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Variability studies in F₂ populations of muskmelon (*Cucumis melo* L.) Standl.) for yield and yield attributing traits

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Abstract
The genetic parameters like PCV, GCV, heritability and genetic advance as percent of mean were generated using appropriate breeding and biometrical approaches for high yield and yield contributing traits in the F₂ population of four crosses (VRMM-310 × VRMM-37, VRMM-35 × VRMM-29, VRMM-310 × VRMM-7, VRMM-37 × VRMM-7), these crosses referred to as cross 1, 2, 3 and 4. Higher genotypic and phenotypic coefficients of variation, as well as high heritability estimates, were observed for the yield of fruit per vine in all four crosses; for the weight of fruit, average diameter in crosses 1, 2, and 4; and for average pulp thickness in crosses 2 and 4, indicating the existence of more variability and additive gene effects among all the traits that can be enhanced by the simple selection.

Keywords: Muskmelon, genotypic coefficient of variation, phenotypic coefficient of variation, heritability, genetic advance

Introduction
Muskmelon (*Cucumis melo* L.) is a major cucurbitaceous vegetable grown as a desert crop. Chromosome number of a crop is $2n = 2x = 24$ and is thought to have originated in Tropical Africa, specifically south of the Sahara Desert, but its diversification and domestication are thought to have occurred in Central Asia. *Cucumis* genera contain a large number of species and subspecies (Brickell *et al*., 2004) [2], Naudin (1985) [11] was the first to attempt to categorize the numerous muskmelon varieties. *Cucumis melo* var. *reticulatus* or *Cucumis melo* var. *cantaloupensis* are edible melons.

In order to make the most use of genetic potential in a breeding plan, it is essential to have a thorough understanding of the inheritance of yield and qualities that are connected to yield. Effective plant breeding techniques are needed to boost production. It is essential to consider the kind, extent, and trait transmission rate of genetic diversity. The variability of a population can be divided into heritable and non-heritable components, such as phenotypic and genotypic coefficients of variation (PCV and GCV), heritability and genetic advance, on which efficient selection can be performed (Singh *et al.* 1986) [14]. PCV and GCV estimates showed significant amount of variation among genotypes for all of the characters under this study. Higher PCV and GCV estimates indicate a greater possibility of individual selection within the population. The greater the variability of the population, the greater the possibility of selection (Frankel, 1947) [6].

Material and Methods
The experiment was carried out at Dr. Y.S.R. HU, College of Horticulture in Venkataramannagudem, West Godavari District. Four promising F₁ hybrids were chosen by comparing growth, yield and quality traits to the control. The best performing F₁ hybrids were chosen and they were selfed to produce F₂, those are evaluated in a randomised block design with two replications during *Rabi* 2022. Observations on different yield characteristics were recorded in all F₂ generation plants for number of fruits per vine, yield per vine (Kg), average weight of fruit (g), average length of fruit (cm), average diameter of fruit (cm), average pulp thickness (cm), Seed Cavity (cm²), GCV, PCV (Burton,1953) [3], Heritability analysis and Genetic Advance (Allard, 1960) [1].

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Genotypical and phenotypical coefficient of variations
Genotypic and phenotypic coefficient of variation can be calculated with the help of the following formulae.

$$PCV = \frac{\sqrt{\sigma p\,2}}{\bar{x}} \times 100$$

$$GCV = \frac{\sqrt{\sigma g\,2}}{\bar{x}} \times 100$$

Where as,

$\sigma g\,2$ = Genotypic variance = $\dfrac{TrMSS - EMSS}{r}$

$\sigma e\,2$ = Environment variance = $\dfrac{EMSS}{r}$

$\sigma p2$ = Phenotypic variance = $\sigma g2 + \sigma e2$

x = General means

PCV and GCV were classified as shown below.

Low = 0-10%

Moderate =10-20%
High = 21% and above

Heritability in Broad sense [h²(b)]

$$h^2\,(b) = \frac{\sigma g\,2}{\sigma p\,2}$$

Where,
$h^2\,(b)$ = Heritability estimates in a broad sense
σg^2 = Genotypic variance
σp^2 = Phenotypic variance

As suggested by Johnson *et al.* (1955) [7], h²(b) estimates were categorized as
Low = 0-30%
Medium = 31-60%
High = 61% and above

Genetic advance (GA)
This was estimated as per the formula proposed by Allard (1960) [1]

GA = K x σp x h² (b)

Where,
K = Selection differential at 5 percent selection intensity (2.06)
h²(b) = Heritability in broad sense
σp = Phenotypic standard deviation

$$GA \text{ as percent of mean} = \frac{Genetic\ advance}{Population\ mean} \times 100$$

Low = 0–10
Moderate = 10–20
High = >20

Results and Discussion
Table number 1, 2, 3, and 4 show the means, GCV, PCV, heritability, and genetic advance as a percentage of mean. In the present study, the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) in all four crosses, namely cross 1 (VRMM-310 × VRMM-37), cross 2 (VRMM-35 × VRMM-29), cross 3 (VRMM-310 × VRMM-7) and cross 4 (VRMM-37 × VRMM-7), indicating the influence of environmental factors during expression of the characters. Identical outcomes have been reported by Sravani *et al.* (2021) [15] in the F₂ generation, Durga *et al.* (2021) [5] in the F₃ generation of ridge gourd; Deepa *et al.* (2018) [4] in cucumber.

High PCV and GCV values were recorded in fruit yield per vine in all crosses, average weight and average diameter of fruit in crosses 1, 2, and 4, and average pulp thickness (crosses 2 and 4), indicating greater variability among all traits recorded and ample scope for enhancement of those characters through selection. This results have been confirmed by Sumarani *et al.* (2009) [16] and Kanimozhi *et al.* (2015) [9] in Ash pumpkin.

The number of fruits per vine (cross 3 and 4), average weight of fruit, average diameter and pulp thickness all had moderate PCV and GCV. These the result was contradictory to Kanal *et al.* (2019) [8] in F₄ population of pumpkin as these characteristics demonstrated a high PCV and GCV.

Lower PCV and GCV was observed for average length of fruit and seed cavity (all crosses). This indicated that these characters have low variability, which is a constraint for genetic improvement through selection. Rani *et al.* (2014) [13] found similar results in bitter gourd and Kannan *et al.* (2019) [10] in ridge gourd.

The success of trait improvement through selection is dependent on heritability combined with genetic advancement. The magnitude of heritability indicates the efficacy with which genotype selection can be based on phenotypic performance. A high heritability value indicates that the character's phenotype strongly reflects the genotype and points to the importance of genotypic constitution in character expression. From a breeding standpoint, such traits are regarded as dependable.

For the number of fruits, the yield per vine, weight of fruit, diameter of fruit and pulp thickness (cross 1, 2, 3, and 4), high heritability was observed, indicating that heritability was primarily due to additive gene effects. So, selection was highly effective for these traits. These findings are in contradictory with Sravani *et al.* (2021) in the F₂ generation, Durga *et al.* (2021) [5] in the F₃ generation of ridge gourd.

Table 1: Means, Genotypic coefficient of variation, Phenotypic coefficient of variation, heritability and genetic advance in F_2 population of VRMM-310 × VRMM-37

Serial Number	Parameters	Means	Range		Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	h^2	Genetic Advance	Genetic advance as percent of mean (%)
			Min	Max					
1	Number of fruits per vine	3.03	2.41	4.5	21.39	20.21	89.29	89.29	39.34
2	Yield of fruit per vine (Kg)	1.83	0.9	2.5	59.11	57.96	96.15	2.14	117.08
3	Average weight of fruit (gm)	583.00	425	660	23.61	22.85	93.66	5.59	45.56
4	Average length of fruit (cm)	18.48	10	19	3.01	2.45	66.13	0.76	4.10
5	Average diameter of fruit (cm)	15.24	10	16	20.30	20.03	97.39	6.21	40.72
6	Average pulp thickness (cm)	1.57	1.0	1.8	15.60	14.24	83.33	0.42	26.78
7	Seed Cavity (cm^2)	8.37	5.6	9.5	7.27	6.27	74.32	0.93	11.13

Table 2: Means, Genotypic coefficient of variation, Phenotypic coefficient of variation, heritability and genetic advance in F_2 population of VRMM-35 × VRMM-29.

Serial Number	Parameters	Means	Range		Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	h^2	Genetic Advance	Genetic advance as percent of mean (%)
			Min	Max					
1	Number of fruits per vine	3.03	2.10	5.1	21.39	20.21	89.29	89.29	39.34
2	Yield of fruit per vine (Kg)	1.83	0.5	2.6	59.11	57.96	96.15	2.14	117.08
3	Average weight of fruit (gm)	583.00	210	750	23.61	22.85	93.66	5.59	45.56
4	Average length of fruit (cm)	18.48	10	19	3.01	2.45	66.13	0.76	4.10
5	Average diameter of fruit (cm)	15.24	9.3	16	20.30	20.03	97.39	6.21	40.72
6	Average pulp thickness (cm)	1.57	0.6	1.7	15.60	14.24	83.33	0.42	26.78
7	Seed Cavity (cm^2)	8.37	4.2	10.2	7.27	6.27	74.32	0.93	11.13

Table 3; Means, Genotypic coefficient of variation, Phenotypic coefficient of variation, heritability and genetic advance in F_2 population of VRMM-310 × VRMM-7.

Serial Number	Parameters	Means	Range		Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	h^2	Genetic Advance	Genetic advance as percent of mean (%)
			Min	Max					
1	Number of fruits per vine	3.03	1.6	5.0	21.39	20.21	89.29	89.29	39.34
2	Yield of fruit per vine (Kg)	1.83	0.7	2.2	59.11	57.96	96.15	2.14	117.08
3	Average weight of fruit (gm)	583.00	312	760	23.61	22.85	93.66	5.59	45.56
4	Average length of fruit (cm)	18.48	6	19	3.01	2.45	66.13	0.76	4.10
5	Average diameter of fruit (cm)	15.24	7	16	20.30	20.03	97.39	6.21	40.72
6	Average pulp thickness (cm)	1.57	0.6	1.6	15.60	14.24	83.33	0.42	26.78
7	Seed Cavity (cm^2)	8.37	6	9	7.27	6.27	74.32	0.93	11.13

Table 4: Means, Genotypic coefficient of variation, Phenotypic coefficient of variation, heritability and genetic advance in F_2 population of VRMM-37 × VRMM-7

Serial Number	Parameters	Means	Range		Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	h^2	Genetic Advance	Genetic advance as percent of mean (%)
			Min	Max					
1	Number of fruits per vine	3.03	2.41	4.5	21.39	20.21	89.29	89.29	39.34
2	Yield of fruit per vine (Kg)	1.83	0.9	2.5	59.11	57.96	96.15	2.14	117.08
3	Average weight of fruit (gm)	583.00	121	800	23.61	22.85	93.66	5.59	45.56
4	Average length of fruit (cm)	18.48	9.2	18	3.01	2.45	66.13	0.76	4.10
5	Average diameter of fruit (cm)	15.24	9	16	20.30	20.03	97.39	6.21	40.72
6	Average pulp thickness (cm)	1.57	0.9	2.2	15.60	14.24	83.33	0.42	26.78
7	Seed Cavity (cm^2)	8.37	7	8.2	7.27	6.27	74.32	0.93	11.13

Conclusions

The experiment was carried out in F_2 generations of four crosses (VRMM-310 × VRMM-37, VRMM-35 × VRMM-29, VRMM-310 × VRMM-7, VRMM-37 × VRMM-7) for high yield and yield attributing characters in muskmelon. Appropriate breeding and biometrical approaches generated data on genetic parameters like PCV, GCV, heritability and genetic advance as a percent of mean.

For all the traits studied, PCV was significantly higher than GCV, confirming the environmental intervention. High Genotypic and phenotypic coefficient of variation values were recorded for fruit yield per vine in all crosses, average weight of fruit in crosses 1, 2, and 4, and average diameter of fruit (crosses 1, 2, and 4 indicating greater variability among all traits recorded). Average fruit length and seed cavity (cross 3) have low PCV and GCV in F_2 generation, which may be due to low genetic influence among the crosses.

For the number of fruits per vine, yield per vine, average weight, average diameter, and average pulp thickness (crosses 1, 2, 3, and 4), high heritability was observed, indicating that the heritability was primarily due to additive gene effect and that selection would be highly effective for the characters. Crop improvement in muskmelon for fruit yield per vine could be concentrated on the yield of fruit per vine in all crosses, average weight of fruit in crosses 1, 2, and 4, and the average diameter of fruit (crosses 1, 2, and 4), which were controlled by additive gene effects as indicated by high heritability combined with high genetic advance as percent of mean. They also had high PCV and GCV, indicating high variability.

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