

Bigger Pods, Smaller Gene Pools? Trade-offs in *Inga edulis* Cultivation Systems

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Inga edulis Mart. (Fabaceae)

Why *Inga edulis*?

- Fast-growing, nitrogen-fixing tree.
- Native to Central and South America. Widely distributed across the Amazon Basin.
- Traditionally cultivated for food, shade and soil improvement.
- The fruit contains a sweet, juicy white pulp that has a soft cotton wool texture and taste like vanilla ice cream.

Do agroforests favor larger pods?

- Agroforestry practices promote selection for larger pod phenotypes.
- Farmers select for yield-related traits.
- Pod size drives its use in agroforestry systems.

Where is genetic diversity higher?

- Home gardens exhibit greater genetic diversity than agroforestry systems. Less selection pressure for uniform traits such as pod size.
- Seed sharing among households and communities seems to maintain genetic heterogeneity.

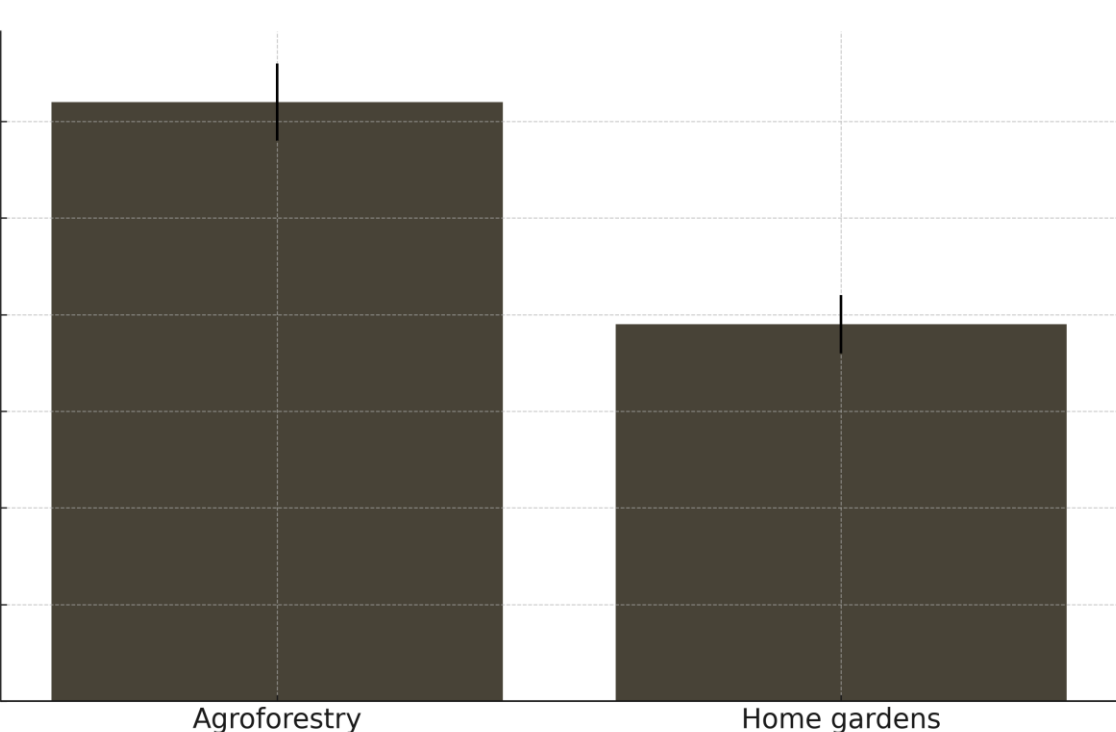
Implications

- Home gardens act as *in farm* reservoirs of genetic diversity. They are crucial for the conservation of *Inga edulis*.
- Home gardens should be included in biodiversity conservation strategies alongside more productive systems.

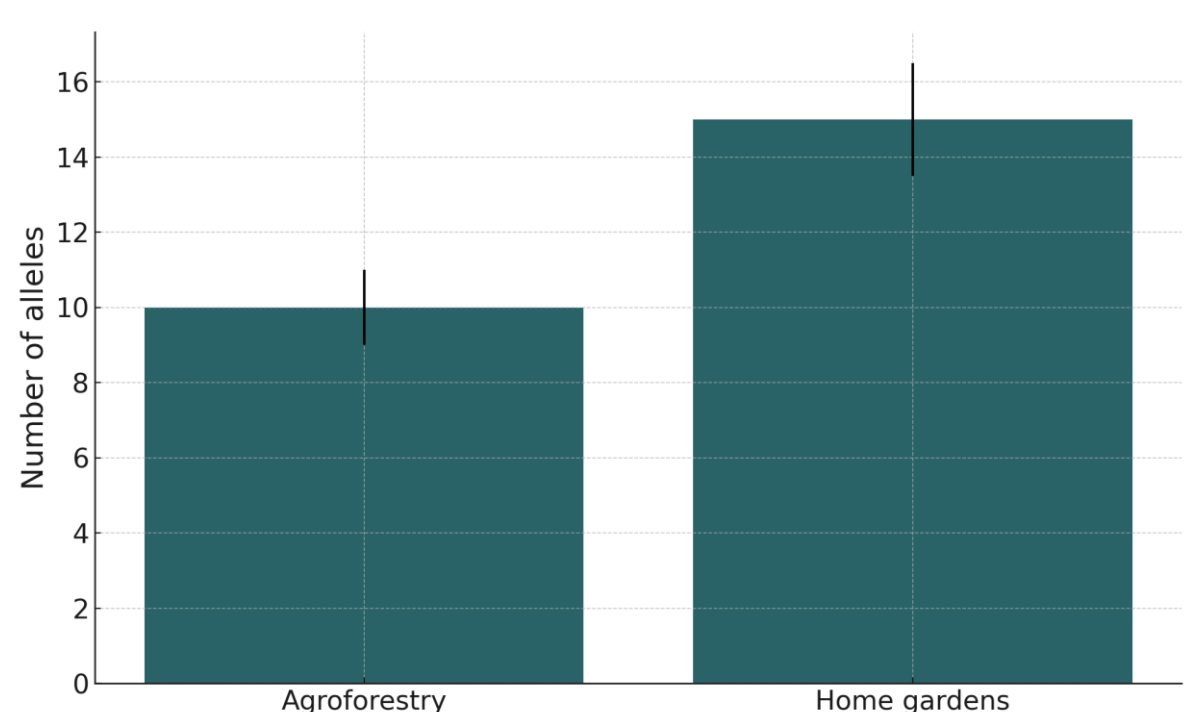
How we did this?

In this preliminary analysis, we collected a total of 82 individuals of *Inga edulis* from two contrasting cultivation systems in the region: 42 from agroforestry plantations and 40 from home gardens.

We evaluated morphological traits, particularly pod length, through direct field measurements. To assess genetic diversity, we extracted DNA from leaf tissue and genotyped samples using 10 microsatellite markers. Allele richness was analyzed using standard population genetics tools, including allele count metrics.



Mean pod length (cm) of *Inga edulis* across cultivation systems. Pods were significantly longer in agroforestry systems compared to home gardens ($p < 0.05$). Error bars represent the standard error.



Genetic diversity of *Inga edulis* based on the mean number of alleles per individual. Home gardens showed significantly higher allelic richness ($p < 0.05$) compared to agroforestry systems (mean ≈ 10 alleles). Error bars represent the standard error.

Funding

This work was supported by FCT—Fundação para a Ciência e a Tecnologia, I.P., Portugal, through project reference UIDB/00329/2020 (CE3C) UID/00239/2025 (CEF), 10.54499/LA/P/0092/2020, and under the Scientific Employment Stimulus—Individual Call (CEEC Individual—2021.01107.CEECIND/CP1689/CT0001(IM).