

W118 Adding value to *T. cacao* germplasm collections combining GWAS and genome sequence analysis

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Large germplasm collections exist for the conservation of *Theobroma cacao* genetic resources. These collections have been extensively characterised for many cocoa useful traits. Genotyping of these genetic resources provide valuable information to decipher the genetic and molecular bases of *T. cacao* useful traits using genome wide association studies (GWAS). Due to reduced confidence interval of the trait/marker associations, compared to classical QTL studies, the search for candidate genes at the origin of trait variations is facilitated when exploring the genome sequence recently produced.

An example is given for the study of quality traits carried out in a collection of genetic resources corresponding to an hybrid « Nacional » pool, cultivated in Ecuador and characterised by its floral flavor allowing to classify it as fine flavor cocoa.

Quality traits of each of the 170 individuals of this population has been characterised for sensorial and biochemical (108 volatils and 7 non volatils) traits evaluated on non roasted and roasted cocoa beans, and potentially linked to quality. The population was genotyped with 180 SSR. Many marker/trait associations were revealed for sensorial and biochemical traits.

The search for candidate genes involved in the trait variation was made with the Criollo genome sequence. Several candidate genes have been identified, and particularly for polyphenols, fat and terpenes compound variation.

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