

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

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.

Responsable :

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