Combining ability analysis for drought related traits in maize (*Zea mays* L.)

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SUMMARY

Experiments were carried out to identify best lines for GCA effects and best hybrids for and SCA effects and high heterosis for three drought tolerant traits *viz.*, SPAD chlorophyll meter reading (SCMR), specific leaf area (SLA) and proline content and grain yield. Twelve lines and three testers were crossed to develop 36 hybrids which have been raised along with their parents in Zonal Agricultural Research Station, V.C. Farm, Mandya under Randomized Complete Block Design with two replications. Seven lines *viz.*, 1410-1, 2422, 262-55, 634-2, NAI-137-2, MAI-105 and SKV-50 have shown desirable GCA effect for SCMR, SLA and grain yield, on the other hand tester HKI-164-4-1-3 exhibited desirable GCA effect for SCMR and proline content. Two cross combinations *viz.*, MAI-105 x CML411 and SKV-50 x HKI-164-4-1-3 were found to be promising as these revealed significant positive SCA effects for yield and two important features of drought tolerance *viz.,* SCMR and proline content.

Key Words : Combining ability, SCMR, SLA, Proline content, GCA, SCA

Exploitation of heterosis in maize is achieving highest growth rate in productivity(73 kg/ha/year) as compared to other cereal crop (DMR, 2013) and which is meeting increasing demand from poultry and livestock sectors in the country.In India, about 95 per cent of maize area in tropics is rainfed and major growing season, *Kharif* accounts more than 80 per cent of total maize area in the country.Drought is a major abiotic factor frequently affecting maize yield under rainfed condition for short or long period. The extent of yield loss depends on degree, duration and time of drought occurrence. Recently in 2009-10 maize has experienced severe drought caused yield reduction from 19.7 mt to 16.7 mt and productivity has decreased from 2414 kg/ha to 2024 kg/ha. Again in 2012 the crop experienced moderate to severe drought during the early season especially in Karnataka, Rajasthan and Gujarat. Development of drought tolerant and high yielding maize hybrids will be the most appropriate solution to mitigate this problem.

Osmotic adjustment is one of the major physiological phenomena vital for sustaining growth of plants under moisture stress condition (Serraj and Sinclair, 2002). Accumulation of a variety of compatible solutes such as proline and betaine, as an adaptive mechanism of tolerance to drought (Ashraf and Harris, 2004; Ashraf and Foolad, 2007). In this study we have focussed on three drought tolerance attributing traits *viz.*, free proline content, leaf chlorophyll content (SPAD) and specific leaf area (SLA) along with grain yield.Hence, present investigation was undertaken to explore the possibility of identifying some best general combiner inbred lines and also the best single cross hybrids with high SCA effects for drought

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tolerant traits and yield.

MATERIAL AND METHODS

Twelve lines and three testers collected from Zonal Agricultural Research Station, V.C. Farm, Mandya were crossed in the Summer 2012. During *Kharif* 2012, 36 F_1s and along with their fifteen parents and two checks (NAH-2049 and NAH-1137) were raised by following Randomized Complete Block Design in two replications with a spacing of 75 cm (between rows)× 30 cm (between hills). Observations were recorded on grain yield (t/ha.) and drought related traits *viz.*, free proline content, leaf chlorophyll content (SPAD) and specific leaf area (SLA). Mean of five randomly selected plants on each character for each entry was subjected to line x tester analysis and variance of combining ability was estimated (Kempthorne, 1957). General and specific combining ability variances were estimatedby fallowing Griffings (1956) method II Model I.

Proline content in leaf tissue of maize genotypes was estimated by the method as suggested by Bates *et al.* (1973)when crop was of 45 days old which had experienced 20 days of moisture stress.Moisture stress was induced by withholding irrigation. Leaf chlorophyll content(SPAD chlorophyll meter reading) was measured in third leaf from the apex of plant under normal sunlight hour between 9 am to 4 pm by using a device developed by Minolta Company, New Jersey USA (SPAD-502). To measure specific leaf area (cm²/ g) fully expanded leaf of the middle region was selected. Leaves were oven dried at 70^0 C for 3 days and dry weight of leaf was measured.

RESULTS AND DISCUSSION

Analysis of variance showed that mean sum of square due to genotypes were significant for all the traits under study. The parents and hybrids significantly differed for all the traits, indicates the prevalence of genetic variability for all the traits. Mean sum of squares for parents vs. hybrids were also significant for all the traits, indicates the possibility of exploitation of heterosis in all traits.

Analysis of variance for general combining ability for drought tolerant traits and yield, lines differed in their general combining ability variance for all the traits studied and on the other hand testers also differed significantly for all traits except SLA (Table 1).

The general combining effects are of direct utility todecide the next phase of breeding program since the general view is that, better general combiner inbreds may yield better hybrid combination and can be directly utilized in development of synthetics as short term approach.The estimate of general combining ability effects in parental lines *i.e.* line NAI-137-2 exhibited significant desirable GCA effect for SCMR value, proline content and grain yield and significant negative GCA effect for SLA. Line 1410-1, 2422, 2-62-55, 634-2, NAI-137-2, MAI-105, SKV-50 showed significant desirable GCA effect for SCMR value, proline content and grain yield. Line 1201 only had shown desirable GCA effect for SLA. Among the testers HKI-164-4-1-3 had shown significant desirable GCA effects for SCMR value and proline content and tester CML-411 for grain yield (Table 2). Among the three drought tolerant characters studied, SCMR values manifested higher degree of SCA variance as compared to GCA variance. Similar results were also reported by Milla and Reich (2007) and Schepers *et al.* (1992). SLA also manifested higher degree of SCA variance as compared to GCA variance. Same trend was observed by Zebarth *et al.* (2002) and Costa *et al.* (2001).

Among the hybrids with significant SCA effects, the ones with high magnitudes were considered as superior. The hybrids from different combinations of the parents with high/low GCA effects are referred as H x H (High x High), H x L (High x Low) and L x L (Low x Low) combinations.Among 36 crosses, 19 crosses registered significant SCA effects, which ranged from -5.93 to 4.4 inSCMR. The estimates of SCA effects varied both in magnitude and direction. 10 crosses exhibited significant positive SCA effects (Table 3). The cross 1232 x CML-411 (H x H) had highest significant SCA effects followed by Mai-105 x HKI-193-2 (H x L) and NAI-137-2 x HKI-164-4-1-3 (L x H). The involvement of high combiners

Table 1 : Analysis of variance for drought tolerance attributing traits and yield in maize

Sources of variation		Mean sum of squares			
	d.f	SCMR values	Specific leaf area (SLA)	Free proline	Yield per plot (g)
Replication	1	34.70	1945.17	1.101	0.106
Genotypes	50	90.42**	660.63**	337.43**	2.84**
Parents	14	29.13**	896.21**	139.88**	2.1**
Hybrids	35	104.38**	515.77**	382.34**	2.88**
Parents vs. Crosses	1	459.75**	2432.82**	1531.3**	11.9**
Lines	11	284.03**	581.14**	909.78**	6.41**
Testers	2	26.94**	181.41	60.91**	0.75**
Line x Testers	22	21.6**	513.47	147.84**	2.1**
Error	50	1.34	212.11	1.38	0.07

**indicates significance of value at P=0.01

Table 2 : General combining ability effects of lines and testers for drought tolerance contributing characters and yield

Lines	SCMR values	Specific leaf area (SLA)	Free proline	Yield per plot (kg)
1232	-7.35**	6.71	-8.21**	-0.67**
1005	-6.40**	-1.11	-7.48**	-0.81**
1201	-6.95**	15.28*	-17.49**	-1.31**
1396	-8.93**	7.81	-19.93**	-1.69**
772-2	-8.08**	1.43	-10.51**	-0.86**
1410-1	8.82**	-6.56	3.61**	0.33**
2422	6.64**	4.81	6.22**	0.61**
262-55	2.34**	4.28	12.41**	0.98**
634-2	2.97**	-0.15	10.59**	0.78**
NAI-137-2	5.30**	-24.64**	17.16**	1.63**
MAI-105	5.29**	-4.36	3.21**	0.23**
SKV-50	6.35**	-3.50	10.42**	0.79**
S.E.±	0.50	6.39	0.47	0.10
C.D. (P=0.05)	0.98	12.52	0.92	0.20
C.D. (P=0.01)	1.29	16.46	1.21	0.26
Males				
HKI-164-4-1-3	1.13**	3.12	1.53**	0.08
HKI-193-2	-0.16	-1.08	-1.65**	-0.20**
CML-411	-0.97**	-2.05	0.12	0.12*
S.E.±	0.25	3.19	0.23	0.05
C.D. (P=0.05)	0.49	6.25	0.45	0.10
C.D. (P=0.01)	0.64	8.22	0.59	0.13

Table 3 : Specific combining ability effects of single cross hybrids for drought tolerant contributing characters and yield in maize

Single cross hybrids	SCMR values	Specific leaf area (SLA)	Free proline	Yield per plot (kg)
1232xHKI-164-4-1-3	-0.65	-4.06	0.76	0.04
1232xHKI-193-2	-3.75**	2.81	1.53	-0.03
1232xCML411	4.40**	1.25	-2.29**	-0.01
1005x HKI-164-4-1-3	1.00	7.30	5.92**	0.52**
1005x HKI-193-2	-0.20	-14.94	-0.55	0.15
1005x CML411	-0.80	7.64	-5.37**	-0.67**
1201x HKI-164-4-1-3	-0.60	17.06	4.39**	0.37*
1201x HKI-193-2	2.45**	-19.55	-2.63**	-0.40
1201x CML411	-1.85*	2.49	-1.76*	0.03
1396x HKI-164-4-1-3	-0.37	-14.87	-3.93**	-0.20
1396x HKI-193-2	2.08*	-9.77	-2.40**	0.19
1396x CML411	-1.72	24.64*	1.53	0.01
772-2x HKI-164-4-1-3	-4..87**	17.44	-12.44**	-0.88**
772-2x HKI-193-2	3.23**	-4.42	-1.62	-.25
772-2x CML411	1.63	-13.01	14.06**	1.13**
1410-1x HKI-164-4-1-3	-0.92	-10.60	5.19**	0.59**
1410-1x HKI-193-2	0.43	-0.61	12.47**	1.02**
1410-1x CML411	0.48	11.22	-17.66**	-1.61**
2422x HKI-164-4-1-3	3.62**	23.24*	-5.38**	-1.10**
2422x HKI-193-2	-0.14	-5.09	3.35**	064**
2422x CML411	-3.48**	-18.15	2.03*	0.46*
262-55x HKI-164-4-1-3	2.87**	2.15	-2.06*	-0.16
262-55x HKI-193-2	-1.79*	10.50	5.92**	0.62**
262-55x CML411	-1.08	-12.65	-3.86**	-0.46*
634-2x HKI-164-4-1-3	-1.27	-26.74*	6.36**	0.74**
634-2x HKI-193-2	-0.92	17.71	-6.97**	-0.98**
634-2x CML411	2.18*	9.03	0.61	0.24
NAI-137-2x HKI-164-4-1-3	3.75**	-3.07	-1.06	-0.06
NAI-137-2x HKI-193-2	-1.70	6.41	1.82*	0.27
NAI-137-2x CML411	-2.05*	-3.34	-0.76	-0.21
MAI-105x HKI-164-4-1-3	-5.93**	6.62	-2.01*	-0.26
MAI-105x HKI-193-2	4.06**	-0.68	-13.58**	-0.13**
MAI-105x CML411	1.87*	-5.94	15.59**	1.29**
SKV-50x HKI-164-4-1-3	3.35**	-14.46	4.27**	0.42*
SKV-50x HKI-193-2	-3.75**	17.64	-2.15*	-0.20
SKV-50x CML411	0.40	-3.18	-2.12*	-0.22

* and ** indicate of significance of values at P = 0.05 and P = 0.01, respectively

in first cross revealed the importance of additive gene action and high and low combiners in second and third crosses revealed significance of over dominance, epistasis genetic variance and non-additive gene action. Zebarth *et al.* (2002) also reported good specific combiner for this trait.

The magnitude of SCA effects in SLA (cm^2/g) ranged from -26.74 to 24.64. Among the crosses, 3 crosses recorded significant SCA effects of which the cross 634-2 x HKI-164-4-1-3 exhibited highest negative SCA effect. Whereas, 2 crosses 1396 x CML-411 followed by 2422 x HKI-164-4-1-3 exhibited high significant SCA effects in positive direction. The involvement of both high general combiners indicating importance of additive gene action. Markham and Stoltenberg (2009), Milla and Reich (2007) reported good specific combiners for this trait.

The SCA effects of crosses in proline content (μg g dry weight^{-1}) ranged from –17.66 to 15.59.Sixteen crosses recorded significant SCA effects in negative direction and twelve in positive direction. The crosses 1410-1 x CML-411and MAI-105 x HKI-193-2 recorded highest SCA effect in negative direction,whereas the crosses MAI-105 x CML-411 and 772-2 x CML-411 in positive direction

For grain yield per plant, the magnitude of SCA effects was from -1.61 to 1.29. Among thirty crosses, eleven crosses were in the positive direction. The crosses *viz.*, MAI-105 x CML-411 (H x H), 772-2 x CML-411 (L x H) and 1410-1 x HKI-193-2 (L x L) were top three specific combiners in the desirable direction. The first cross showed the additive gene action for this trait. In second cross non-additive gene action may be imperative and in the third cross involvement of parents both with low GCA indicating the importance of over

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dominance and epistasis for this trait.Ananth (2004) and Abhishek (2006) reported that grain yield per plot was predominantly governed by non-additive gene action.

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