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Genetic Analysis of Grain Yield, its Components and Grain Micronutrients

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A B S T R A C T

This study aimed to find the gene action, GCA and SCA effects for yield, its components and micronutrients and their association with each other. For this, thirty six crosses (hybrids), nine parents and two checks ICTP 8203 Fe and ICMB 98222 (totalling 47 genotypes) were evaluated during *Kharif* 2014 at three locations *viz*., IARI, New Delhi (zone A), IARI Regional Centre, Dharwad (zone B) and National Bureau of Plant Genetic Resources, Regional Station, Jodhpur (zone A_1). These locations represented all pearl millet growing zones. Pooled analysis of variance revealed significant differences among genotypes for all the traits studied. Analysis of variance for combining ability exhibited significant differences among parental lines and hybrids for all the traits. The mean squares of GCA and SCA were highly significant for all the traits indicating that both GCA and SCA played an important role in the inheritance of these traits. Thus, the present study highlighted gene action and association among yield and its contributing traits as well as grain micronutrients. Two (ICMR 07999 x IPC 1518 and ICMR 07999 x PPMI 701) of the four hybrids that showed high significant SCA effects for seven traits were also found adaptable over test environments for one or more traits.

Introduction

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] Is a major warm season cereal grown on more than 27 million ha in some of the harshest environments in the arid and semi-arid tropical regions of Africa (17 million ha) and Asia (10 million ha).

Yield is a complex trait dependent on different component traits.

Some of the traits have greater effect on grain yield than others.

To know the relative importance of component traits, association of these traits with grain yield can be estimated.

Materials and Methods

Plant material used for generation of new crosses

The basic experimental material consisted of nine elite inbred/restorer lines *viz*., HTP 94/54, H77/833-2-202, ICMR 06222, ICMR 07999, IPC 1518, PPMI 162, PPMI 295, PPMI 683 and PPMI 701.

Development of experimental crosses

Above mentioned selected lines were crossed in half diallel fashion at ICAR-IARI, Regional Centre, Dharwad during *summer* 2014 and thirty-six crosses were generated excluding reciprocals.

Field evaluation

Field trials of these thirty six hybrids, nine parents and two checks ICTP 8203 Fe and ICMB 98222 were conducted at three locations namely ICAR-Indian Agricultural Research Institute, New Delhi, ICAR-IARI Regional Centre, Dharwad and ICAR-National Bureau of Plant Genetic Resources, Regional Station, Jodhpur. These locations were decided by taking into consideration all the pear millet growing zones.

For example Jodhpur represents the A_1 zone, Delhi, the A zone and Dharwad represents B zone. Forty-five entries along with two checks were evaluated in Randomized Complete Block Design with three replications at all the three locations.

The plot size for each entry consisted of two rows of 4 meter length. Distance between rows was 50 cm and plant to plant was 12 cm. All the normal cultural practices were followed during the crop growing period.

Data recorded on various traits were subjected to analysis and softwares SAS 9.3, OPSTAT and Genstat 14.0 version, VSN International were used.

After testing the error variance for homogeneity, the data over locations were combined and analysis was performed.

For combining ability analysis, thirty six hybrids and nine parents were used and two check varieties were not included. The estimates of general combining ability (GCA) and specific combining ability (SCA) effects were obtained following Griffing's method 2 model 1 (fixed model) (Griffing 1956), which included F_1s and parents. Significance of GCA and SCA was determined by a t- test (Griffing, 1956).

Both GCA and SCA effects were estimated from inbred parents and crosses respectively. Since the combining ability mean squares were calculated based on cross means of each genotype from each location, error mean squares calculated for crosses were used to test the significance of GCA and SCA interactions with location.

The GCA effects of parents were calculated as a deviation of the parents mean from all hybrids' mean following Singh and Chaudhary (1985).

The SCA effects were calculated as a deviation of each cross mean from all hybrids' means adjusted for corresponding GCA effects of parents.

The SCA effects were also computed as suggested by Singh and Chaudhary (1985).

Results and Discussion

Analysis of variance

The analysis of variance for eleven characters *viz*., days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), panicle girth (cm), number of productive tillers per plant, panicle weight (gm), 1000- grain weight (gm), grain yield (q/ha), iron and zinc content in grain (Tables 1–3).

Highly significant differences were observed for all the traits at Delhi. However, number of effective tillers per plant was the exception at Dharwad and Jodhpur locations. After testing the homogeneity of error variance, the data across locations was pooled. The pooled analysis of variance showed significant differences among genotypes for all the characters.

Table.1 Analysis of variance for different traits across three test locations

Traits	Location	Genotypes	EMS	LSD	C.V.
d. f.	2	46	92		
Days to 50% flowering	164.36	12.00**	4.47	0.28	2.46
Days to maturity	155.62	11.07**	1.54	0.29	1.59
Plant height (cm)	3716.50	10783.88**	61.18	1.83	4.68
Panicle length (cm)	1456.97	88.11**	3.22	0.42	7.92
Panicle girth (cm)	4.61	1.44**	0.02	0.03	6.51
Number of effective tillers per plant	55.20	0.81**	0.46	0.16	24.48
Single panicle wt. (gm)	6.98	77.99**	3.64	0.45	5.82
1000- grain wt. (gm)	16.23	7.42**	0.31	0.13	6.29
Grain yield (q/ha)	547.24	143.22**	7.49	0.64	8.78
Iron (ppm)	2455.62	897.54**	27.50	1.23	9.10
Zinc (ppm)	27973.33	232.75**	25.57	1.19	13.59

Table.2 Analysis of variance and mean squares of the crosses and parents

S.N.	Traits	Replication	Genotypes	Error
	d. f	2	44	88
1	Days to 50% flowering	13.47	8,232.82**	5.03
2	Days to maturity	15.48	8,790.72**	3.87
3	Plant height (cm)	24.43	6,618.10**	7.21
4	Panicle length (cm)	94.95	5,468.68**	39.61
5	Panicle girth (cm)	7.18	7,776.86**	8.48
6	Number of effective tillers per plant	7.53	7,267.04**	5.49
7	Single panicle wt. (gm)	2.02	6,761.80**	5.67
8	1000- grain wt. (gm)	6.58	6,938.45**	4.40
9	Grain yield (q/ha)	6.14	5,693.95**	4.85
10	Iron (ppm)	1.43	5,010.82**	3.51
11	Zinc (ppm)	3.15	3,992.34**	4.35

Table.3 Analysis of variance and mean squares for combining ability

S.N.	Traits	GCA	SCA	Error
	d.f	8	36	88
1	Days to 50% flowering	5,999.36**	8,729.14**	1.68
2	Days to maturity	13992.74**	7634.72**	1.29
3	Plant height (cm)	7,563.76**	6,407.95**	2.40
4	Panicle length (cm)	5,690.22**	5,419.45**	13.20
5	Panicle girth (cm)	4,780.81**	8,442.65**	2.83
6	Number of effective tillers per plant	6,357.21**	7,469.22**	1.83
7	Single panicle wt. (gm)	8,174.75**	6,447.82**	1.89
8	1000- grain wt. (gm)	8,548.35**	6,580.69**	1.47
9	Grain yield (q/ha)	6,233.61**	5,574.02**	1.62
10	Iron (ppm)	3,417.89**	5,364.80**	1.17
11	Zinc (ppm)	2,099.48**	4,412.98**	1.45

The mean squares of GCA and SCA were highly significant for all the traits indicating that both GCA and SCA played an important role in the inheritance of these traits. Preponderance of additive gene action was observed for days to maturity, plant height, panicle length, single panicle weight, 1000-grain weight and grain yield. However, characters like days to 50% flowering, panicle girth, number of effective tillers per plant, iron and zinc content in grain showed non-additive gene action. GCA effects indicated that none of the parents was good combiner for all the eleven traits. Parent HTP 94/54 was observed to be good combiner for five traits. Similarly, H77/833-2-202, IPC 1518 and PPMI 162 were identified as good combiners for four traits.

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