



Hanoi VIETNAM

11-14 Sept. 2023 Melia Hanoi Hotel

BOOK OF ABSTRACTS

  29th Conference
Asic **2023**

Agronomy | Chemistry | Technology | Physiological effects

WELCOME

Agronomy | Chemistry | Technology | Physiological effects

ASIC (Association for the Science and Information on Coffee) has been existing for 56 years already and has organized regularly conferences on coffee science most usually every second year, trying to alternate coffee producing and consuming countries.

I would like to take this opportunity to warmly thank, on behalf of ASIC and the scientific community working on coffee, the Vietnamese authorities who have accepted to organize this 29th conference.

Vietnam is the second largest coffee producing country in the world and the largest producer of Robusta coffee. In the north of the country, Arabica coffee is also grown in the mountain areas.

This conference represents a unique opportunity to gather specialists from all over the world working on different aspects of coffee science and technology. During the conference, all possible aspects of coffee science will be developed and the participants will be able to hear and share novelties on the different following topics:

- **agronomy:** genetics, botany, agrotechnology, pests and diseases, agroecology, etc.;
- **chemistry:** coffee analysis, chemical composition, aroma, etc.;
- **technology:** green coffee processing, roasting, grinding, extraction, decaffeination, etc.;
- **physiological effects:** coffee and health.

As the President of ASIC, I am cordially inviting all scientists working in the field of coffee and interested in sharing their research data to presently take good care of themselves and families. Do not forget to add to your agenda the next **29th ASIC Conference** that will be held in **Hanoi, Vietnam, from 11 Sept. - 14 Sept. 2023** which will allow taking advantage of all nice meeting and learning opportunities offered by the event. We will be very happy to welcome you in Hanoi next year.



Astrid NEHLIG, President of ASIC

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*Registration, accommodation
Sponsorship and exhibition*

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Could genes allocated to S_H3 loci contribute to other resistance factors?

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Rationale:

Leaf rust is one of the most harmful coffee diseases. *Coffea* spp. resistance factors S_H1-S_H9 are known. S_H3 resistance factor from *C. liberica* has been valued because it delivers durable resistance to the leaf rust. Leaf rust is caused by the fungus *Hemileia vastatrix*, and at least 15 physiological races were identified in Brazil. We recently proposed structural models for six *C. liberica* SH3-Rx-CC-NBS-LRR gene variants. Working *in silico* we recently demonstrated that S_H3 loci are complex and can display four up to eight SH3-NBS-LRR gene variants placed in chromosomes 3 from different *Coffea*, with additional variants identified in chromosomes 6 for some species. The variant placement resemble the complexity observed at the *C. arabica* cv. IAPAR59 S_H3 locus, accessed a decade ago. This work aims to contribute for SH3-NBS-LRR variant divergence analyses, which are highly interesting to investigate structure x species-specific pathogen effector recognition

Methods:

Via PACBio target-sequencing, S_H3 genes from a *C. arabica* plant with introgression from *C. liberica* (BA10 series), from differential genotypes C1FC H147/1, H151/1 and H153/2 used for *H. vastatrix* race typing, and a *C. arabica* var. Caturra selection were accessed. These five coffee genotypes express S_H2-3, S_H2-5, S_H-5, S_H1,3,-5, and S_H5, respectively. PACBio Hi-Fi reads were subjected to correction and assembly using the *canu* algorithm (v2), and to an additional round of *contig* assembling with a minimum of 97% identity throughout 3000 bases. Pairwise distance between aligned *contigs* were calculated (dnadist) and clustering was performed by the maximum likelihood method (without a molecular clock). Software were set to the default values (Phylip v3.698)

Results:

Contigs/variants produced had open reading frames for NBS-LRR resistance proteins, being seven from the BA10 coffee plant, three *contigs*/variants from each differential genotypes, and four from *C. arabica* var. Caturra. One additional *contig* for each differential genotype had no NBS-LRR-like open reading frame. Taking 2000 bases of carboxy-termini, directly involved in pathogen effector species-specific recognition, and relaying on the differential genotypes, clusters of S_H3, and S_H3,5 related variants were obtained.

Conclusions & Perspectives:

Coffee SH3-NBS-LRR variant seems to diverge according to their species-specificity, and could possibly interact with different fungus physiological races. SH3-NBS-LRR variant number/diversity could determine resistance to one or more fungus physiological race(s). This preliminary result shall be tested by variant expression analyses.