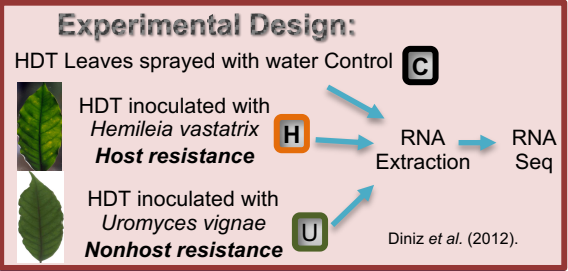
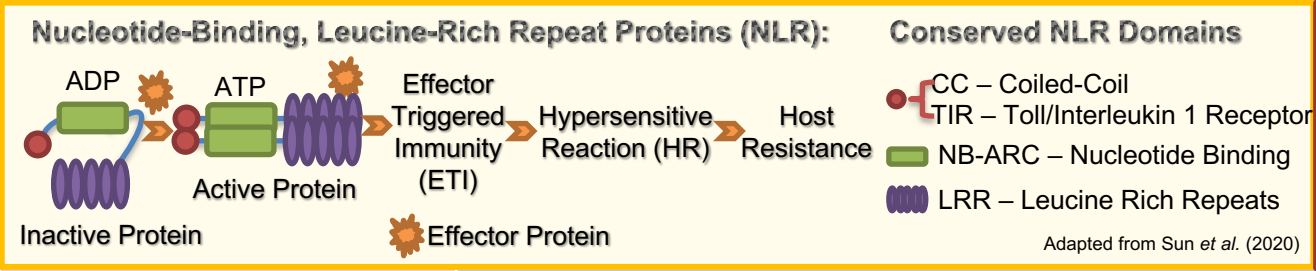




Identification of NLR proteins in the coffee genotype HDT 832/2 challenged with *Hemileia vastatrix* (host resistance) and *Uromyces vignae* (nonhost resistance)

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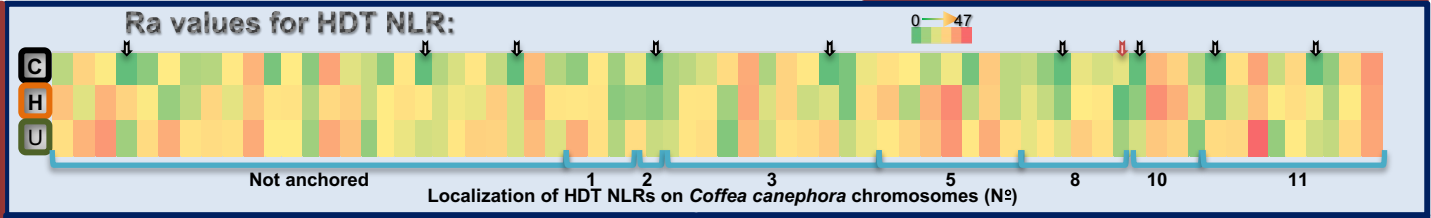
Identification of HDT NLR:

SEQ: **C** **H** **U**

Mapped To *Coffea canephora* genome

Functional Annotation Blast2Go PFAM search Functional categories

Relative abundance (Ra) of HDT transcripts was calculated according to Vega-Arrequin *et al.* (2009)



HDT NLRs Expression

We identified 68 different putative NLR proteins that showed at least one of the conserved domains of NLRs:

- > Most NLR mRNA sequences with higher Ra compared to the control were upregulated in leaves inoculated with *H. vastatrix* and *U. vignae*;
- > 8 NLR mRNA sequences were present only in inoculated HDT leaves; ⇒
- > 1 NLR mRNA was not expressed in leaves inoculated with *H. vastatrix*. ⇒

HDT NLRs Localization in *C. canephora* Chromosomes

> NLRs present in HDT transcriptome were in higher number located at chromosome 3. Although chromosome 11 in *C. canephora* genome has the highest number of predicted NLR proteins, it is in chromosome 3 that NLR clusters are predominant, it is also the predicted localization of *SH3* gene, which has been linked to *Hemileia vastatrix* resistance (Denoeud *et al.* 2014).

Conclusions & Perspectives

- ❖ High number of NLRs in the transcriptome of HDT 832/2 reflects the high number of NLRs in plant genomes – Redundancy or Diversification?
- ❖ Most of HDT NLR sequences seem to have a low transcription level, and are unaltered when compared to the control – Fine-tuning?

- ❖ The identification of NLRs from other coffee genotypes with high spectrum of resistance to *H. vastatrix*, such as HDT derivatives and the Kawisari hybrid (*C. arabica* x *C. liberica*), under a new project named CoffeeRES that will contribute to unveil the role of these proteins in the immune system of coffee plants.

References

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 Denoeud, *et al.* (2014) *Science* 345:1181-1184 (doi:10.1126/science.1255274)
 Vega-Arrequin, *et al.* (2009) *BMC Genomics* 10:299 (doi:10.1186/1471-2164-10-299)

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