

**Titre de la communication :**  
**Synténie et génome évolution chez le caféier allotétraploïde (*Coffea arabica*): Etude de la région S<sub>H3</sub>**

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**Texte :**

Coffee leaf rust caused by the obligate parasitic fungus *Hemileia vastatrix* is an economically important disease and a major limiting factor for arabica coffee (*Coffea arabica*) production. While the rust resistance genes identified in *C. arabica*, a recent allotetraploid species (CaEa), have not provided durable resistance, resistance genes from diploid related coffee species such as *C. liberica* (i.e. S<sub>H3</sub> gene) and *C. canephora* have provided long-lived protection under field conditions. Positional cloning of the S<sub>H3</sub> gene has been therefore undertaken in order to enhance opportunities for genomics-enabled breeding and to gain molecular insight into rust durable resistance.

Hence, we explored the possibility to utilize the exponentially increasing sequence information from model plants such as *Arabidopsis* and Tomato. By combining a search of *Arabidopsis* sequences homologous to coffee BAC-end sequences belonging to the related S<sub>H3</sub> BAC contig and use of orthologous sequence markers, we demonstrated microsynteny between coffee and *Arabidopsis* duplicated counterparts. The complex duplication history of *Arabidopsis* did not prevent the use of *Arabidopsis* as model for coffee species. Furthermore, an extended colinearity between the coffee and tomato genomes was revealed for the chromosome arm carrying the S<sub>H3</sub> locus using comparative genetic molecular mapping. This finding highlights the possibility to share genomic and genetic information among these two related crop plants. Finally, the complete sequences of homeologous coffee BAC clones (i.e. belonging to the two different genomes) from the S<sub>H3</sub> region were determined. Preliminary analysis showed a low sequence divergence and a highly conserved colinearity between the corresponding segments of the C<sub>a</sub> and E<sub>a</sub> genomes.