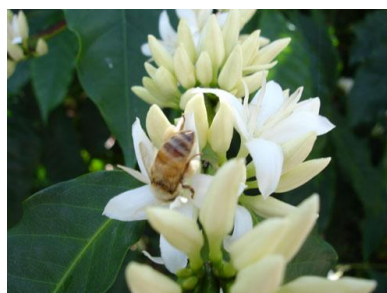


## Coffee Tree Genome has been Sequenced

An international study coordinated by researchers from IRD, the CEA (Genoscope), CIRAD, the CNRS, and the University of Buffalo (United States), and involving many laboratories, helped identify a reference genome sequence for coffee trees for the first time. This discovery is important in two ways: first, it is fundamental as it improves understanding of the organisation of the genome, its function, and its evolution; secondly, it also offers new possibilities for selection or improvement of coffee tree varieties.



Coffee seedlings



Coffee in bloom

In the study published in *Science*, the researchers were interested in Robusta coffee because of its average sized genome (710 million pairs of DNA bases) and its diploid nature (contrary to *Coffea arabica*, which is tetraploid). The genetic map of the coffee tree studied, produced in the 1980s by IRD in Cote d'Ivoire, also had the advantage of being a homozygous plant (two identical sets of eleven chromosomes), which is easier to analyse than natural heterozygotes.

By using several sequencing technologies, Genoscope (CEA) coordinated the mapping of the DNA sequence for the coffee tree, assembled in large fragments able to be used in various types of analysis. The IRD and CIRAD teams then anchored these sequence fragments to a high-density genetic card to reconstruct the pseudo-chromosomes. A catalogue of genes and repeated sequences was then created and validated, allowing for a comparison with other plants.

### Key findings

Thus, the researchers established a reference genome sequence for coffee trees (including for the species *Coffea arabica*), and more generally for the Rubiaceae, one of the largest families of flowering plants (containing nearly 12,500 species).

A comparative analysis of genomes by the international consortium also revealed that the organisation of the coffee tree genome is best preserved in the Asteridae (the family to which potatoes and tomatoes belong) and is very close to that of the ancestral species from which all true Dicotyledons (or Eudicotyledons) descended through evolution. Lastly, the study of the genome improves knowledge of the secondary metabolism of plants and its diversification. A comparative analysis with the cacao tree genome also shows that the biosynthesis of caffeine is due to enzymes unique to each species, which appeared at various moments in their evolution.

Over the longer term, the identification of the coffee tree genome sequence opens up new possibilities for varietal improvement, knowledge of the specific functions of the

genes (in particular those specific to coffee trees), the possibility of transferring results to other species, and refining diagnostic tools for the function of the plant.



Coffee fruits in bearing

The research will facilitate the completion of applied projects, such as the selection or creation of coffee tree varieties with improved technological and/or qualitative characteristics; more resistant to environmental constraints and to bioaggressors, such as for example orange leaf rust. In fact, this disease still has a considerable impact on coffee cultivation and the economy of small producer countries in Central America such as Guatemala, Honduras, and Costa Rica. Lastly, it should help guide producers toward ecologically intensive agriculture.

These results in detail were published in the journal *Science* on 5 September 2014.

**Source:**

<http://www.sciencedaily.com/releases/2014/11/141104111412.htm>

The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. *Science*, 2014; 345 (6201): 1181 DOI: 10.1126/science.1255274