Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2019; 8(6): 2498-2501
Received: 10-09-2019
Accepted: 12-10-2019

Muttappa Hosamani
University of Agricultural Sciences, Raichur, Bengaluru, Karnataka, India

I Shankergoud
University of Agricultural Sciences, Raichur, Bengaluru, Karnataka, India

PH Zaidi
International Maize and Wheat Improvement Center (CIMMYT)-Asia, ICRISAT Campus, Patancheru, Hyderabad, Telangana, India

Ayyanagouda Patil
University of Agricultural Sciences, Raichur, Bengaluru, Karnataka, India

MT Vinayan
International Maize and Wheat Improvement Center (CIMMYT)-Asia, ICRISAT Campus, Patancheru, Hyderabad, Telangana, India

PH Kuchanur
University of Agricultural Sciences, Raichur, Bengaluru, Karnataka, India

K Seetharam
International Maize and Wheat Improvement Center (CIMMYT)-Asia, ICRISAT Campus, Patancheru, Hyderabad, Telangana, India

Somasekhar
University of Agricultural Sciences, Raichur, Bengaluru, Karnataka, India

Corresponding Author:
PH Kuchanur
University of Agricultural Sciences, Raichur, Bengaluru, Karnataka, India

Genotypic variability in testcrosses derived from heat tolerant multi-parental synthetic populations of maize

Muttappa Hosamani, I Shankergoud, PH Zaidi, Ayyanagouda Patil, MT Vinayan, PH Kuchanur, K Seetharam and Somasekhar

Abstract
Understanding the genotypic variability, heritability and genetic advance of traits in any plant population is an important pre-requisite for selection programme. This study was designed to assess the genotypic variability, heritability and genetic advance for various characters of maize testcrosses derived from two heat tolerant multi-parental synthetic (MPS 1 and MPS 2) populations. The trial consisted of 407 testcrosses of MPS 1 and 475 testcrosses of MPS 2. They were evaluated in Alpha lattice design with two replications at Main Agriculture Research Station, Raichur, Karnataka during spring season where the most part of reproductive stage, starting from tassel emergence until late grain filling, was exposed to heat stress. Analysis of variance revealed that the mean sum of squares due to genotypes in MPS 1 differed significantly for grain yield and MPS 2 showed significant variation among genotypes for all the characters studied, indicating the presence of variability for all the traits in the germplasm utilized for present study. Phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the characters studied. High to moderate estimates of PCV and GCV were recorded for grain yield and anthesis-silking interval suggesting sufficient variability for the traits, thus offering scope for genetic improvement through selection. Heritability and genetic advance were low for all the traits. These results suggested that the traits *viz.*, days to 50 per cent anthesis, days to 50 per cent silking, anthesis-silking interval, plant height (cm), ear height (cm) and grain yield (t ha^{-1}) were under the control of non-additive gene action in both the MPS populations.

Keywords: Maize, testcrosses, multi-parent population (MPS), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (PCV), heritability and genetic advance

Introduction
Maize (*Zea mays* L.; 2n=20), the sole cultivated member of genus *Zea* and tribe *Maydeae,* ranks as one of the three important cereal crops in the world after wheat and rice. It is the principal staple food in many developing countries in tropics contributing in their food security and income. There is no cereal on the earth which has so immense potentiality and that is why it is called "Queen of Cereals". Most of the area under this crop is in the warmer parts of tropical regions and in humid-subtropical climate. Highest production is in area having the warmest month isotherms from 21^0 to 27 ^{0}C and a frost-free season of 120 to 180 days duration. It can be grown in soils ranging from 5.5 to 8.0 pH, but it is sensitive to salinity.

Globally, maize is cultivated in an area of 183.24 m ha with the production of 1036.07 m t and productivity of 5.65 t ha^{-1} (Anon, 2018) [3]. Among the maize growing countries, USA stands first followed by Brazil, China, Mexico. India stands sixth among the maize producing countries in the world with an area, production and productivity of 9.6 m ha, 27.15 m t and 2.83 t ha^{-1}, respectively (Anon, 2018) [3]. Further, 2.83 t ha^{-1} productivity is lower than world average, may be due to 70-75 per cent area is under rainfed condition, where, crop suffers from heat and/or drought stress. Karnataka is one of the major maize producing states in the country with an area of 1.18 m ha, production 3.27 m t and productivity 2773 kg ha^{-1} (Anon, 2017) [2]. The other states contributing to the national production are Madhya Pradesh, Uttar Pradesh, Bihar, Tamil Nadu, Maharashtra, Andhra Pradesh, Rajasthan and Gujarat.

Heat stress can be defined as exposure to temperatures (maximum and/or minimum) above a threshold level for a period of time that causes irreversible damage to crop growth and development and is a function of the intensity, duration and rate of increase in temperature (Zaidi *et al*., 2016) [16]. It has been predicted that growing season temperatures in the tropics and subtropics will exceed even beyond the most extreme seasonal temperatures so far (Battisti and Naylor, 2009) [4].

Maize is highly productive under optimal growing conditions and crop management conditions and does reasonably well under sub-optimal conditions, but susceptible to severe drought and heat. Every year an average of 15 to 20 per cent of the world maize production is lost due to drought and heat stresses. High temperatures have profound impact on yield compared to drought in maize (Lobell *et al*., 2011) [11]. Being grown is diverse conditions and throughout the year, maize is at highest risk of extreme temperatures compared to wheat and soybean worldwide (Deryng *et al*., 2014) [6].

The basic information on the existence of genetic variability and diversity in a population and the relationship between different traits is essential for any successful plant breeding programme. Genetic improvement through conventional breeding approaches depends mainly on the availability of diverse germplasm and presence of enormous genetic variability. The characterization and evaluation such diversity is the important pre-requisites for effective utilization of germplasm and also to identify sources of useful genes. An insight into the nature and magnitude of genetic variability present in the gene pool is of immense value for starting any systematic breeding programme because the presence of considerable genetic variability is the basis that ensures better chances of developing desirable plant type. Hence, an attempt was made to estimate the extent of variation for yield attributing traits in 405 testcrosses of MPS 1 and 470 testcrosses of MPS 2 by studying the genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance, for formulation of suitable selection indices for improvement of heat stress tolerance in maize. Keeping these points in view, the present investigation was undertaken to assess the genetic variability, heritability and genetic advance for various characters of maize testcrosses of multi-parental synthetic (MPS 1 and MPS 2) populations under heat stress condition.

Material and methods

The experimental material comprised of 405 $F_{2:3}$ testcrosses derived from MPS 1 which belongs to heterotic group A and crossed with tester CML 451 belongs to heterotic group B and 470 $F_{2:3}$ testcrosses from a heterotic group B population, *i.e.* MPS 2, crossed with tester CL02540 belongs to heterotic group A. The testcrosses of MPS 1 were evaluated along with two popular commercial checks (31Y45 and DKC9108), while the testcrosses of MPS 2 were evaluated with five popular commercial checks (31Y45, DKC9108, HTMH5401, NK6240 and Pio3396) in spring season in India. The testcrosses were evaluated in Alpha lattice design with two replications at Main Agriculture Research Station, Raichur, Karnataka during spring season, where trial was exposed to high temperature regime (Tmax 37 to > 40 ºC) during summer-2014 (March-May). Each entry was raised in single row of 4 m length with a spacing of 60 cm x 20 cm.

After thorough land preparation, sowing was done by hand dibbling of seeds with two seeds per hill and later thinned to retain one seedling per hill. Then the plot was irrigated. The recommended dose of fertilizers (150 N, 75 P_2O_5 and 37.5 K_2O kg ha^{-1}) was given to the crop. The entire dose of P_2O_5, K_2O and one third of nitrogen was applied as basal dose and remaining two-third nitrogen was top dressed in two equal splits at fourth and seventh week after planting. Standard package of practices were adopted to raise a healthy crop.

Phenotypic data were collected on days to 50 per cent anthesis, days to 50 per cent silking, anthesis-silking interval, plant height (cm), ear height (cm) and grain yield per plot (which was later scale to t ha^{-1} at 12% grain moisture).

Genetic variability was measured and subjected to statistical analysis as suggested by Panse and Sukhatme (1967) [13]. Heritability (broad sense) and genetic advance (GA) were worked by following the method suggested by Falconer (1981) [7] and Johnson *et al*. (1955) [8].

Results and discussion

Phenotypic and genotypic coefficient of variation in testcrosses of MPS populations

Genotypic variability plays an important role in crop breeding. An insight in to the magnitude of variability present in crop species is of utmost importance as it provides the basis of selection and further improvement. Genetic variability studies are also helpful to know about the nature and extent of variability that can be attributed to different causes, sensitivity of crop to environment, heritability of the character and genetic advance. The mean sum of squares due to genotypes showed highly significant differences for all the characters in MPS 2 and grain yield in MPS 1 population (Table 1) indicating the presence of adequate variability for improvement among the families. Similar results were reported by Angadi (2014), Ranganath (2015) [14] and Dinesh (2015) [5] under heat stress condition.

The estimates of mean, range, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean are presented in Table 2. The trait, plant height (108.33 to 176.65 cm) revealed highest range followed by days to 50 per cent silking (51.00 to 65.00), days to 50 per cent anthesis (48.50 to 60.50) and ear height (47.25 to 105.17 cm). While, the grain yield and anhesis-silking interval showed a range of 0.85 to 10.25 t ha^{-1} and 0.00 to 7.00 days, respectively in MPS 1. Whereas in MPS 2, plant height (75.83 to 191.00 cm) showed highest range followed by ear height (62.16 to 114.16 cm), days to 50 per cent silking (50.00 to 62.00), days to 50 per cent anthesis (48.00 to 58.50). While, the range for grain yield and anthesis-silking interval by 2.13 to 11.50 t ha^{-1} and-1.50 to 7.50 days, respectively. Hence, a breeder can concentrate more on these traits which can provide him ample scope for selection. Similar results have been reported by Angadi (2014) [1] and Ranganath (2015) [14] under heat stress condition.

The phenotypic coefficient of variation and genotypic coefficient of variation are presented in Table 2. As expected, the PCV values were greater than the GCV values for all the characters in MPS populations, indicating considerable influence of environment on the expression of these characters under field conditions. In MPS 1 and MPS 2, the values for PCV ranged from 4.51 to 41.66 per cent and 4.15 to 41.99 per cent, respectively. The values for GCV in MPS1 and MPS 2 obtained for different characters ranged from 0.77 to 19.37 per cent and 1.87 to 13.33 per cent, respectively. Among the trait studied in MPS 1 and MP 2 populations, the coefficients of variation at phenotypic and genotypic levels were high to moderate for grain yield and anthesis silking interval under heat stress condition indicating major role of additive gene action in the inheritance of these traits and hence phenotypic selection for these trait could be effective. Moderate PCV values but low GCV were recorded for plant height and ear height in MPS populations indicating the role of non-additive gene action in the inheritance of these traits. Similarly, days to 50 per cent anthesis and days to 50 per cent silking showed non-additive gene action as indicated by their low PCV and GCV values. Similar results were earlier reported by Khodarahmpour and Choukan (2011) [9], Khodarahmpour (2012) [10], Angadi (2014) [1], Ranganath (2015) [14] and Dinesh (2015) [5] under heat stress condition.

Rupinder Kaur and Saxena (2011) [15] also reported additive and non-additive gene actions for these traits under optimum and heat stress conditions.

Table 1: Analysis of variance for various characters in testcrosses derived from multi-parental synthetic (MPS 1 and MPS 2) populations of maize evaluated under heat stress condition

Source of variance	DF	MPS 1						DF	MPS 2					
		AD	SD	ASI	PH	EH	GY		AD	SD	ASI	PH	EH	GY
Replication	1	0.21	34.66	17.08	239.78	69.94	103.16	1	160.14	69.14	18.74	325.36	627.33	3.68
Block(Rep)	80	7.72	9.14	2.91	430.96	283.32	6.10	94	5.21	5.71	2.95	212.01	111.60	3.48
Treatments	406	5.44	7.54	2.44	293.10	179.97	5.33*	474	6.38**	6.63**	2.55**	210.268*	129.93*	4.96**
Error	326	5.18	8.07	2.48	305.80	178.61	4.23	380	3.56	4.01	1.91	175.53	107.61	3.83

* Significant at P =0.05, ** Significant at P =0.01

AD: Days to 50% anthesis; SD: Days to 50% silking; ASI: Anthesis to silking interval; PH: Plant height (cm); EH: Ear height (cm); GY: Grain yield (t ha-1)

Table 2: Variability parameters for various characters in testcrosses drived from multi-parental synthetic (MPS 1 and MPS 2) populations of maize evaluated under heat stress condition

Characters	MPS 1							MPS 2						
	Range		Mean	PCV (%)	GCV (%)	h^2_{bs} (%)	GA (%)	Range		Mean	PCV (%)	GCV (%)	h^2_{bs} (%)	GA (%)
	Min.	Max.						Min.	Max.					
Days to 50% flowering	48.50	60.50	53.64	4.51	0.95	4.50	0.22	48.00	58.50	52.97	4.23	2.22	27.60	1.27
Days to 50% silking	51.00	65.00	57.09	4.82	0.77	2.60	0.14	50.00	62.00	56.30	4.15	1.87	20.40	0.98
Anthesis-silking interval	0.00	7.00	3.45	37.79	10.53	7.80	0.20	-1.50	7.50	3.32	41.19	13.33	10.50	0.29
Plant height (cm)	108.33	176.65	147.32	12.34	1.26	1.10	0.39	75.83	191.00	161.08	9.38	3.08	10.80	3.35
Ear height (cm)	47.25	105.17	81.61	17.35	1.21	1.80	0.14	62.16	114.16	90.25	12.17	3.96	10.60	2.40
Grain yield (t ha^{-1})	0.85	10.25	5.57	41.66	19.37	21.60	1.03	2.13	11.59	6.98	29.44	10.05	11.70	0.49

PCV= Phenotypic coefficient of variation; GCV= Genotypic coefficient of variation; h^2_{BS}=Broad sense heritability; GA = Genetic advancement at 5 per cent level

Heritability and genetic advance

The effectiveness of selection for any yield component depends not only on the magnitude of variability, but also how much of it is heritable to the next generation. The coefficient of variation indicates only the extent of variation and does not discriminate the variability into heritable and non-heritable. Heritability value alone cannot provide information on the amount of progress that would result from selection of best individuals. Johnson *et al*. (1955) [8] reported that heritability estimates along with genetic gain would be more useful than the former alone in predicting the effectiveness of selecting the best individuals. Therefore, it is essential to consider the predicted genetic advance along with heritability estimate as a tool in the selection programme for better efficiency in the selection.

A relative comparison of heritability values and expected genetic gain expressed as percentage of mean gives an idea about the nature of gene action governing a particular character. High heritability coupled with high genetic advance reveals the presence of lesser environmental influence and prevalence of additive gene action in their expression of traits (Panse, 1957) [12]. But lower values of genetic advance indicate the prevalence of narrow range of variability, high G × E interaction or non-additive gene action. For moderate values of genetic advance, both additive and non-additive gene actions might be responsible for the expression of traits.

In the present investigation, all the character studied in MPS populations under heat stress condition showed low heritability coupled with low genetic advance indicating the influence of environmental effects on the traits thus implying for presence of non-additive gene action in the population. This may be due the high levels of heterozygosity existed in the population. Similar trends were observed under heat stress by Ranganath *et al*. (2015) [14] and Dinesh *et al.* (2015) [5] for anthesis-silking interval, ear length and ear girth.

It is concluded that genotypic variability in testcrosses derived from MPS 1 differed significantly for grain yield and MPS 2 showed significant variation among genotypes for all the characters studied, indicating the presence of variability for all the traits in the germplasm utilized for present study. PCV was in higher magnitude than GCV for all the characters under study. In MPS 1 and MP 2 populations, PCV and GCV levels were high to moderate for grain yield and anthesis-silking interval under heat stress condition indicating major role of additive gene action in the inheritance of these traits and hence phenotypic selection for these trait could be effective. Moderate PCV values but low GCV were recorded for plant height and ear height indicating the role of non-additive gene action in the inheritance of these traits. Similarly, days to 50 per cent anthesis and days to 50 per cent silking showed non-additive gene action as indicated by their low PCV and GCV values. Similarly, heritability and the genetic advance were also low for all the traits. These results suggest that these characters are under the control of non-additive gene action in the MPS populations under heat stress condition.

Acknowledgements

Technical support and valuable germplasm provided for this study under ‘Heat tolerant maize for Asia’ project funded by United State Agency for International Development (USAID) is duly acknowledged.

Reference

1. Angadi S. Evaluation of maize (*Zea mays* L.) inbred lines and hybrids for heat tolerance. M. Sc. (Agri.) Thesis, Univ. Agric. Sci., Raichur, Karnataka (India), 2014.
2. Anonymous. Ministry of Agriculture, Govt. of India, 2017. www.indiastat.com.

3. Anonymous. World agricultural production. USDA, Washington, DC, 2018, 1-31.
4. Battisti DS, Naylor RL. Historical warnings of future food insecurity with unprecedented seasonal heat. Science. 2009; 323:240-244.
5. Dinesh A. Genetic architecture of reproductive traits in tropical maize under heat stress situation. M. Sc. (Agri.) Thesis, Univ. Agric. Sci., Raichur, Karnataka (India), 2015.
6. Deryng D, Conway D, Ramankutty N, Price J, Warren R. Global crop yield response to extreme heat stress under multiple climate change futures. Environ. Res. Lett. 2014; 9:e03-4011.
7. Falconer DS. Introduction to quantitative genetics. 2nd Edition, Longman Group Ltd., Longman House, Harrow, England, 1981, 350.
8. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agron. J. 1955; 47:314-318.
9. Khodarahmpour Z, Choukan R. Study of the genetic variation of maize (*Zea mays* L.) inbred lines in heat stress condition using cluster analysis. Seed and Plant J. 2011; 4:1-27.
10. Khodarahmpour Z. Morphological classification of maize (*Zea mays* L.) Genotypes in heat stress condition. J Agri. Sci, 2012, 1-14.
11. Lobell DB, Banziger M, Magorokosho C, Vivek B. Nonlinear heat effects on African maize as evidenced by historical yield trials. Nature Climate Change. 2011; 1:42-45.
12. Panse VG. Genetics of quantitative characters in relation to plant breeding. Indian J Genet. 1957; 17:318-328.
13. Panse VG, Sukhatme PV. Statistical Methods for Agricultural Workers, 2nd Ed. ICAR publication, New Delhi, India, 1967, 381.
14. Ranganatha CN. Early generation testing in maize for heat stress tolerance. M. Sc. (Agri.) Thesis, Univ. Agric. Sci., Raichur, Karnataka (India), 2015.
15. Rupinder Kaur, Saxena VK. Genetics of heat tolerance traits in spring maize (*Zea mays* L.). Indian. J Pl. Physiol. 2011; 168(16):1987-1992.
16. Zaidi PH, Zaman-Allah M, Trachsel S, Seetharam K, Cairns JE, Vinayan MT. Phenotyping for abiotic stress tolerance in maize heat stress: a field manual, CIMMYT, Asia, Hyderabad, India, 2016, 1-32.