

First look into the genetic diversity of Cashew (*Anacardium occidentale* L.) in East-Timor

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Introduction

The cashew tree (*Anacardium occidentale* L.) is a tropical cash crop of the Anacardiaceae family, native from Brazil.

Introduced in Africa during the second half of the 16th century, after European contact with the Americas as part of The **Columbian Exchange** event.



Nowadays, is widely distributed across tropical countries, where is considered an export-oriented crop, due to its high value cashew nuts, the main export product.

Recently, in East Timor cashew has been introduced as a source of economic revenue, as a viable alternative to coffee, the main export agriculture commodity (*Coffea arabica*).



In this study, an extensive genetic diversity assessment of cashew within East Timor was performed using microsatellites or Simple Sequence Repeat (SSR) markers, in order to determine for the first time, the potential of a in-country genetic signature for an added-value opportunity for cashew.

Material & Methods

Material collection



DNA quantification and integrity



16 SSRs molecular markers were selected to uncover intra-specific diversity

Benefiting from cashew material from other countries, namely Mozambique and Indonesia that will allow to provide a regional biogeographical knowledge of cashew diversity

Results

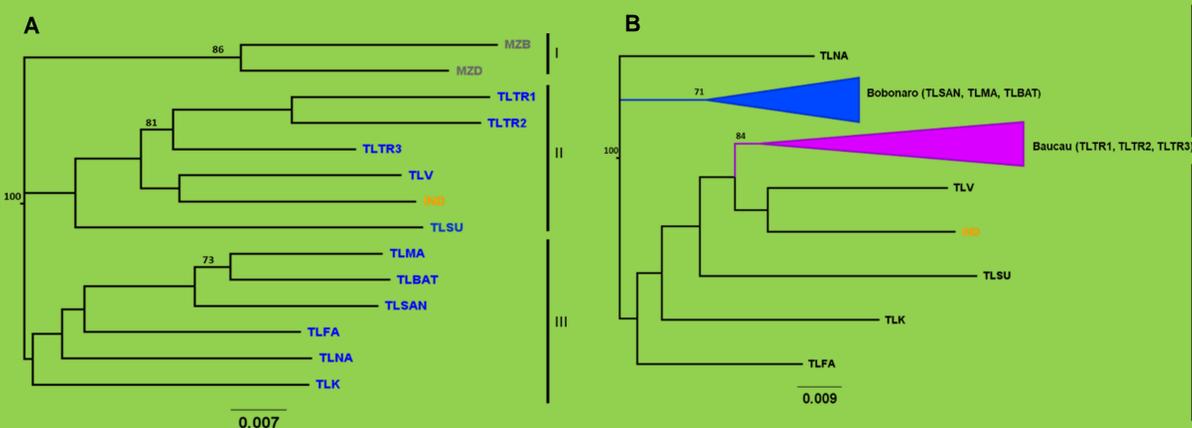
Genetic diversity indices of cashew populations by countries. Data are provided by total SSRs, following by a country analysis.

Countries	Sample size	Na	Na SD	H _e	H _e SD	H _o	H _o SD	Private Alleles	F
East Timor	164	10.38	4.44	0.69	0.03	0.40	0.01	5.94	0.41
Indonesia	16	3.25	1.84	0.54	0.006	0.37	0.03	0.44	0.28
Mozambique	27	5.13	2.13	0.71	0.02	0.45	0.02	1.63	0.37

Countries-Mozambique (2 populations), Indonesia (1 population) and East Timor (11 populations). Populations: 14 different populations. Genetic diversity indices for each group were assessed by expected heterozygosity (H_e) and observed heterozygosity (H_o) with corresponding standard deviation (SD) values, inbreeding/fixation coefficient (F), and mean alleles per locus (Na).

Population Structuring Analysis

1) Based on genetic distances using East-Timor, Mozambique and Indonesia (A) and using only East-Timor Populations (B) using Indonesia population as outgroup

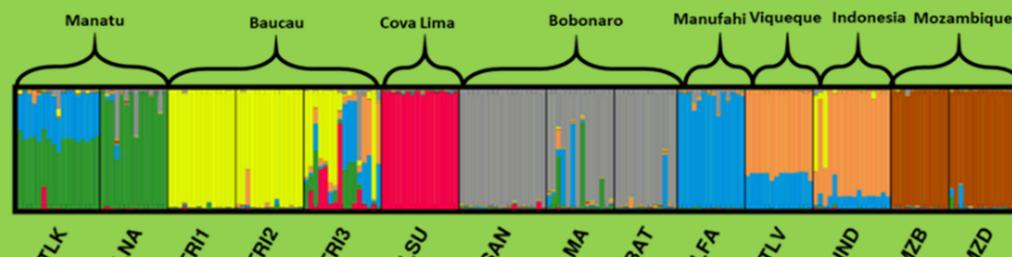


Neighbor-Joining tree generated from FreeNA using matrix DC^{INA} respectively, representing the population from East Timor, Indonesia and Mozambique. Grey colors represent Mozambique populations, blue populations from East Timor and Indonesia in orange.

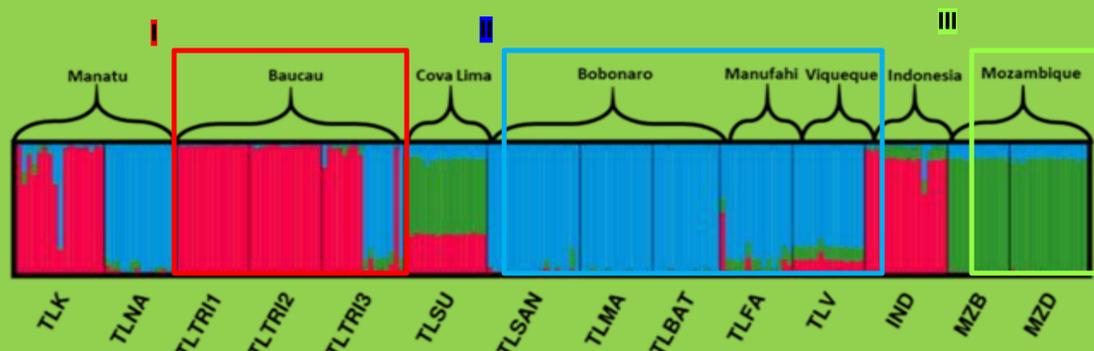
Neighbor-Joining tree generated from FreeNA using matrix DC^{INA} , respectively, representing the population from East Timor and Indonesia, at blue it is the Bobonaro populations and at purple is the Bacau populations grouped.

2) Based on individual- based clustering using a Bayesian analysis (STRUCTURE):

Clustering based on SSR data using STRUCTURE (K = 7) for populations of East Timor, Indonesia and Mozambique.



Clustering based on SSR data using STRUCTURE (K = 3) for populations of East Timor and Indonesia and Mozambique



Conclusions

This study is the first assessment of the genetic diversity in cashew population from East Timor, where this crop is viewed as alternative cash crop to coffee.

Our results provides clues on the most genetically diverse population, i.e. TLK and Baucau populations, which should be conserved *in situ* for future characterization of varieties adapted to different climatic conditions.

Identification of a genetic signature at East-Timor country, with cashew agrobiodiversity *in situ* hotspots.

The three pillars by which cashew should be implemented as a cash crop in East-Timor



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