



EPOSTER FLASH PRESENTATION

S01 - Session P2 - Some *Coffea liberica* SH3-LRR-coding sequences are highly distinguishable

🕒 Monday, August 15, 2022 2:00 PM to 2:05 PM · 5 min. (Europe/Paris)

📍 Angers Congress Centre

📄 S01 Breeding and effective use of biotechnology and molecular tools in horticultural crops

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Genes in the SH3 locus are involved in the interaction with the fungus *Hemileia vastatrix*. Previously we found, by comparison to data published for *Coffea arabica* cv. IAPAR59, that the SH3 loci are multi-allelic and complex in *C. arabica* var. Caturra, *C. eugenioides* and *C. canephora* publicly available genomes. The above cited SH3 loci hold different numbers of copies of a CC-NBS-LRR gene in distinctive organizations. *C. liberica* is considered to display the SH3 ideal configuration providing durable resistance to coffee leaf rust, which is highly desirable, hence pursued in breeding. The coffee CC-NBS-LRR genes allocated to the SH3 loci display highly conserved as well as hypervariable regions. So, sets of primers designated to amplify the hypervariable LRR-carboxy terminals were used to clone and sequence SH3 variants in *C. liberica* and 'IAPAR59'. Sanger sequencing was used to access the cloned variants and neighbor-joining was used to represent pairwise divergence indexes between the sequences. 'IAPAR59' was re-accessed as a testimonial for the effectiveness of the approach because it was possible to verify that all the variants for the SH3 genes in 'IAPAR59' BAC clones already reported elsewhere, were also cloned using our primer sets. Indeed, it was considered that all the variants present in the accessed *C. liberica* plant had been cloned too. This was checked by contrasting the restriction fragment maps generated from genomic DNA x cloned amplicons in the two genotypes: patterns for both DNA sources of a same genotype were equal, and diverged from those in the other genotype. Regarding sequences, at least three out of six carboxy-terminal variants found in *C. liberica* seem to be exclusive when contrasted to the other four genotypes accessed. Differences found in the restriction maps and sequences are very likely related to susceptibility or resistance reactions verified during [coffee plants - *H. vastatrix* physiological races] interactions.

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Type of sessions

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Type of broadcast

In person

Keywords

gene-to-gene interaction leucine rich repeats plant-pathogen recognition

Room

Amphitheatre Jardin - Screen 2



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Researcher, Dr.
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