Tropentag, September 20-22, 2017, Bonn

"Future Agriculture:
Socio-ecological transitions and bio-cultural shifts"

Genetic Structure in Wild and Cultivated Populations of Inga Edulis Mart. (Fabaceae) in Peruvian Amazon

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Abstract

Inga edulis has been improved through history by human selection focusing on edible fruit. Inga trees were also cultivated to provide shade for other cultivated crops. In the present study we aimed at comparing genetic structure of the wild with cultivated populations *I. edulis* spanning the Peruvian Amazon. In total 259 individuals were evaluated and divided according to its origin into two subgroups: cultivated 197 and wild 62 trees. The samples were divided into 27 populations according to their geographic and wild or cultivated origin. For each individual a voucher specimen was kept. Total genomic DNA was extracted as described in Rollo et al. (2016). We used four microsatellite primers Pel5, Inga03, Inga08 and Inga33. The amplifications conditions also followed the protocol stated in the same study. Afterwards the reactions were loaded on an ABI PRISM 310 Genetic Analyzer (Applied Biosystems, Forest City, CA, USA) and run according to the manufacture's protocol. Allele sizes were determined using the ROX500 internal size standard and GeneMarker® v2.4 software. An individual was declared null (lacking to amplify at a locus) and treated as missing data after at least two amplification failures. The diagnostic results using MICRO-CHECKER (van Oosterhout et al. 2004) found no evidence of stuttering or large allele drop-out for any of the loci. To assess the population structure we used Structure version 2.3.3 software (Pritchard et al. 2000) to estimate the number of genetic clusters (K) and to fractionally assign individuals sampled from cultivated and wild populations to the inferred groups. Due to a weak population structure characterised by very low FST values (0.069), we used a "locprior" model, which incorporated a priori sampling location information (Hubisz et al. 2009), i.e. a "locprior" model. Two groups of populations were used as priors, i.e. cultivated and wild populations. The number of clusters (K) was set at each value from one through twenty-eight, and the simulation was run ten times at each K value to confirm the repeatability of the results.

Keywords: DNA, genetic structure, *Inga edulis* Mart., microsatellite locus, PCR, peruvian Amazon, population

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