

# Genetic bases of fruity and flora aroma of the Nacional cocoa variety

Renaud Boulanger<sup>1</sup>

Kelly Colonges<sup>2</sup>, Gaston Rey Loor Solorzano<sup>3</sup>, Claire Lanaud<sup>4</sup>, Edward Seguine<sup>5</sup>, Juan-Carlos Jimenez<sup>6</sup>

<sup>1</sup>CIRAD

<sup>2</sup>CIRAD

<sup>3</sup>INIAP

<sup>4</sup>CIRAD

<sup>5</sup>Guittard

<sup>6</sup>INIAP

## ABSTRACT

Cocoa is classified into two types of products: so-called standard cocoa, which has a pronounced cocoa taste and so-called fine aromatic cocoa, which is characterised by floral and fruity notes. The production of fine aromatic cocoa therefore represents about 5% of world production. Some Latin American countries produce almost exclusively fine cocoa, which is a significant source of income for them. One of the characteristics of Nacional cocoa, the emblematic cocoa of Ecuador, is its aromatic ARRIBA flavour. This aroma is mainly composed of floral and fruity notes whose genetic and biochemical origin is not well-known. This research objective is to study the genetic and biochemical determinism of the floral aroma of modern Nacional cocoa variety from Ecuador. Genome-Wide Association Study (GWAS) was conducted on a population of 152 genotypes of cocoa trees belonging to the population variety of modern Nacional. Genome-Wide Association Study was conducted by combining SSR and SNP genotyping, assaying biochemical compounds, and sensory evaluations from various tastings. A large number of association zones have been identified. A total of 60 association zones were characterised in relation to sensory taste notes (fruity (22) and floral (38)). And a total of 895 association zones were identified with volatile compounds, 480 with fruity characteristic and 355 with floral characteristic. In a second step, a search for candidate genes in these association zones was undertaken, which made it possible to find genes potentially involved in the biosynthesis pathway of the biochemical compound identified in associations. 556 candidate genes involved in the biosynthetic pathways of volatile compounds identified in association areas were detected. Five main metabolic pathways were identified as involved in the fruity traits of the Nacional population: the protein degradation pathway, the sugar degradation pathway, the fatty acid degradation pathway, the monoterpene pathway, and the L-phenylalanine pathway against two for the floral traits (the monoterpene biosynthesis pathway and the L-phenylalanine degradation pathway).

**Keywords:** GWAS analysis, aroma compounds, candidate genes