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Studies on genetic variability of garlic on growth, yield and quality parameters

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Abstract
The present study was conducted to know genetic variability for growth, yield and quality attributes in garlic (*Allium sativum* L.) at herbal garden of Department of Horticulture, College of Agriculture, UAS, Raichur with twenty eight garlic genotypes with three replications to know the extent of genetic variability, heritability, genetic advance as percent mean. High degree of variation was observed for all the characters studied. Phenotypic co-efficient of variance (PCV) in general was higher than genotypic co-efficient of variance (GCV) with smaller differences which reflects the role of environment is very less. Genotypic coefficient of variation varied from 1.97% (pH) to 49.49% (reducing sugar), while phenotypic coefficient of variation varied from 3.42% (pH) to 49.60% (reducing sugar) among the various characters studied. Higher estimates of heritability found for most of the characters studied. Genetic advance as percent mean was observed as moderate and high for most of the characters except pH and sprouting percent. The characters are governed by additive gene effects. Selection on the basis of the characters will be more useful for the crop improvement towards attaining higher yield.

Keywords: Heritability, additive gene, garlic, co-efficient of variance

Introduction
Garlic belongs to the family Alliaceae with botanical name *Allium sativum* L. and it is a diploid species (2n=16). Alliaceae family comprises of approximately 600 known species distributed over the whole Northern hemisphere. The wild species *Allium longicuspis* Regel is considered as closest relative and ancestor of garlic. It is one of the ancient cultivated vegetable having pungency. It is native to Central Asia and Southern Europe especially Mediterranean region. It is being grown in India and China in larger areas.

Characteristic of *Allium* species are of herbaceous, perennial bulbous plants with a typical leek odour. The bulb of garlic is of a compound nature, consisting of numerous bulblets called cloves of different size and the whole surrounded by layers of white scale leaves. The ovoid cloves are 3-4 sided with an acute summit, narrowed into a thread like portion of fibre and the base is tunicate. Each clove is separately enclosed in a white scale and covered with a pinkish-white skin. From the central clove, the plant shoots a quill-like, round, hollow and unbranched stalk, which is encased at the bottom by long, narrow and flat grass-like leaves. The whitish flowers are placed at the end of a stalk rising directly from the bulb and grouped together in a globular head. The flowers develop numerous egg-shaped bulbils, which have an important function in the propagation of the plant.

The breeding works primarily based on the measure of variability of plant populations. Knowledge of variability in yield and yield contributing characters in crops germplasm is needed for performing selection. The variability of any trait induced by the genetic constitution differences of the genotypes as well as the variations that arise owing to the environmental circumstances. Selection efficacy, primarily based on variability in genetic constituents as it controls the expression of various characters in the population directly. The non-genetic variability constituents, on the contrary, are the results of genetic and environmental interactions and are not so much of helpful to breeders as they cannot be carried from one generation to another.

Genetic variability is the basis for all crop improvement programmes. A wide range of variability in any crop provides better chance of selecting desirable types. Importance of genetic variability was perceived by Vavilov (1951) [12] for the first time and advocated that wide range of variability provides better scope of selecting desirable genotypes.

Materials and Methods

The experiment was undertaken at Herbal garden of Department of Horticulture, College of Agriculture, UAS, Raichur. Twenty eight garlic genotypes were taken for the study. Planting of cloves was done to the main field during *rabi* season. The experiment was laid out by adopting Randomized Block Design with three replications with spacing of 15 x 10 cm. Genotypic co-efficient of variation (GCV) and Phenotypic co-efficient of variation (PCV) were estimated using formula of Burton and De vane (1953) [3] and expressed in terms of percentage. Heritability was estimated using formula of Hanson *et al.* (1956) [6] and expressed in terms of percentage. Genetic advance as percent of mean was given by Johnson *et al.* (1955) [7].

Table 1: List of genotypes for the studies on genetic variability of garlic on growth, yield and quality parameters

Treatments/ Genotypes	Source of collection	Treatments / Genotypes	Source of collection
T_1 - DOGR-92	DOGR, Pune	T_{15} - DOGR-24	DOGR, Pune
T_2 - DOGR-552	DOGR, Pune	T_{16} - DOGR-425	DOGR, Pune
T_3 - DOGR-419	DOGR, Pune	T_{17} - DOGR-189	DOGR, Pune
T_4 - DOGR-662	DOGR, Pune	T_{18} - AC-50	DOGR, Pune
T_5 - DOGR-531	DOGR, Pune	T_{19} - Godavari	DOGR, Pune
T_6 - DOGR-18	DOGR, Pune	T_{20} - GG-2	DOGR, Pune
T_7 - DOGR-30	DOGR, Pune	T_{21} - BRG-14	DOGR, Pune
T_8 - DOGR-377	DOGR, Pune	T_{22} - G-12-2	DOGR, Pune
T_9 - DOGR-323	DOGR, Pune	T_{23} - G-324	DOGR, Pune
T_{10} - DOGR-695	DOGR, Pune	T_{24} - SJG-16-01	DOGR, Pune
T_{11} - DOGR-31	DOGR, Pune	T_{25} – Bhima Purple	DOGR, Pune
T_{12} - DOGR-367	DOGR, Pune	T_{26} - Ranebennur local	Ranebennur
T_{13} - DOGR-112	DOGR, Pune	T_{27} - Bidar local	Bidar
T_{14} - DOGR-139	DOGR, Pune	T_{28} - Gulbarga local	Gulbarga

Results and Discussion

The extent of variability with respect to various characters in different genotypes was measured in terms of range, mean, genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), heritability (h^2) and genetic advance as percent of mean (GAM) (Table 2).

Genotypic co-efficient of variation

Genotypic coefficient of variation varied from 1.97 percent (pH) to 49.49 percent (reducing sugar). Parameter like pH (1.97%) followed by sprouting (5.71%), days to maturity (5.96%) and plant height (10.01%) parameters were shown between 1-10 percent and thus these characters referred as low GCV.

The number of leaves per plant (11.97%) followed by leaf length (10.26%), leaf width (10.42%), neck thickness (12.41%), fresh weight of plant (18.94%), dry weight of plant (20.09%), dry matter content (10.84%), bulb diameter (11.21%), bulb length (12.38%), clove length (12.31%), ascorbic acid (16.10%) and volatile oil content (15.83%) parameters were found between 10.1-20 percent and hence these characters referred as moderate GCV.

The bulb weight (29.14%), clove diameter (20.96%), hundred clove weight (27.60%), yield per hectare (27.47%), sulphur content (26.66%), total sugar (28.51%), reducing sugar (49.49%) and non reducing sugar (34.58%) parameters were in range 20.1 and above percent and hence these characters referred as high GCV indicating greater scope for selection due to high variation in genotypes. The results are in conformation with Andrade Junior *et al*. (2019) [1], Bagchi *et al*. (2020) [2], Divya *et al.* (2021) [4] and Khadi *et al*. (2022) [8].

Phenotypic co-efficient of variation

Phenotypic coefficient of variation varied from 3.42 percent (pH) to 49.60 percent (reducing sugar %). Characters like pH (3.42%), sprouting (9.39%) and days to maturity (6.13%), and total soluble solids (10.03 °Brix) parameters were in between 1-10 percent and these characters are thus referred as low PCV.

Plant height (11.25%) followed by number of leaves per plant (13.63%) leaf length (12.01%), leaf width (12.58%), neck thickness (15.44%), fresh weight of plant (19.79%), dry matter content (15.02%), bulb diameter (12.54%), bulb length (13.59%), clove length (14.24%), ascorbic acid content (16.34%) and volatile oil content (16.24%) parameters were found in between 10.1-20 percent and these characters referred as moderate PCV.

Dry weight of plant (21.61%) followed by average bulb weight (30.19%), number of cloves per bulb (44.04%), clove diameter (22.15%), hundred clove weight (28.10%), yield per hectare (28.40%), sulphur content (26.91%), total sugar (28.59%), reducing sugar (49.60%) and non reducing sugar (34.64%) parameters were in range between 20.1 and above percent and these characters referred as high PCV. These results indicate that genotypes under study can offer scope for improvement through selection of the genotypes for the characters those showed high genotypic as well as phenotypic coefficient of variation. These results are in agreement with Andrade Junior *et al*. (2019) [1], Bagchi *et al*. (2020) [2], Divya *et al.* (2021) [4] and Khadi *et al.* (2022) [8].

Heritability Broad Sense

The genotypic coefficient of variation does not offer full scope to estimate the variations that are heritable and therefore, estimation of heritability becomes necessary. Burton and De Vane (1953) [3] suggested that genetic co-efficient of variations along with heritability estimates would give a reliable indication of expected amount of improvement through selection. Heritability which denotes the proportion of genetically controlled variability expressed by a genotype for a particular character or a set of character is very important biometrical tool for guiding plant breeders for adoption of appropriate breeding procedures. High heritability in broad sense is helpful in identifying appropriate character

for selection and enables the breeder to select superior genotypes on the basis of phenotypic expression of quantitative characters. The estimated values of heritability in broad sense were classified as low (0-30%), moderate (30.1-60%) and high (60.1% and above).

Heritability broad sense percent of variation varied from 33.30 percent (pH) to 99.70 percent (Non-reducing sugar). Parameter which shows between 0-30 percent such is referred as low heritability. This is indicative of the fact that this character is rather more influenced by the environment and may not respond much to selection. Dry matter content (52.10%), pH (33.30%) and sprouting percentage (37.00%) parameters were between 30.1-60 percent referred as moderate heritability.

Plant height (79.20%) followed by number of leaves per plant (77.70%), leaf length (72.90%), leaf width (68.50%), neck thickness (64.50%), fresh weight of plant (91.60%), dry weight of plant (86.50%), days to maturity (94.80%), average bulb weight (93.20%), bulb diameter (79.90%), bulb length (83.00%), number of cloves per bulb (96.90%), clove length (74.80%), clove diameter (89.50%), hundred clove weight (96.40%), yield per hectare (93.50%), total soluble solids (95.50%), ascorbic acid (97.10%), sulphur content (98.10%), volatile oil content (95.10%), total sugar (99.40%), reducing sugar (99.60%) and non reducing sugar (99.70%) parameters were found between 60.1 and above percent and thus these characters referred as high heritability. Higher values of heritability of these characters expressed that they were least influenced by environmental modification. It reflected that the phenotypes were the representative of their genotypes and selection based on phenotypic performance would be reliable. The results are in conformation with Panthee *et al.* (2006) [9], Gupta *et al.* (2007) [5], Tsega *et al*. (2011), Sandhu *et al.* (2015) [10] and Divya *et al.* (2021) [4].

GAM (Genetic advance as percent mean)

Heritability however, indicates only the effectiveness with which selection of a genotype can be based on phenotypic performance, but fails to indicate the genetic progress. Heritability estimates along with genetic gains are more effective and reliable in predicting the improvement through selection (Johnson *et al*., 1955) [7]. Estimates of genetic advance helps to predict the extent of improvement that can be achieved for improving the different characters. The estimated values of genetic advance as percentage of mean are classified as high (more than 20%), moderate (11-20%) and low (less than 11%).

GAM revealed that variation varied from 2.34 percent (pH) to 101.72 percent (reducing sugar). Parameters like pH (2.34%) and sprouting percent (7.15%) were found between 1-10 percent and these characters are referred as low GAM which indicated that were highly influenced by environmental effects and consequently selection for these traits may not be rewarding.

Plant height (18.36%), leaf length (18.05%), leaf width (17.77%), dry matter content (16.12%), days to maturity (11.97%) and total soluble solids (19.73%) parameters were appeared between 10.1-20 percent and these characters referred as moderate GAM, indicating the prevalence of additive gene action in their inheritance denoting the selection based on these traits to be quite effective.

Number of leaves per plant (21.67%) followed by fresh weight of plant (37.34%), dry weight of plant (38.49%), average bulb weight (57.97%), bulb diameter (20.65%), neck thickness (20.53%), bulb length (23.24%), number of cloves per bulb (87.92%), clove length (21.94%), clove diameter (40.84%), hundred clove weight (55.83%), yield per hectare (54.70%), ascorbic acid content (32.67%), sulphur content (54.41%), volatile oil content (31.81%), total sugar (58.56%), reducing sugar (101.72%) and non reducing sugar (71.13%) parameters were noticed between 20.1 and above percent and these characters referred as high GAM. This estimate of genetic advance as percent of mean helps to predict the extent of improvement that can be achieved for improving the different characters. The results are in accordance with the findings of Panthee *et al.* (2006) [9], Gupta *et al.* (2007) [5], Tsega *et al.* (2011) [11], Sandhu *et al.* (2015) [10] and Divya *et al.* (2021) [4].

Table 2: Estimates of variability, heritability and genetic advance as percent mean for different characters in garlic genotypes

Sl. No	Characters	Range		Mean	GCV (%)	PCV (%)	h^2BS (%)	GAM (%)
		Min	Max					
1	Plant height (cm)	40.22	64.16	52.37	10.01	11.25	79.20	18.36
2	Number of leaves per plant	7.86	12.32	9.38	11.97	13.63	77.70	21.67
3	Leaf length (cm)	31.39	47.51	37.83	10.26	12.01	72.90	18.05
4	Leaf width (mm)	9.68	15.63	12.43	10.42	12.58	68.50	17.77
5	Neck thickness (mm)	6.11	12.27	9.20	12.41	15.44	64.50	20.53
6	Sprouting (%)	75.23	96.86	85.45	5.71	9.39	37.00	7.15
7	Fresh weight of plant (g)	12.07	25.23	18.88	18.94	19.79	91.60	37.34
8	Dry weight of plant (g)	5.69	14.01	9.51	20.09	21.61	86.50	38.49
9	Dry matter content (%)	43.12	68.49	50.81	10.84	15.02	52.10	16.12
10	Days to maturity	107.50	143.33	124.35	5.96	6.13	94.80	11.97
11	Average bulb weight (g)	3.24	18.50	9.29	29.14	30.19	93.20	57.97
12	Bulb diameter (mm)	20.08	36.62	30.52	11.21	12.54	79.90	20.65
13	Bulb length (mm)	17.01	31.58	26.01	12.38	13.59	83.00	23.24
14	No. of cloves per bulb	5.35	24.07	9.54	43.35	44.04	96.90	87.92
15	Clove length (mm)	13.17	23.43	19.84	12.31	14.24	74.80	21.94
16	Clove diameter (mm)	5.62	17.31	13.07	20.96	22.15	89.50	40.84
17	100 clove weight (g)	40.54	153.35	106.50	27.60	28.10	96.40	55.83
18	Yield per hectare (t ha^{-1})	1.64	6.18	3.88	27.47	28.40	93.50	54.70
19	Total soluble solids (ºBrix)	24.31	40.70	32.65	9.80	10.03	95.50	19.73
20	pH	5.46	6.20	5.87	1.97	3.42	33.30	2.34
21	Ascorbic acid (mg/100gm)	3.92	7.36	5.24	16.10	16.34	97.10	32.67

22	Sulphur content (%)	0.09	0.34	0.19	26.66	26.91	98.10	54.41
23	Oil content (%)	0.43	0.86	0.70	15.83	16.24	95.10	31.81
24	Total sugar (%)	2.20	7.77	4.62	28.51	28.59	99.40	58.56
25	Reducing sugar (%)	1.09	4.48	2.15	49.49	49.60	99.60	101.72
26	Non reducing sugar (%)	1.07	5.10	2.51	34.58	34.64	99.70	71.13

GCV and PCV: 1-10% (low), 10.1-20% (moderate), 20.1% and above (high); Heritability (Broad sense): 0-30% (low), 30.1-60% (moderate), 60.1% and above (high); GAM: 0-10% (low), 10.1-20% (moderate), 20.1% and above (high); GCV: Genotypic co-efficient of variation; PCV: Phenotypic co-efficient of variation; h^2 BS: Broad sense heritability; GAM: Genetic advancement as percent of mean

Conclusion

High genetic variability in GCV and PCV indicating that characters offers great scope for selection due to high variation in genotypes. High heritability coupled with high GAM permits greater effectiveness for selection by separating out the environmental influence from total variability and thereby allowing the accurate selection of potential genotypes. Therefore simple selection would be helpful for the improving these characters as they are governed by action of additive gene.

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