

RETRO-COF

LTR-retrotransposons (LTR-RTN) to decipher the structure, diversity and origin of the *Coffea arabica* genome.

ABSTRACT

Transposable elements constitute the main part of plant genomes. They have been identified and annotated from the Robusta coffee tree genome (*C. canephora*), one of the two diploid ancestors of the cultivated allotetraploid Arabica genome (*C. arabica*), and so from the *C. arabica* genome. TEs represent 49% et 59% of *C. canephora* and *C. arabica* genomes, respectively. LTR retrotransposons (LTR-RTN) is a particular class of TEs that represent altogether 42% and 52% of *C. canephora* and *C. arabica*. In *C. canephora*, LTR-RTNs are not randomly distributed along chromosomes, drawing TE rich and poor-regions similar to heterochromatin and euchromatin regions observed in plant chromosomes. The analysis of our LTR-RTN databases allowed identifying a new group of non-autonomous elements, devoid of the enzymatic machinery involved in their mobility (Chaparro et al., 2015). Members in this group, called TR-GAG, are relatively short (In addition to cultivated species, 10 genomes of wild species from West Africa, East Africa and Madagascar were partially sequenced (> 100,000 sequences each), and the diversity and copy numbers of LTR-RTNs studied. The analysis highlighted one LTR-RTN family, called SIRE (Copia), not present in species from East Africa and Madagascar, but showing a large diversity in species from West Africa, like *C. canephora* and *C. arabica*. Two SIRE elements, were finally used as genetic markers with the REMAP technology to analyze the diversity of a set of 96 DNA sample from wild and cultivated *C. arabica*, *C. eugenioides* and *C. canephora*. Preliminary data suggest that these LTR-RTN are particularly informative to reveal the genetic diversity of *C. arabica* genotypes.

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PERSPECTIVES

The analysis of the *C. arabica* genome and its comparison with the diploid ancestor *C. canephora* will allow in the near future to highlight variation of the TE insertion profiles. Those profiles will be exploited to understand the evolution and origin of the *C. arabica* genome.