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Genetic variability, heretability and genetic advance studies for yield and yield related traits in pearlmillet [*Pennisetum glaucum* (L.) R. Br.]

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Abstract

The study was initiated to determine the genetic variability, heritability and genetic advance analysis for yield and yield related traits. The materials comprised of nine parents *viz.*, RVS-08/6, R-16419, R-15114, R-15134, R-15261, R-15510, R-15762, R-18428, ASRT-111 and their 36 F_1's developed through half diallel cross. The trial was carried out in randomized block design (RBD) with two replications. Heritability is a measure of possible genetic advancement under selection. Some characters recorded high value of heritability and genetic advance, indicating effectiveness in selection of these traits. Higher heritability was observed for Seed setting %, panicle length, panicle index per plant, plant height, days to 50% flowering and effective tiller per plant, pollen viability %, grain yield per plant while moderate heritability exhibited for canopy temperature at vegetative stage, canopy temperature at post anthesis and flag leaf temperature. Higher genetic advance as per cent of mean was found for three characters that is for effective tillers per plant, panicle length and grain yield per plant. The moderate genetic advance was found for plant height that makes simple selection should lead to a fast genetic improvement of the genotypes used in this study.

Keywords: Genetic variability, heretability, genetic advance,pearlmillet, traits

Introduction

Pearlmillet [*Pennisetum glaucum* (L.) belongs to the family poaceae and genus *Pennisetum.* It is a highly cross pollinated crop with protogynous flowering. It is diploid (2n=2x=14) in nature and commonly known as Bajra, cat tail millet and Bulrush millet in different part of the world. (Lakshmana, 2008) [13]. Pearl millet is a rich source of protein, calcium, phosphorus and iron Jambunathan *et al.,* (1988) [10] and Rai *et al.,* (1999) [17]. In spite of having superior nutritional quality, the people of developing countries who consume this cereal are subjected to severe malnutrition owing to some of its inherent defects. For instance, these contains some antinutritional factors such as polyphenols, goittrogen and phytic acid. These factors reduce bioavailability of nutrients present in crop produce or induce other toxic effects (Gibson *et al.*, (2000) [8] and Gargari *et al.*, (2007) [7]. It is world's sixth and India's fourth important cereal food crop after rice, wheat and maize. Pearl millet is an important food and fodder crop of short duration in India (Govindaraj *et al.*, 2011) [9]. Pearl millet accounts for about 50% of the total global production of millets. India is the largest single producer of the crop, both in terms of area (7million hectares) and production (9.25 million tons) (Anonymous 2015) [1]. In India mainly cultivated in the states of Rajasthan, Uttar Pradesh, Maharashtra, Haryana, Gujarat, Madhya Pradesh, and Tamil Nadu. Progress of any crop improvement depends mainly on the magnitude of genetic variability and heritability present in the source material. The extent of variability is measured by GCV and PCV which provides information about relative amount of variation in different characters. Hence, to have a thorough comprehensive idea, it is necessary to have an analytical assessment of yield components. Since heritability is also influenced by environment, the information on heritability alone may not help in pin pointing characters enforcing selection. Nevertheless, the heritability estimates in conjunction with the predicted genetic advance will be more reliable (Johnson *et al.*, 1955) [11]. Heritability gives the information on the magnitude of inheritance of quantitative traits, while genetic advance will be helpful in formulating suitable selection procedures (Sumathi *et al.*, 2010) [24].

Materials and Methods

The experimental material used in the present study comprised of thirty six hybrids obtains from nine parents (RVS-08/6, R-16419, R-15114, R-15134, R-15261, R-15510, R-15762, R-18428, and ASRT-111) through half diallel mating design and material were evaluated in a completely randomized block (RCBD) design with two replications at Research Farm College

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Agriculture, Gwalior during *kharif*-2015. Each entry was sown in single row of 1 m length adopting a row spacing of 50 cm. Observations were recorded on five plants basis. The observations were recorded on days to 50% flowering, canopy temperature at post anthesis stage (°C), pollen viability (%), flag leaf temperature (°C), Plant height (cm), effective tillers per plant, canopy temperature at vegetative stage (°C), panicle length (cm), seed setting (%), panicle index per plant (%) and grain yield per plant (g).

Statistical analysis
Analysis of variance was analyzed by following the procedure given by Panse and Sukhatme (1967) for randomized block design. The phenotypic and genotypic coefficients of variation in per cent were computed by the following formulae given by Burton (1952) [5].

$$GCV\% = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

$$PCV\% = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

Where
PCV = Phenotypic coefficient of variation
GCV = Genotypic coefficient of variation
The coefficient of variation were categorized as proposed by Sivasubramanian and Madhava Menon (1973) [21].

0-10%	- Low
10-20%	- Moderate
>20%	- High

The heritability estimate of a trait was computed as the ratio between estimate of genetic variance and phenotypic variance. Coefficient of variability (CV), Heritability (Broad Sense) and Genetic Advance estimate was worked out as procedures outline by Singh and Chaudhry (1985) [20].

$$\text{Heritability (h}^2\text{)} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

Heritability values are categorized as low, moderate and high (Robinson *et al*., 1949) [18] and are given below,

0-30%	- Low
30-60%	- Moderate
60% and above	- High

The estimates of expected genetic advance from selection, G(s), was obtained by the formula suggested by Robinson *et al.*, (1949) [18].

$$G(s) = k \times h^2 \times \sigma_p$$

Where' k = Selection differential in standard deviation units which is 2.06 for 5% selection intensity, h^2 = Heritability in broad sense, and σ_p = Phenotypic standard deviation
Genetic advance was expressed as percentage of mean by using the formula suggested by Johnson *et al*., (1955) [11].

$$\text{Genetic advance as percentage of mean} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

Genetic advance as percent of mean was classified as low, moderate and high (Johnson *et al*., 1955) [11] and values are given below:

| 0-10% | - Low |
| 10-20% | - Moderate |
| 20% and above | - High |

Results and Discussion
Analysis of variance (Table1) exhibited significant differences among the studied traits, which revealed that sufficient variability was observed for days to 50% flowering, canopy temperature at post anthesis, pollen viability %, flag leaf temperature, plant height, tillers per plant, canopy temperature at vegetative stage panicle length, seed setting, panicle index and grain yield per plant. Naik *et al.,* (1996) reported similar result in their experiment. The GCV, PCV, Heritability and genetic advance presented in (Table 2). Almost equal magnitude of GCV and PCV showed for days to 50% flowering, pollen viability %, plant height, panicle length, seed setting %, and panicle index per plant indicating that these characters are less influenced by the environment. While, canopy temperature at post anthesis, flag leaf temperature, effective tillers per plant and canopy temperature at post anthesis exhibited high value of PCV over its GCV value, indicating large amount of variation for these characters were due to environment only. Present finding are in confirmation with Sumathi *et al.,* (2010) [24], Drabo *et al*., (2013) [6], Subi *et al.,* (2013) [23], Sathya *et al.*, (2014) [19] and Kumar *et al.,* (2015) [19]. High heritability was observed for Seed setting, panicle length, panicle index per plant, plant height, days to flowering, effective tiller per plant, pollen viability, and grain yield per plant. While, moderate heritability exhibited for canopy temperature at vegetative stage, canopy temperature at post anthesis, and flag leaf temperature. Since heritability estimates are influenced by environment, genetic material and also other factors hence their utility will be restricted. Thus, heritability values coupled with genetic advance would be more reliable and useful in formulating selection criteria. Present finding are in confirmation with Lakshman and guggari (2001) [14] and Mahawar *et al.,* (2003) [15]. High estimates of heritability value coupled with high genetic advance were recorded for traits effective tillers per plant, panicle length and grain yield per plant indicating the presence of additive variances and suggested simple mass selection for the improvement of these traits. Present finding were confirmed with Aryana *et al.,* (1996) [2], Solanki *et al*., (2002) [22], Bortkhataria *et al.,* (2005), Varu *et al.*, (2005) [25] and Bhoiet *et al*., (2008). Heritability will provide the magnitude of inheritance of characters, while genetic advance is useful to formulate the suitable selection strategies. When the selection is based on both the high heritability combined with high genetic advance for the character will be more consistent and useful. A wide range of variation observed in the population would provide a huge chance of exploiting qualitative and quantitative traits for the development of new pearl milletrosses.

Table 1: Analysis of variance for yield and its attributing characters of parents and their different crosses in Pearl millet

Source of Variation	df	Days To 50% Flowering	Canopy Temp. at Post Anthesis (°C)	Pollen Viability (%)	Flag Leaf Temp. (°C)	Plant Height (Cm)	Effective Tillers Per Plant	Canopy Temp. at Vegetative Stage (°C)	Panicle Length (cm)	Seed Setting (%)	Panicle Index Per Plant (%)	Grain Yield Per Plant (g)
Replication	1	0.54	1.10**	0.10	2.27**	0.02	0.04	1.43**	1.55	3.60*	7.98	80.28
Genotypes	44	2.69**	0.24**	5.40**	0.35**	153.46**	0.36**	0.62**	9.54**	20.27**	15.79**	165.13**
Crosses	35	1.22**	0.10	5.52**	0.32**	119.43**	0.34**	0.21	8.70**	20.95**	14.97**	142.33**
Parents	8	0.88**	0.36**	1.48	0.37*	66.25**	0.16**	1.34**	1.38*	2.75**	20.66**	257.15**
C vs P	1	68.82**	3.90**	32.46**	1.20**	2042.04**	2.74**	9.37**	104.37**	136.41**	5.68	226.89**
Error	44	0.26	0.08	1.44	0.13	10.81	0.04	0.19	0.39	0.56	2.39	34.12

*, ** significant at 5% and 1% level respective
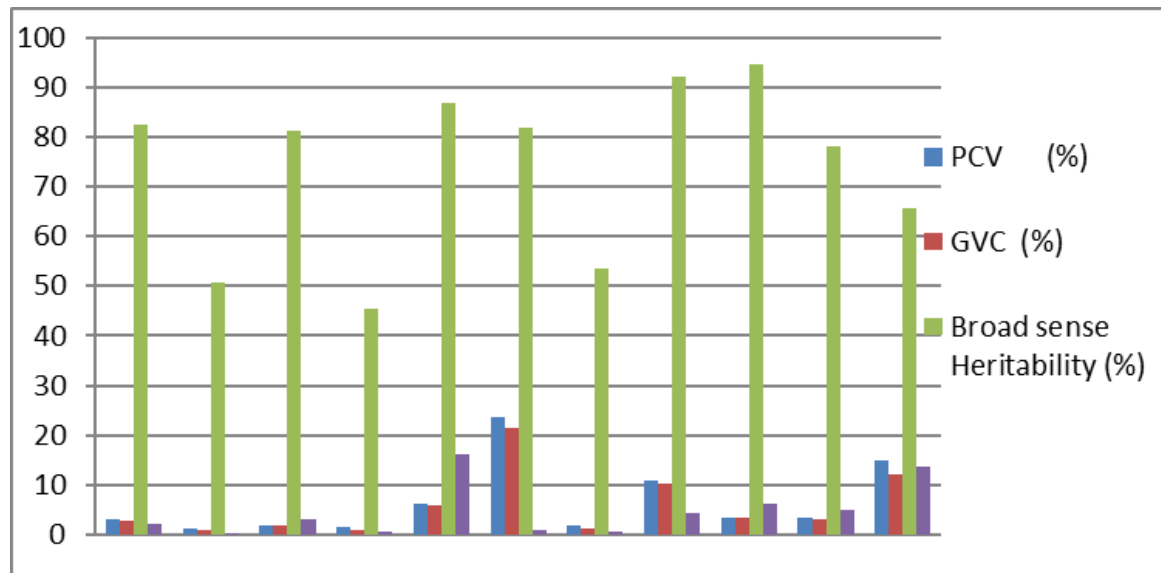
Fig 1: Variability present among various traits of pearl millet parents and their different crosses in Pearl millet

Table 2: Analysis of Genetic parameters for yield and its attributing characters of parents and their different crosses in Pearl millet

S. No	Characters	Mean	Range	PV	GV	PCV (%)	GCV (%)	Broad sense Heritability (%)	Genetic advance	Genetic advance as % of mean
1	Days to 50% flowering	40.37	37.7-42.7	1.48	1.22	3.01	2.73	82.44	2.06	5.11
2	Canopy temp. at post anthesis (°C)	32.16	31.3-32.6	0.16	0.08	1.23	0.88	50.58	0.41	1.28
3	Pollen viability %	94.96	92.2-99.8	3.67	2.98	1.95	1.48	81.14	3.20	3.25
4	Flag Leaf Temp. (°C)	34.24	33.4-35.8	0.24	0.11	1.43	0.97	45.33	0.46	1.34
5	Plant height (cm)	147.21	130.4-158.6	82.13	71.33	6.16	5.74	86.84	16.21	11.01
6	Effective tillers per plant	1.89	1.1-2.8	0.20	0.16	23.66	21.41	81.92	0.76	39.92
7	Canopy temp. at vegetative stage (°C)	36.25	35.3-37.9	0.41	0.22	1.76	1.29	53.65	0.70	1.94
8	Panicle length (cm)	20.63	15.6-24.6	4.97	4.58	10.80	10.37	92.12	4.23	20.50
9	Seed setting (%)	94.54	84.5-98.5	10.41	9.86	3.41	3.32	94.65	6.29	6.66
10	Panicle index per plant (%)	87.80	81.3-92.6	4.97	4.58	2.54	2.44	92.12	4.23	4.82
11	Grain yield per plant (g)	67.38	50.4-85.1	99.62	65.51	14.81	12.01	65.76	13.52	20.07

PV = Phenotypic Variance, GV =Genotypic variance, PCV =Phenotypic coefficient of variance, GCV = Genotypic Coefficient of variance

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