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Introduction

Coffea humblotiana Baill., also called “Caféier de Humblot”, is the sole *Coffea* species endemic to the Comoro archipelago (Figure 1). It was probably consumed by the past. The remarkable feature of *C. humblotiana*, is the absence of caffeine in seeds and leaves, shared by most species from Madagascar, Mascarene Islands and some species from East and Central Africa. Caffeine is produced in the young leaves and immature fruits of African coffee species mainly, with a maximum level in *C. canephora* (2.4–3.3% dmb). The caffeine biosynthesis pathway involves three methylation steps catalyzed by different N-methyltransferase genes (*NMT*): *XMT*, *MXMT* and *DXMT*. As output trait for the industry, caffeine as well as chlorogenic acid (CGA) compounds are of a great interest since they participate in producing metabolites which activates five human bitter taste receptors, therefore contributing to an inferior final cup quality. To understand the mechanism of the absence of caffeine in *C. humblotiana*, we sequenced and assembled the genome at the chromosome level.

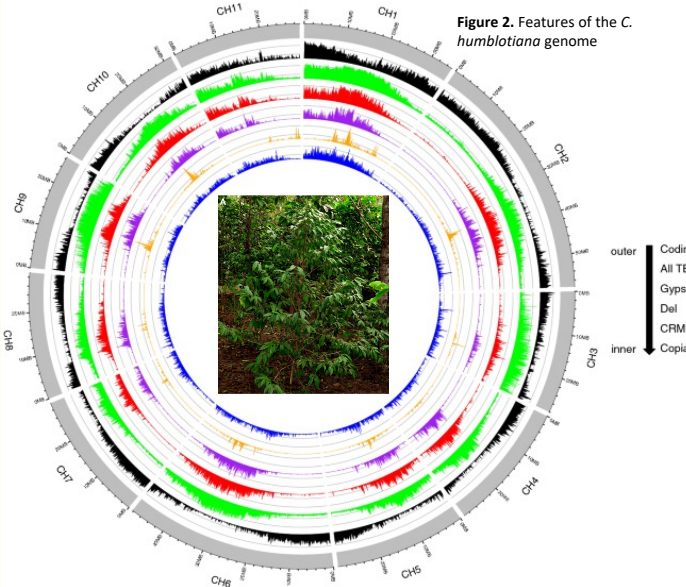


Figure 2. Features of the *C. humblotiana* genome

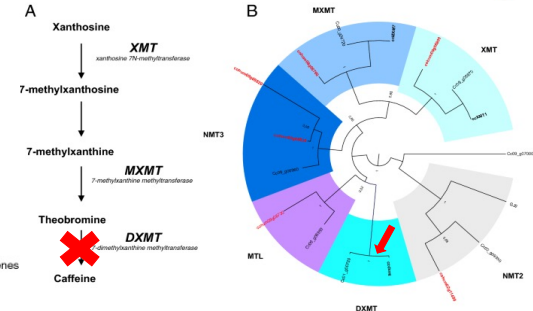


Figure 2. A Methylation steps of the Caffeine biosynthesis. B. Phylogenetic analysis of NMT proteins in *C. humblotiana* (red) and *C. canephora* (black).

Results/Discussion

Using PacBio, Illumina and Hi-C, we assembled 422 Mb of sequences into 11 pseudochromosomes (Figure 1). 32,874 predicted genes were identified. Among them, N-methyltransferases similar to *XMT*, *MXMT* and *DXMT* genes in *C. canephora* were carefully researched. It appears that the *DXMT* gene (Caffeine synthase), converting Theobromine to Caffeine, is absent from the *C. humblotiana* genome. Together with the biochemical absence of caffeine, low accumulation of Theobromine in leaves, and low expression of *XMT* and *MXMT* genes, we conclude to a probable regulation of the Caffeine pathway in *C. humblotiana*.

Conclusion/Perspectives

The assembly of *C. humblotiana* provides the first high-quality reference genome for the *Coffea* genus. It provides valuable information for promoting its preservation and it represents a resource for genomic and evolutionary studies on *Coffea*. It is also of interest in helping to develop new strategies for characterizing coffee cup-quality traits. However, additional and substantial efforts will be necessary to develop strategies for improving coffee cultivars. In this regard, the absence of caffeine of *C. humblotiana* beans, that reduce the bitterness of coffee beverage, is an interesting avenue to follow.

References

Raharimalala, N., Rombauts, S., McCarthy, A. et al. The absence of the caffeine synthase gene is involved in the naturally decaffeinated status of *Coffea humblotiana*, a wild species from Comoro archipelago. *Sci Rep* 11, 8119 (2021). <https://doi.org/10.1038/s41598-021-87419-0>