

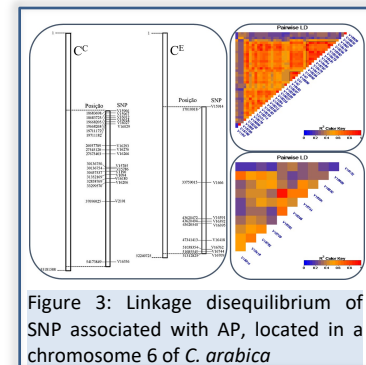
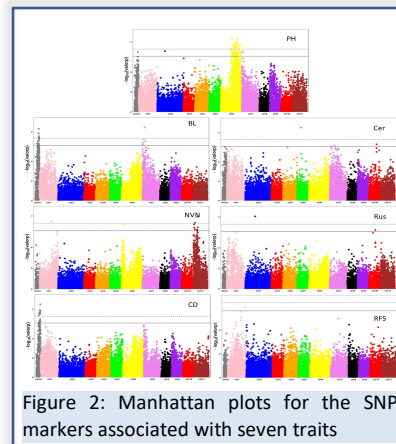
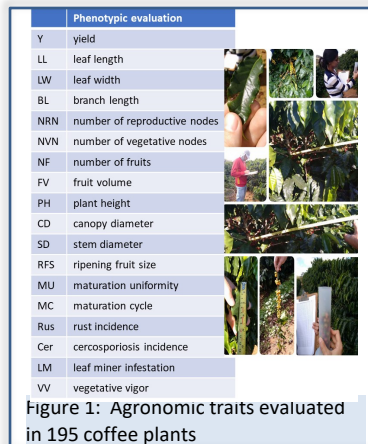
# Genome-wide association study for morphological and yield components traits in *Coffea arabica*

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**Introduction:** Genome-wide association study (GWAS) has been successfully applied in several annual and perennial plant species. However, few GWAS works have addressed *Coffea arabica*. The incorporation of this methodology in coffee breeding programs is important to explore the low variability of this species, maximize genetic gains and make the breeding process faster and more efficient.

**Materials/Methods:** A phenotypic evaluation of 18 agronomic traits (Fig. 1) were performed in breeding population of 195 individuals of *C. arabica*, in three consecutive ears. The phenotypic data were corrected for years, plots, and years  $\times$  plots interactions, using the REML/BLUP methodology. The population was also genotyping using Capture-Seq methodology. The genetic structure of the population was obtained through the Principal Component Analysis, using prcomp (software R). PCA were used as covariates in the GWAS model, to detect SNP associated with phenotypic traits.



**Results/Discussion:** Coffee trees, besides being phenotyped, were genotyped with 20,477 SNP widely distributed in the genome. By GWAS, 110 SNPs were significantly associated ( $p < 0.05$ ) with seven of the analyzed traits (PH, BL, NVN, CD, Cer, Rus and RFS) (Fig.2). Plant height (PH) showed the highest number of significant associations SNP (56 SNP), and the data suggested a major QTL in the control of this trait, located on chromosome 6 (Fig.3). The effects of each associated SNP were obtained, allowing to identify favorable allele and markers for future use in assisted selection. The genes with the significant SNP was analyzed and 19 candidate genes were identified.

**Conclusion/Perspectives:** The efficiency of the GWAS methodology for coffee was confirmed. Molecular marker were identified associated with main agronomic traits, including disease resistance, morphological and yield component traits. Our results provide new insights into the genetic architecture of these traits, and will be helpful in assisted *C. arabica* breeding program.