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Research Article

Genetic variability and association analysis in the segregating population of extra early barnyard millet [*Echinochloa frumentaceae* (Roxb.) Link] involved crosses

S. Monika[1], C. Vanniarajan[1*], R. Chandirakala[1] and R. Renuka[2]

[1]Department of Plant Breeding and Genetics,Agricultural College and Research Institute, Madurai- 625104, Tamil Nadu, India.
[2]Department of Biotechnology, Agricultural College and Research Institute, Madurai- 625104, Tamil Nadu, India.
***E-Mail**: vanniarajan.c@tnau.ac.in

Abstract
An investigation was conducted to evaluate the F_2 population of two crosses of barnyard millet *viz.,* cross I, ACM-15-343 X IEC 82 and cross II, Co (Kv) 2 X IEC 107 for extra earliness. Genetic variability and association analyses were carried out for sixteen biometrical traits. In both the crosses, high PCV and GCV was observed for the width of flag leaf, length of a lower raceme, number of racemes and grain yield per plant. Low PCV and GCV was observed for days to maturity. The minimum difference between PCV and GCV was observed for all the traits in both crosses, indicating the negligible effect of environment on the expression of the characters. Moderate to high heritability with moderate to high genetic advance in all the traits revealed the predominance of additive gene action. A positive significant correlation was noted for grain yield with plant height, days to flowering, days to maturity, the number and length of nodes, the number of basal tillers, stem diameter and single ear head weight. Path analysis disclosed a high positive direct effect of the number of basal tillers and single ear head weight on yield. These results together help in the selection of superior segregants based on the number of basal tillers and single ear head weight in forwarding them to successive generations.

Key words: Barnyard millet, F_2, Variability, Association analysis

INTRODUCTION

Barnyard millet [*Echinochloa frumentaceea* (Roxb.) Link] is an annual grass grown predominantly as a rainfed crop. It is one of the oldest millets to be domesticated in the semi arid areas of Tropical Asia and Africa (Sood *et al*., 2020). India is the leading producer of barnyard millet with an area of 0.146 million hectares, production of 0.151 million tonners (Vetriventhan *et al*., 2020) and productivity of 1034 kg/ha and was reported for the past three years (Renganathan *et al*., 2020). It is an endurable crop, which can withstand several biotic and abiotic stresses. It can serve as a dual crop providing both food and fodder. It is the fastest growing crop giving voluminous fodder (Meena *et al*., 2021). It is rich in micronutrients such as iron and zinc, which is the maximum among cereals (Renganathan *et al*., 2017). Though the cultivation of barnyard millet remained dormant for the past few decades, its agronomic and nutritional benefits, make them more preferable for cultivation at present. The duration of present-day varieties in Tamil Nadu remains to be 95-105 days (Vanniarajan *et al*., 2018). Development of extra early maturing (60-75 days) cultivars with high yield would help the farmers to mitigate the present day climate change issues. In the present scenario, barnyard millet is grown in rabi season. Reduced plant height with early maturity would be suitable for cultivation in all seasons and also for intercropping. This would support the agronomic and economic self-sustainability of small and marginal farmers relying on rainfed farming. Knowledge on the extent of variation prevailing in the population for different traits forms the pillar for the success of a breeding program. Literature regarding genetic variability and association studies in segregating the population of barnyard millet is scanty. The current study focuses on determining the variability and association parameters acting in two F_2 populations of barnyard millet crosses, which would help in the improvement of the crop for further generations.

MATERIALS AND METHODS

The present investigation was conducted during *Kharif,* 2020 at the experimental farm, Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Tamil Nadu Agricultural University, Madurai. The experimental material comprised of F_2 seeds of two crosses, executed between late and early maturing lines namely, ACM-15-343 X IEC 82 and Co (Kv)2 X IEC 107. The details of the four parents used are presented in **Table 1**. The plants were raised in rows of 3 m length with a spacing of 30 cm between rows and 15 cm between plants in a non-randomized design. Recommended crop management practices were carried out with caution for the better development of the crop. Out of 500 F_2 plants raised, 250 superior plants were selected and observations were taken down for sixteen quantitative traits such as plant height, days to flowering, days to maturity, the number of nodes, length of node, the number of basal tillers, stem diameter, length of flag leaf, the width of flag leaf, length of inflorescence, the width of inflorescence, length of the peduncle, length of the lower raceme, the number of racemes, single ear head weight and grain yield per plant.

Phenotypic, Genotypic and Environmental variances for non-replicated segregating population were computed as follows:

$$\text{Phenotypic variance} = \text{Variance } (F_2)$$
$$\text{Environmental variance} = (P_1+P_2) / 2$$
$$\text{Genotypic variance} = \text{Phenotypic variance} - \text{Environmental variance}$$

Where, P_1 and P_2 are the variances of Parent 1 and Parent 2, respectively.

Phenotypic, genotypic co-efficient of variations were computed following the method given by Burton (1952) and interpreted following the classification of Sivasubramanian and Madhavamenon (1973). Broad sense heritability was calculated by the formula said by Lush (1940). Genetic advance as per cent of mean was analyzed as given by Johnson *et al*. (1955a). Both were classified following the suggestion of Johnson *et al*. (1955a). The above-mentioned variability analyses were carried out in Microsoft office EXCEL 2013. Correlation and path co-efficients were deliberated by adopting the procedure suggested by Johnson *et al*. (1955b) and Dewey and Lu (1959) respectively. These two association analyses were performed using the GENRES software version – 7.01 (Arunachalam and Vanniarajan, 2012)

RESULTS AND DISCUSSION

First and second order statistics applied for genetic variation analysis would help in finding the best performing progenies (Shanmuganathan, 2010), based on the genotype avoiding the impact of the environment. In both the crosses, high PCV and GCV was recorded for the width of flag leaf, length of lower racemes, the number of racemes and grain yield per plant (**Table 2**) which is similar to the results of Nandini *et al*. (2016) in the F_3 generation of little millet, Shet *et al*. (2009) in the second filial generation of finger millet, Shanmuganathan (2010) and Anil kumar *et al*. (2019) in F_2 population of pearl millet, Vemanna *et al*. (2013) and Nirosh *et al*. (2021) in F_2 population of sorghum. The contradictory results were reported by Renganathan *et al*. (2018) in the F_2 population of Barnyard millet, where it was moderate for grain yield per plant. This result may be due to the differences in duration and height of the varieties chosen. The parents chosen in the present study were early maturing with reduced plant height. The high magnitude of PCV and GCV indicated a large amount of variation prevailing in the population. Moderate PCV and GCV was observed for the number of nodes, length of nodes, length

Table1. Details of the parents used in the study

Crosses	Line / Variety	Parentage / Origin	Source	Duration
Cross I	ACM-15-343	A cross derivative of ACM- 10-161 X ACM-10-012	Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai	95-105 days
	IEC 82	Germplasm collected from India	ICRISAT, Hyderabad	60 days
Cross II	Co (Kv) 2	Pure line selection from EF 79	Department of Millets, Tamil Nadu Agricultural University, Coimbatore	95-105 days
	IEC 107	Germplasm collected from India	ICRISAT, Hyderabad	63 days

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Table 2. Genetic variability parameters of sixteen quantitative traits in barnyard millet crosses

S.No.	CHARACTERS	PCV (%)		GCV (%)		Heritability (%)		GAM (%)	
		Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
1	Plant height	18.52	20.28	16.9	17.67	83.2	75.95	31.75	31.74
2	Days to 50% flowering	11.31	10.93	11.02	9.78	95.03	80.23	22.15	18.06
3	Days to maturity	8.17	9.02	8.06	8.19	97.4	82.46	16.4	15.31
4	Number of nodes	16.27	18.22	12.21	14.31	55.83	61.64	18.71	23.15
5	Length of nodes	17.84	19.19	13.48	16.07	57.1	70.18	20.98	27.74
6	Number of basal tillers	20.45	27.91	16.62	25.85	66.06	85.76	27.83	49.32
7	Stem diameter	28.18	20.70	26.75	17.29	90.1	69.74	52.3	29.74
8	Length of flag leaf	18.63	19.74	15.02	17.86	64.98	81.84	24.94	33.28
9	Width of flag leaf	23.7	24.20	20.88	22.54	77.61	86.88	37.88	43.31
10	Length of inflorescence	17.82	14.58	16.02	11.84	80.79	65.97	29.67	19.82
11	Width of inflorescence	30.91	21.36	30.41	19.94	96.8	87.25	61.64	38.38
12	Length of lower racemes	29	32.15	26.55	30.12	83.82	87.76	50.07	58.12
13	Length of peduncle	13.73	22.46	9.8	19.36	51	74.30	14.41	34.38
14	Number of racemes	24.56	25.62	22.8	23.91	86.15	87.16	43.58	45.99
15	Single ear head weight	20.98	20.92	18.6	17.31	78.56	68.53	33.94	29.53
16	Grain yield/plant	40.17	39.93	37.78	38.28	88.46	91.88	73.2	75.58

of flag leaf and length of inflorescence, identical to the reports of Nandini *et al*. (2016), Shanmuganathan (2010), Anil kumar *et al*. (2019), for both PCV and GCV and to Subhashini *et al*. (2019) exclusively in PCV, for the trait, inflorescence length. Moderate PCV and GCV meant the occurrence of notable variation for the above traits in the present segregating population. High PCV and moderate GCV was detected for single ear head weight, uniform with the outcomes of Subhashini *et al*. (2019) for both PCV and GCV whereas, with Renganathan *et al*. (2018) and Anil kumar *et al*. (2019) solely for GCV. Low PCV and GCV were spotted for days to maturity. This indicated that genetic improvement through selection for this trait often would not be effective and require special breeding procedures. This is in accordance with the answers of Renganathan *et al*. (2018), Nandini *et al*. (2016), Vemanna *et al*. (2013) and Nirosh *et al*. (2021). In cross I, high PCV and GCV was expressed by stem diameter and width of inflorescence and moderate PCV and GCV were noticed for plant height and days to flowering. Similar results were mentioned by Nandini *et al*. (2010) in the finger millet F_2 population, Shanmuganathan (2010) for both PCV and GCV and Nandini *et al*. (2016) and Anil kumar *et al*. (2019), Subhashini *et al*. (2019) for PCV of plant height. In cross II, high PCV and GCV was observed for the number of basal tillers, homogeneous with the results of Nandini *et al*. (2010), Shanmuganathan (2010) and Anil kumar *et al.* (2019). High PCV and moderate GCV was revealed by the number of basal tillers in cross I, and by plant height, stem diameter, the width of inflorescence, length of peduncle in cross II. Analogous results were reported by Vemanna *et al*. (2013) and Nirosh *et al*. (2021) for stem diameter for GCV alone. Length of peduncle marked moderate PCV and low GCV in cross I and similar results were found for days to flowering in cross II. In both the crosses studied, the difference between PCV and GCV is low for all the traits, which unfolds the negligible effect of the environment and the resistance of these traits to the environmental alterations (More *et al*., 2019)

Heritability in conjunction with genetic advance provides an outlook of gain under selection. The outcome of genetic advance relies on the estimates of variability, heritability and selection intensity of the population (Subhashini *et al*., 2019). High heritability was found for the traits such as, plant height, days to flowering, days to maturity, the number of basal tillers, stem diameter, length of flag leaf, the width of flag leaf, length of inflorescence, the width of inflorescence, length of the lower raceme, the number of racemes, single ear head weight and grain yield per plant in cross I which are in agreement with Renganathan *et al*. (2018) in barnyard millet, Nandini *et al*. (2010) in finger millet, Shanmuganathan (2010) and Anil kumar *et al*. (2019) for plant height, the number of basal tillers and grain yield per plant in pearl millet, Nirosh *et al*. (2021) in sorghum leaving moderate heritability for the number of nodes, length of nodes and length of the peduncle. Moderate heritability shows that the additive gene effect operates, which can be improved by mass selection (Nandini *et al*., 2016). Genetic advance as per cent of the mean (GAM) was high for all the traits, which coincides with Nandini *et al*. (2010) Shanmuganathan (2010). GAM of days to maturity, the number of nodes and the length of peduncle were moderate. They were similar to the results of Nandini *et al*. (2016) and Nirosh *et al*. (2021) for days to maturity and with Vemanna *et al*. (2013) for the number of nodes. In cross II, all the traits revealed high heritability and moderate GAM was indicated by days to flowering and maturity, correspondent to the sequels of Nandini *et al*. (2016) for days to maturity and length of inflorescence as described by Anil kumar *et al*. (2019).

As proposed by Allard (1960), high heritability was perceived as a minor influence of environment on the expression of the particular character. Since, broad sense heritability aids in the selection based on phenotypic utterance and may incur additive or non-additive gene effects (dominance and epistasis), additional information about genetic advance would nourish the indirect selection process. In the present study, nearly all the traits disclosed moderate to high heritability with moderate to high genetic advance in both the crosses, which indicates the preponderance of additive gene action and this would be rewarding for effective selection of desirable segregants to be forwarded for succeeding generation.

Yield is a complex trait influenced by several other quantitative traits. Hence, useful information about the relationship between different traits and yield would aid in the concomitant genetic amelioration of these attributes. In both the crosses, correlation studies indicated a positive significant correlation of grain yield per plant with plant height, days to flowering, days to maturity, the number of nodes, the number of basal tillers, stem diameter and single ear head weight. Renganathan *et al*. (2017) reported a similar association in F_2 population and germplasm of barnyard millet, Nandini *et al*. (2016) in F_3 population of little millet, Nandini *et al*. (2010) in F_2 population of finger millet, Subhashini and Selvi (2019) in the F_2 generation of sorghum. Thus, indirect selection relying on the above characters can help in identifying the high yielding lines in the population. Plant height exhibited a positive significant correlation with every other trait involved in the study, identical to the trends of Renganathan *et al*. (2017). Days to flowering and days to maturity showed a strong positive correlation with each other with significance. This portrays a tight linkage between the genes responsible for these traits. Days to flowering and maturity were strongly correlated with single ear head weight in a positive direction. These two traits should be taken into consideration, such that a balance of yield and duration should be maintained while selecting superior segregants. Correlation between different traits for the cross I and cross II are presented in **Tables 3 and 5,** respectively. Negatively correlated traits must be given less importance in selection.

Path co-efficient splits the correlation into direct and indirect effects. It gives the cause and effect relationship between the independent attributes and the dependent trait, the grain yield per plant. In both crosses, the traits, number of basal tillers and single ear head weight showed a high positive direct effect on grain yield per plant. Similar results were reported by Renganathan *et al*. (2017),

Table 3. Correlation co-efficient for sixteen quantitative traits in cross I

	PH	DF	DM	NN	LON	NBT	SD	LFL	WFL	LOI	WOI	LLR	LOP	NOR	SEW	GY/P
PH	1.000															
DF	0.313**	1.000														
DM	0.322**	0.952**	1.000													
NN	0.660**	0.307**	0.321**	1.000												
LON	0.617**	0.027	-0.004	0.079	1.000											
NBT	0.175**	0.141*	0.128*	0.108	0.139**	1.000										
SD	0.205**	0.351**	0.322**	0.251**	0.026	0.085	1.000									
LFL	0.409**	-0.021	-0.014	0.299**	0.327**	0.072	0.113**	1.000								
WFL	0.243**	0.004	-0.015	0.194**	0.135**	0.122	0.239**	0.395**	1.000							
LOI	0.545**	-0.033	-0.036	0.336**	0.400**	0.157*	0.082	0.428**	0.390**	1.000						
WOI	0.367**	0.005	-0.007	0.216**	0.263**	0.133*	0.032	0.341**	0.298**	0.518**	1.000					
LLR	0.382**	0.040	0.017	0.195**	0.314**	0.127*	0.114**	0.351**	0.190**	0.521**	0.694**	1.000				
LOP	0.248**	0.035	0.024	0.065	0.357**	0.052	0.045	0.200**	0.008	0.237**	0.231**	0.270**	1.000			
NOR	0.249**	0.219**	0.180**	0.248**	0.114**	0.110	0.308**	0.165**	0.177**	0.192**	0.051	0.073	0.055	1.000		
SEW	0.275**	0.786**	0.770**	0.229**	0.042	0.211**	0.236**	-0.014	0.009	-0.060	-0.006	0.033	0.016	0.164**	1.000	
GY/P	0.299**	0.605**	0.586**	0.245**	0.112**	0.637**	0.230**	0.064	0.099	0.044	0.077	0.082	0.033	0.254**	0.730**	1.000

* Significant at 5% level   ** Significant at 1% level.

PH-Plant height; DF- Days to flowering; DM- Days to maturity; NN- Number of nodes; LON- Length of nodes; NBT-Number of basal tillers; SD-Stem diameter; LFL-Length of flag leaf; WFL-Width of flag leaf; LOI- Length of flag leaf; WOI- Width of inflorescence; LLR-Length of lower raceme; LOP-Length of peduncle; NOR- Number of racemes; SEW- Single ear head weight: GY/P- Grain yield per plant.

Table 4. Direct (diagonal) and indirect effects of yield contributing components with grain yield per plant in cross I

	PH	DF	DM	NN	LON	NBT	SD	LFL	WFL	LOI	WOI	LLR	LOP	NOR	SEW	GY/P
PH	**0.0110**	0.0185	0.0112	0.0111	0.0087	0.0877	-0.0072	0.0100	0.0038	-0.0279	0.0105	-0.0082	-0.0031	0.0224	0.1449	**0.299****
DF	0.0034	**0.0592**	0.0331	0.0052	0.0004	0.0707	-0.0012	-0.0005	0.0001	0.0017	0.0001	-0.0009	-0.0004	0.0196	0.4149	**0.605****
DM	0.0035	0.0563	**0.0348**	0.0054	-0.0001	0.0643	-0.0011	-0.0003	-0.0002	0.0019	-0.0002	-0.0004	-0.0003	0.0162	0.4066	**0.586****
NN	0.0072	0.0182	0.0112	**0.0168**	0.0011	0.0054	-0.0009	0.0073	0.0030	-0.0172	0.0062	-0.0042	-0.0008	0.0223	0.1209	**0.245****
LON	0.0067	0.0016	-0.0001	0.0013	**0.0140**	0.0698	-0.0001	0.0080	0.0021	-0.0205	0.0076	-0.0067	-0.0044	0.0102	0.0221	**0.112****
NBT	0.0019	0.0083	0.0045	0.0018	0.0020	**0.5019**	-0.0003	0.0018	0.0019	-0.0080	0.0038	-0.0033	-0.0007	0.0098	0.1113	**0.637****
SD	0.0022	0.0208	0.0112	0.0042	0.0004	0.0424	**-0.0035**	0.0028	0.0037	-0.0042	0.0009	-0.0024	-0.0006	0.0276	0.1244	**0.230****
LFL	0.0045	-0.0012	-0.0005	0.0050	0.0046	0.0363	-0.0004	**0.0245**	0.0061	-0.0219	0.0098	-0.0075	-0.0025	0.0148	-0.0076	**0.064**
WFL	0.0027	0.0003	-0.0005	0.0033	0.0019	0.0613	-0.0008	0.0097	**0.0155**	-0.0199	0.0086	-0.0041	-0.0001	0.0159	0.0049	**0.099**
LOI	0.0060	-0.0020	-0.0013	0.0057	0.0056	0.0788	-0.0003	0.0105	0.0060	**-0.0512**	0.0149	-0.0112	-0.0029	0.0172	-0.0317	**0.044**
WOI	0.0040	0.0003	-0.0002	0.0036	0.0037	0.0665	-0.0001	0.0084	0.0046	-0.0265	**0.0287**	-0.0149	-0.0029	0.0046	-0.0029	**0.077**
LLR	0.0042	0.0023	0.0006	0.0033	0.0044	0.0638	-0.0004	0.0086	0.0029	-0.027	0.0199	**-0.0214**	-0.0034	0.0066	0.0173	**0.082**
LOP	0.0027	0.0021	0.0008	0.0011	0.0050	0.0264	-0.0005	0.0049	0.0001	-0.0121	0.0066	-0.0058	**-0.0125**	0.0049	0.0085	**0.033**
NOR	0.0027	0.0129	0.0063	0.0042	0.0016	0.0548	-0.0011	0.0040	0.0027	-0.0098	0.0015	-0.0016	-0.0007	**0.0899**	0.0864	**0.254****
SEW	0.0030	0.0465	0.0268	0.0039	0.0005	0.1059	-0.0008	-0.0004	0.0002	0.0031	-0.0002	-0.0007	-0.0002	0.0147	**0.5278**	**0.730****

Residual effect = 0.454

Table 5. Correlation co-efficient for sixteen quantitative traits in cross II

	PH	DF	DM	NN	LON	NBT	SD	LFL	WFL	LOI	WOI	LLR	LOP	NOR	SEW	GY/P
PH	1.000															
DF	0.194**	1.000														
DM	0.193**	0.924**	1.000													
NN	0.775**	0.138*	0.136*	1.000												
LON	0.596**	0.115**	0.071	0.504**	1.000											
NBT	0.191**	-0.041	-0.053	0.153*	0.137*	1.000										
SD	0.294**	0.199**	0.189**	0.241**	0.165v	0.079	1.000									
LFL	0.524**	0.026	0.001	0.407**	0.427**	0.174**	0.362**	1.000								
WFL	0.529**	0.069	0.075	0.440**	0.342**	0.128*	0.262**	0.603**	1.000							
LOI	0.440**	-0.137*	-0.149*	0.371**	0.325**	0.139*	0.193**	0.422**	0.308**	1.000						
WOI	0.322**	0.131*	0.119	0.289**	0.260**	0.132*	0.266**	0.309**	0.293**	0.275**	1.000					
LLR	0.494**	0.139*	0.127*	0.361**	0.387**	0.180**	0.215**	0.409**	0.434**	0.329**	0.541**	1.000				
LOP	0.598**	0.168**	0.139*	0.424**	0.601**	0.158*	0.108**	0.467**	0.487**	0.223**	0.217**	0.440**	1.000			
NOR	0.048	-0.012	-0.044	0.121	-0.048	0.026	0.171**	0.054	-0.021	0.302**	0.065	-0.115	-0.202**	1.000		
SEW	0.285**	0.877**	0.788**	0.183**	0.226**	0.002	0.170**	0.080	0.141*	-0.066	0.150*	0.209**	0.314**	-0.020	1.000	
GY/P	0.270**	0.477**	0.409**	0.203**	0.203**	0.763*	0.181**	0.196**	0.163*	0.082	0.159*	0.222**	0.265**	0.055	0.564**	1.000

* Significant at 5% level ** Significant at 1% level

PH-Plant height; DF- Days to flowering; DM- Days to maturity; NN- Number of nodes; LON- Length of nodes; NBT-Number of basal tillers; SD-Stem diameter; LFL-Length of flag leaf; WFL-Width of flag leaf; LOI- Length of flag leaf; WOI- Width of inflorescence; LLR-Length of lower raceme; LOP-Length of peduncle; NOR- Number of racemes; SEW- Single ear head weight: GY/P- Grain yield per plant.

Table 6. Direct (diagonal) and indirect effects of yield contributing components with grain yield per plant in cross II

	PH	DF	DM	NN	LON	NBT	SD	LFL	WFL	LOI	WOI	LLR	LOP	NOR	SEW	GY/P
PH	**-0.0761**	0.0159	-0.0062	0.0185	-0.0097	-0.1467	0.0062	0.0279	-0.0060	0.0121	-0.0096	-0.0063	0.0003	0.0014	0.1543	**0.270****
DF	-0.0147	**0.0825**	-0.0298	0.0033	-0.0019	-0.0312	0.0042	0.0014	-0.0079	-0.0038	-0.0039	-0.0017	0.0001	-0.0004	0.4741	**0.477****
DM	-0.0146	0.0762	**-0.0322**	0.0033	-0.0012	-0.0407	0.0039	0.0000	-0.0009	-0.0041	-0.0035	-0.0016	0.0001	-0.0013	0.4262	**0.409****
NN	-0.0600	0.0114	-0.0044	**0.0239**	-0.0082	-0.1173	0.0050	0.0217	-0.0050	0.0102	-0.0086	-0.0046	0.0002	0.0037	0.0991	**0.203****
LON	-0.0455	0.0095	-0.0023	0.0120	**-0.0163**	0.1056	0.0035	0.0228	-0.0039	0.0089	-0.0077	-0.0049	0.0003	-0.0015	0.1224	**0.203****
NBT	-0.0145	-0.0033	0.0017	0.0036	-0.0022	**0.7688**	0.0017	0.0093	-0.0015	0.0038	-0.0039	-0.0023	0.0001	0.0008	0.0008	**0.763****
SD	-0.0223	0.0164	-0.0061	0.0057	-0.0027	0.0610	**0.0209**	0.0193	-0.0030	0.0053	-0.0079	-0.0028	0.0001	0.0052	0.0917	**0.181****
LFL	-0.0398	0.0022	-0.0001	0.0097	-0.0070	0.1341	0.0076	**0.0533**	-0.0069	0.0116	-0.0092	-0.0052	0.0002	0.0016	0.0434	**0.196****
WFL	-0.0402	0.0057	-0.0024	0.0105	-0.0056	0.0984	0.0055	0.0322	**-0.0114**	0.0085	-0.0087	-0.0055	0.0003	-0.0006	0.0761	**0.163****
LOI	-0.0334	-0.0112	0.0048	0.0089	-0.0053	0.1069	0.0040	0.0225	-0.0035	**0.0275**	-0.0082	-0.0042	0.0001	0.0091	-0.0357	**0.082**
WOI	0.0245	-0.0108	-0.0038	0.0069	-0.0042	0.1014	0.0056	0.0165	-0.0033	0.0075	**-0.0297**	-0.0069	0.0001	0.0020	0.0808	**0.159****
LLR	-0.0376	0.0114	-0.0041	0.0086	-0.0063	0.1385	0.0045	0.0218	-0.0049	0.0091	-0.0161	**-0.0128**	0.0002	-0.0035	0.1131	**0.222****
LOP	-0.0455	0.0138	-0.0045	0.0101	-0.0098	0.1214	0.0023	0.0249	-0.0055	0.0061	-0.0065	-0.0056	**0.0005**	-0.0061	0.1698	**0.265****
NOR	-0.0036	-0.0010	-0.0014	0.0029	0.0008	0.0200	0.0036	0.0029	0.0024	0.0083	-0.0019	-0.0015	-0.0001	**0.0302**	-0.0106	**0.055**
SEW	-0.0217	0.0723	-0.0254	0.0044	-0.0037	0.0012	0.0036	0.0043	-0.0016	-0.0018	-0.0044	-0.0026	0.0002	-0.0006	**0.5406**	**0.564****

Residual effect = 0.303

PH-Plant height; DF- Days to flowering; DM- Days to maturity; NN- Number of nodes; LON- Length of nodes; NBT-Number of basal tillers; SD-Stem diameter; LFL-Length of flag leaf; WFL-Width of flag leaf; LOI- Length of flag leaf; WOI- Width of inflorescence; LLR-Length of lower raceme; LOP-Length of peduncle; NOR- Number of racemes; SEW- Single ear head weight: GY/P- Grain yield per plant.

Nandini *et al*. (2010) for single ear head weight. The selection based on these traits will improve the yield. Other traits such as plant height, days to flowering, number of nodes, length of flag leaf and number of racemes exerted a negligible positive effect on it. In cross I, stem diameter, length of inflorescence, lower raceme and peduncle and in cross II, days to maturity, length of nodes, the width of flag leaf and inflorescence, length of lower raceme exhibited a negligible negative effect on grain yield. Due to negative indirect effects and non -significant associations, these traits may not be useful in selection for high yield. Plant height, number of nodes and tillers and stem diameter provided low positive indirect effect through single ear head weight, similar to the sequels of Subhashini *et al*. (2019) for plant height. This strongly assured the role of single ear head weight in increasing the yield. The direct and indirect effect of different traits on yield for the cross I and cross II are presented in **Tables 4 and 6,** respectively.

The residual effect was observed as 0.454 and 0.303 for the cross I and cross II respectively. This indicated that these traits are reliable in contributing to yield. However, 45.4% and 30.3% of variability remain unnoticed in the two crosses respectively and there exist some other traits, which may contribute to increased yield in these two crosses.

Thus, the present investigation was carried out to identify new barnyard millet genotype with early maturity, reduced plant height and high yield. The parents chosen show extreme differences in plant height and maturity. Transgressive segregants were obtained for all the characters under study particularly for plant height, days to maturity and grain yield per plant. Thus, high PCV, GCV, heritability and genetic advance indicate the minimum influence of environment and effective selection of the traits. Association analysis indicates that selection for the number of basal tillers and single ear head weight would be promising for increasing the yield. These results together help in the isolation of best performing segregants to be forwarded to the successive generation.

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