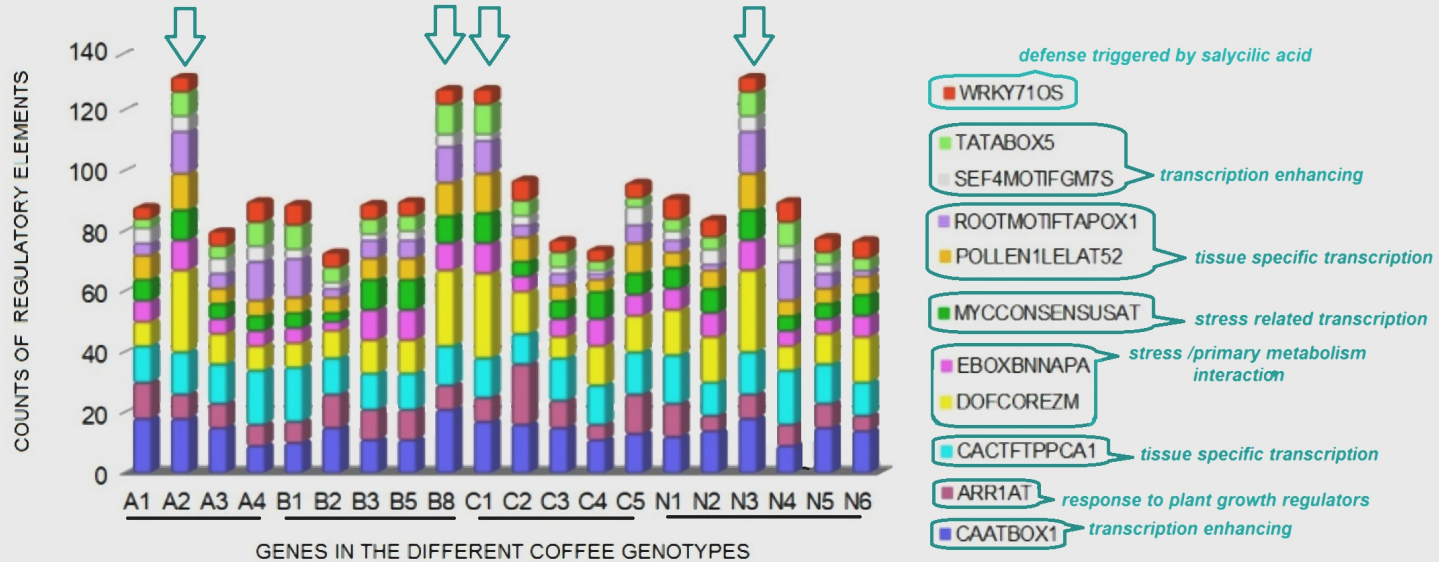


Paula C. S. Angelo (paula.angelo@embrapa.br), Caroline Ariyoshi, Eveline Teixeira, Luiz Filipe P. Pereira

RATIONALE: The **SH3 locus** is implicated in plant defense against the **leaf rust disease** caused by *Hemileia vastatrix*, which reduces coffee plant production. A **cluster of genes coding for CC-NB-LRR proteins** is allocated to this *locus*. Investigating the **gene regulatory regions** can be worthy as basic knowledge and economically.

METHODS: The cis-acting elements 2000 pb upstream translation start on **20 genes** allocated to paralogous SH3 *loci* in **four Coffea spp.** genotypes were identified and counted (<http://www.dna.affrc.go.jp/place>). Frequency data were analyzed using Sigma Plot.



The ten most frequent regulatory elements 2 kb upstream the translation initiation site of CC-NBS-LRR genes clustered in SH3 paralogous loci of *C. arabica* cv. Caturra (A1 - 4), *C. eugenioides* (B1 - 5), *C. canephora* (C1 - 4) and *C. arabica* native from Ethiopia (N1 - 6). B8 and C5 are isolated copies identified in chromosome number 6. The probable function of the different regulatory elements is indicated. The gene copy displaying the highest number of regulatory elements in each genotype is indicated by the empty arrows.