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Genetic Variability for Grain Iron, Zinc and Yield Contributing Traits in Pearl Millet [*Pennisetum glaucum* (L.) R. Br.]

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Genetic variability of grain iron, zinc, yield and its contributing traits in pearl millet were

studied in 30 genotypes (R-line). An experiment was carried out during *Kharif*-2018 at the Research Farm of ICAR-AICRP on Pearl Millet, Project Coordinating Unit, Mandor,

Jodhpur. Analysis of variance showed high significant variance among the genotypes for

all the characters, under study, indicated availability of wide spectrum of variability among

the genotypes. Highest magnitudes of PCV and GCV were observed for zinc content

whereas, the lowest for days to maturity. High estimate of heritability along with high genetic advance as percentage of mean were observed for days to 50% flowering, plant

height, number of productive tiller per plant, panicle length, panicle diameter, stover yield per plant, grain yield per plant, 1000 grain weight, harvest index, iron content and zinc

content suggested additive gene action for expression of these characters. Hence, these

characters may be proved as effective criteria for selection to improve seed yield in pearl

millet whereas high heritability values with moderate genetic advance as percentage of

ABSTRACT

Keywords

Pearl Millet, Genetic variability; Heritability; Genetic advance, Iron, Zinc, Yield

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Introduction

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is commonly known as Bajra, Cat-tail or Bulrush millet in different parts of the world. It belongs to family Poaceae (Gramineae). Pearl millet is a diploid species having chromosomes number 2n=14. It is a highly cross-pollinated crop due to protogynous nature.

Pearl millet is an outstanding crop and is endowed with enormous variability for agronomically important traits in populations adapted to diverse agro-ecological conditions. Pearl millet is an important cereal crop in an arid and semi-arid region of the world. It is predominantly grown as a staple food grain and source of feed and fodder. It is believed to have originated in Africa (Vavilov, 1950), from where it's spread to India and other

mean were observed for days to maturity and protein content.

countries. Indian subcontinent is the largest producer of Pearl millet.

The grain contains 8.5 to 15 percent protein, 5.03 to 6.0 percent fat, 5 to 70 percent carbohydrates, Fe content ranging from18 to 135 ppm and Zn content 22 to 92 ppm (Rai *et al.*, 2012). Micronutrients, including iron and zinc, are essential elements for a balanced human nutrition, required in small amounts. These two minerals are essential for human well-being and an adequate iron and zinc supply helps prevent, respectively, iron deficiency anemia and strengthen the immune system, which are two frequent problems in developing countries (Blair *et al.*, 2009).

In 2017-18, pearl millet was cultivated in country on about 7.5 million hectares with a production of 9.07 MT and an average productivity of 1305 kg/ha (Anonymous, 2017-18). Rajasthan, Gujarat, Uttar Pradesh and Haryana are the major pearl millet growing states in India. In the state of Rajasthan, the area under this crop is 42.36 lakh ha, which is 56.48% of the national acreage. The total production of pearl millet in the state is 48.40 lakh tonnes, which is 53.36% of the national production with an average productivity of 1143 kg/ha (Anonymous 2017-18).

Genetic variability defined as the formation of individuals differing in genotype, or the genotypically different presence of individuals, in contrast to environmentally induced differences which, as a rule, cause only temporary, nonheritable changes of the phenotype. The possibility of achieving improvement in any crop plants depends on magnitude of genetic variability. the Heritability specifies the proportion of the genotypic variance to the total phenotypic variance. It is a good index for the transmission of characters from parents to the offspring's (Falconer, 1960).

Genetic advance is the difference between the mean genotypic value of selected lines and mean genotypic value of parental population (original population before selection). The study of genetic advance is equally important as it measures the genetic gain based on the selection in a particular character. High genetic advancement coupled with high heritability estimates offers the most suitable condition for selection (Johnson et al., 1955). improvement Therefore, for any crop programme through selection, the study of genetic variability and heritability together with genetic advance will be more useful.

Materials and Methods

The investigation was conducted during the principal cropping season; kharif-2018, at Research farm of ICAR-AICRP on Pearl Millet, Project Coordinating Unit, Mandor, Jodhpur. The material comprised of 30 genotypes (R-line) of pearl millet which were sown in a Randomized Block Design (RBD) with three replications. Each genotype was sown in 4 m length of two rows with spacing of 60 cm between rows and 15 cm between plants. The recommended agronomic practices were followed to raise a good crop. The observations were based on the five randomly selected plants from each genotype and replication for different agromorphological traits *i.e.* plant height (cm), number of productive tillers per plant, panicle length (cm), panicle diameter (cm), stover yield per plant (g), grain yield per plant (g), 1000-grain weight (g) and harvest index (%). The observation for days to 50% flowering and days to maturity was recorded on the plot basis. Iron and Zinc estimation was done by using Atomic Absorption Spectrophotometer by following the method proposed by Jackson (1973). While, the nitrogen content of pearl millet genotypes was determined by the Kjeldhal method using a KEL PLUS distillation unit (Pelican Equipment, Chennai,

India). The crude protein content of the sample was calculated as 6.25 times its nitrogen content and expressed as percentage. The data was subjected to analysis of variance (Panse and Sukhatme, 1985), coefficients of variation (Burton, 1652 and Johnson *et al.*, 1955), heritability in broad sense and genetic (Johnson *et al.*, 1955) as per the standard statistical methods. Statistical analysis was performed using WindoStatversion 9.1 software.

Results and Discussion

In the present study, the analysis of variation showed highly significant differences among the genotypes for all the 13 characters indicating the existence of considerable genetic variation in the 30 genotypes of pearl millet. The analysis of variance (Table 1) showed highly significant differences among the genotypes for all the thirteen traits viz., days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, panicle length (cm), panicle diameter (cm), stover yield per plant (g), grain yield per plant (g), 1000-grain weight (g), harvest index (%), protein content (%), iron content (ppm) and zinc content (ppm) indicating the presence of considerable genetic variability among the experimental material. Present results showed similar trend with earlier reported by Sumathi *et al.*, (2010), Amiribezadi et al., (2012), Mukesh et al., (2013), Subi and Idris (2013), Vinodhana et al., (2013), Bika and Shekhawat (2015), Sumathi et al., (2016), Bhasker et al., (2017), Nehra et al., (2017), Kausik et al., (2018) and Sharma *et al.*, (2018).

High magnitudes of PCV and GCV were observed (Table 2) for the traits viz., zinc content recorded PCV (42.63%) and GCV (42.01%) followed by number of productive tiller per plant (38.31%, 35.33%), grain yield per plant (36.30%, 32.51%), stover yield per plant (35.80%, 31.76%), iron content (33.65%, 33.31%), 1000 grain weight (27.85%, 26.99%), panicle length (24.66%, 24.22%), panicle diameter (24.41%, 23.14%) and harvest index (24.10%, 21.51%). These results indicated greater scope for selection of these characters for further improvement programme because of substantial variability present in genotypes (R-lines) for these traits. This finding is substantiated by similar results reported by Sumathi et al., (2010) reported high GCV and PCV for the trait panicle length, panicle diameter, plant height, grain yield per plant and number productive tiller per plant, Vinodhana et al., (2013) reported high GCV and PCV for grain yield per plant, panicle length, 1000 grain weight and number of productive tiller per plant. Nehra et al., (2017) reported high GCV, PCV for panicle diameter, number of productive tiller per plant and 1000 grain weight. Talawar et al., (2017) reported the high values of GCV, PCV for number of productive tiller per plant, panicle length and grain yield per plant.

Moderate GCV and PCV reported for plant height (17.64%, 16.78%) and days to 50 % flowering (13.45%, 13.02%), this result indicates that there was the little role of an environmental component in the observed variation. Similar results found by Bika and Shekhawat (2015) reported moderate GCV, PCV for trait days to 50 % flowering, plant height. Talwar *et al.*, (2017) also reported moderate GCV, PCV for plant height and days to 50 % flowering.

Low GCV and PCV were reported for protein content (9.80%, 8.08%) and days to maturity (6.61%, 6.48%). That indicated the selection of these characters might not be effective. Similar works were reported by Choudhary *et al.*, (2012) report low GCV, PCV for protein content. Bhasker *et al.*, (2017) reported low GCV and PCV for days to maturity.

Source	DF	Mean sum of squares												
		Days to	Days to	Plant	Number	Panicle	Panicle	Stover	Grain	1000	Harvest	Protein	Iron	Zinc
		50%	maturity	height	of	length	diameter	yield per	yield per	grain	index	content	content	content
		flowering		(cm)	productive	(cm)	(cm)	plant (g)	plant (g)	weight	(%)	(%)	(ppm)	(ppm)
					tillers per					(g)				
					plant									
Replication	2	6.34	1.20	58.03	0.27	1.61	0.05	314.07	54.53	0.50	0.27	1.24	16.63	22.01
Genotype	29	130.65**	89.6**	1507.92**	2.83**	66.3**	0.75**	1622.42**	251.91**	12.44**	119.17**	3.01**	863.32**	795.87**
Error	58	2.83	1.19	50.90	0.16	0.80	0.03	134.21	19.166	0.26	9.35	0.41	5.80	7.91
*, ** significant at 5% and 1% levels, respectively														

Table.1 Analysis of variance (ANOVA) for grain iron, zinc, yield and its contributing traits

Table.2 Mean, Range, Genotypic and Phenotypic coefficient of variation, Heritability (broad sense) and Genetic advance as % of mean for grain iron, zinc, yield and its contributing traits

Character	Mean	Range		Coefficient	of variation	Heritability (%)	Genetic advance	
		Min	Max	Genotypic	Phenotypic	(broad sense)	as % mean at 5%	
Days to 50% flowering	50	34	66	13.02	13.45	93.78	25.98	
Days to maturity	84	77	101	6.48	6.61	96.12	13.09	
Plant height (cm)	131.3	92.9	188.4	16.78	17.64	90.51	32.89	
Number of productive tillers per	2.7	1.0	4.3	35.33	38.31	85.05	67.12	
plant								
Panicle length (cm)	19.3	12.1	31.5	24.22	24.66	96.46	49.01	
Panicle diameter (cm)	2.1	1.5	3.2	23.14	24.41	89.94	45.22	
Stover yield per plant (g)	70.1	30.2	133.5	31.76	35.80	78.71	58.04	
Grain yield per plant (g)	27.1	9.0	47.5	32.51	36.30	80.19	59.97	
1000 grain weight (g)	7.5	4.2	14.9	26.99	27.85	93.95	53.89	
Harvest index (%)	28.1	12.3	40.5	21.51	24.10	79.66	39.55	
Protein content (%)	11.5	9.3	13.8	8.08	9.80	67.92	13.71	
Iron content (ppm)	50.6	29.7	106.1	33.31	33.65	98.01	67.94	
Zinc content (ppm)	38.6	19.2	96.7	42.01	42.63	97.08	85.26	

In the present study, high heritability coupled with high genetic advance as per cent of mean were observed for days to 50% flowering, plant height, number of productive tiller per plant, panicle length, panicle diameter, stover yield per plant, grain yield per plant, 1000 grain weight, harvest index, iron content and zinc content indicating lesser influence of environment in expression of these characters and may be governed by additive gene action, hence effective for simple selection. Similar results were in accordance with Vinodhana *et al.*, (2013), Bika and Shekhawat *et al.*, (2015), Nehra *et al.*, (2017).

High heritability with moderate genetic advance as percent of mean was recorded for the characters *viz*, days to maturity and protein content. This indicates the presence of additive and dominance gene action and hence selection would be ineffective for these traits. These findings were reported by Choudhary *et al.*, (2012).

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