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Genetic parameters and correlation studies for fruit and seed characteristics in half-sib progenies of *Cinnamomum zeylanicum* Blume

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Abstract

Cinnamomum zeylanicum Blume is an economically important tree spice valued for its bark, leaves and increasingly for its fruits. The present study was undertaken to assess genetic variability, heritability and inter-relationships among fruit and seed traits in half-sib progenies of *C. zeylanicum* under humid tropical conditions of the Western Ghats, India. Six-year-old half-sib progenies representing five seed sources were evaluated during 2023-2025 in a randomized complete block design. Genetic parameters including genotypic and phenotypic coefficients of variation, heritability and genetic advance were estimated, along with genotypic and phenotypic correlations among traits.

Substantial variability was observed for most fruit and seed characters. Fruit traits such as mature fruit length (84.58%), fruit width (60.26%) and test weight (69.92%) exhibited high heritability coupled with moderate genetic gain, indicating predominance of additive gene action and suitability for direct selection. Seed length (81.33%) and seed dry weight (73.72%) recorded high heritability and moderate genetic gain, suggesting strong genetic control and potential for improving seed quality and vigour. Traits related to fruit number and fruit set showed greater environmental influence and lower selection efficiency. Correlation analysis revealed strong positive associations among size and weight-related fruit traits, as well as among seed morphological traits, indicating that selection for one trait could lead to simultaneous improvement of related characters. The study identifies key selection traits for cinnamon improvement and provides valuable insights for breeding, conservation and sustainable cultivation of *C. zeylanicum*.

Keywords: Genetic variability, heritability, genetic gain, correlation, fruit and seed traits

Introduction

Cinnamomum zeylanicum Blume (Lauraceae), commonly known as cinnamon or Dalchini, is an evergreen spice tree of high economic and medicinal value. Indigenous to Sri Lanka and southern India, the species has been cultivated for centuries for its aromatic bark, leaves and fruits, which are extensively used in culinary, pharmaceutical and traditional medicinal systems. Recent scientific investigations have highlighted the presence of bioactive compounds in different plant parts, contributing to antioxidant, antimicrobial and therapeutic properties (Zare *et al.*, 2019; Lima *et al.*, 2005) ^[22, 10]. These attributes have increased interest in cinnamon not only as a spice crop but also as a potential source of natural health products. Although the dried inner bark remains the principal commercial product, cinnamon trees also yield essential oils from leaf, stem bark and root bark, each differing in chemical composition and functional applications (Wijesekera *et al.*, 1975) ^[21]. In recent years, cinnamon fruits-particularly immature fruits-have gained considerable importance in southern India. In Karnataka, immature fruits are widely harvested for the preparation of spice powders and masala products, offering enhanced income opportunities to farmers and expanding the economic relevance of fruit-based traits (Hanumantha, 2020; Hanumantha and Vasudeva, 2022) ^[6, 4].

In tree improvement programmes, the estimation of genetic parameters such as genotypic and phenotypic variances, heritability and genetic advance is fundamental for understanding the inheritance of quantitative traits and predicting selection response (Falconer and Mackay, 1996) ^[2]. Genetic parameters are important to understand the strength of genetic control of specific traits. Heritability estimates along with expected genetic gains are more useful for selecting best

genotypes (Zobel and Talbert, 1984) [23]. Heritability estimates are useful in making selection of superior phenotypes (plus trees) on the basis of phenotypic performance of quantitative characters (Vasudeva *et al.*, 2004) [20]. Correlation studies is also very essential for selecting the trees based on dependent traits; as associations between fruit and seed characteristics can influence breeding strategies and enable indirect selection for complex traits like yield and quality (Hanumantha, 2000; Hanumantha *et al.*, 2001) [5, 7]. Positive correlations among economically important traits may enhance selection efficiency, whereas negative correlations may impose constraints on genetic improvement.

Fruit and seed traits are also influenced by phenological behaviour and environmental factors such as temperature, rainfall and pollinator activity, which affect flowering, fruit development and seed maturation (Leith, 1974; Fenner, 1998). Previous studies in perennial spice crops have demonstrated wide variability in reproductive traits and highlighted the importance of genetic analysis for identifying superior genotypes (Haldankar *et al.*, 2004; Miniraj *et al.*, 2023; Vasudeva *et al.*, 2004) [3, 12, 20]. However, despite the growing commercial importance of cinnamon fruits, information on genetic parameters and inter-relationships among fruit and seed traits in *C. zeylanicum* progenies remains limited, particularly under the humid tropical conditions of the Western Ghats.

Therefore, the present investigation was undertaken to estimate genetic parameters and assess phenotypic and genotypic correlations among fruit and seed characteristics in half-sib progenies of *Cinnamomum zeylanicum* Blume. The results are expected to provide critical insights into the genetic control of reproductive traits and support the identification of superior genotypes for use in cinnamon improvement, conservation and sustainable cultivation programmes.

Materials and Methods

The study was carried out over a period of two years (2023-2025) at the College of Forestry, Sirsi, and at an established progeny trial located in Kangod village, Uttara Kannada district, Karnataka, India. The investigation focused on assessing variability in fruit and seed traits among half-sib progenies of *C. zeylanicum* and on estimating genetic parameters associated with these reproductive characters. Uttara Kannada district lies within the central Western Ghats region of India, extending between 13°55' and 15°32' N latitude and 74°05' and 75°05' E longitude, and encompasses a geographical area of approximately 10,291 km². The district is bounded by Goa and Belagavi districts to the north, Dharwad, Haveri and Shivamogga districts to the east, Udupi district to the south, and the Arabian Sea along the western margin, forming a narrow coastal belt of about 120 km. The region experiences a humid tropical climate with high rainfall, creating favourable conditions for the growth and development of cinnamon.

The progeny evaluation trial was conducted in a farmer-managed field at Kangod village (14°32'-14°33' N latitude and 74°48'-74°50' E longitude) in Sirsi taluk of Uttara Kannada district. The experimental material consisted of six-year-old half-sib progenies of *C. zeylanicum*, which were originally established during 2020-2021 following a Randomized Complete Block Design (RCBD) (Hanumantha, 2020) [6]. Based on prior performance records, twenty progenies representing five distinct seed sources were selected for detailed evaluation. Meteorological data including rainfall, relative humidity and temperature for the study period from July 2024 to July 2025 were obtained from the Agricultural Research Station, Sirsi as

shown in table 01. Rainfall showed a distinct monsoonal pattern, with the highest precipitation recorded in July 2024 (1598.4 mm), followed by a gradual decline in the post-monsoon months. The lowest rainfall was recorded in January and February 2025 (0.0 mm), while a secondary peak occurred in May 2025 (322.8 mm) during the pre-monsoon showers. Rainfall began to increase again in June 2025 (692.2 mm) with the onset of the southwest monsoon. The annual mean maximum and minimum temperatures were 29.91 °C and 19.45 °C, respectively. Minimum temperatures were recorded in December and January (17.7 °C and 14.9 °C), whereas maximum temperatures were observed in March and April 2025, peaking at 34.7 °C in March. Morning relative humidity remained consistently high (85-91%) throughout the year, while evening humidity varied widely, reaching as low as 42 per cent in March 2025 and remaining elevated (82-83%) during the monsoon months. The total rainfall during the 13-month observation period was 4594.6 mm, with average morning and evening relative humidity values of 89.18 per cent and 63.49 per cent, respectively. These climatic conditions are typical of the monsoon-dependent ecosystem of the Western Ghats, where plant growth and reproductive behaviour are closely associated with seasonal rainfall and humidity fluctuations.

The data obtained for all the measured characters were subjected to analysis of variance (ANOVA) following the procedure described by Panse and Sukhatme (1961). The ANOVA was used to test the significance of differences among progenies, considering replication and error effects in a Randomized Complete Block Design. The genotypic, phenotypic, and environmental variances were estimated using the following formulas:

$$V_g = \frac{(M_t - M_e)}{r}, V_e = \frac{M_e}{r}, V_p = V_g + V_e$$

where V_g represents genotypic variance, V_e environmental variance, V_p phenotypic variance, M_t mean sum of squares due to progenies, M_e mean sum of squares due to error, and r number of replications. Coefficients of variability were computed according to the method proposed by Burton and Devane (1953) [1]. Heritability and genetic advance were estimated following the procedures of Falconer and Mackay (1996) [2]. These analyses helped quantify the genetic variability and inheritance pattern of reproductive traits among half-sib progenies of *C. zeylanicum* under field conditions in the Western Ghats region of Karnataka.

Results and Discussion

Genetic and phenotypic variation for fruit traits

The genetic analysis (Table 01) revealed wide variation in genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) across fruit traits, indicating substantial genetic diversity. Estimation of genetic parameters is essential for facilitating tree selection and higher heritability and genetic gain simplify the selection process (Hanumantha, 2000; Niharika, 2023) [6, 14]. The number of fruits per inflorescence exhibited the highest GCV (37.08%) and PCV (60.10%), suggesting strong environmental influence on this trait. Similar findings were reported by Sarma *et al.* (2010) [15] in *C. verum*, where fruit yield traits showed high environmental sensitivity.

Moderate GCV values were observed for immature fruit dry

weight (14.74%), fresh weight (12.56%), and test weight (11.42%), and suggesting potential for genetic improvement through selection. Traits like mature fruit length and width showed comparatively lower GCV-PCV differences, indicating stable expression and stronger genetic control. Heritability estimates varied widely, with the highest for mature fruit length (84.58%), followed by test weight (69.92%) and mature fruit width (60.26%), implying that these traits are largely heritable and amenable to direct selection (Johnson *et al.*, 1955) [8]. High heritability coupled with high genetic advance, as observed for fruit length (20.62%) and test weight (19.67%), suggests additive gene action. Conversely, fruit set per cent showed low heritability (26.93%) and low genetic gain (12.76%), indicating predominant environmental control and limited selection response (Nayak *et al.*, 2020) [13]. Niharika (2023) [14] also reported variation for GCV, PCV, heritability and genetic gain among cinnamon progenies for growth and leaf parameters. Overall, mature fruit length, fruit width, and test weight were identified as stable and heritable traits, suitable as primary selection indices for genetic improvement of fruit quality in *C. zeylanicum*.

Genetic and phenotypic variation for seed traits

Analysis of genetic parameters (Table 02) revealed that seed dry weight recorded the highest GCV (27.68%) and PCV (32.23%), followed by seed fresh weight (GCV = 18.47%). High variability for weight-related traits suggests scope for genetic enhancement (Ravindran *et al.*, 2004; Hanumantha, 2020) [6]. In contrast, seed length and width showed lower GCV values (12.37% and 12.28%), indicating relative stability. Heritability estimates were high for seed length (81.33%) and seed dry weight (73.72%), suggesting strong genetic control and effectiveness of selection. The genetic gain was highest for seed dry weight (48.96%), followed by seed fresh weight (31.71%), indicating additive genetic control and potential for direct selection (Johnson *et al.*, 1955) [8]. Similar trends were reported by Kumar *et al.* (2018) [9] in tree spices, where seed morphological traits displayed high heritability and moderate genetic advance. The combination of high heritability and high genetic gain for seed dry weight and seed length underscores their importance as selection criteria in cinnamon breeding programs aimed at enhancing seed vigour and yield potential.

Correlation among fruit traits

Genotypic and phenotypic correlation coefficients among fruit traits (Table 03) revealed strong and highly significant positive associations among weight- and size-related characters. Immature fruit fresh weight showed a nearly perfect correlation with immature fruit dry weight ($r = 0.997^{**}$), and strong associations with mature fruit length ($r = 0.954^{**}$) and width ($r = 0.960^{**}$). These relationships indicate that fruit biomass accumulation during early stages strongly determines final fruit size and weight. Mature fruit width also showed strong correlation with test weight ($r = 0.910^{**}$), suggesting that fruit girth contributes directly to seed yield potential.

Number of fruits per inflorescence correlated moderately with fruit set percentage ($r = 0.672^{**}$), but not significantly with fruit weight, implying that fruit number and size are independently controlled-consistent with findings in nutmeg and cardamom (Thomas *et al.*, 2017; Sreekumar and Mathew, 2020) [19, 17]. At the phenotypic level, the correlation magnitudes were slightly lower, reflecting environmental influences. Nonetheless, the consistent positive associations across levels suggest that early selection for heavier immature fruits can indirectly enhance mature fruit weight and seed yield (Shashidhar *et al.*, 2021) [16].

Correlation among seed traits

The correlation matrix (Table 04) demonstrated strong positive associations among all seed traits. Seed width showed highly significant correlations with seed fresh ($r = 0.986^{**}$) and dry weight ($r = 0.972^{**}$), while seed length was strongly correlated with seed width ($r = 0.958^{**}$) and seed dry weight ($r = 0.911^{**}$). These findings indicate that seed size and weight are closely related, and selection for one trait can lead to simultaneous improvement of others. Phenotypic correlations followed the same trend, though with slightly reduced magnitudes, suggesting that environmental variation had limited impact. These results are consistent with previous studies in *Cinnamomum* species and other tree spices, where seed morphological traits were found to be interrelated and genetically determined (Liyanage *et al.*, 2021; Thomas *et al.*, 2019) [11, 18]. Such strong genetic interrelationships among seed traits suggest that selection based on seed width or fresh weight could effectively enhance overall seed quality, vigor, and yield potential (Burton and DeVane, 1953) [1].

Table 1: Genetic and phenotypic variation for fruit traits in half-sib progenies of *C. zeylanicum*

Sl. No.	Genetic parameters	No. of fruits per inflorescence	Fruit set at immature stage	FW of immature fruit (g)	DW of immature fruit (g)	Mature fruit length (mm)	Mature fruit width (mm)	Test weight/100 fruit weight (g)
1	SE(m)	12.30	9.39	0.26	0.08	0.38	0.42	3.84
2	C.D @ 5%	35.34	26.99	0.75	0.22	1.09	1.20	11.04
3	GCV	37.08	11.94	12.56	14.74	10.88	10.06	11.42
4	PCV	60.10	23.01	21.49	24.59	11.83	12.96	13.66
5	Heritability (Broad sense)	38.06	26.93	34.14	35.92	84.58	60.26	69.92
6	Genetic advance	21.21	10.50	0.39	0.12	2.92	1.42	17.48
7	Genetic gain	47.12	12.76	15.12	18.20	20.62	16.09	19.67

Table 2: Genetic and phenotypic variation for seed traits in half-sib progenies of *C. zeylanicum*

Sl. No.	Genetic Parameters	Seed length (mm)	Seed width (mm)	Seed fresh weight (gm)	Seed dry weight (gm)
1	SE(m)	0.44	0.44	0.39	0.31
2	C.D @ 5%	1.27	1.25	1.12	0.89
3	GCV	12.37	12.28	18.47	27.68
4	PCV	13.72	15.94	22.17	32.23
5	Heritability (Broad sense)	81.33	59.31	69.43	73.72
6	Genetic advance	2.96	1.45	17.42	15.92
7	Genetic gain	22.98	19.47	31.71	48.96

Table 3: Correlation among fruit traits of cinnamon progenies

	No. of fruits/ inflorescence	Per cent fruit set	FW of immature fruit (g)	DW of immature fruit (g)	Mature fruit length (mm)	Mature fruit width (mm)	Test weight/100 fruit weight (g)
No. of fruits/ inflorescence	--	0.672**	0.139 ^{NS}	0.313*	0.138 ^{NS}	0.019 ^{NS}	0.006 ^{NS}
Per cent fruit set	0.494**	--	0.190 ^{NS}	0.411**	0.524**	0.188 ^{NS}	0.331*
FW of immature fruit (gm)	0.095 ^{NS}	0.047 ^{NS}	--	0.997**	0.954**	0.960**	0.743**
DW of immature fruit (gm)	0.115 ^{NS}	0.111 ^{NS}	0.837**	--	0.983**	0.934**	0.889**
Mature fruit length (mm)	0.032 ^{NS}	0.198 ^{NS}	0.496**	0.577**	--	0.930**	0.926**
Mature fruit width (mm)	0.095 ^{NS}	0.069 ^{NS}	0.383*	0.379*	0.741**	--	0.910**
Test weight/100 fruit weight (gm)	0.001 ^{NS}	0.106 ^{NS}	0.402**	0.419**	0.709**	0.797**	--

~ Above genotypic correlation ~ Below phenotypic correlation

* = significant at 5 per cent, ** = significant at 1 per cent and NS = non-significant

Table 4: Correlation among seed traits in different half-sib progenies of cinnamon

	Seed length (cm)	Seed width (cm)	Seed fresh weight (g)	Seed dry weight (g)
Seed length (cm)	--	0.958**	0.889**	0.911**
Seed width (cm)	0.746**	--	0.986**	0.972**
Seed fresh weight (gm)	0.677**	0.679**	--	0.970**
Seed dry weight (gm)	0.717**	0.668**	0.945**	--

~ Above genotypic correlation ~ Below phenotypic correlation

* = significant at 5 per cent, ** = significant at 1 per cent and NS = non-significant

Summary and Conclusion

The present study assessed genetic variability, heritability and trait associations for fruit and seed characteristics in half-sib progenies of *Cinnamomum zeylanicum* Blume under Western Ghats conditions. Considerable genetic and phenotypic variation was observed for most reproductive traits, indicating a broad genetic base and good scope for selection in cinnamon improvement programmes. Fruit traits related to size and weight, particularly mature fruit length, fruit width and test weight, exhibited high heritability with moderate to high genetic advance, suggesting predominance of additive gene action and effectiveness of direct selection. In contrast, fruit set percentage and number of fruits per inflorescence showed greater environmental influence and lower selection efficiency. Seed traits, especially seed dry weight and seed length, showed high heritability and genetic gain, indicating strong genetic control and their suitability as reliable selection criteria for improving seed quality and vigour.

Correlation analysis revealed strong positive associations among weight and size related fruit traits, indicating that early fruit biomass accumulation strongly influences final fruit and seed yield. Similarly, seed traits exhibited strong interrelationships, suggesting that improvement of one trait would lead to simultaneous enhancement of others. Overall, mature fruit length, fruit width, test weight, seed length and seed dry weight emerged as key selection traits. The study highlights the importance of progeny evaluation in identifying elite genotypes and provides a scientific basis for genetic improvement, conservation and sustainable cultivation of *C. zeylanicum* under humid tropical conditions.

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