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RESEARCH PAPER

Genetic variability studies in pearl millet for yield & yield components, multiple disease resistance

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Abstract : Genetic variability for rust, blast, yield and yield components was carried out for 150 inbred lines (Dharwad and Vijayapur) along with two susceptible checks ICMB-94555 and ICMB-92777. Significant differences ($p<0.05$) were revealed by the analysis of variance statistically, which showed the genetic variability's existence for various characteristics in inbred lines. Maximum heritability was documented for grain yield (kg/ha) followed by panicle length and plant height. Maximum genetic advances in means were observed by grain yield, fodder yield, height of plant (cm) and panicle length (cm). High broad sense heritability was noticed for all the traits indicating that simple selection process is indicative of genetic improvement in desired direction.

Key words: Blast, Inbred lines, Rust, Variability

Introduction

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] belongs to the family Poaceae (Graminae) and sub family Penicedae, having relatively small diploid genome ($2n = 2x = 14$).It is considered to be originated in Africa from where it was imported to India. Pearl millet is a C4 plant with high photosynthetic efficiency and dry matter production capacity. It is usually grown under the most adverse agro-climatic conditions where other crops like rice, sorghum and maize fail to produce economic yields. Pearl millet has the ability to respond to favourable environments due to its short developmental stages and capacity for high growth rate. It is an excellent crop for short growing seasons under improved crop management. Pearl millet is cultivated in more than 30 countries of five continents *viz.*, Asia, Africa, North America, South America and Australia.

In India, pearl millet is the fourth most important crop after Rice, Wheat and Sorghum. In India, it is cultivated over an area of 6.93 m ha. with an average production of 8.61 mt. with the national average productivity of 1243 kg/ha during 2018-19 (Anonymous, 2020). The major Pearl millet growing states are Rajasthan, Maharashtra, Gujarat, Uttar Pradesh and Haryana which account for more than 90% of Pearl millet acreage in the country. Most of pearl millet in India is grown in *kharif* season (June-September). It is also cultivated during the summer season (February-May) in parts of Gujarat, Rajasthan and Uttar Pradesh; and during the *rabi* season (November-February) at a small scale in Maharashtra and Gujarat. In Karnataka, pearl millet is one of the major *kharif* crop, grown on an area of 3.22 lakh hectares with an annual production of 3.67 lakh tonnes with the average productivity of 1140 kg/ha (Anonymous, 2020).

Selection efficacy depends on the amount of the genetic variation existing for a specific trait. Phenotypic variance is a measure of degree of variance resulting from difference in phenotypic trait. However, the genotypic variance tests the degree of variance resulting from phenotypical or genotypical values. The degree of the variability is not the only thing that matters most in the success of the selection system, but also the degree of variation that is heritable.

Material and methods

Genetic variability for rust, blast and yield and yield components was done for 150 inbred lines at Dharwad and Vijayapur along with two susceptible checks. Screening for rust and blast was done for 150 inbred lines and two susceptible checks ICMB-94555 and ICMB-92777. In each entry, severity was recorded by considering lower leaves, middle leaves and top leaves of pearl millet and the disease reaction was explained detail in next experiment during *kharif*-2018 at Vijayapur and during *kharif*-2019 at Dharwad. Each entry was planted in a 3 m long row with a 45 cm x 15 cm spacing in three replications. A NPK fertilizer dose of 50:25:0 kg/ha was applied at the time of seeding. To ensure a suitable number of plants, thinning was performed twenty one days after seedling emergence.

The blast and rust disease severity was recorded at the time of flowering, grain filling and maturity using 0-9 scale as per the method suggested by Mayee and Datar (1986) by randomly selecting five plants in each genotype. In each entry, severity was recorded by considering lower leaves, middle leaves and top leaves of pearl millet and based on the disease reaction, genotypes were categorized into immune, resistant, moderately resistant, moderately susceptible, susceptible and highly susceptible. Further, these scales were converted to Per cent Disease Index (PDI) using the formula given by Wheeler (1969).

$$\text{Per cent Disease Index} = \frac{\text{Sum of individual disease ratings}}{\text{No.of leaves assesed x Max. grade}} \text{ x } 100$$

Pearl millet inbred lines were later grouped into different categories based on their reaction to blast disease under unprotected conditions.

Results and discussion

The analysis ofvariance of various characters studied in the inbred lines are specified in Table 1. The mean sum of squares due to genotypes were substantial for every trait studied. In contrast, the mean sum of squares due to replication was not substantial for all the traits.The results pertaining to genetic parameters *viz.*, range, mean, phenotypic coefficient of variation

Table 1. Analysis of variance (Mean sum of squares) of 152 inbred line with respect to morpho-physiological characters, rust and blast diseases in pearl millet

Sources of variation	Degrees of freedom	Plant height (cm)	No. of productive tillers per plant	Panicle Length (cm)	Panicle Girth (cm)	Grain yield	Dry fodder yield	Rust	Blast
Replication	1	166.09	0.25	3.80	0.11	25.00	807.00	5.37	27.11
Treatments	151	770.10**	0.56**	24.01**	0.16**	69151.00**	74490.00**	60.29**	43.05**
Error	151	66.30	0.07	1.41	0.03	733.00	15350.00	6.43	7.95
S. Em.±		5.76	0.18	0.84	0.13	19.14	87.61	1.79	1.99
CD @ 5%		16.09	0.51	2.35	0.37	53.49	244.80	5.01	5.57
CD @1%		21.24	0.67	3.10	0.48	70.63	323.22	6.61	7.36

Note: *Significance at 5% probability, **significance at 1% probability

Table 2. Estimates of genetic variability parameters of 152 inbred lines for morpho-physiological traits, rust and blast diseases in pearl millet

Characters	Mean	Range		σ^2 p	σ^2g	GCV	PCV	h^2_{bs}	GA	GAM
		Min	Max			(%)	(%)	(%)		(%)
Plant height (cm)	153.02	101.30	207.30	418.20	351.90	12.26	13.36	84.15	34.45	23.17
No. of productive tillers per plant	1.99	0.80	3.10	0.32	0.25	25.02	28.19	78.81	0.91	45.76
Panicle Length (cm)	20.59	10.80	32.00	12.71	11.30	16.32	17.31	88.90	6.53	31.70
Panicle Girth (cm)	2.68	1.92	3.40	0.10	0.06	9.27	11.56	64.30	0.41	15.31
Grain yield	270.425	99.960	1078.00	34942.23	34209.22	68.40	69.12	97.90	376.99	139.41
Dry fodder yield	1163.771	745.000	1980.00	44920.22	29569.77	14.78	18.21	65.83	287.40	24.70
Rust (PDI)	12.31	2.22	36.00	33.36	26.93	42.15	46.91	80.73	9.60	78.01
Blast (PDI)	15.86	6.67	36.00	25.50	17.55	26.42	31.85	68.83	7.16	45.16

σ^2 p = Phenotypic variance, σ^2 g = Genotypic variance, GCV = Genotypic covariance, PCV = Phenotypic covariance, GA = Genetic advance, GAM = Genetic advance Mean

(PCV), genotypic coefficient of variation (GCV), broad sense heritability (h^2_{bs}), genetic advance (GA) and genetic advance as per cent over mean (GAM) were computed to identify the degree of variability existing in the one hundred and fifty two inbred lines for productivity traits are specified in Table 2.

The variability study showed moderate level estimate of PCV and GCV for plant height. The variability analysis showed high estimate of heritability. Further, less difference amongst PCV and GCV indicated, any selection force driven on these traits may assist for improvement at early generations. Similar outcomes were described by Sumathi *et al.* (2010); Govindaraj *et al.* (2010); The variability analysis displayed high magnitude of GAM indicating the variation mainly due to additive gene effects. Similarly, medium values of GAM were testified by Navale *et al.* (1991) and Yadav *et al.* (2001).

The variability study disclosed high estimations of GCV and PCV for Number of productive tillers per plant. The values of high variability were conveyed earlier by Hepziba *et al.* (1993); Sharma (2002) and Vetriventhan and Nirmalakumari (2007). The variability analysis showed that reasonably high values of heritability registered for this trait. Similar outcomes were also reported by Mukherji *et al.* (1980); Pethani and Kapoor (1990); Sharma (2002); Varu *et al.* (2005) and Sumathi *et al.* (2010). The estimate of GAM was high for the trait, productive tillers per plant. Various research workers registered reasonably high value of genetic GAM as conveyed by Sharma (2002) and Varu *et al.* (2005). High GCV, PCV, heritability together with high GAM indicating that the heritability might be due to additive gene effects governing the trait and selection might be effective.

The variability study for panicle length displayed moderate PCV and GCV. Relatively moderate values of heritability were obtained for the trait, similar outcomes have been noted previously by Vidyadhar *et al.* (2007) and Shanthi *et al.* (2014). The study also showed high estimates of genetic advance as per cent over mean.

The variability study for panicle girth displayed moderate level of PCV and low level of GCV. Comparable outcomes were registered by Sumathi *et al.* (2010); Shanthi *et al.* (2014). Relatively high values of heritability were obtained for the trait. Similar consequences were registered Kunjir and Patil (1986) and Shanthi *et al.* (2014). The variability analysis also displayed comparatively moderate estimates of GAM. Similar outcomes were registered by Shanthi *et al.* (2014).

The variability study showed relatively high PCV and GCV for grain yield per hectare. The study of variability also displayed high heritability for grain yield per plot. Similar outcomes were revealed by Kunjir and Patil (1986) and Navale *et al.* (1991). The estimate of GAM was also relatively high, other scientists in their study on variability presented fairly high estimates of GAM for this trait, noticed by Lakshmana *et al.* (2003) and Mukesh *et al.* (2013). The study of variability disclosed fairly moderate assessments of PCV and GCV for dry fodder yield per hectare. The variability study also showed high estimate of heritability for this trait. The estimate of GAM was high for the trait.

The study on variability disclosed high estimates of PCV and GCV for rust disease. Observations for higher variability have been reported earlier by Shivukumar *et al,* (2011) ,Yadawad

e*t al.* (2015); Suresh *et al*, 2021. The analysis of variability indicated high value of heritability. The estimate of GAM was relatively high for rust disease. The study on variability disclosed high estimates of PCV and GCV for blast disease (Table 2). Observations for higher variability have been reported earlier by Immanuel *et al*. (2011), Hosagoudar *et al*. (2015). The analysis of variability indicated high value of heritability. Similar outcomes were registered by Sharma *et al.* (2021). The estimate of GAM was relatively high for blast disease.

Conclusion

Genetic variability study in the inbred lines revealed moderate and high values of GCV, PCV, GAM for plant height, number of productive tillers per plant, panicle length, panicle girth, grain yield per hectare and dry fodder yield per hectare, rust and blast severity expressed in terms of PDI. High broad sense heritability was noticed for all the traits mentioned earlier indicating that simple selection would be sufficient for these traits to bring genetic improvement in desired direction.

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