

# COULD $S_H3$ GENES CONTRIBUTE FOR THE ACQUISITION OF DIFFERENT RESISTANCE TRAITS?

Plant Resistance  
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Leaf rust is one of the most harmful coffee diseases. We recently cloned and proposed structural models for six *C. liberica*  $S_H3$ -Rx-CC-NBS-LRR resistance gene variants. Working *in silico*, we demonstrated that  $S_H3$  loci are complex and can display **four up to eight  $S_H3$ -NBS-LRR gene variants** placed in chromosomes 3 from different *Coffea*.

The introgression of multiple avirulence alleles from BA-10 genitors, which are sources of RF3 was reported (Conceição et al, 2005).

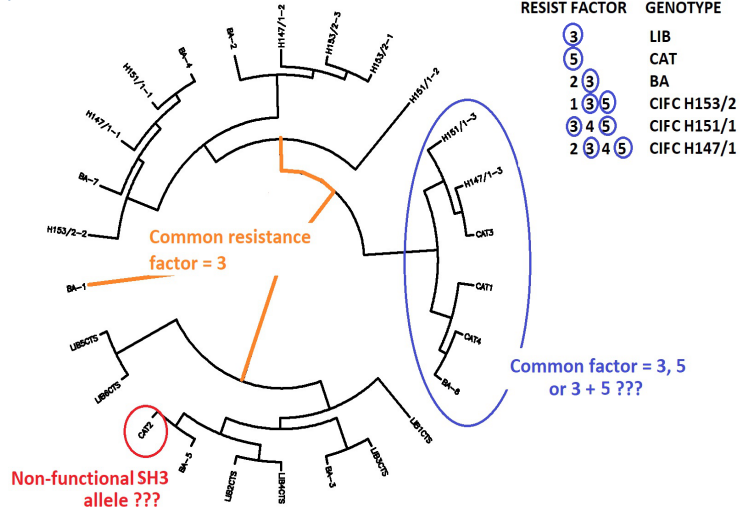
Differentials with resistance based exclusively on RF5 have not been reported yet (Zambolim and Caixeta, 2021).

So, could some of the gene variants allocated to  $S_H3$  loci contribute to the expression of additional RFs?

- *contigs* of PACBio reads resulted in  $S_H3$  different variants, being 3 for each CIFC differential, 4 for Caturra Amarelo, 7 for BA-10;

- constraints were not imposed while thinking about RFs expressed by the plants x variants/alleles analyzed. The common RF at each cluster, which should be exclusively RF3, was identified (Figure 1).

$S_H3$  variants from Caturra (which expresses RF5), clustered mostly with H151/1 and H147/1 (which express RF3 and 5 among others), and with BA-10 T1C4P2 (which expresses RFs 2,3). We considered possible that some of the variants placed in  $S_H3$  loci can contribute to the expression of RF5. Otherwise, those variants in the 'blue' cluster (Fig. 1) could be non-functional variants.



**Figure 1:** distribution of  $S_H3$  variant second exon sequences in *Coffea arabica* var. Caturra Amarelo, *C. liberica*, BA-10, and three differential genotypes. PACBio targeted sequencing reads were subjected to canu2 correction and assembled as *contigs*. Sanger sequencing was applied as an aid for *C. liberica* variant sequences determination.