

Deciphering the genetic basis of adaptation to environment in *T. cacao* using resequenced genomes

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ABSTRACT

Theobroma cacao is native to the Upper Amazon. The species has undergone centuries of environmental and human selection and has spread throughout Latin America. The *T. cacao* germplasm is characterized by a high genetic diversity with at least ten major genetically differentiated groups. Little is known about the environmental and climatic drivers, as well as the genomic basis of adaptation in the species. Yet, a better understanding of how plants adapt to their environment is crucial to improve predictions of species' adaptive capacities and to provide accurate conservation strategies of genetic resources in the context of increasing environmental pressure. Environmental changes along altitudinal gradients allow the identification of functionally important genes contributing to the adaptive potential of species at a restricted geographic scale. In this study, using landscape genomics approaches, we deciphered the genomic basis of cocoa tree adaptation to temperature and precipitation from accessions sampled along an altitudinal gradient. A total of 102 geolocalised accessions of cacao trees collected in Ecuador along an altitudinal gradient ranging from 200 to 1000 m above sea level have been re-sequenced to identify genome-wide biallelic single nucleotide polymorphism (SNP) markers and presence/absence gene variation (PAV). The climate variables associated with sampled locations were obtained from the public database WorldClim. Using genome-scan, we detected genes under selection along the altitudinal gradient and potentially involved in trees adaptation to climate. Then, we searched for significant associations between genomic variation and the climate variables by conducting genome-environment association studies. Functional categories of genes associated with adaptation to elevation were investigated. This work will enhance our understanding of *T. cacao* response to continued climatic change. It allows to better characterize the available adaptive

genetic diversity, to better understand the mechanisms of adaptation to climate and to apply them to crop breeding.

Keywords: Climate adaptation, Genome sequencing, Genetic diversity