-896×PDW-291	-0.28	-0.28	-0.44*	-0.33*	1.38**	-0.31	0.30	0.45
46	RAJ-1555×PDW-274	-0.14	-0.01	-0.29	-0.15	0.57	1.15**	2.83**	1.51**
47	RAJ-1555×PDW-233	-0.30	0.14	0.11	-0.02	0.96*	0.31	2.54**	1.27**
48	RAJ-1555×PDW-314	-0.13	-0.25	-0.36	-0.25	1.14*	1.15**	1.84**	1.38**
49	RAJ-1555×PDW-291	-0.52*	0.35	-0.10	-0.09	1.52**	-2.44**	3.74**	0.94**
50	PDW-274×PDW-233	-0.86**	0.47	-0.73**	-0.37**	1.97**	0.85*	4.22**	2.34**
51	PDW-274×PDW-314	-0.73**	-0.00	-0.82**	-0.52**	1.86**	1.18**	5.09**	2.71**
52	PDW-274×PDW-291	0.92**	-0.03	1.19**	0.69**	0.86	3.36**	0.61	1.61**
53	PDW-233×PDW-314	0.56*	-0.47	0.57**	0.22	1.69**	5.68**	-0.02	2.45**
54	PDW-233×PDW-291	0.62*	0.17	1.05**	0.62**	1.58**	3.01**	0.87	1.82**
55	PDW-314×PDW-291	-0.06	-0.15	-0.77**	-0.33*	-1.34**	3.41**	-1.60**	0.16
Standard error									
	Gi	0.07	0.07	0.06	0.04	0.14	0.11	0.17	0.08
	Gi-Gj	0.11	0.11	0.09	0.06	0.21	0.17	0.26	0.12
	Sii	0.22	0.22	0.19	0.12	0.42	0.34	0.52	0.25
	Sij	0.25	0.25	0.21	0.14	0.46	0.38	0.58	0.28
	Sij-ik	0.37	0.37	0.31	0.20	0.68	0.56	0.85	0.41
	Sij-Skl	0.35	0.35	0.30	0.19	0.65	0.54	0.81	0.39

*, ** Significant at 5 per cent and 1 per cent respectively

Table 15 GCA and SCA effects for chlorophyll content (mg), and chlorophyll stability index

SN	Genotype	Chlorophyll content (mg)				Chlorophyll stability index			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	HI-8737	0.05*	0.05**	0.05*	0.05**	0.49**	0.47**	0.49**	0.48**
2	NIDW-295	0.09**	0.09**	0.09**	0.09**	0.47**	0.46**	0.47**	0.46**
3	HI-8498	0.03	0.03	0.03	0.03*	0.11	0.11	0.11	0.11
4	HI-8663	-0.04	-0.04	-0.04	-0.04*	0.20	0.19	0.19	0.19**
5	WH-896	0.14**	0.14**	0.14**	0.14**	-0.02	-0.02	-0.02	-0.02
6	RAJ-1555	-0.16**	-0.16**	-0.16**	-0.16*	-0.83**	-0.81**	-0.83**	-0.82*
7	PDW-274	-0.07**	-0.07**	-0.07**	-0.07*	-0.75**	-0.73**	-0.75**	-0.74*
8	PDW-233	-0.07**	-0.07**	-0.07**	-0.07*	-0.05	-0.04	-0.05	-0.05
9	PDW-314	0.07**	0.07**	0.07**	0.07**	0.52**	0.50**	0.52**	0.51**
10	PDW-291	-0.05*	-0.05*	-0.05*	-0.05*	-0.14	-0.14	-0.14	-0.14
11	HI-8737×NIDW-295	0.27**	0.27**	0.27**	0.27**	0.30	0.29	0.30	0.30
12	HI-8737×HI-8498	0.06	0.06	0.06	0.06	0.24	0.23	0.24	0.24
13	HI-8737×HI-8663	-0.39**	-0.39**	-0.39**	-0.39**	-1.38**	-1.35**	-1.38**	-1.37**
14	HI-8737×WH-896	-0.56**	-0.56**	-0.55**	-0.55**	2.15**	2.09**	2.14**	2.13**
15	HI-8737×RAJ-1555	-0.18*	-0.18**	-0.18**	-0.18**	-2.43**	-2.37**	-2.44**	-2.41**
16	HI-8737×PDW-274	-0.06	-0.06	-0.06	-0.06	-1.75**	-1.70**	-1.74**	-1.73**
17	HI-8737×PDW-233	0.16*	0.16*	0.16*	0.16**	1.05*	1.02**	1.05*	1.04**
18	HI-8737×PDW-314	0.29**	0.30**	0.29**	0.29**	0.25	0.24	0.25	0.25
19	HI-8737×PDW-291	0.11	0.11	0.11	0.11**	0.55	0.54	0.55	0.54*
20	NIDW-295×HI-8498	0.02	0.02	0.02	0.02	0.32	0.31	0.32	0.32
21	NIDW-295×HI-8663	-0.17*	-0.17**	-0.17*	-0.17**	0.53	0.52	0.53	0.53*
22	NIDW-295×WH-896	0.21**	0.21**	0.21**	0.21**	0.56	0.55	0.56	0.56*

SN	Genotype	Chlorophyll content (mg)				Chlorophyll stability index			
		E1	E2	E3	Pool	E1	E2	E3	Pool
23	NIDW-295×RAJ-1555	-0.41**	-0.40**	-0.40**	-0.40**	-2.29**	-2.24**	-2.30**	-2.28**
24	NIDW-295×PDW-274	-0.36**	-0.36**	-0.36**	-0.36**	-2.26**	-2.20**	-2.26**	-2.24**
25	NIDW-295×PDW-233	0.24**	0.23**	0.23**	0.23**	0.18	0.18	0.18	0.18
26	NIDW-295×PDW-314	0.05	0.05	0.05	0.05	0.80	0.78*	0.80*	0.79**
27	NIDW-295×PDW-291	0.10	0.10	0.10	0.10**	-1.15*	-1.12**	-1.15**	-1.14**
28	HI-8498×HI-8663	0.21**	0.21**	0.21**	0.21**	0.89	0.86*	0.89*	0.88**
29	HI-8498×WH-896	0.00	0.00	0.00	0.00	2.34**	2.28**	2.34**	2.32**
30	HI-8498×RAJ-1555	-0.32**	-0.32**	-0.32**	-0.32**	1.55**	1.52**	1.55**	1.54**
31	HI-8498×PDW-272	-0.39**	-0.39**	-0.39**	-0.39**	-1.60**	-1.57**	-1.61**	-1.59**
32	HI-8498×PDW-233	0.15*	0.15*	0.15*	0.15**	-2.19**	-2.14**	-2.19**	-2.17**
33	HI-8498×PDW-314	0.21**	0.20**	0.21**	0.21**	-2.33**	-2.28**	-2.34**	-2.32**
34	HI-8498×PDW-291	-0.12	-0.12	-0.12	-0.12**	-0.44	-0.42	-0.44	-0.43
35	HI-8663×WH-896	0.31**	0.31**	0.31**	0.31**	0.84	0.82*	0.84*	0.83**
36	HI-8663×RAJ-1555	0.34**	0.34**	0.33**	0.33**	1.47**	1.43**	1.47**	1.46**
37	HI-8663×PDW-274	-0.27**	-0.27**	-0.27**	-0.27**	2.99**	2.92**	2.99**	2.96**
38	HI-8663×PDW-233	-0.25**	-0.25**	-0.25**	-0.25**	0.57	0.56	0.57	0.57*
39	HI-8663×PDW-314	-0.32**	-0.32**	-0.32**	-0.32**	0.13	0.12	0.12	0.12
40	HI-8663×PDW-291	0.00	0.00	0.00	0.00	-0.76	-0.74	-0.76	-0.75**
41	WH-896×RAJ-1555	0.16*	0.16*	0.16*	0.16**	-1.81**	-1.77**	-1.81**	-1.80**
42	WH-896×PDW-274	0.34**	0.34**	0.34**	0.34**	3.38**	3.30**	3.38**	3.35**
43	WH-896×PDW-233	0.05	0.05	0.05	0.05	-2.71**	-2.65**	-2.71**	-2.69**
44	WH-896×PDW-314	-0.07	-0.07	-0.07	-0.07	-2.50**	-2.44**	-2.50**	-2.48**
45	WH-896×PDW-291	-0.21**	-0.21**	-0.22**	-0.21**	1.94**	1.90**	1.94**	1.93**

SN	Genotype	Chlorophyll content (mg)				Chlorophyll stability index			
		E1	E2	E3	Pool	E1	E2	E3	Pool
46	RAJ-1555×PDW-274	0.67**	0.66**	0.67**	0.67**	-0.97*	-0.94*	-0.97*	-0.96**
47	RAJ-1555×PDW-233	-0.24**	-0.24**	-0.24**	-0.24**	0.05	0.05	0.05	0.05
48	RAJ-1555×PDW-314	-0.25**	-0.24**	-0.25**	-0.25**	2.75**	2.68**	2.75**	2.73**
49	RAJ-1555×PDW-291	0.50**	0.50**	0.50**	0.50**	1.80**	1.76**	1.80**	1.79**
50	PDW-274×PDW-233	0.00	0.00	0.00	0.00	1.39**	1.36**	1.39**	1.38**
51	PDW-274×PDW-314	0.41**	0.41**	0.41**	0.41**	-2.01**	-1.96**	-2.01**	-1.99**
52	PDW-274×PDW-291	0.25**	0.26**	0.25**	0.25**	-1.24**	-1.21**	-1.23**	-1.23**
53	PDW-233×PDW-314	-0.37**	-0.37**	-0.37**	-0.37**	1.32**	1.29**	1.31**	1.31**
54	PDW-233×PDW-291	-0.24**	-0.24**	-0.24**	-0.24**	-1.52**	-1.48**	-1.52**	-1.51**
55	PDW-314×PDW-291	-0.31**	-0.31**	-0.31**	-0.31**	-1.20*	-1.17**	-1.19**	-1.19**
Standard error									
	Gi	0.02	0.02	0.02	0.01	0.14	0.12	0.12	0.07
	Gi-Gj	0.03	0.03	0.03	0.02	0.20	0.17	0.18	0.11
	Sii	0.07	0.06	0.06	0.04	0.41	0.35	0.36	0.22
	Sij	0.07	0.06	0.07	0.04	0.46	0.39	0.40	0.24
	Sij-ik	0.11	0.09	0.10	0.06	0.68	0.57	0.59	0.35
	Sij-Skl	0.10	0.09	0.09	0.06	0.65	0.54	0.56	0.34

*, ** Significant at 5 per cent and 1 per cent respectively

Table 16 GCA and SCA effects for heat injury index (%), and canopy temperature depression ($^{\circ}\text{C}$)

SN	Genotype	Heat injury index (%)				Canopy temperature depression ($^{\circ}\text{C}$)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	HI-8737	-3.55**	-3.45**	2.10**	-1.63*	1.27**	0.02	0.48	0.59**
2	NIDW-295	1.62**	1.88**	-1.27**	0.74**	0.57**	-0.09	1.41**	0.63**
3	HI-8498	4.92**	4.87**	-1.70**	2.70**	0.05	0.02	0.62*	0.23*
4	HI-8663	1.78**	1.74**	0.90*	1.47**	-0.66**	0.15	0.22	-0.10
5	WH-896	-1.85**	-1.89**	-0.11	-1.28*	-0.07	-0.13	0.43	0.08
6	RAJ-1555	-3.51**	-3.56**	1.10**	-1.99*	-0.33*	0.31*	-0.80**	-0.27*
7	PDW-274	-0.81*	-0.85*	1.91**	0.08	0.11	0.26*	-0.53	-0.05
8	PDW-233	-0.31	-0.35	0.72	0.02	-0.29*	-0.02	-0.98**	-0.43*
9	PDW-314	0.98**	0.94**	-0.06	0.62**	-0.17	-0.27*	-0.67*	-0.37*
10	PDW-291	0.72*	0.68*	-3.59**	-0.73*	-0.49**	-0.25	-0.18	-0.31*
11	HI-8737×NIDW-295	6.14**	5.72**	0.63	4.16**	0.80	2.61**	-0.83	0.86*
12	HI-8737×HI-8498	6.01**	5.90**	2.71*	4.87**	-0.45	-0.38	-0.10	-0.31
13	HI-8737×HI-8663	-5.87**	-5.98**	-0.82	-4.22**	-0.54	0.11	0.20	-0.08
14	HI-8737×WH-896	-0.21	-0.32	1.96	0.48	-0.17	0.25	-0.18	-0.03
15	HI-8737×RAJ-1555	-0.99	-1.10	2.18	0.03	1.73**	-1.97**	-0.08	-0.11
16	HI-8737×PDW-274	-4.12**	-4.23**	0.74	-2.54**	0.66	2.24**	0.48	1.12**
17	HI-8737×PDW-233	-1.16	-1.27	2.14	-0.10	0.16	0.69	0.26	0.37
18	HI-8737×PDW-314	-3.30**	-3.41**	2.65*	-1.35*	-1.03*	-1.53**	0.72	-0.61
19	HI-8737×PDW-291	-3.70**	-3.81**	-4.63**	-4.05**	0.65	-0.38	0.40	0.22
20	NIDW-295×HI-8498	-9.88**	-10.15**	-0.48	-6.84**	-0.45	-0.84	-0.52	-0.60
21	NIDW-295×HI-8663	-7.97**	-8.24**	-4.20**	-6.80**	0.92*	-0.22	1.33	0.68
22	NIDW-295×WH-896	5.13**	4.86**	2.87*	4.29**	-0.47	-1.83**	-0.81	-1.04**

SN	Genotype	Heat injury index (%)				Canopy temperature depression (°C)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
23	NIDW-295×RAJ-1555	5.47**	5.20**	-1.76	2.97**	0.70	0.13	0.28	0.37
24	NIDW-295×PDW-274	4.45**	4.18**	-0.36	2.75**	-0.28	-0.87*	-0.06	-0.40
25	NIDW-295×PDW-233	2.50*	2.23*	-2.55*	0.73	-0.37	-0.15	1.26	0.25
26	NIDW-295×PDW-314	3.93**	3.66**	-0.66	2.31**	0.23	1.59**	-0.22	0.53
27	NIDW-295×PDW-291	3.47**	3.20**	3.72**	3.46**	-0.28	0.64	1.30	0.55
28	HI-8498×HI-8663	2.45*	2.49*	-7.21**	-0.76	0.13	1.68**	-0.01	0.60
29	HI-8498×WH-896	3.83**	3.87**	-7.86**	-0.05	-0.52	0.97*	-0.41	0.01
30	HI-8498×RAJ-1555	6.92**	6.96**	-5.50**	2.80**	-0.50	0.18	0.31	-0.00
31	HI-8498×PDW-272	5.14**	5.18**	4.03**	4.78**	1.80**	-1.38**	0.27	0.23
32	HI-8498×PDW-233	2.85*	2.89*	6.26**	4.00**	-0.96*	0.10	0.69	-0.06
33	HI-8498×PDW-314	3.21**	3.25**	3.84**	3.43**	-0.72	0.93*	0.08	0.09
34	HI-8498×PDW-291	0.88	0.92	-2.42	-0.21	0.29	0.08	0.43	0.27
35	HI-8663×WH-896	6.53**	6.57**	-5.81**	2.43**	0.26	-1.53**	-0.08	-0.45
36	HI-8663×RAJ-1555	8.76**	8.80**	-8.75**	2.94**	-0.12	1.16**	-0.02	0.34
37	HI-8663×PDW-274	11.71**	11.76**	4.88**	9.45**	-0.85	1.05*	-0.57	-0.12
38	HI-8663×PDW-233	7.99**	8.03**	2.78*	6.27**	-1.11*	0.41	-2.58*	-1.10**
39	HI-8663×PDW-314	6.48**	6.53**	5.38**	6.13**	-0.78	0.80	-0.16	-0.05
40	HI-8663×PDW-291	-8.39**	-8.34**	4.71**	-4.01**	0.01	-1.24**	-0.41	-0.55
41	WH-896×RAJ-1555	1.73	1.77	4.35**	2.62**	1.23**	1.39**	-0.56	0.68
42	WH-896×PDW-274	-1.71	-1.67	2.57*	-0.27	-0.71	-0.10	-0.14	-0.32
43	WH-896×PDW-233	-4.29**	-4.25**	-5.47**	-4.67**	0.76	0.79	1.31	0.95*
44	WH-896×PDW-314	-2.75*	-2.71*	-6.97**	-4.14**	-0.23	-0.10	0.27	-0.02
45	WH-896×PDW-291	-1.98	-1.93	-1.86	-1.92**	-0.55	-0.45	0.72	-0.09

SN	Genotype	Heat injury index (%)				Canopy temperature depression (°C)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
46	RAJ-1555×PDW-274	-6.96**	-6.92**	-2.83*	-5.57**	-1.09*	0.23	-0.48	-0.44
47	RAJ-1555×PDW-233	-5.68**	-5.64**	0.94	-3.46**	-0.38	0.76	-0.23	0.05
48	RAJ-1555×PDW-314	-5.98**	-5.94**	1.41	-3.50**	-0.48	0.65	0.10	0.09
49	RAJ-1555×PDW-291	-4.97**	-4.92**	0.23	-3.22**	0.08	-0.39	-2.39*	-0.90*
50	PDW-274×PDW-233	-6.06**	-6.01**	-2.97*	-5.01**	0.05	-0.90*	-0.93	-0.60
51	PDW-274×PDW-314	-6.04**	-6.00**	-3.24*	-5.10**	1.06*	0.44	0.65	0.72
52	PDW-274×PDW-291	-1.37	-1.33	-9.14**	-3.94**	0.14	0.36	0.00	0.17
53	PDW-233×PDW-314	-0.70	-0.66	-8.79**	-3.38**	0.70	0.25	0.67	0.54
54	PDW-233×PDW-291	2.22	2.26*	-7.13**	-0.88	0.24	0.74	-1.68	-0.23
55	PDW-314×PDW-291	4.85**	4.89**	-6.21**	1.18	-0.41	-0.56	0.31	-0.22
	Standard error								
	Gi	0.34	0.33	0.37	0.20	0.13	0.13	0.29	0.12
	Gi-Gj	0.50	0.50	0.55	0.30	0.20	0.19	0.44	0.17
	Sii	1.01	1.01	1.12	0.60	0.40	0.39	0.89	0.35
	Sij	1.13	1.12	1.24	0.67	0.45	0.44	0.99	0.39
	Sij-ik	1.66	1.65	1.83	0.99	0.66	0.64	1.46	0.57
	Sij-Skl	1.58	1.58	1.74	0.94	0.63	0.61	1.39	0.55

*, ** Significant at 5 per cent and 1 per cent respectively