

**A NEW INSIGHT IN THE NUCLEAR AND CYTOPLASMIC DIVERSITY OF *T. CACAO* :
CONSEQUENCES FOR THE *T. CACAO* CLASSIFICATION**

Boccaro M.¹, Fouet O.¹, Argout X.¹, Allegre M.¹, Pot D.¹, Motilal LM.², Lachenaud P.³, Thévenin JM.³, Zhang D.⁴, Umaharan P.², LooSolorzano RG.⁵, Lanaud C.¹

¹ CIRAD, UMR 1334 AGAP, TA 108/03- 34398, Montpellier, Cedex 5, France.

² University of the West Indies, Cocoa Research Unit (CRU), St Augustine, Trinidad and Tobago.

³ CIRAD, Biological Systems Department, UPR Bioagresseurs, 97387 KourouCedex, French Guiana.

⁴ USDA-ARS: 5601 Sunnyside Avenue, Beltsville, MD 20705-5139, USA.

⁵ INIAP: EET-Pichilingue. CP 24.Km5 vía Quevedo El Empalme. Ecuador.

SUMMARY

An extended diversity study was carried out on a collection of 650 *T. cacao* accessions representing the different geographic origins of native cocoa populations as well as cultivated populations. These populations were genotyped with 837 SNP markers defined in genes with a putative known function. Classical genetic parameters were calculated to characterize the diversity existing inside and between populations, highlighting a classification of the *T. cacao* species in three main genetic groups. SNP alleles, specific to some populations could be identified. A cytoplasmic diversity, based on SNP identified in chloroplastic and mitochondrial genomes, also allowed for a refinement of the *T. cacao* classification. An estimation of linkage disequilibrium, reflecting the extend of physical linkage conserved between markers and genetic mixing was made in each population. In parallel with the exploitation of linkage disequilibrium as a genome mapping approach, the detection of outlying loci concerning genetic differentiation provides a complementary strategy for identifying genome regions and candidate genes related to adaptive traits. This strategy was applied to the set of SNP presented in this study considering the genetic structure previously highlighted. Some SNP markers located in the vicinity of annotated genes, exhibited diversity patterns consistent with evidence of selection events, suggesting their potential interest to monitor breeding efforts for adaptive traits such as disease resistance or environmental changes.