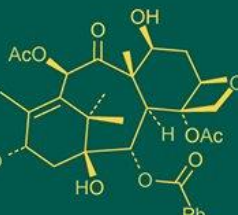
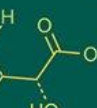
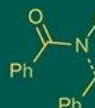


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Assessment of genetic variability and heritable components governing growth, flowering, yield and quality attributes in an F_2 population of sponge gourd [*Luffa cylindrica* (L.) Roem.] Derived from the cross HR-6 $\times$ SG-3

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Abstract

The present study estimated genetic variability, heritability and genetic advance for twenty growth, flowering, yield and quality traits in the F_2 population of sponge gourd (*Luffa cylindrica* (L.) Roem.) derived from the cross HR-6 $\times$ SG-3, raised during the late kharif season at KRCCH, Arabhavi. Two growth traits, number of primary branches at 45 DAS (PCV 11.05%, GCV 10.07%) and vine length at 45 DAS (PCV 11.17% and GCV 9.69%), showed moderate coefficients of variation, while the remaining eighteen traits remained in the low (<10%) category. Heritability was high (>60%) for seventeen of the twenty traits, being highest for average fruit weight (95.30%), node at which the first female flower appears (92.52%) and total leaf area (91.21%) and total soluble solids was the only trait with moderate heritability (57.31%). Genetic advance as per cent of mean did not exceed 20% for any trait but was moderate (10-20%) for thirteen traits, led by number of primary branches at 45 DAS (18.89%), node at first female flower appearance (17.36%) and vine length at 45 DAS (17.32%). The combination of moderate coefficients of variation, high heritability and the highest genetic advance recorded for the two early growth traits indicates a comparatively strong additive genetic component for vegetative vigour in this cross, making them the most promising traits for direct selection, whereas total soluble solids and fruit diameter, with the lowest genetic advance recorded, are likely to require alternative breeding strategies for improvement.

Keywords: Sponge gourd, HR-6 $\times$ SG-3, F_2 population, GCV, PCV, heritability, genetic advance

Introduction

Sponge gourd (*Luffa cylindrica* (L.) Roem.; $2n = 2x = 26$) is grown throughout the warmer parts of India for its tender fruits, valued for their high moisture content and dietary fibre and its cultivation continues to expand even though the crop has received comparatively little attention from organised breeding programmes (Wehner *et al.*, 2020 and Halder *et al.*, 2022) [1, 2]. For any quantitative trait, the success of a selection programme is governed by how much of the observed phenotypic variation is genetic in origin and how reliably that genetic variation is transmitted across generations. The genotypic (GCV) and phenotypic (PCV) coefficients of variation quantify the extent of variability present in a population (Burton and De Vane, 1953) while broad-sense heritability estimates the proportion of that variability attributable to genotype. Because heritability alone can be inflated by non-additive genetic variance, particularly in an early segregating generation, it is generally interpreted together with genetic advance as per cent of mean (GAM) to judge whether a trait is likely to respond well to direct phenotypic selection (Johnson *et al.*, 1955) [7].

An F_2 population, obtained by selfing the F_1 of a hybrid cross, segregates for the alleles contributed by both parents and therefore offers breeders an early opportunity to assess the genetic architecture of growth, flowering, yield and quality traits before investing in a longer breeding cycle.

This study was undertaken to independently assess the genetic variability, heritability and genetic advance for twenty growth, flowering, yield and quality traits in the F_2 population of

the cross HR-6 × SG-3, so as to identify the traits offering the greatest scope for improvement through direct selection within this specific parental combination.

2. Materials and Methods

The investigation was conducted at the Kittur Rani Channamma College of Horticulture (KRCCCH), Arabhavi, during the late kharif season, using the F₂ population obtained by selfing the F₁ of the cross HR-6 × SG-3.

The twenty growth, earliness/flowering, yield and quality characters recorded for the companion cross were evaluated in this population: vine length at 45 and 90 days after sowing (DAS), number of primary branches at 45 and 90 DAS, total leaf area, days taken for first flowering, days taken for 50 per cent plants flowering, node at which the first female flower appears, per cent fruit set, days taken to first and last harvest, fruit length, fruit diameter, number of fruits per vine, average fruit weight, fruit yield per vine, fruit yield per plot, fruit yield per hectare, total soluble solids and ascorbic acid content.

PCV and GCV were categorised as low (<10%), moderate (10-20%) and high (>20%) following Sivasubramanian and Menon (1973). Heritability in the broad sense was classified as low (<30%), moderate (30-60%) and high (>60%) as per Robinson *et al.* (1949) and GAM was classified as low (<10%), moderate (10-20%) and high (>20%) following Johnson *et al.* (1955)^[7].

As with the companion cross, the specific F₂ population size, number of replications and the procedure used to separate

genotypic from environmental variance were not indicated in the records available for this analysis and the discussion that follows relies strictly on the reported PCV, GCV, h², GA and GAM values for HR-6 × SG-3 without assuming mean or range values, which were likewise not available.

3. Results and Discussion

The estimates of PCV, GCV, heritability and genetic advance recorded for the twenty characters studied in the F₂ population of HR-6 × SG-3 are presented in Table 1.

Unlike growth traits in general, two characters in this cross crossed over from the low into the moderate (10-20%) PCV/GCV class: vine length at 45 DAS (PCV 11.17% and GCV 9.69%) and number of primary branches at 45 DAS (PCV 11.05% and GCV 10.07%), the latter being the only character in this population for which both PCV and GCV simultaneously exceeded 10%. All remaining eighteen characters, including vine length at 90 DAS, primary branches at 90 DAS, all flowering traits and all yield and quality traits, remained in the low (<10%) PCV/GCV class, with average fruit weight (GCV 8.08%) and node at which the first female flower appears (GCV 8.76%) showing the next-highest genotypic variation after the two growth traits noted above. A similar predominance of low-to-moderate PCV and GCV across most growth, flowering, yield and quality traits, with only branching and vine-related characters occasionally crossing into the moderate class, has been reported for sponge gourd germplasm by Khule *et al.* (2011) and Kumar *et al.* (2018)^[15, 16].

Table 1: Estimates of genetic variability parameters for growth, flowering, yield and quality characters in the F₂ population of sponge gourd Cross HR-6 × SG-3

Characters	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)
Growth parameters					
Vine length at 45 DAS	11.17	9.69	75.28	0.55	17.32
Vine length at 90 DAS	7.93	5.98	56.91	0.49	9.30
No of primary branches at 45 DAS	11.05	10.07	83.00	0.80	18.89
No of primary branches at 90 DAS	9.45	8.75	85.72	0.90	16.68
Total leaf area (cm ²)	7.94	7.58	91.21	15.71	14.91
Earliness and flowering parameters					
Days taken for first flowering	8.68	7.04	65.66	4.72	11.74
Days taken for 50% plants flowering	7.75	7.24	87.33	7.30	13.94
Node at which first female flower appears	9.11	8.76	92.52	1.98	17.36
Percent fruit set	8.34	7.90	89.69	11.90	15.41
Days taken to first harvest	7.17	5.89	67.52	5.28	9.98
Days taken to last harvest	6.63	6.20	87.23	12.77	11.92
Yield parameters					
Fruit length (cm)	7.52	6.56	76.14	2.96	11.80
Fruit diameter (cm)	5.79	4.84	69.79	0.29	8.33
Number of fruits per plant	6.16	5.78	88.06	1.59	11.18
Average fruit weight (g)	8.27	8.08	95.30	20.36	16.25
Fruit yield per Vine (kg)	8.54	6.78	63.06	0.25	11.09
Fruit yield per plot (kg)	8.83	7.64	74.86	2.24	13.61
Fruit yield per hectare (tonnes)	7.92	7.49	89.40	2.14	14.59
Quality parameters					
Total Soluble Solids (°Brix)	7.32	5.54	57.31	0.35	8.64
Ascorbic acid (mg/100g)	7.96	7.05	78.32	1.02	12.85

PCV = Phenotypic coefficient of variation; GCV = Genotypic coefficient of variation; h² = Broad-sense heritability; GA = Genetic advance; GAM = Genetic advance as per cent of mean

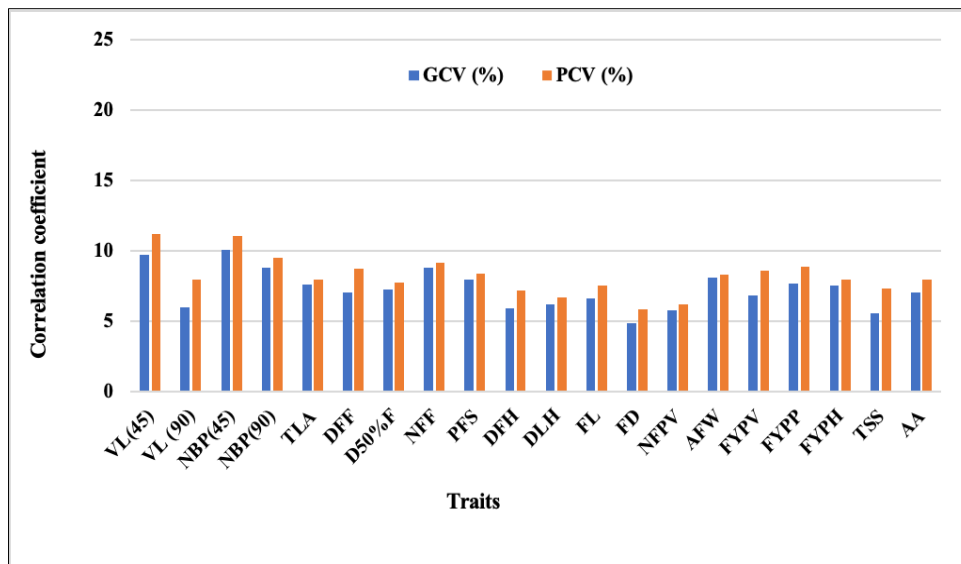


Fig 1: Comparison of variation measured at genotypic and phenotypic levels for different parameters in sponge gourd (HR-6 x SG-3)

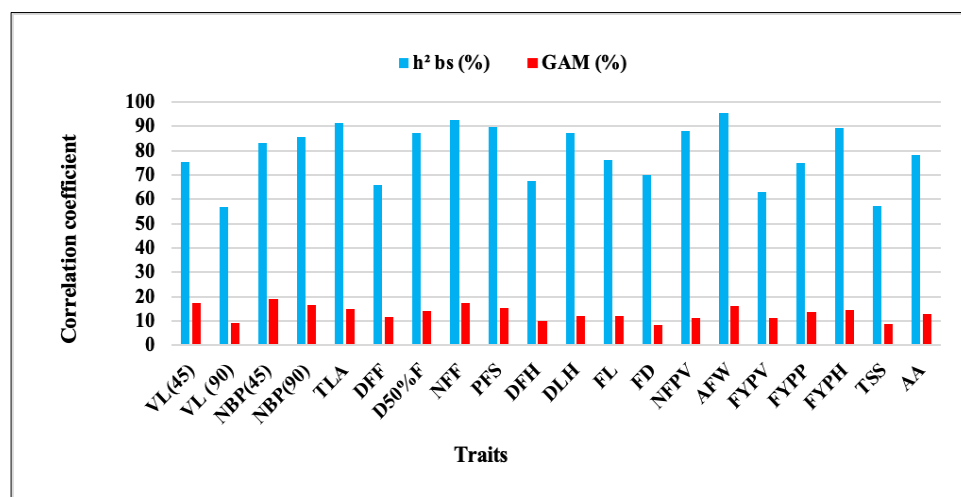


Fig 2: Heritability and genetic advance over mean for different parameters in sponge gourd (HR-6 x SG-3)

VL45- Vine length at 45 DAS (m), VL90- Vine length at 90 DAS (m), PB45- No. of primary branches at 45 DAS, PB90- No. of primary branches at 90 DAS, TLA- Total leaf area (cm²), DFF- Days taken for first flowering, D50F- Days taken for 50% plants flowering, NFF- Node at which first female flower appears, PFS- Fruit set (%), DFH- Days taken to first harvest, DLH- Days taken to last harvest, FL- Fruit length (cm), FD- Fruit diameter (cm), NFPV- No. of fruits per vine, AFW- Average fruit weight (g), FYPV- Fruit yield per vine (kg), FYPP - Fruit yield per plot (kg), FYPH - Fruit yield per hectare (t), TSS - Total soluble solids (°Brix), AA - Ascorbic acid (mg/100 g)

Heritability was high (>60%) for seventeen of the twenty characters, the highest being recorded for average fruit weight (95.30%), node at which the first female flower appears (92.52%), total leaf area (91.21%) and per cent fruit set (89.69%). Only total soluble solids (57.31%), vine length at 90 DAS (56.91%) and fruit yield per vine (63.06%, borderline high) recorded comparatively lower heritability, total soluble solids being the single trait with moderate rather than high heritability in this cross. This predominance of high heritability across most growth, flowering and yield characters parallels the pattern reported for the majority of yield-contributing traits in bitter melon by Sagar *et al.*

(2024) [18] and for ridge gourd, a closely related *Luffa* species, by Rai *et al.* (2025) [17].

Genetic advance as per cent of mean again did not reach the high (>20%) class for any character, but the moderate (10-20%) class was more heavily populated than in the companion cross, comprising thirteen characters. The highest GAM values were recorded for number of primary branches at 45 DAS (18.89%), node at which the first female flower appears (17.36%), vine length at 45 DAS (17.32%), number of primary branches at 90 DAS (16.68%) and average fruit weight (16.25%). Low GAM (<10%) was confined to seven characters, the lowest being fruit diameter (8.33%) and total soluble solids (8.64%). This ceiling on genetic advance, with no character reaching the high class despite several traits combining high heritability with only moderate GAM, mirrors observations made across quantitative traits in sponge melon by Kumar *et al.* (2018) [16], reinforcing the likelihood of a substantial non-additive component even where heritability alone appears very high. The two growth characters that moved into the moderate PCV/GCV class in this cross, vine length at 45 DAS and number of primary branches at 45 DAS, mark the clearest point of divergence from the pattern generally reported for early vegetative traits in sponge melon, where branching and vine length have variously been reported to show low,

moderate or high coefficients of variation depending on the parental material used (Panwar *et al.*, 1977 and Som *et al.*, 2020) [9, 11]. Their appearance here alongside comparatively high heritability (83.00% and 85.72%, respectively for the two branching stages) and the two highest GAM values recorded in the entire dataset (18.89% and 16.68%) is consistent with additive gene action being unusually prominent for early-stage branching and vine extension in this particular parental combination and marks these two traits as strong early candidates for phenotypic selection, a conclusion broadly in line with that reached for branching traits in ridge gourd by Choudhary and Kumar (2011) [14] and consistent with the high heritability and genetic advance reported for vine length and branch number across bottle gourd genotypes by Singh *et al.* (2021) [19].

For the majority of the remaining traits, the pattern of high heritability combined with only moderate genetic advance, seen for average fruit weight (h^2 95.30%, GAM 16.25%), node at first female flower appearance (h^2 92.52%, GAM 17.36%) and total leaf area (h^2 91.21%, GAM 14.91%), points to the same interpretive caution raised by Johnson *et al.* (1955) [7] and heritability estimated on an F_2 population reflects both additive and non-additive components of variance and traits for which GAM lags behind an otherwise very high heritability are likely still carrying an appreciable dominance component that phenotypic selection on F_2 plants alone cannot fully exploit. A broadly similar combination of high heritability with moderate rather than high genetic advance for fruit weight and flowering-node traits has been reported for sponge gourd germplasm by Abhijeet *et al.* (2018) and Kousthubha *et al.* (2023) [8, 12].

Fruit diameter and total soluble solids stood out as the two traits with the lowest genetic advance in this cross and total soluble solids was also the only trait with moderate rather than high heritability (57.31%). A comparable moderate-heritability, low-GAM pattern for total soluble solids has been noted in gourd crops by Kumar *et al.* (2013) [10], while the somewhat higher heritability recorded here for ascorbic acid content (78.32%) alongside moderate genetic advance (12.85%) is broadly consistent with the heritability estimated for vitamin C content in the related crop ridge gourd by Arizoo *et al.* (2024) [13]. Taken together, these two quality traits appear to be governed by a more balanced mix of additive and non-additive effects than most of the growth and yield traits in this cross and are correspondingly less amenable to rapid improvement through simple phenotypic selection. Notably, fruit diameter does not behave uniformly across cucurbits: Singh *et al.* (2021) [19] recorded very high PCV, GCV and genetic advance for this trait in bottle gourd, underscoring that its low genetic advance in the present cross is a feature of this particular parental combination rather than an inherent property of the trait itself.

Days taken to first harvest and fruit yield per vine, both of which combined high heritability with comparatively low GAM (9.98% and 11.09%, respectively), mirror the pattern reported for fruit-set and earliness traits in an unrelated F_2 gourd population by Kumar *et al.* (2013) [10], reinforcing the general observation that earliness-related characters in *Luffa* often carry a smaller additive fraction than fruit-size and fruit-number traits even when their heritability appears numerically high. Similar moderate genetic advance for earliness and flowering-related characters, despite comparatively high heritability, has also been documented in sponge gourd by Khule *et al.* (2011) [15].

4. Conclusion

In the F_2 population of HR-6 $\times$ SG-3, number of primary branches at 45 DAS and vine length at 45 DAS were the only two traits, among the twenty studied, to record moderate genotypic and phenotypic coefficients of variation and all other traits remained in the low category. Both of these growth traits also combined high heritability with the highest genetic advance recorded in this cross, indicating a comparatively strong additive component and identifying them as the most promising traits for direct phenotypic selection within this specific parental combination, along with node at which the first female flower appears and average fruit weight, which likewise combined high heritability with above-average genetic advance.

Total soluble solids, the only trait with moderate rather than high heritability in this cross, together with fruit diameter, showed the lowest genetic advance recorded, suggesting that gains for these two traits through simple selection on the F_2 population are likely to be limited and a hybridisation-based or later-generation selection approach would be more appropriate for their improvement. Overall, the comparatively higher genetic advance recorded for growth and branching traits in this cross, relative to the companion cross of the same study, suggests that HR-6 $\times$ SG-3 offers somewhat greater scope for early selection gains in vegetative vigour, though this observation is specific to the present dataset and would need to be verified through replicated multi-generation evaluation.

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