



RESEARCH ARTICLE

Trait interrelationships and composite bio-yield potential index-based selection of *Pongamia pinnata* (L.) Pierre genotypes for biofuel feedstock improvement

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Abstract

Pongamia pinnata (L.) Pierre is a promising non-edible, leguminous tree-borne oilseed species with strong potential as a feedstock for biofuel and sustainable aviation fuel (SAF). This study evaluated 20 *P. pinnata* genotypes from different parts of Tamil Nadu to quantify variability in pod, seed and shell traits and to identify superior genotypes. Substantial variation was observed with pod length, pod breadth, seed length and 100 seed weight (130.5–205.4 g). Shell percentage showed wide variation (36.2–57.8 %) and was negatively correlated with 100-seed weight ($r = -0.48$), whereas seed traits exhibited strong positive correlations with seed weight ($r = 0.62-0.78$), indicating their collective influence on kernel biomass. Principal component analysis (PCA) explained 72.4 % of the total variation in the first 3 components and, together with heatmap clustering, grouped trees into distinct performance categories. To integrate key bioresource traits, a composite bio-yield potential index (BPI) was formulated from standardized pod yield, 100 seed weight and shell percentage and it ranged from 0.60–0.84. Five genotypes viz., PP14, PP11, PP19, PP10 and PP2 were identified as elite, combining heavier seeds with lower shell proportions (36–49 %), traits favourable for improved oil recovery. Overall, integrating trait interrelationships with multivariate and composite index approaches proved effective for identifying high-yielding *P. pinnata* trees. The selected elite genotypes provide a strong foundation for genetic improvement, seed orchard development and the establishment of suitable feedstock resources to support India's expanding biofuel and SAF sectors.

Keywords: biofuels; composite selection index; genetic improvement; morphometric variability; *Pongamia*; sustainable aviation fuel

Introduction

Global energy systems are undergoing rapid transformation as nations work to reduce greenhouse gas emissions, diversify energy sources and strengthen long-term sustainability. The transport and aviation sectors remain major contributors to fossil fuel consumption and global carbon output (1). In this context, sustainable biofuels derived from non-edible, perennial oilseed crops have gained prominence because they can be cultivated on marginal lands while simultaneously supporting ecological restoration and rural development (2, 3). The aviation sector's transition has gained momentum as global adoption of sustainable aviation fuel (SAF) increases, offering substantial life-cycle greenhouse gas reductions compared with conventional jet fuel and being compatible with existing aircraft engines and infrastructure (4). India has recently announced an initial 1 % SAF blending mandate for domestic flights by 2027 as part of its national strategy for low-carbon aviation (5). Achieving these targets will require reliable, scalable and regionally adaptable

feedstocks capable of supporting sustained biofuel production without competing with food crops.

Given these evolving energy demands, *Pongamia pinnata* (L.) Pierre – syn. *Milletia pinnata* has gained prominence as a strategic tree-borne oilseed species. *P. pinnata* is a hardy, nitrogen-fixing legume well-adapted to arid, saline and resource-poor soils across India (6). Its seeds contain 30–40 % non-edible oil, making it suitable for renewable fuel applications, including biodiesel and SAF pathways (6, 7). Importantly, *P. pinnata* can be cultivated on 6–8 million hectares of underutilized land, allowing expansion without affecting food production systems. Beyond oil yield, the species contributes significantly to soil improvement, carbon sequestration and livelihood support in rural regions (8, 9). Its by-products viz., seed cake, pod shells and woody residues can be converted into briquettes, biochar, organic manure or soil amendments (10, 11), further integrating the species into circular bioeconomy frameworks (11). Thus, *P. pinnata* presents a promising multipurpose feedstock for India's evolving SAF supply chains.

P. pinnata, exhibits wide phenotypic and genotypic variability in pod, seed and reproductive traits due to cross-pollination, environmental heterogeneity and genetic recombination (12, 13). This diversity offers valuable opportunities for identifying genotypes with superior yield and oil characteristics. Previous studies from India and Indonesia have reported significant variation in pod size, seed weight, oil content and shell proportion, although relationships among these traits often vary by region (14, 15). Importantly, while seed oil remains a primary criterion for selection, traits such as pod weight, shell percentage and crown productivity strongly influence overall bioresource recovery (8, 12). Pod shells account for 35–60 % of total pod biomass and can be used for pyrolysis, activated carbon production and bioenergy applications (16, 17). Although earlier work has documented variation in seed weight and oil content (18, 19), comprehensive evaluations that also include shell biomass and pod morphological traits remain limited, highlighting the need for holistic trait assessment to support circular bioenergy systems.

Tamil Nadu contains diverse on-farm and natural *P. pinnata* populations, providing an excellent resource base for evaluating genetic variation and identifying elite genotypes. Integrating shell biomass, pod and seed morphological traits with multivariate and index-based approaches would facilitate the selection of elite genotypes capable of supporting biodiesel and SAF-oriented production chains. Therefore, the present study evaluated twenty genotypes of *P. pinnata* across 3 different parts of Tamil Nadu with the objectives of assessing variability in pod, seed and shell traits, examining correlations among key reproductive and yield components and identifying high-performing genotypes suitable for integration into biofuel and SAF value chains. The findings underscore the strategic value of *P. pinnata* in advancing genetic improvement efforts and building a reliable, sustainable feedstock base for India's emerging SAF and low-carbon energy sectors.

Materials and Methods

Study area and site description

Twenty *Pongamia pinnata* (L.) Pierre genotypes were selected from 3 districts viz., Sivaganga, Dharmapuri and Krishnagiri of

Tamil Nadu. Mature, healthy trees aged 20–30 years were identified in farmer's fields, roadside plantations, riverbeds and institutional plantations based on vigour and consistent pod-bearing capacity. Tree age was estimated from local plantation records wherever available and maturity indices observed in the field. Geographic coordinates were recorded using a handheld GPS and each tree was coded PP 1–PP 20 for evaluation during the 2023–2024 fruiting season (Fig. 1, Table 1).

Morphological measurements

Tree height (m), basal girth (BG, cm), girth at breast height (GBH, cm), crown width (m) and number of primary branches of selected *P. pinnata* genotypes were recorded. Height was measured using a clinometer, GBH at 1.37 m using a measuring tape and crown width as the mean of 2 perpendicular canopy diameters. Annual pod yield per tree was estimated by harvesting mature pods from 2 representative branches, calculating the mean yield and extrapolating the value by multiplying it with total number of branches of the entire tree. These measurements were used to quantify structural variation and productivity among genotypes (Fig. 2).

Pod and seed trait evaluation

The 100 fully mature pods were randomly collected from all crown directions of each genotype during peak harvest. Pods were sun-dried for 10 days to achieve uniform drying and to equilibrate moisture content. Pod length and breadth (mm) were measured with a digital Vernier caliper (± 0.01 mm). Extracted seeds were assessed for seed length (mm) and seed breadth (mm) using digital Vernier caliper and 100-seed weight (g) using an electronic balance (± 0.01 g). All measurements were taken with 5 replications from whole set of pods from each genotype and mean values were used for analysis. These traits were chosen for their direct influence on seed development, oil accumulation and reproductive suitability in *P. pinnata* (Fig. 3).

Shell content and biomass partitioning

For each genotype, the weights of 100 pods, 100 seeds and 100 shells were recorded after thorough drying. The shell percentage was calculated using the formula:

Table 1. Location, morphological and yield characteristics of *Pongamia pinnata* genotypes

Genotypes	Location	Latitude	Longitude	Height (m)	BG (cm)	GBH (cm)	NoB	Crown width (m)	Yield* (kg)
PP 1	Mittareddihalli	12.041453	78.157874	11	134	75	11	6.5	80
PP 2	Laligam	12.044028	78.147822	10	154	86	9	8.5	100
PP 3	Errapaati	12.090001	78.133222	12	170	155	11	8	75
PP 4	Mulli-Karamadai	11.211068	76.818968	15	250	142.5	10	10.25	75
PP 5	Melur slope	11.230692	76.748798	16	235	184	16	12.3	75
PP 6	Mulli-Pilloor	11.230691	76.748792	10	143	84.5	7	10.07	70
PP 7	Belluhalli	12.314467	77.946471	11	180	160	13	10	70
PP 8	Mittareddihalli	12.041557	78.157764	9	138	134	15	9.75	75
PP 9	Dharmapuri	12.102106	78.144696	13	180	132	11	10.2	80
PP 10	Belrampatti	12.308811	77.968616	9	220	105	13	22.2	75
PP 11	Kanavenahalli	12.318757	78.012221	11	195	132.5	14	11.1	70
PP 12	Mettupalayam	11.327660	76.935318	8	120	80.25	10	8.5	80
PP 13	Thiruvengampattu	9.820113	78.801168	14	155	105	14	10.8	105
PP 14	Kallal	9.988061	78.660873	9	95	80	12	8	70
PP 15	Thiruvengampattu	9.830335	78.784376	10	112	82	9	7.5	80
PP 16	Sivaganga	9.821604	78.798307	12	160	130	13	11.7	100
PP 17	Mettupalayam	11.329756	76.903309	12	103	81	14	11.5	85
PP 18	Mettupalayam	11.325358	76.935506	10	195	165	12	10.75	80
PP 19	Mettupalayam	11.296335	76.932756	9	166	146	11	8.85	80
PP 20	Kuttaiyur	11.275888	76.949189	12	160	120	9	9.5	90

BG: basal girth; GBH: girth at breast height; NoB: number of branches. * Represent pod yield/ tree in current season.

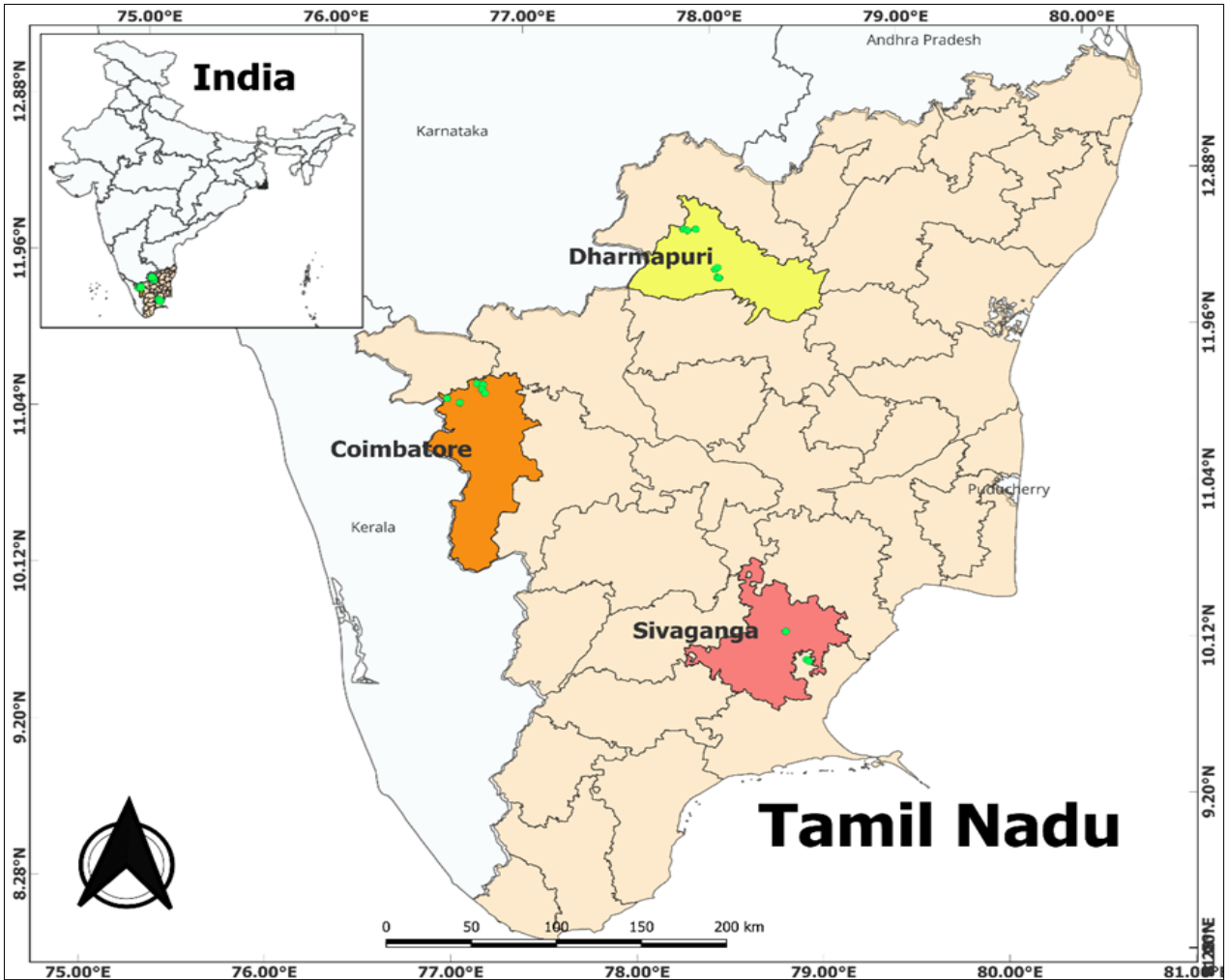


Fig. 1. Location of twenty *Pongamia pinnata* genotypes from Tamil Nadu (using GPS Handheld survey instrument with map display).

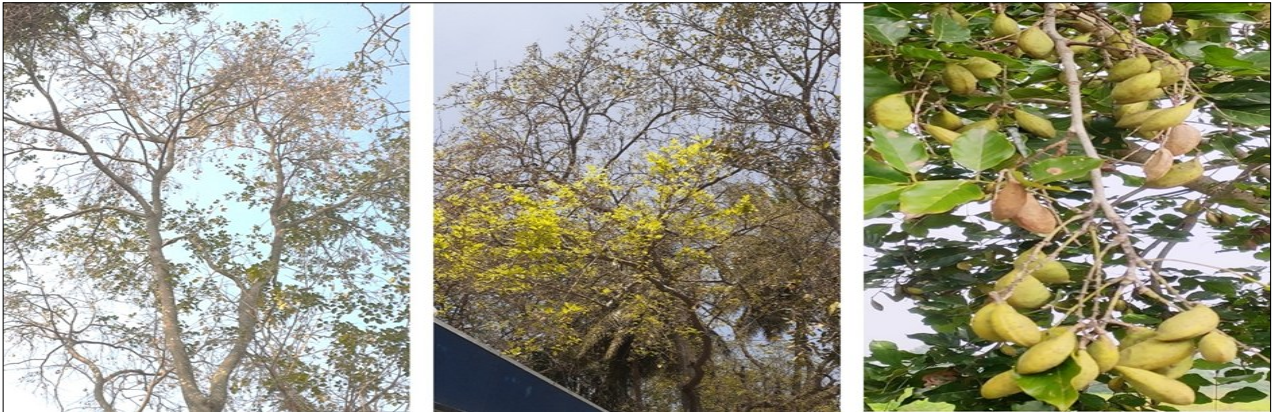


Fig. 2. Promising *Pongamia pinnata* genotypes.



Fig. 3. Variation in pods and seeds of *Pongamia pinnata* genotypes.

$$\text{Shell (\%)} = (100 \text{ shell weight} / 100 \text{ pod weight}) \times 100$$

This parameter represents the proportion of pod biomass invested in shell tissue. This parameter provides insight into seed-to-shell ratio and potential for value-added uses of shell biomass (e.g., biochar, briquettes), complementing seed-based yield assessment.

Statistical analysis

Descriptive statistics (mean and SD) were computed to quantify variability among genotypes. Pearson's correlation coefficients were used to examine relationships among pod, seed and shell traits. Multivariate analyses including principal component analysis (PCA) and hierarchical clustering were performed on standardized (z-score) data to classify genotypes based on overall morphological similarity and divergence. Data visualization was generated using R version R 4.4.1. Heat map was developed using pheatmap package in R and PCA was performed using prcomp function from ggpubr, ggplot2, factoextra and extrafont packages.

Selection of superior genotypes

A composite bio-yield potential index (BPI) was constructed to identify elite genotypes by integrating pod yield, 100-seed weight and shell percentage. All traits were standardized using z-scores; standardized shell percentage values were multiplied by -1 to invert their direction of influence, as shell biomass is a non-productive component; this ensured that genotypes with lower shell percentage received higher index scores and contributed positively to the overall Index. Bio-yield potential index for each genotype was calculated as the mean of the 3 standardized scores and trees were ranked accordingly. Approximately the top 25 % of genotypes was designated as elite genotypes for future propagation and breeding programs aimed at improving *P. pinnata* productivity.

Results and Discussion

Morphological characteristics of *P. pinnata* genotypes

Twenty *P. pinnata* genotypes (n=20) showed significant variation in basic morphological attributes, including tree height, basal girth,

GBH, crown width and pod yield (Table 1). Tree height ranged from 8–16 m, while basal girth varied widely (95–250 cm), indicating considerable structural diversity across Tamil Nadu. Several genotypes namely, PP 4, PP 5, PP 10, PP 11, PP 16 and PP 18 displayed larger crown widths (>10 m) and higher numbers of branches, traits that contribute to greater photosynthetic surface area and potentially higher reproductive output. These trends align with earlier observations that *P. pinnata* trees with broader crowns and thicker trunks generally accumulate more biomass and show superior reproductive vigor (6, 12). Variation in pod yield (70–105 kg tree⁻¹) also followed site-specific patterns, with Dharmapuri and Sivaganga genotypes showing relatively higher productivity; similar regional differences in yield were reported in Karnataka and Tamil Nadu populations, where local soil fertility and rainfall patterns strongly influenced pod production (14, 19). Although replication-based statistical comparisons were not feasible due to the nature of plus-tree sampling, the clear phenotypic differences observed here are consistent with previous reports of large inter-tree variability in *P. pinnata* collections and support the selection of structurally vigorous, wide-canopied trees for further breeding and improvement.

Variation in pod and seed physical traits

Substantial variation was observed among the 20 *P. pinnata* genotypes for pod and seed physical traits, including pod length, pod breadth, seed length, seed breadth, seed L/B ratio and 100-seed weight (Table 2). PP 7, PP 10, PP 11, PP 14, PP 19 and PP 20 genotypes recorded higher pod dimensions and seed size, reflecting superior reproductive morphology. The wide range in 100-seed weight (107.8–205.4 g) further indicates significant seed development differences, with PP 10, PP 11, PP 14, PP 19 and PP 20 appearing as the heaviest-seeded genotypes. Similar degrees of variability in pod and seed characteristics were previously reported in *P. pinnata* populations from Karnataka and Andhra Pradesh, where seed weight and pod size showed strong inter-tree divergence linked to genetic and site effects (20, 21). Variation in seed length: breadth ratio (1.25:1.66) suggests diversity in seed shape biology, a trait known to influence kernel packing efficiency and oil recovery in tree-borne oilseeds such as neem (*Azadirachta*

Table 2. Variations in pod and seed physical traits of *Pongamia pinnata* genotypes

Genotypes	Pod length (mm)	Pod breadth (mm)	Seed length (mm)	Seed Breadth (mm)	Seed L/B Ratio (mm)	100 seed weight (g)
PP 1	42.47*	24.41*	18.13	14.51	1.25	107.8
PP 2	42.11*	22.03*	22.27*	15.59*	1.43	162.2*
PP 3	39.03	19.89	21.54	13.26	1.63*	162.8*
PP 4	44.22*	22.17	20.48	14.20	1.46	144.0
PP 5	27.36	19.11	20.77	13.37	1.55	134.8
PP 6	34.26	21.16	21.62	14.91	1.45	138.8
PP 7	46.84*	25.06*	21.21	16.88*	1.26	156.8
PP 8	37.92	22.20*	21.33	15.63*	1.36	164.0*
PP 9	35.76	21.52	20.20	14.41	1.32	139.3
PP 10	46.16*	26.47*	22.68*	16.56*	1.37	194.6*
PP 11	45.16*	21.98*	22.57*	14.50	1.56	205.4*
PP 12	38.39	19.72	20.81	13.66	1.52	144.6
PP 13	42.66*	18.85	18.90	13.20	1.43	150.3
PP 14	39.39	19.45	23.70*	14.25	1.66*	203.2*
PP 15	42.42*	18.54	20.21	13.23	1.53	123.6
PP 16	43.26*	18.58	18.82	13.35	1.41	120.6
PP 17	43.31*	18.01	21.92	14.34	1.53	119.5
PP 18	35.10	19.49	22.09	14.01	1.61*	124.9
PP 19	33.70	21.61	22.81*	14.81	1.54	197.0*
PP 20	41.32*	24.18*	23.55*	16.30*	1.44	191.0*
Mean	40.04	21.22	21.28	14.55	1.47	154.3
SEd	0.63	0.31	0.51	0.44	0.05	1.36
CD (0.05)	1.24	0.62	1.01	0.88	0.10	2.70

L/B ratio: length: breadth ratio; *Significance at 5 %.

indica) and mahua (*Madhuca longifolia*) (22, 23). Consistent with previous studies in *P. pinnata* germplasm, higher seed length and breadth values in the present genotypes are associated with greater 100-seed weight, reinforcing their value as key selection traits for early yield-focused screening (24). Overall, the observed variability demonstrates the phenotypic diversity of the sampled *P. pinnata* population and highlights several promising genotypes with superior pod–seed characteristics suitable for further improvement.

Pod and seed biomass allocation

Marked variation was observed among the 20 genotypes for 100-pod weight, 100-seed weight and shell percentage, indicating substantial differences in biomass allocation patterns (Fig. 4). Genotypes such as PP 10, PP 11, PP 14, PP 19 and PP 20 showed consistently higher pod and seed weight values, while also maintaining comparatively lower shell percentages (< 45%), an ideal combination for maximizing oil recovery. Lower shell proportion is desirable because shell biomass contributes little to oil yield and negatively influences seed weight, a trend widely reported in *P. pinnata* and other oilseed tree species (25, 26). In contrast, genotypes such as PP 4, PP 5, PP 6 and PP 15 displayed higher shell percentages (> 50%), which corresponded with reduced seed weight, supporting the negative association between shell mass and seed development. Similar relationships have been documented in neem (*Azadirachta indica*) and mahua (*Madhuca longifolia*), where excessive pericarp thickness reduces kernel proportion and thereby limits extractable oil (22, 23). The superior combinations observed in PP 10, PP 11, PP 14, PP 19 and PP 20 therefore indicate efficient biomass partitioning toward seed tissue, reinforcing their suitability for high-yielding *P. pinnata* improvement and selection programs.

Pattern of morphological diversity identified through PCA

The PCA revealed clear patterns of phenotypic divergence among the 20 *P. pinnata* genotypes, with PC1 (47.6%) and PC2 (25.6%) together explaining a substantial 73.2% of the total variation (Fig. 5). The strong loadings of seed weight, pod breadth, seed breadth and pod length on PC 1 indicate that these yield-related traits were the primary contributors to inter-genotype variability. Genotypes such as A 10, A 20, A 14 and A 19, positioned far along the positive PC 1 axis, showed a strong association with heavier seeds and larger pod dimensions, reflecting superior kernel development. This pattern aligns with recent findings which reported that seed weight and pod size are the major discriminatory traits in *P.*

pinnata due to their high genetic variance and heritability (12). Similarly, in Indonesian *P. pinnata* plus trees accessions with higher pod breadth and seed weight consistently clustered together in PCA space, confirming that these traits drive genetic differentiation across environments (15). The compact grouping of genotypes near the origin in the present study (A 1, A 2, A 6, A 11) suggests limited morphological divergence, which may reflect either shared ancestry or stabilization of seed traits under similar environmental conditions.

The placement of genotypes along the PC 2 axis was primarily influenced by seed length, seed breadth ratios and pod shape characteristics, indicating secondary but meaningful morphological contrasts. Genotypes such as A 5, A 18 and A 15, which are distinctly positioned along PC 2, may exhibit unique seed shape proportions or pod elongation patterns. Comparable trait-driven separation along secondary components was also observed in North Karnataka *P. pinnata* germplasm, where pod shape indices contributed moderately to accession grouping (14). The wide dispersion observed in the present PCA biplot supports the presence of considerable phenotypic diversity, a trend corroborated by previous Indian studies reporting strong eco-geographic influences on seed size, pod wall thickness and kernel proportion (6, 19).

The superior genotypes aligning with high seed weight vectors likely exhibit enhanced resource partitioning toward kernel tissue, a physiological trend described earlier, in which larger seed mass in *P. pinnata* often reflects higher endosperm accumulation and greater oil productivity (27, 7). Altogether, the PCA analysis not only confirms substantial genetic and morphological divergence in the evaluated population but also highlights a subset of genotypes with promising seed and pod attributes suitable for further improvement and selection programs.

Correlation analysis of pod and seed traits

Correlation analysis revealed clear and biologically meaningful relationships among pod length, pod breadth, seed length, seed breadth and 100-seed weight in the 20 *P. pinnata* genotypes (Fig. 6). Strong and positive correlations were observed among most pod and seed dimensional traits, particularly between seed length and seed breadth ($r > 0.80$) and between pod length and pod breadth across replications ($r = 0.92$ – 0.97). These high correlations suggest that these morphological traits are developmentally linked and tend to increase simultaneously within genotypes.

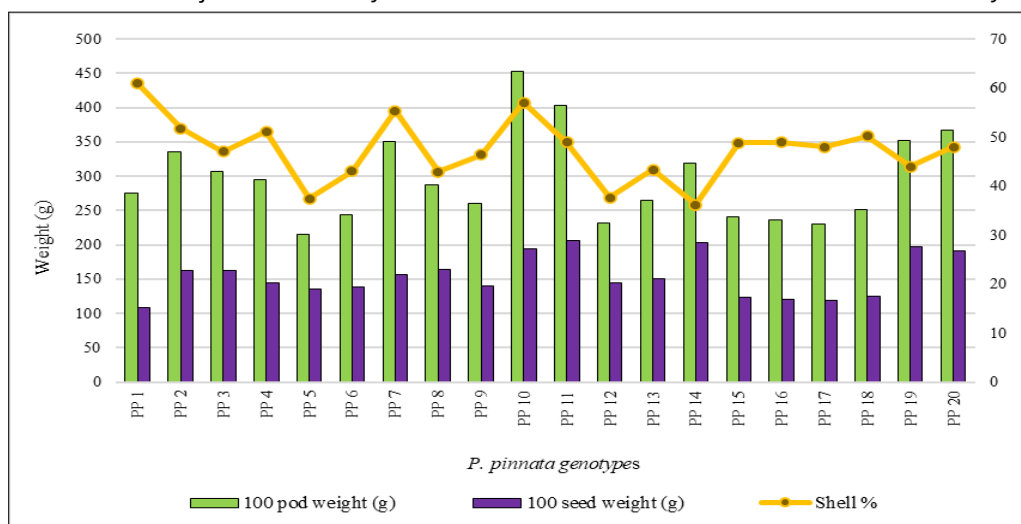


Fig. 4. Variation in shell percentage among *Pongamia pinnata* genotypes. Values represent the mean.

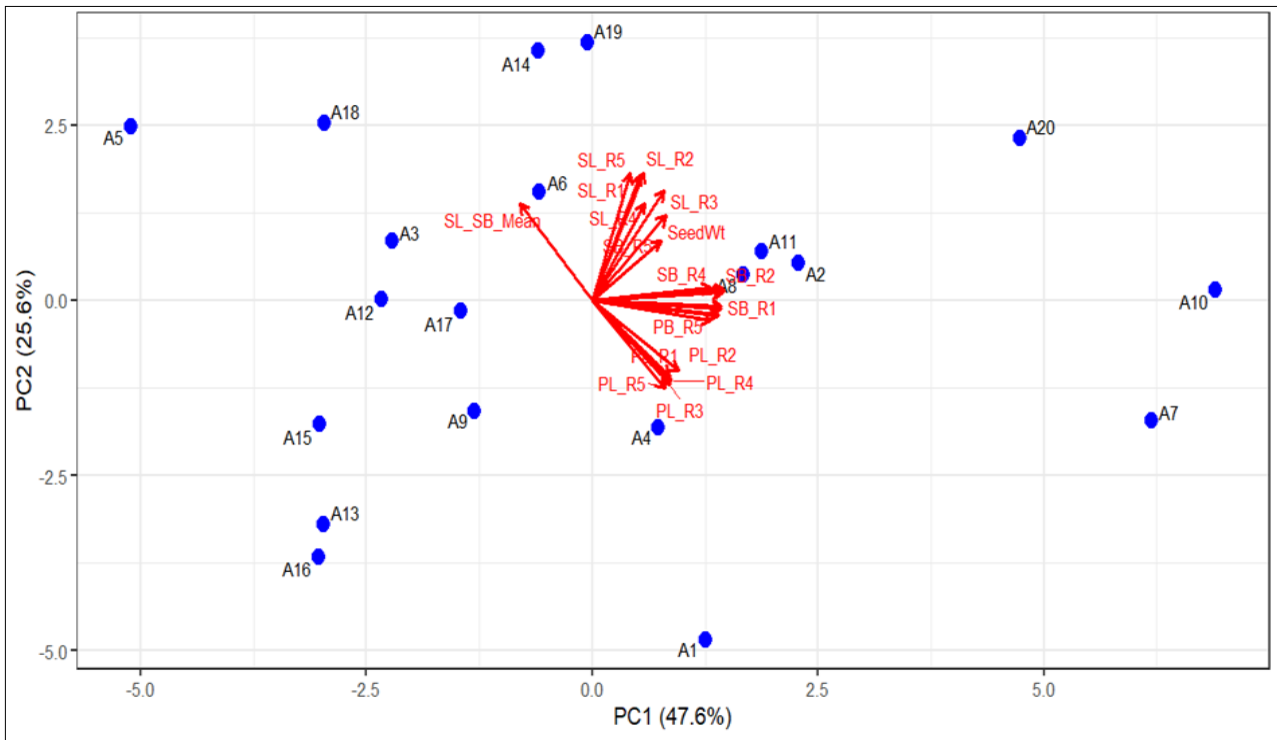


Fig. 5. Principal component analysis biplot of pod and seed traits of *Pongamia pinnata* genotypes.

The first two principal components explained 47.6 % (PC 1) and 25.6 % (PC 2) of the total variation. Blue points represent genotypes, while red vectors indicate the direction and magnitude of trait loadings. Genotypes positioned in the direction of longer vectors exhibit stronger associations with those traits.

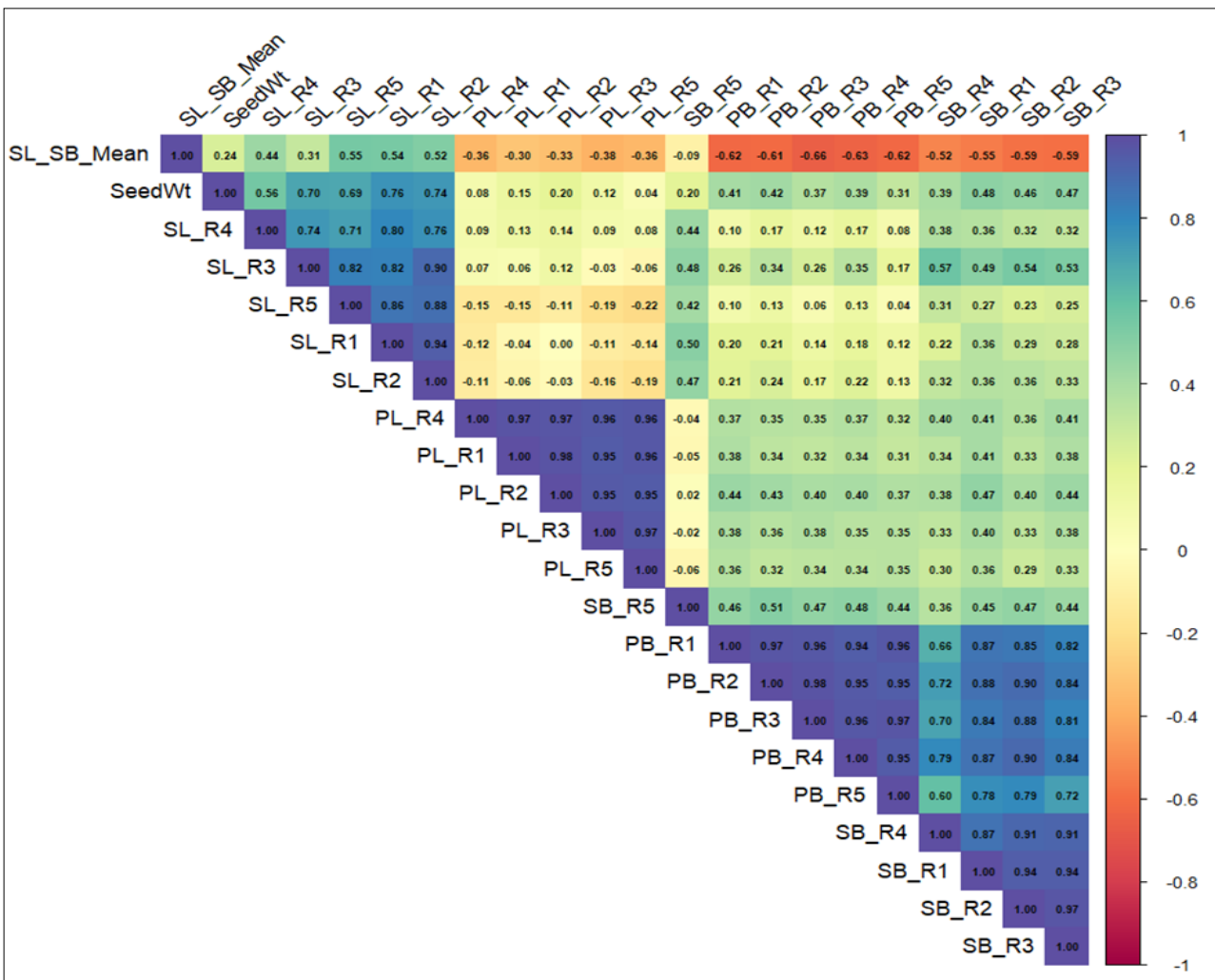


Fig. 6. Correlation matrix of pod and seed traits of *Pongamia pinnata* genotypes.

Positive correlations (blue–green) indicate coordinated increases among pod and seed traits, whereas negative correlations (yellow–red) reflect trade-offs between kernel size and pod wall characteristics.

Seed weights also exhibited moderate to strong positive associations with seed length and seed breadth ($r = 0.54\text{--}0.71$), indicating that genotypes producing larger seeds generally contribute more to total seed mass. Similar trait associations have been widely reported in *P. pinnata* germplasm, where seed dimensions were shown to be reliable predictors of kernel weight and oil-yield potential (12, 27, 7). The present results therefore reinforce the suitability of seed size traits as primary selection criteria in early-stage screening programs.

Negative correlations observed between seed size traits and pod wall or shell-related measures (e.g., SL_SB mean vs. pod-related traits: $r = -0.30$ to -0.62) suggest a trade-off between kernel development and structural pod biomass. This trend is consistent with previous findings from Karnataka and Tamil Nadu, where genotypes with thicker pod walls or heavier shells tended to show reduced seed-to-shell ratios and lower seed mass (14, 19). The positive correlation between pod and seed breadth and seed weight further indicates that genotypes with wider pods can accommodate larger or more fully developed seeds, an observation also reported in Indonesian *P. pinnata* plus trees (15). Collectively, the correlation patterns demonstrate that seed breadth, seed length and pod breadth serve as key determinants for identifying high-yielding genotypes. The strong interdependence among these measurements suggests that selecting for a single trait such as seed breadth, may result in simultaneous improvement in other yield-related traits, thereby accelerating genetic gain in *P. pinnata*

breeding and selection programs.

Hierarchical clustering of pod, seed and 100 seed weight traits

The heatmap and accompanying hierarchical clustering revealed clear grouping patterns among the 20 *P. pinnata* genotypes based on standardized pod, seed and weight traits (Fig. 7). Genotypes that shared similar morphological profiles clustered together, reflecting coordinated expression of pod and seed size traits. The upper cluster predominantly consisted of genotypes exhibiting higher values for seed length, seed breadth and 100-seed weight, as indicated by the strong green–blue intensities in these zones. These clusters align well with PCA findings, in which genotypes with larger seed and pod dimensions were positioned along the positive PC1 axis. Similar clustering behaviour was earlier reported by a researcher, who observed that high seed weight and larger pod characters tend to group genetically related or phenotypically superior *P. pinnata* genotypes (12). Strong clustering of Indonesian *P. pinnata* plus trees with comparable pod and seed measurements, reinforcing that these traits reliably partition genotypes into meaningful morphological groups (15).

The lower cluster of the heatmap contained genotypes consistently associated with lower seed dimensions and reduced seed weight, as indicated by predominant yellow–orange hues. These genotypes likely represent lines with thinner pods, smaller kernel size, or lower resource allocation to seed

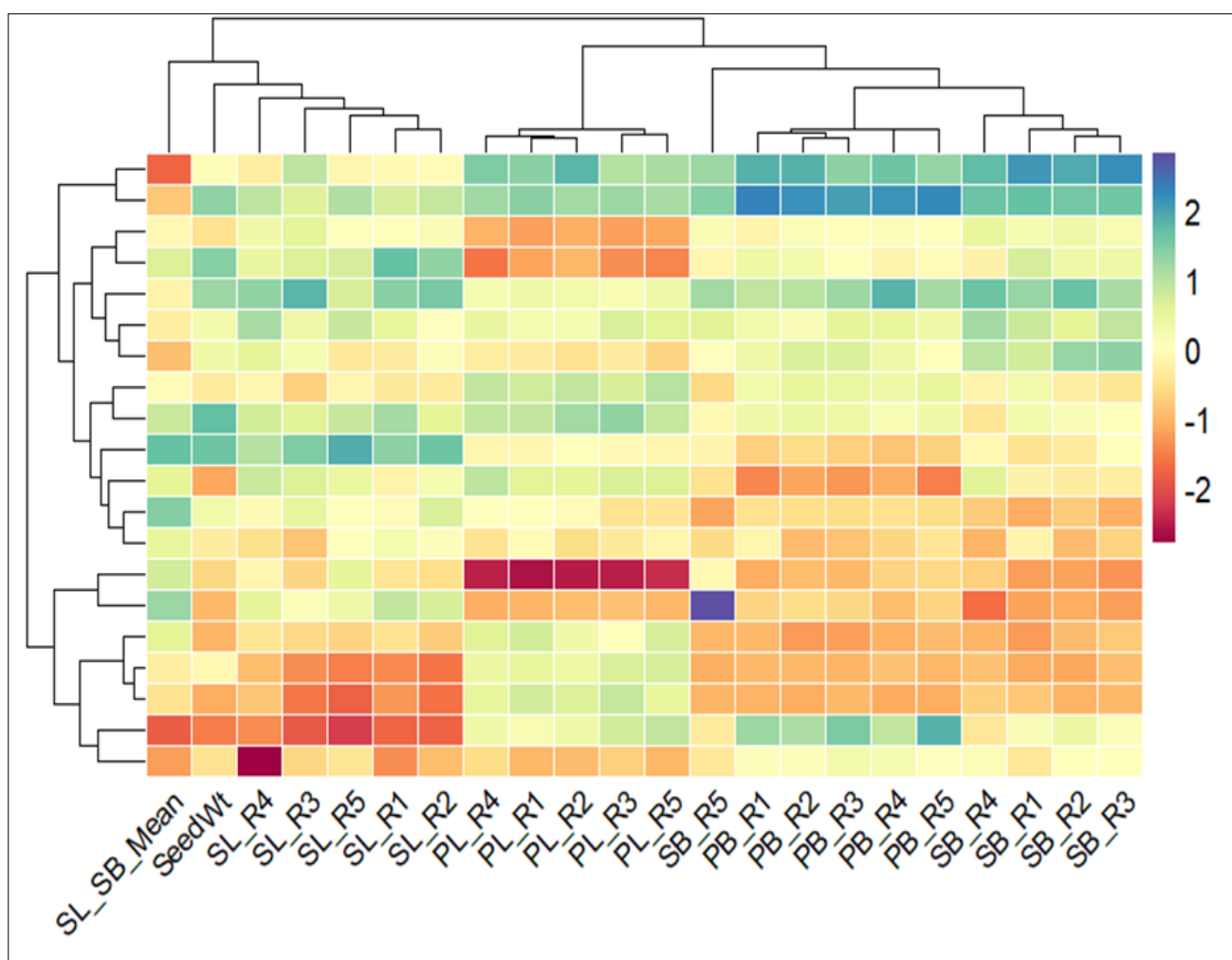


Fig. 7. Heatmap and hierarchical clustering of pod and seed traits in *Pongamia pinnata* genotypes.

Heatmap cells represent standardized trait values, with blue–green shades indicating higher measurements and yellow–red shades indicating lower values. Clustering patterns highlight groups of genotypes with similar pod and seed size profiles.

development. Previous studies from Tamil Nadu and Karnataka similarly identified clusters of low-performing accessions characterized by small seeds and lower kernel–shell ratios (14, 19). The contrasting red bands for specific pod or seed traits in some genotypes also suggest localized specialization or compensatory trade-offs, a phenomenon described earlier in which certain *P. pinnata* morphotypes invest more in pod wall biomass at the expense of seed development (6). The overall heatmap pattern highlights substantial phenotypic heterogeneity within the population and reinforces the value of multi-trait clustering for differentiating promising genotypes. This multivariate structure, together with correlation and PCA outcomes, clearly supports the identification of superior genotypes with desirable seed and pod attributes for breeding and seed orchard development.

Composite performance and elite genotype selection

The composite BPI, developed using pod yield, 100-seed weight and shell percentage, revealed clear variability in productive efficiency among the 20 *P. pinnata* genotypes (Table 3). The BPI values ranged from -0.60 to 0.84, with positive scores indicating superior biomass partitioning toward seed tissue. Five genotypes viz., PP 14, PP 11, PP 19, PP 10 and PP 2, ranked within the top quartile, demonstrating the most favourable combination of high seed weight, moderate to low shell fraction and strong pod yield. PP 14 emerged as the best performer due to its exceptionally low shell percentage (36.2 %) and high seed mass, while PP11 exhibited the highest 100-seed weight (205.4 g) despite a slightly higher shell proportion. PP 19 and PP 10 also showed balanced trait combinations, whereas PP 2 attained elite status primarily through its outstanding pod yield (100 kg tree⁻¹). Such trait combinations mirror earlier findings that heavier seed mass and a low shell-to-kernel ratio are reliable indicators of superior oil-bearing efficiency in *P. pinnata* (14, 24) and that integrating multiple morphological indicators improves genotype discrimination more effectively than single-trait approaches (15).

Trait associations observed in the present study further validate the BPI-based rankings. Strong positive correlations between seed weight and pod/seed dimensional traits, along with a moderate negative correlation between seed weight and shell percentage, support the physiological advantage of genotypes allocating biomass preferentially to seed growth. These patterns are consistent with earlier reports on *P. pinnata* and other tree-borne oilseeds, in which genotypes with coordinated increases in seed length, breadth and mass tend to exhibit higher oil yield potential (8, 22). The clustering of elite genotypes in PCA space and their favorable position in heatmap groupings indicate a shared morphological profile characterized by heavier seeds, broader pods and reduced shell biomass. Together, these findings underscore the robustness of the composite index and affirm that PP 14, PP 11, PP 19, PP 10 and PP 2 represent genetically and

agronomically superior candidates for propagation, breeding and future feedstock development.

The combined evidence from correlation analysis, PCA, heatmap clustering and the BPI provides a coherent and robust basis for identifying superior *P. pinnata* genotypes. Strong positive associations among seed length, seed breadth and seed weight, along with the negative relationship between seed weight and shell percentage, confirm that kernel development is the primary driver of yield efficiency. PCA further distinguished genotypes with larger pod and seed such as PP 14, PP 11, PP 19, PP 10 and PP 2, placing them in distinct high-performing clusters, while the heatmap revealed consistent grouping of these genotypes based on shared seed–pod size profiles. The BPI rankings, which integrate yield, seed mass and shell fraction, reaffirmed these trends by placing the same genotypes in the top quartile, highlighting their superior biomass allocation toward economically valuable seed tissue. When considered together with morphological observations (greater crown spread, pod size, seed mass), the multivariate patterns consistently point to PP 14, PP 11, PP 19, PP 10 and PP 2 as genetically and agronomically elite candidates. These converging analytical outcomes demonstrate that trait-driven, multi-criteria selection is highly effective in discriminating high-yielding *P. pinnata* trees and provides a strong foundation for advancing breeding programs, establishing seed orchards and developing regionally adapted feedstock resources.

Conclusion

This study revealed substantial phenotypic variation among 20 *P. pinnata* genotypes, with multivariate analyses consistently identifying PP 14, PP 11, PP 19, PP 10 and PP 2 as elite genotypes exhibiting superior seed weight, lower shell biomass and overall higher yield efficiency. These traits underline their strong potential for oil-focused value chains and provide a reliable foundation for breeding programs and seed orchard development. Given *P. pinnata*'s adaptability to marginal lands, nitrogen-fixing ability, high non-edible oil content and suitability for sustainable aviation fuel production, the selected genotypes represent promising feedstock resources for India's emerging SAF sector. Their co-products viz., seed cake, pod shells and biomass residues further support circular bioeconomy opportunities through biochar, briquetting and soil amendment applications. Collectively, these findings reinforce *P. pinnata* as a strategic multipurpose species capable of enhancing rural livelihoods, improving feedstock security for SAF production and contributing to long-term decarbonization and sustainability goals. Future research should focus on multi-environment validation of these elite genotypes, coupled with oil content

Table 3. Composite bio-yield potential index (BPI) and ranking of *Pongamia pinnata* genotypes

Genotypes	Yield (kg tree ⁻¹)	100-Seed weight (g)	Shell (%)	Standardized yield (Zy)	Standardized seed weight (Zs)	Inverted shell (Zsh)	Composite BPI score	Rank
PP 14	70	203.2	36.2	-0.09	+1.25	+1.35	0.84	1
PP 11	70	205.4	48.9	0.09	+1.32	+0.24	0.49	2
PP 19	80	197.0	44.0	+0.59	+1.06	+0.61	0.42	3
PP 10	75	194.6	57.0	+0.25	+0.98	-0.18	0.35	4
PP 2	100	162.2	51.7	+2.01	-0.08	+0.11	0.34	5
PP 8	75	164.0	42.9	+0.25	-0.02	+0.70	0.31	6
PP 1	80	107.8	60.9	+0.59	-1.88	-0.51	-0.60	7

BPI: $(Zy + Zs + Zsh) / 3$, where high values of yield and seed weight and low values of shell (%) contribute positively to the index.

profiling and marker-assisted characterization to strengthen selection efficiency and deployment.

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Authors' contributions

SV carried out the research, data collection, analysis and writing original draft. KTP conceptualised the idea, participated in the supervision, validation and review of manuscript. PK involved in genotype identification and pods collection. IS, SVR, Rmand SKR participated in the review and editing. RAR carried out statistical analysis. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

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