



Introduction

Coffee production is an untapped source of revenue for developing countries. The metabolite and lipid diversity among *Coffea canephora* can be harnessed for genomic improvement of high cup quality trait.

Materials/Methods

Genetic diversity among 18 conserved and 30 cultivated coffee genotypes were detected by analyzing 433048 single nucleotide polymorphisms (SNPs) identified through genotyping-by-sequencing. Gas Chromatography–Mass Spectrophotometer and Ultra-performance liquid chromatography coupled with mass spectrometry (UPLC–MS) used to quantify and profile metabolites and lipid molecules on the same genotypes of *C. canephora*.

Conclusion/Perspectives

‘Niaouli’ genotypes could therefore serve as useful germplasm for starting a Nigerian *C. canephora* quality improvement breeding program. This study revealed the narrow genetic base of the coffee germplasm in Nigeria. There is need to initiate research collaboration between Nigeria and other international and national coffee research institutes in other to access available coffee germplasm for high quality improvement.

References:
 Anagbogu et al. 2019 Genet Resour Crop Evol. doi.org/10.1007/s10722-019-00744-2
 Anagbogu et al. 2019 Plants doi:10.3390/plants8100425

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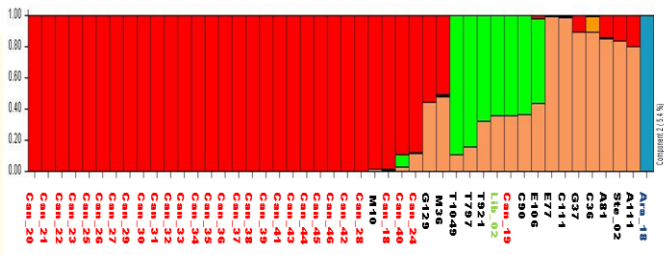


Figure 1: Population structure analysis

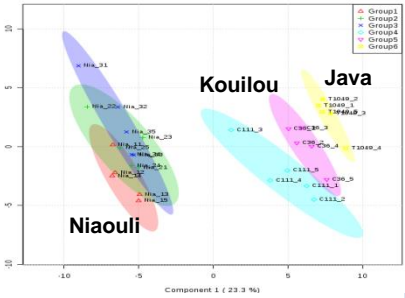


Figure 3: Metabolomic profiles of the 6 genotypes by PLS

Results/Discussion

We found three distinct diversity structures within the *C. canephora* gene pool that were likely be of Congolese origin (Fig.1).

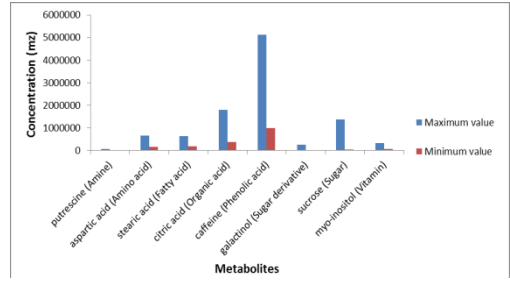


Figure 2: The concentration of levels of the 8 metabolite classes

High uniformity was also found among the cultivated accessions with 99% of them representing *C. canephora* var. Niaouli as their ancestral background. Across genotypes, the sucrose-to-caffeine ratio was low, a characteristic indicative of low cup quality (Fig. 2). The sucrose-to-caffeine ratio was also highly correlated, indicative of common mechanisms regulating the accumulation of these compounds. Nevertheless, this strong correlative link was broken within the ‘Niaouli’ group, as caffeine and sucrose content were highly variable among these genotypes. The most abundance lipid was found to be triacylglycerols followed by fatty acyls while the least abundance was cholesterol ester. The three analyses differentiated ‘Niaouli’ from other genotypes studied (Fig.3).