

Estimation of heritability and genetic gain in height growth of superior clones of *Dacryodes edulis* (G. Don.) H. J. Lam



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Why focus on *Dacryodes edulis*

- *Dacryodes edulis* commonly known as bush butter tree, is the most-collected agroforestry tree product (AFTP) (quantity-wise) with high social and economic importance in southern Cameroon (Schreckenberget al. 2002)
- In 1999, 2,324 tones were sold for a total amount of about US\$ 1.5 million in nine big markets in Cameroon (Awono *et al.*, 2002). This quantity represented only about 14-23 % of total production in the national territory as Isseri and Temple (2000) estimated the 59 national production at 10,000 to 16,000 t.
- Currently, in local market in Yaoundé, the price is comprised between 1,250 and 2,667 FCFA per kg



Challenges for large scale cultivation

- Since the beginning of the tree domestication program by ICRAF and partners in the mid-1990s, research on the species has covered several topics, including accessing priority traits for users (Schreckenberget al. 2002), phenotypic variation (Waruhiu *et al.* 2004) and different propagation options (Mialoundama *et al.* 2020).
- Despite efforts to disseminate these propagation techniques, wide-spread cultivation of the species has not yet happened.
- Users are still expecting from science cultivars that optimize benefits.

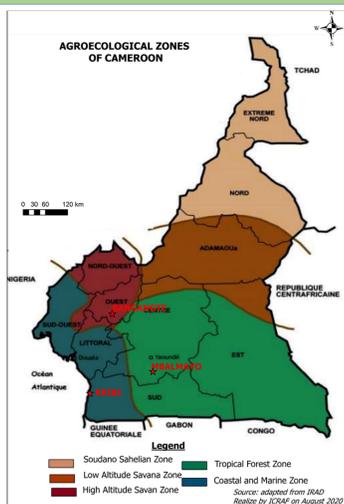
Research objective

To assess narrow-sense heritability (h^2) and genetic gain in height growth (36 months after planting) in *D. edulis* using five accessions from ICRAF's genebank, in view of boosting its cultivation and increasing its production in users' farms.

Methodology

Study sites

- Mbalmayo
- Bangangte and
- Kribi



Different clones under experiment and assessed traits

Table 1: Different clones under experiment and assessed traits

Key traits targeted	Approach used to select plus trees	Population targeted	Size of population	Plus trees accession numbers
Pulp weight	Phenotypic variation assessment between trees	ICRAF field genebank	39 trees (NB: off-springs from parents identifying by farmers as "plus trees" among more than 100 individuals in sampled villages).	- DE/BUM/34 - DE/Mbyo/2-92
Off-season	Farmers' perception	Makenene's population	More than 500 trees	- DE/MA/41 - DE/MA/50 - DE/MA/54 - DE/MA/58

Table 2: Number of plantlets planted per clone and per site

Clones	Number of plantlets		
	Mbalmayo	Kribi	Bangangte
DE/BUM/34	2	2	3
DE/Mbyo/2-92	2	3	2
DE/MA/41	3	3	3
DE/MA/50	3	3	3
DE/MA/54	2	2	2
DE/MA/58	2	2	2

Parameters that are yearly assessed

Height, DBH, collar diameter, crown diameter, flowering, fruiting (fruit number, fruit traits: (fruit mass, pulp mass, pulp color, pulp thickness) fruiting period, pest and diseases sensibility.

Data analysis

Table 3: Analysis of variance

Source of variation	DF	MS	F
Between clones	f-1	MS ₁	MS ₁ /MS ₃
Sites	r-1	MS ₂	
Within clones	f(r-1)	MS ₃	

Table 4: Analysis of variance in height growth

Source of variation	DF	SS	MS	F	P-value
Between clones	5	28.87	5.77	2.96	0.031
Sites	2	10.77	5.38	0.93	0.082
Within clones	10	19.543	1.95		

Procedure for calculation of heritability and genetic gain

$h^2 = V_G/V_P$ } Where, h^2 = narrow sense heritability, V_G = Variations arising from differences in genetic constitution (between accessions variation), V_P = Variations in phenotypic characters, V_E = Variation due to environment (within accessions variation).

From ANOVA (Table 3), $V_G = (MS_1 - MS_3)/r$, where, MS_1 = mean square between clones = $V_E + rV_G$, MS_2 = mean square of sites, MS_3 = Mean square among clones = V_E , r = number of replications = number of clones.

The selection differential (S) was estimated as $S = X_s - X_\mu$, where, S = Selection differential (difference between mean of selected individual and the population mean (Jansson, 2005)), X_μ = Mean of population, X_s = Mean phenotypic value after selection (sample mean)

Genetic gain (G) was estimated as $G = \text{Percentage gain} * h^2$, where, h^2 = Narrow sense heritability.

Key results

- No significant difference ($p = 0.08$) was observed between locations.
- Mean height was significantly different ($p = 0.031$) among the 6 clones studied (Table 4).
- Height and genetic gain varied among the accessions (Table 5).
- Narrow sense heritability (h^2) in height growth was 0.64 indicating that 64% or more of the observed variation in height growth was genetically controlled.

Table 5: Height increment and genetic gain in height growth among 6 clones of *D. edulis*

Accessions	Xs (height)	Genetic gain
DE/MA/41	4.35	23.30682906
DE/MA/50	2.956	1.64701592
DE/MA/58	2.843	-0.108765202
DE/MA/54	2.65	-3.107577207
DE/Mbyo/2-92	2.623	-3.52710013
DE/BUM/34	1.667	-18.38131918

- One clone (DE/MA/41) had a mean height increment above the overall mean performance and was recommended for future selection.
- Growth parameters is one of the top of desirable fruit/nut traits in tree selection which is important because, tree domestication has been identified as an economic incentive for farmers to plant trees, hence an efficient option to restore degraded and deforested landscapes.

Conclusion

At 36 months, there was significant variation in tree heights among clones and this is important for tree breeders who would like to carry out selection as early as possible. It could be concluded that greater gains in high yield of *D. edulis* could be realized by selecting fast growing clones.

Reference

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