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Variability and Heritability Studies in Bittergourd (Momordica charantia. L) Genotypes

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ABSTRACT: The modern breeding programmes depends mostly on creating genetic variability along with simple selection and utilization of that variation present in selected genotypes to generate new breeding materials with traits of interest. Genetic variability among traits is essential for any crop improvement programme and in selecting desirable genetic material. The present investigation was undertaken to study the Variability and heritability studies in bitter gourd (Momordica charantia. L) genotypes. Field evaluation of six bittrgourd genotypes was conducted at the Department of Vegetable Science, College of Agriculture, Vellayani during June to September 2022. The genetic parameters such as component of variance, heritability, genetic advance, correlation and path analysis were studied. Maximum variation was observed for yield per plot (38.36% and 37.81%) followed by fruit length (27.34% and 27.11%) and fruit diameter (26.90% and 26.67%). The heritability estimates of all the traits ranged from 0.82 to 0.99, which indicates the influence of additive gene effect on the expression of traits in bitter gourd. The highest genetic advance was observed for yield per plot (76.76%), followed by fruit length (55.37%) and fruit diameter (54.45%). Yield per plot showed significant and positive genotypic and phenotypic correlation with yield per plant (0.97 and 0.95 respectively), fruit weight (0.89 and 0.85 respectively) and fruit length (0.94 and 0.91 respectively). High heritability, high genetic advance and high GCV values showed that the expression of different traits in bittergourd was less influenced by environmental factors and are controlled by additive genetic effects. Therefore simple selection is adequate in the crop improvement programme for the development of elite genotype.

Keywords: Bittergourd, GCV, PCV, Correlation, Path analysis and Heritability.

INTRODUCTION

Bittergourd (Momordica charantia. L) is one of the commercially cultivated cucurbitaceous vegetable crop grown for its bitter tender fruit. The crop is grown extensively throughout the tropical and sub-tropical regions of the world and is native to Tropical Africa and Asian regions. It is an important vegetable grown for its nutritional and medicinal values. The plant contains higher amount of biologically active compounds such as momordicin and cucurbitacin. The crop being an important vegetable requires a systematic breeding program for improvement in the yield potential and other horticultural traits (Gupta et al., 2015). Yield is one of the complex characters which is highly influenced by the environment. Hence selection based on the yield alone may limit crop improvement. Effective improvement in yield can be brought about by selecting various yield contributing characters, which show association among themselves and also with vield. The selection of traits is very effective when genetic variability is available among different plant population (Chaudhary et al., 2019). The advancement in the selection of genotype for breeding programmes totally depends on the knowledge of correlation, genetic

advance and heritability among the genotypes on various characters. The study of the genetic parameters will also provide valuable information on the mode of inheritance of different characters, which would be useful for selecting plants having desirable characters to develop new varieties (Khan *et al.*, 2015). Correlation among and between the yield and yield attributing characters is important for selecting the genotypes for hybridization programme. Therefore the objective of this study was to evaluate the genetic variability, heritability, correlation and genetic advance among the genotypes, inorder to determine yield potentiality of the genotypes to screen suitable parental lines for future hybridization programmes.

MATERIALS AND METHODS

The field experiment was conducted at the Department of Vegetable Science, College of Agriculture, Vellayani during 2022. The statistical design used for the experiment was Randomised Block Design with 6 genotypes collected from different State Agricultural Universities. The seeds were sown in portrays and 20 days old seedlings were transplanted to the main field with four replications at a spacing of $2m \times 2m$. The standard horticultural practices recommended by KAU (2016) was adopted to raise the crop. Observations were recorded from five randomly selected plants from each replication. The observations recorded were days to first female flower opening (DFF), days to first harvest (DFH), fruit length (FL) (cm), fruit diameter (FD) (cm), fruit weight (FW) (g), yield per plant(YPPL) (g), yield per plot (YPP) (kg).

The genotypic and phenotypic coefficient of variance was calculated according to Burton's methods (1952) and was classified according to Sivasubramanian and Madhavamenon (1973) *i.e.* Low (< 10%), medium (10-25%) and high (> 25%).

The proportion of variation for different traits in a population can be attributed to the inheritance of the genetic factors. Heritability estimates range from 0 to 1 and are often expressed in percentage. The value close to one indicates the highly heritable traits within and between the population (Ozturk and Yildirim 2014).

The range of genetic advance was given by Johnson *et al.*, (1955). i.e. High (>20%), Moderate (10-20%) and Low (<10%).

Genotypic and phenotypic coefficients of variations are useful for detecting the amount of variability present among the genotypes. High degree of variation was observed in the phenotypic and genotypic variance among the different genotypes studied. The estimates of coefficient of variability revealed that the magnitude of phenotypic coefficient of variation for different traits was higher than the magnitude of genotypic coefficient of variation (Table 1). The result was found to be in concordance with the findings of Alekar et al. (2019); Prashanth et al. (2020). Maximum variation was observed for yield per plot (38.36% and 37.81%) followed by fruit length (27.34% and 27.11%) and fruit diameter (26.90% and 26.67%) which indicates less influence of environmental factors on the expression of the characters (Reddy et al., 2021). Most of the characters showed narrow differences between the values of GCV and PCV as given in table 1. This narrow difference may be due to the genetic constitution which indicates the better scope of selection for these traits for improvement.

RESULTS AND DISCUSSION

	PCV (%)	GCV (%)	Heritability	GA (%)
DFF	2.86	2.58	0.82	4.82
DFH	2.53	2.32	0.84	4.39
FD	26.90	26.67	0.98	54.45
FL	27.34	27.11	0.98	55.37
FW	17.99	17.68	0.96	35.76
YPPL	21.14	21.08	0.99	43.29
YPP	38.36	37.81	0.97	76.76

Table 1: Estimation of Components of Variance of 6 bitter gourd genotypes.

PCV- Phenotypic coefficient of variation, GCV- Genotypic coefficient of variation, GA- Genetic advance, DFF- Days to first female flower, DFH- Days to first harvest, FD- Fruit diameter, FL- Fruit length, FW- Fruit weight, YPPL- Yield per plant, YPP- Yield per plot

Heritability is the proportion of phenotypic variance among the individuals in the population due to the heritable genetic effects. Heritability close to the value zero indicates that variation in the plant traits are highly influenced by environmental factors than the genetic effect. Heritability estimates of all the traits ranged from 0.82 to 0.99, which indicates less influence of environmental factor on the expression of different characters. Similar results were reported by Islam et al., (2009); Rajput (2012); Pathak (2014); Alekar et al., (2019); Prashant et al. (2020) in bittergourd. High genetic advance was observed for most of the characters. It ranged from 4.39% to 76.76%. The highest genetic advance was observed for yield per plot (76.76%), followed by fruit length (55.37%) and fruit diameter (54.45%). Low genetic advance was observed

for days to first harvest (4.39%), followed by days to first flowering (4.82%). The high heritability coupled with the highest genetic advance indicates that the various traits in bittergourd was inherited by additive genetic effects (Reddy *et al.*, 2021).

Genotypic correlation was slightly higher than the phenotypic correlation for all the characters except days to first flowering. This indicates that these traits have strong inherent association at the genotypic level, which was in agreement with Singh *et al.* (2013); Reddy *et al.* (2021). In both genotypic and phenotypic correlation, yield per plot showed significant and positive correlation with yield per plant, fruit weight and fruit length and showed significant negative correlation with fruit diameter, days to first harvest and days to first flowering as given in table 2 and table 3 respectively.

	DFF	DFH	FD	FL	FW	YPPL	YPP
DFF	1	0.83**	0.54^{*}	-0.69*	-0.73**	-0.77**	-0.82**
DFH		1	0.52^{*}	-0.71**	-0.78**	-0.78**	-0.81**
FD			1	-0.60^{*}	-0.72**	-0.36 ^{Ns}	-0.45*
FL				1	0.94**	0.90^{**}	0.91**
FW					1	0.81^{**}	0.85^{**}
YPPL						1	0.95**
YPP							1

Table 2: Phenotypic correlation among 7 characters of bittergourd.

** Significant at 1% level * Significant at 5% DFF- Days to first female flower, DFH- Days to first harvest, FD- Fruit diameter, FL- Fruit length, FW- Fruit weight, YPPL- Yield per plant, YPP- Yield per plot

Fruit diameter had significant positive correlation with days to first flowering $(0.54^* \text{ and } 0.62^*)$ and days to first harvest $(0.52^* \text{ and } 0.58^*)$ at phenotypic and genotypic level (Gupta *et al.*, 2015). It was observed that days to first flowering and days to first harvest showed significant negative phenotypic and genotypic correlation with fruit length (-0.69 and -0.78), fruit weight (-0.73 and -0.82), yield per plant (-0.77 and -0.83) and yield per plot (-0.82 and -0.91), whereas positive correlation with days to first harvest (0.83 and 0.28), which indicates that earliness in flowering leads to early harvest which significantly increases the number of harvests and yield.

The path analysis showed the direct and indirect effect of different characters individually and in combination

with other characters on yield per plot (Table 4). The results showed that fruit length (2.68) had maximum positive direct effect on yield per plot followed by fruit diameter (0.33), while days to first flowering (-0.84), days to first harvest (-0.30), fruit weight (-1.60) and yield per plant (-0.98) have negative direct effect on yield per plot. The highest indirect positive effect was showed by fruit length on fruit weight (2.59) followed by fruit weight on yield per plant (2.45). Similar result was reported by Maurya *et al.* (2019). Fruit length (0.94), fruit weight (0.89) and yield per plant (0.97) showed positive genotypic correlation with yield per plot as given in Table 4.

	DFF	DFH	FD	FL	FW	YPPL	YPP
DFF	1	0.28^{*}	0.62^{*}	-0.78**	-0.82**	-0.83**	-0.91**
DFH		1	0.58^{*}	-0.81**	-0.87**	-0.85**	-0.91**
FD			1	-0.61*	-0.72**	-0.37 ^{Ns}	-0.47*
FL				1	0.97^{**}	0.91**	0.94**
FW					1	0.84^{**}	0.89**
YPPL						1	0.97^{**}
YPP							1

** Significant at 1% level * Significant at 5% levelDFF- Days to first female flower, DFH- Days to first harvest, FD- Fruit diameter, FL- Fruit length, FW- Fruit weight, YPPL- Yield per plant, YPP- Yield per plot

	Fable 4: Path coefficient anal	ysis of y	yield contributing	characters of bitter g	gourd.
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	DFF	DFH	FD	FL	FW	YPPL	GC YPP
DFF	-0.84	-0.31	0.20	-2.10	1.31	0.82	-0.92
DFH	-0.87	-0.30	0.19	-2.16	1.39	0.83	-0.91
FD	-0.52	-0.17	0.33	-1.63	1.16	0.37	-0.48
FL	0.66	0.24	- 0.20	2.68	-1.55	-0.89	0.94
FW	0.69	0.26	- 0.24	2.59	-1.60	-0.82	0.89
YPPL	0.70	0.25	-0.12	2.45	-1.33	-0.98	0.97

DFF- Days to first female flower, DFH- Days to first harvest, FD- Fruit diameter, FL- Fruit length, FW- Fruit weight, YPPL-Yield per plant, YPP- Yield per plot *Bold values shows direct effect, GC YPP- Genotypic correlation with yield per plot

CONCLUSIONS

The phenotypic coefficient of variation was found to be slightly higher than genotypic coefficient of variation. This provides better scope for crop improvement programme in bittergourd. Heritability and genetic advance of almost all the characters are higher, which indicates the additive genetic effect of the inherited characters. Genotypic correlation was higher than the phenotypic correlation, except for days to first female flowering. This suggested the greater effectiveness of selection due to the less influence of environment. Path analysis showed that the fruit length was having higher positive direct effect on yield.

FUTURE SCOPE

On the basis of the component of variation, correlation and path analysis for yield, it could be stated that simultaneous selection based on the yield characters could help the breeders for selecting the bitter gourd genotypes for future studies.

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Conflicts of interests. None.

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