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Combining Ability of Lowland Adapted Ethiopian Sorghum Hybrids for Yield

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ይህ ጥናት አላማ አድረጎ የተነሳው በአጭርና በመካከለኛ ጊዜ ከሚደርሱ የማሽላ ዝርያዎች የተገኙ ድቃይ የማሽላ ዝርያዎችን ለመገምገም በማሰብ ወደዚህ የምርምር ስራ ተገብቷል። በጥናቱ ውስጥ 95 የድቃይ ማሽላ ዝርያዎች ከሶስት ቀደም ሲል ከተለቀቁ የማሽላ ዝርያዎች ጋር በማካተት በሜኢሶና በሽራሮ የሙከራ ንዑስ ጣቢያዎች ውስጥ በ2009/10 ዓ.ም የምርት ዘመን ተዘርተው ጥናቱ ተካሂዷል። ለቡቃያው የሚያስፈልገውን እንክብካቤ በሙሉ በጊዜ፣ በዓይነትና በመጠን በመለየት ወቅቱን ጠብቆ ተደርጓል። በዚህም መሰረት ለጥናቱ አስፈሊጊ የሆኑ መረጃዎች በወቅቱ ተሰበሰቡ። የተሰበሰቡ መረጃዎችን ለማስላት አስፈሊጊ የስታትስቲክስ ፓኬጆችን በመጠቀም እንዲሰላ ተደርጎ በሙከራ ዝርያዎቹ መካከል የተሰበሰሰበውን መረጃ ስሌት መንስዔ በማድረግ የባህሪ ልዩነት እንዳለ ተረጋገጠ። በመሆኑም የጥናቱን ውጤት መነሻ በማድረግ በጥናቱ ውስጥ ከተካተቱት ውስጥ ዘረ-መል ቁጥር (እናት ዝርያ) ICSV96143፣ICSR93034፣IESV92168-DC እና ETSL101565 ለድቃይ ማሽላ ዝርያ ምርታማነትና ሌሎች ለምርታማነት አስፈላጊ ለሆኑ የማሽላ ባህሪያት ከፍተኛ ጠቀሜታ እንዳላቸው ታውቋል። በተመሳሳይ ከተጠኑት ድቃዮች መካከል 15 የሚሆኑት ቀደም ሲል በምርምር ከተለቀቁ ሶስት ዝርያዎች ጋር ሲወዳደሩ በምርታማነታቸው የላቁ መሆናቸውን በጥናት ተደርሶበታል። ከነዚህም ድቃዮች ውስጥ ከፍተኛው የተመዘገበው በMARC6A x IESV23010DL (78%) ሲሆን በማስከተልም TX623A x ETSL101859 (71%) እና TX623A x ETSL100684 (67%) በቅደም ተከተል ይገኙበታል። እነዚህን የተሻሉ የማሽላ ድቃዮችን በአስተማማኝነት ለምርታማነት ለመልቀቅ ተጨማሪ ጥናት እንደሚያስፈልግ በጥናቱ ተጠቁሟል። ከዚህ ጥናት የሚገኘው ውጤት በቀጣይ በማሽላ ምርትና ሌሎች ባህሪያት ማሻሻል ላይ ለሚሰሩ አዳቃዮችና ተመራማሪዎች እንደ ግብዓት ሆኖ ያገለግላል።

Abstract

This study was conducted with the objective to assess the performances of hybrids developed from early and medium maturing lowland adapted Ethiopian sorghum inbred lines. A total of 95 hybrids and three checks were tested using alpha lettuce design with two replications at Meiso and Sheraro. All agronomic practices were done on time as recommended. Based on the results obtained from the analysis positive and significant GCA values among the female lines were recorded by ICSV96143, ICSR93034, IESV92168-DC and ETSL101565. Likewise, tester TX623A were identified as most promising parents having good general combining ability for grain yield and almost all its major yield components. Similarly, for grain yield, 15 hybrid combinations had significant advantage over their respective standard check Melkam. Among these hybrids the highest was obtained from MARC6A x IESV23010DL (78%) followed by TX623A x ETSL101859 (71%) and TX623A x ETSL100684 (67%). The information generated *from the present study can be used for breeders who want to improve yield and yield-contributing traits of sorghum by understanding the genetic relationship among inbred lines.*

Introduction

Even though, Ethiopia is the center of origin and domestication for sorghum with a wide range of sorghum collections for various agro ecologies their heterotic performance and the magnitude of heterosis between different racial groups of sorghum are not well studied. In addition, there are no more sorghum hybrids unlike to maize that will increase the present sorghum production i.e. around 2 tons per ha to 4-5 tons per ha. Combining ability studies of germplasm facilitates its exploitation in breeding and the choice of suitable parents for superior hybrid combinations (Akinwale *et al*., 2014). Combining ability is the capacity of an individual to transmit superior performance to its offspring. It provides information on gene effects in controlling inheritance of traits of interest and helps in selecting the parents to be included in cultivar improvement or hybridization programs. The objective of this study was to determine the combining abilities of selected landraces for morphological traits under dry lowland environments to increase hybrid breeding efficiency.

Materials and Methods

Materials

A total of ninety-five hybrids and three checks were used in this experiment. The hybrids were developed from 50 lines and 3 testers using line by tester design at Werer agricultural research center in the off-season with the collaboration of the national sorghum improvement program based at Melkassa agricultural research center (MARC).

Experimental design and field management

The experiment was conducted at Mieso (9°14′N, 40°45′E, 1394 m), and Sheraro (14.4N, 37.9 E, 1179 m). The areas are located in potential sorghum production areas of the country and each with a distance of 293km and 1095km from the capital Addis Ababa respectively. Each plot has two rows of 5m long with spacing of 0.75m and 0.15m inter and intra rows, respectively. Seed rates of 10kg/ha was used in drill and planting was done at the onset of the main rainy season at the respective testing environment. Fertilizer was applied at the rates 100kg/ha Urea and 100kg/ha DAP. Split application was used for Urea half of it at planting time and the remaining half at knee stage period. In addition to land preparation and hand-weeding all other cultural practices was applied as per the recommendation for sorghum production at respective areas. The hybrids were evaluated and the detail agronomic and morphological data were collected at both experimental sites.

Data collection and analysis

All appropriate agronomic data were collected on plot and plant bases using sorghum descriptors (IBPGR/ICRISAT, 1993) and analysis of variance was computed using SAS software ver. 9.3 (SAS, 2003). Then both general and specific combing ability were calculated using a modification of the Line by Tester-SAS program (Zhang and Kang, 1997).

Entry means adjusted for block effects as analyzed according to lattice design (Cochran and Cox, 1957) were used to perform combining ability analysis. Further analysis was done according to the line x tester analysis to partition the mean square due to crosses into lines, tester and line by tester effects (Dabholkar, 1992, Singh and Chaudhary, 1985) using SAS computer program. For traits that showed significant differences among crosses. Further genetic analyses were carried out for traits that showed significant differences among the genotypes excluding the checks according to line x tester analysis methods as suggested by (Kempthorne, 1957) to partition the mean square due to crosses in to lines (GCAf), tester (GCAm) and line x tester interactions (SCAfm) using SAS software program. The significant of GCA and SCA effects were tested by dividing the corresponding GCA and SCA values by their respective standard error and comparing the obtained t with tabular t-value at error degree of freedom.

Result and Discussion

Analysis of variance for the evaluated hybrids

Mean squares of the nine characters from analysis of variance (ANOVA) combined over the two locations are presented in Table 1. Hybrids displayed highly significant differences ($p<0.001$ and $p<0.01$) in all traits except panicle weight. The entry main effects and their interactions was further partitioned into various components; hybrids, checks and checks versus crosses. The sum of squares of hybrids was partitioned into variations due to lines, testers, and line x tester interactions. The current result showed that mean squares of lines were highly significant at $p\leq 0.001$, for days to 90% maturity, plant height, number of panicles plot^{-1}, panicle length and grain yield. Highly significant differences at $p\leq 0.05$ were only observed for days to 50% anthesis. The remaining panicle weight, hundred grain weight and disease score were not significant (Table 1).

The mean squares due to testers were significant at $p\leq0.05$, for only panicle length. The mean squares for testers were not significant for days to 50% anthesis, days to 90% maturity, plant height, and number of panicles plot^{-1}, panicle weight, hundred grain weight, disease score and grain yield. The line x tester mean squares showed significant differences at $p\leq 0.001$ for days to 90% maturity, plant height, and panicle length, significant differences at $p\leq 0.01$ for days to 50% anthesis, number of panicles plot^{-1} and hundred grain weight. No significant differences for panicle weight, disease score and grain yield (Table 1). The present finding is in agreement with previously done by Thakare (2014).

Estimates of general combining ability

The estimates of GCA effects of 12 inbred lines evaluated in a line x tester cross for grain yield and agronomic traits are presented in Table 2. The inbred lines varied significantly in GCA for all traits. Inbred line L3 (ICSV 96143) exhibited the maximum GCA effect of 2.86, whereas L1 (ICSR 14) exhibited the lowest GCA effect of -2.58. Inbred lines L2 (1.97), L3 (2.86), L9 (1.24) and L11 (1.55) showed significant positive GCA (additive) effects for grain yield. These inbred lines are desirable parents for hybrid development as well as for inclusion in the breeding program, as the lines may contribute favorable alleles in the synthesis of new varieties. In contrast, L1 (-2.58), L4 (-1.38), L6 (-1.27) and L8 (-1.77) had significant negative GCA effects for grain yield, indicating that these lines were poor general combiners for grain yield. From the tester, T1 (TX623A) was the best general combiner while T2 (MARC 6A) and T3 (MARC 4A) were poor general combiner for grain yield. Both positive and negative GCA effects were reported in sorghum by several investigators (Hariprasanna *et al*., 2012).

Both negative and positive GCA effects were observed for days to anthesis and maturity. Lines, L7 and L10 showed highly negative and significant GCA effects for days to anthesis and maturity, respectively. Whereas inbred line eight showed positive and significant GCA effects for both days to anthesis and maturity. Lines L7 (M204) (-0.99 days) and L10 (03MW6049) (-0.91 days) were good general combiners while L8 (01MS7013) (0.97 days) was poor general combiners for days to anthesis (Table 2). Lines L7 (-0.75 days) and L10 (-0.63 days) were good general combiners while L8 (0.83 days) was poor general combiners for days to maturity (Table 2). The negative value implies that the inbred lines are good combiners as it indicates the tendency of earliness and the reverse is true for those with positive GCA effects. It can be useful in further breeding for earliness. The findings of Kenga *et al*., (2004), Girma *et al*., (2010) and Premalatha *et al*., (2006) support the result in this study. For plant height, L1 (-11.51) and L7 (-9.71) were found to be good general combiners while L6 (ETSL100318) (16.42) and L11 (ETSL101565) (9.47) were poor general combiners (Table 2). This indicates that L1 has a tendency to reduce whereas L6 has a tendency to increase plant height in the hybrid sorghum progenies.

Estimates of specific combining ability

For grain yield, both positive and negative and significant estimates of SCA effects were observed among the crosses, indicating that the crosses performed better or poorer than what would be expected from the GCA effects of their respective parents. Therefore, six crosses namely; IESV23005DL x TX623A (4.58), IESV92168-DC x MARC4A (2.74), ICSR 93034 x MARC4A (2.2), ETSL101565 x MARC6A (2.05), ICSV96143 x MARC6A (2.02) and ETSL100318 x TX623A (1.59) showed positive and significant SCA effects for grain yield (Table 3). These crosses were good specific combiners with favorable SCA estimates for grain yield. Crosses that exhibited negative and significant SCA effects for grain yield were IESV23005DL x MARC6A (-3.02), IESV92168-DC x TX623A (-2.88), ETSL101565 x MARC4A (-2.79), IESV23005DL x MARC4A (-1.57) and ICSV 96143 x TX623A (-1.34). These crosses were not good specific combiners for grain yield (Table 3). However, to get the best SCA results it is not necessarily from crosses between two good general combiners. The current study showed that the combination of a parents with negative and a parent with positive GCA value resulted in a hybrid with positive SCA values in some cases. For example, the combination of a parent with negative and a parent with positive GCA values IESV23005DL (-1.38) x TX623A (0.42), IESV92168-DC (1.24) x MARC4A (-0.26), ICSR93034 (1.97) x MARC4A (-0.26), ETSL101565 (1.55) x MARC6A (-0.26), ICSV96143 (2.86) x MARC6A (-0.26) and ETSL100318 (-1.27) x TX623A (0.42) resulted in positive SCA values of, 4.58, 2.74, 2.2, 2.05, 2.02 and 1.59 respectively. Vassal *et al*, (1992) argued that positive SCA effects indicate that lines are in opposite heterotic groups while negative SCA effects indicate that lines are in the same heterotic group. Among the 36 crosses, four F_1s showed significant and positive SCA effects for plant height whereas, six crosses recorded significant and negative SCA effects. The F_1s with significant positive SCA are ICSR14 x MARC6A, IESV23005DL x TX623A, SILA x MARC4A and M204 x MARC4A with 6.52, 13.10, 7.35 and 8.43 SCA values, respectively. They were identified as best for the plant height as along as significant and positive SCA effects recorded highest average values (298.20cm, 295.70cm, 294.30cm and 289.15cm respectively) as represented in the Table 3. For panicle length, out of 36 F_1s, five hybrids showed significant and positive SCA effects i.e. ICSR14 x TX623A (1.06), ETSL101565 x TX623A (0.70), 03MW6049 x MARC4A (0.55), IESV92168-DC x MARC6A (0.54) and ETSL101565 x MARC6A (0.49) with the mean performance at 36.28cm, 34.90cm, 34.36cm, 33.15cm and 32.28cm respectively. However, the hybrids with negative SCA are ICSR 14 x MARC 4A (-0.60), ICSR 93034 x TX623A (-0.54) and ICSV 96143 x TX623A (-0.50).

Out of the 36 hybrids (F_1s), five hybrids showed the highest significant and positive SCA effects while three hybrids noted significant and negative SCA effects for number of panicles/plot. The crosses identified as good for number of panicles/plot on the basis of significant SCA and average mean value are M204 x TX623A (3.73 and 61.00), ETSL101565 x MARC6A (3.56 and 63.00), ETSL100661 x MARC6A (3.23 and 58.00), ICSR93034 x MARC4A (3.16 and 56.25) and M204 x TX623A (3.06 and 56.50). However, the F1s with negative SCA are M204 x MARC6A (-5.44), ETSL100318 x MARC6A (-4.11) and M204 x MARC4A (-3.46) as shown in Table 3.The importance of non-additive genetic variance for days to anthesis has been reported by Khandelwal *et al*. (2004), while in the present study the additive variance was higher in magnitude.

With regard to panicle weight, out of 36 crosses, six crosses were showed positive and significant SCA effects. These crosses are ICSR 14 x MARC 6A (150..34), ICSR 14 x MARC 4A (111.8), SILA x MARC 4A (149.3), M204 x TX623A (154.51), IESV 92168-DC x TX623A (129.51) and ETSL 101565 x TX623A (187.84) with the average values of 2850gm, 2600gm, 2900gm, 3250gm, 3200gm and 3300gm respectively as shown in Table 3. On the other hand five crosses exhibited negative and significant SCA effects i.e. ICSR 14 x TX623A (-262.16), SILA x TX623A (-187.16), M204 x MARC 6A (-120.49), IESV 92168-DC x MARC 4A (-184.03) and IESV 92168-DC x MARC 4A (-137.16). With respect to number of days to maturity, crosses ETSL 100318 x MARC 6A, ICSR 14 x TX623A, ICSR 93034 x MARC 6A, M204 x MARC 6A and IESV 92168-DC x MARC 4A showed positive and significant SCA effects with the values 1.0, 0.66 0.63, 0.59 and 0.44 respectively, whereas negative and significant SCA effects were observed in crosses ETSL 100318 x TX623A, ETSL 101565 x MARC 6A, ICSR 14 x MARC 6A and M204 x TX623A with the values of -0.80, -0.58, -0.54 and -0.47 (Table 3).

Table 1. Combined analysis of variance and means for grain yield and other agronomic traits of hybrids evaluated at Mieso and Sheraro in 2016 cropping season

Source of variation	Df	DTA (days)	DTM (days)	PHT (cm)	NPPP (#)	PAL (cm)	PAW (g)	HGW (g)	DS (#)	GYD (t/ha)
Location (L)	1	237.4***	370.9***	384000***	17678.7***	236.9***	898685	12.7***	0.02	14121***
Hybrids	94	9.74***	6.5***	2359.8***	218.2***	36.4***	390239	0.33**	0.09*	132.8**
GCA	51	8.3	6.2***	2325.4***	251.7***	30.2***	488079*	0.4	0.08	152**
SCA	41	9.8*	6.6***	2240.3***	152.5*	33.2	418109	0.4*	0.09	112*
Hybrids x L	94	5.4*	3.1*	1419.6***	85.6	4.1	408831	0.17	0.09	93.3
GCA x L	51	4.5	2.6	1206.1	86.0	5.5	515322*	0.25	0.11	90.8
SCA x L	41	7.8	3.3	1763.5***	118.0	4.6	360167	0.32	0.12	108.2
Error	189	6.5	2.6	677.5	93.4	7.3	333899	0.28	0.11	76.2
Mean		71.6	110.4	242.7	46.3	26.8	2864.8	2.4	1.1	30.5
SE(m)		2.5	1.6	36	9.6	2.7	577	0.5	0.33	8.7
CV (%)		3.6	1.5	10.7	20.8	10.1	20.2	22.2	30.3	28.6

, ** and * significant at $P \leq 0.05$, $P \leq 0.01$ and $P \leq 0.001$; CV (%) = coefficient of variation; Df= degree of freedom; DTA= days to anthesis; DTM= days to maturity; PHT= plant height; NPPP= number of panicles per plot; PAL= panicle length; PAW= panicle weight; HGW= grain weight; DS= disease score; GYD= grain yield t/ha; SE (m) =standard error of the mean*

Table 2. General combining ability effects (GCA) of 12 inbred lines for grain yield and agronomic traits evaluated at Mieso and Sheraro, 2016

Line	DTF (day)	DTM (day)	PHT (cm)	NPPP (#)	PAL (cm)	PAW (g)	HGW (g)	DS (#)	GYD (t/ha)
L1	0.51	0.13	-11.51***	-0.06	0.45*	-197.22***	-0.01	-0.03	-2.58***
L2	0.26	0.08	4.21	0.36	-0.55**	-51.39	-0.06	0.05	1.97**
L3	0.26	-0.04	-2.90	-2.02	-0.25	198.61***	0.08*	0.01	2.86***
L4	0.22	-0.17	-0.96	-0.81	-0.67**	-55.55	-0.04	-0.03	-1.38*
L5	0.26	0.33	-2.26	-1.60	0.39	-84.72	-0.11**	0.1***	-0.37
L6	-0.20	0.33	16.42***	-1.77	0.81***	-43.05	0.18***	-0.03	-1.27*
L7	-0.99**	-0.75**	-9.71**	3.32*	0.67***	23.61	-0.17***	-0.03	-0.06
L8	0.97**	0.83***	-0.19	-1.64	-1.15***	-18.05	0.02	-0.03	-1.77**
L9	-0.7*	-0.54*	0.79	-0.39	-0.37	23.61	-0.10**	0.1***	1.24*
L10	-0.91**	-0.63**	-6.13	1.82	-0.55	190.28***	0.13***	-0.03	-0.39
L11	0.34	0.42	9.47**	2.44	1.24	15.28	0.16***	0.01	1.55*
L12	-0.03	-0.04	2.72	0.40	-0.06	-1.39	-0.04	-0.03	0.23
GCASE	0.34	0.23	3.50	1.5	0.22	52.25	0.04	0.03	0.65
SE	1.23	0.92	16.80	5.33	1.17	342.59	0.24	0.16	5.17
T1	-0.1***	-0.03	-6.14**	0.15	0.47*	12.16	-0.05**	0.04***	0.42***
T2	0.02	0.04*	3.55	0.19*	-0.22	37.16***	-0.01	-0.01	-0.26*
T3	0.07*	-0.02	2.58	-0.33***	-0.27	-49.30***	0.08***	0.02*	-0.26*
GCASE	0.03	0.02	2.45	0.08	0.20	8.61	0.02	0.01	0.13
SE	0.29	0.22	4.04	1.28	0.28	13.29	0.06	0.04	1.24

**, ** and *** = $P < 0.05$, $P < 0.01$ and $P < 0.001$ respectively, DTA= days to anthesis; DTM= days to maturity; PHT= plant height; NPPP= number of panicles plot^{-1}; PAL= panicle length; PAW= panicle weight; HGW= hundred grain weight; DS= disease score; GYD= grain yield t/ha*

Conclusions

Based on the present combining ability study indicated that both general and specific combining ability effects are important but predominance of non-additive genetic variance indicate the presence of hetrozygosity in the population. As such this type of genetic variance is non-fixable hence, breeding is effective for crop improvement. Grain yield, number of panicles plot^{-1}, panicle length and panicle weight should be taken into consideration either simultaneously or alone for selecting high yielding genotypes as well as hybrids of sorghum. Among the female lines, ICSV96143 followed by ICSR93034, IESV92168-DC, ETSL101565, and male line TX623A were identified as most promising parents due to having good general combining ability for grain yield and almost all its major components. The crosses showing significant and desirable SCA effects in order of the merit for yield and yield contributing traits were MARC6A x ETSL101565, MARC4A x IESV92168-DC, TX623A x ETSL100318, TX623A x IESV23005DL, MARC6A x ICSV96143, and MARC4A x ICSR 93034. Besides these, the high SCA effects for earliness were observed in MARC6AxICSR14 followed byTX623A x ETSL100318, TX623A x M204, and MARC6A x ETSL101565, whereas TX623A x M204, MARC6A x IESV23005DL, TX623A x SILA, TX623A x ETSL101565, MARC 4A x ICSR93034 and MARC 6A x ETSL100318 possessed considerable SCA effects for dwarfness and recommended for heterosis breeding. Therefore, it may be concluded that use of suitable lines and testers in developing hybrids would be useful for attaining a quantum jump in sorghum yield.

Table 3. Estimation of specific combining ability (SCA) effect of lines and testers for studied traits of lowland sorghum in line x tester mating fashion at Mieso and Sheraro 2016

Cross	DTA (day)	DTM (day)	PHT (cm)	NPPP (#)	PAL (cm)	PAW (g)	HGW (g)	DS (#)	GYD (q/ha)
L1 x T1	0.27*	0.66**	-5.91	1.23	1.06***	-262.16***	-0.16***	0.00	-0.06
L1 x T2	-0.23*	-0.54*	6.52*	-1.94	-0.44	150.34**	0.14**	0.01	-0.42
L1 x T3	-0.03	-0.10	-0.61	0.70	-0.60*	111.80*	0.01	-0.02	0.47
L2 x T1	-0.36**	-0.30	3.75	-1.19	-0.54*	-20.49	0.05	0.04	-1.19
L2 x T2	0.27*	0.63**	3.71	-1.98	0.44	79.51	-0.04	0.05	-1.03
L2 x T3	0.10	-0.31	-7.45*	3.16*	0.12	-59.03	-0.04	-0.10*	2.20***
L3 x T1	0.39***	0.20	5.86	-0.82	-0.50*	-20.49	-0.10*	-0.04	-1.34*
L3 x T2	-0.23*	-0.12	-3.86	2.64	0.27	-20.49	-0.01	0.09*	2.02**
L3 x T3	-0.15	-0.06	-1.99	-1.84	0.25	40.97	0.10*	-0.06	-0.69
L4 x T1	0.06	0.07	13.10**	-0.78	0.40	58.67	0.14**	0.00	4.58***
L4 x T2	-0.19	0.00	-9.64**	2.44	-0.19	-103.83	-0.10*	0.01	-3.02**
L4 x T3	0.14	-0.06	-3.45	-1.67	-0.19	45.13	-0.06	-0.02	-1.57**
L5 x T1	0.52***	0.20	-8.46**	-0.86	0.00	-187.16***	-0.06	0.00	-0.37
L5 x T2	-0.10	-0.37	1.13	0.98	-0.33	37.84	0.01	-0.12**	1.11
L5 x T3	-0.40**	0.19	7.35*	-0.13	0.35	149.30**	0.02	0.11**	-0.75
L6 x T1	-0.52**	-0.80**	5.02	2.06	-0.36	21.17	0.05	0.00	1.59*
L6 x T2	0.61***	1.00***	-7.35*	-4.11**	0.03	-28.83	0.03	0.01	-1.24
L6 x T3	-0.07	-0.19	2.34	2.04	0.34	7.63	-0.10*	-0.02	-0.36
L7 x T1	0.02	-0.47*	-12.20**	3.73**	0.19	154.51**	-0.06	0.00	0.54
L7 x T2	0.27*	0.59**	3.78	-5.44**	-0.40	-120.49*	0.13**	0.01	-0.95
L7 x T3	-0.28*	-0.10	8.43**	1.71	0.23	-34.03	-0.09*	-0.02	0.40
L8 x T1	0.56***	0.20	4.75	3.06*	-0.17	-3.83	0.06	0.00	-0.53
L8 x T2	-0.44**	-0.12	-2.14	0.39	-0.06	21.17	-0.06	0.01	0.61
L8 x T3	-0.11	-0.06	-2.60	-3.46**	0.24	-17.37	-0.02	-0.02	-0.09
L9 x T1	-0.77**	-0.18	-3.63	-1.44	-0.37	129.51*	-0.03	0.00	-2.88**
L9 x T2	0.23*	-0.25	4.18	0.14	0.54*	54.51	-0.10*	-0.12**	0.13
L9 x T3	0.56***	0.44*	-0.55	1.29	-0.14	-184.03**	0.11**	0.11**	2.74***
L10 x T1	0.18	0.16	4.91	-2.40	-0.21	-87.16	-0.01	0.00	-0.01
L10 x T2	-0.06	0.09	-1.53	0.06	-0.32	87.84	0.00	0.01	0.16
L10 x T3	-0.11	-0.23	-3.38	2.33	0.55*	-0.70	-0.01	-0.02	-0.16
L11 x T1	-0.32**	0.24	-7.81*	-1.03	0.70**	187.84***	0.06	-0.04	0.73
L11 x T2	-0.19	-0.58**	5.50	3.56**	0.49***	-137.16**	-0.07	-0.03	2.05**
L11 x T3	0.51***	0.35	2.32	-2.55	-1.17	-50.70	-0.01	0.06	-2.79***
L12 x T1	-0.32**	0.07	0.64	-1.61	-0.10	29.51	-0.04	0.00	-1.11
L12 x T2	-0.19	-0.25	-0.28	3.23*	0.02	-20.49	-0.02	0.01	0.59
L12 x T3	0.51***	0.19	-0.35	-1.63	0.10	-9.03	0.04	-0.02	0.52
SCASE	0.12	0.23	3.4	1.42	0.26	57	0.044	0.04	0.67
SE	0.33	0.59	9.09	3.23	2.03	103.39	0.41	0.28	2.95

**, ** and *** = $P < 0.05$, $P < 0.01$ and $P < 0.001$, respectively DTA= days to anthesis; DTM= days to maturity; PHT= plant height; NPPP= number of panicles plot^{-1}; PAL= panicle length; PAW= panicle weight; HGW= hundred grain weight; DS= disease score; GYD= grain yield t/ha*

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