

# 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 :**

**Date de démarrage :** 01/10/2012

**Date de clôture :** 31/12/2014

**Montant :**

