

Diversity in the regulatory region of genes in the S_H3 locus

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RATIONALE

The S_H3 locus is implicated in plant defense against the leaf rust disease caused by the fungi *Hemileia vastatrix*, which reduces coffee plant production. A cluster of genes coding for NB-LRR proteins is allocated to this locus. Investigating the regulatory region of these genes can be worthy in knowledge and economically.

METHODS

The cis-acting elements (cis-els, conserved motifs for the interaction with transcription machinery) in the promoters (2000 pb up-stream translation start) of 20 genes allocated to paralogous S_H3 loci in four *Coffea* spp. genotypes were identified and counted (www.dna.affrc.go.jp/place). Data were analyzed using Sigma Plot.

RESULTS

Cis-els more frequently identified are depicted in Fig. 1 (in average, 3.5 times/promoter for SEF4MOTIFGM7S up to 14.1 times for CAATBOX1). Genes diverged for the frequency of cis-els. At least one gene/genotype was found in the highest cis-el frequency class ($11.46 < N3, A2, C1, B8 > 11.9$ copies of each cis-el), probably displaying complex patterns of induction. Genotypes did not diverge.

CONCLUSIONS & PERSPECTIVES

Information presented here are going to be correlated with the transcription level of different genes.

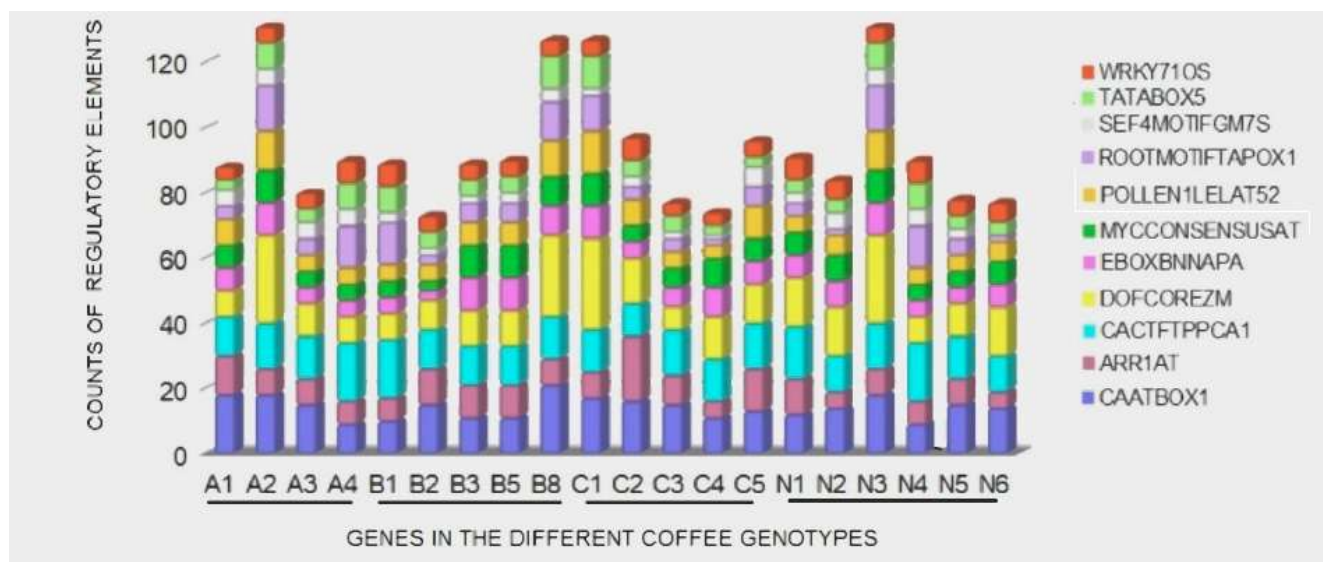


Fig. 1. Cis-acting elements in the regulatory region of genes clustered in S_H3 paralogous loci of different *Coffea* genotypes. A1-4 and N1-6: *C. arabica*; B1-8: *C. eugenioides*; C1-5: *C. canephora* genes. Besides ROOTMOTIFTAPOX1 and CACTFTPPCA1, which are possibly involved in tissue specific transcription in the roots and mesophyll cells, and WRKY71OS, which is involved in SA-triggered defense, most of the cis-elements identified are transcription enhancers.