



XIX ANNUAL MEETING OF THE PORTUGUESE ASSOCIATION FOR EVOLUTIONARY BIOLOGY

XIX ENBE 2023

18-19 Dezembro, Lisboa

Hosted by Instituto Superior de Agronomia & Faculdade de Ciências
University of Lisbon, Portugal

<https://enbe2023.rd.ciencias.ulisboa.pt>



A pantropical population genetics study on cashew crop: uncovering genetic diversity and agrobiodiversity hotspots

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Cashew (*Anacardium occidentale* L.) is a crop currently grown in several tropical countries because of the economic importance of cashew nuts. It is assumed that in the middle of the sixteenth century the Portuguese brought the cashew tree from Brazil (center of origin) to India, and later expanded to Southeast Asia, and introduced in Africa at the same time in Mozambique. The socio-economic importance of the cashew tree in tropical regions is recognized, and in recent decades, the demand for cashew has increased at the global market. Despite its enormous economic worth, limited research has been conducted on the molecular diversity of cashew genetic resources. In this work, we present the current research performed in characterizing cashew genetic diversity under a population genetics approach, across different tropical regions, from Brazil (South America) to Guinea-Bissau and Mozambique (Africa) and East Timor, Indonesia (Asia), using CPLP countries as a case study, which also cover cashew pantropical distribution. More than 350 individual cashew trees were analyzed with 16 cashew-specific SSRs, covering a pantropical approach and a more in-depth analysis on East-Timor diversity. In terms of diversity by population, Guinea-Bissau and East-Timor populations were found to display the greatest diversity, and not the center of origin of the crop (Brazil). The population structuring revealed that genetic diversity scattering does follows a geographical trend under a continental distribution. When analyzing East-Timor populations alone, a higher allelic richness was found and population structuring analysis revealed that the genetic diversity of cashew populations in was higher than previously reported. Moreover, our study showed that cashew populations in East Timor are grouped into two dissimilar genetic groups, which may suggest multiple cashew introductions over time. Overall, our data reports the first comprehensive study on cashew intraspecific diversity using a continental approach thus highlighting the need to perform conservation programs focused on a country standpoint. This is especially important considering that the result of a limited gene flow across countries were observed, which may be due to local selection of accessions within each country. Therefore, this study provides useful information regarding genetic diversity and population structure that can be harnessed to improve cashew world production. This data is also important for creating a country-specific genetic cashew signature to increase cashew market value. Ongoing work is being developed under the Project GenoCash (PTDC/ASP-AGR/0760/2020) on associating environmental variable to genetic diversity across a pantropical distribution, to understand current genetic diversity panorama. Besides, a pangenomics study is undergoing in order to identify genome regions with regional significance that could be associated to agronomical traits performance.

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