

Comparative characterization of resistance proteins in Coffea species

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Introduction

Plants have molecular mechanisms that allow them to fight against multitude of pathogens. The main function of R proteins is to detect pathogens in a direct or indirect way and develop an immune response. Identify and study R proteins and their action mechanisms on different plant species and varieties is essential to, for example, elaborate action plans against the attack of pests. In our study, we identify and characterize the R genes present in *Coffea arabica, Coffea canephora and Coffea eugenioides.* Finally, we also analysed homology, syntheny, and chromosomal distribution of these proteins in the three Coffea species.





References: 1. Osuna-Cruz CM, Paytuvi-Gallart A, Di Donato A, Sundesha V, Andolfo G, Aiese Cigliano R, Sanseverino W, Ercolano MR. PRGdb 3.0: a comprehensive platform for prediction and analysis of plant disease resistance genes. Nucleic Acids Research 2017.

Figure 2. characterization of the R proteins domains in each chromosome of each species

Results/Discussion

The percentage of the proteome dedicated to resistance proteins in the three studied Coffea species ranges between 7.98% and 9.17%. This percentage is considerably higher than values observed in most plant species (usually ranging between 0.5 and 1.8%). Overall, 5366, 2345, and 3295 R protein were found in *C. arabica, C. canephora, and C. eugeniodies*, respectively. The number of exclusive and shared proteins among the three Coffea species is shown in **figure 1**. Chromosomes 2 and 11 consistently showed the largest number of R proteins, being kinase the domain most frequently found in these proteins. The distribution of the different types of R proteins per chromosome is shown in **figure 2**. The genomic location of most of the homologous R proteins is maintained across species, as shown in **figure 3**.



Conclusion/Perspectives

Knowing and studying R proteins in order to develop long-lasting and effective strategies that allow crops to deal with pests occupies an increasingly important position in plant research. Our work sheds light on the molecular structure, distribution, and evolutionary history of R genes in *C. canephora, C. arabica, and C. eugenioides*. Using this knowledge and the implemented methodology, a stepping stone is established for the study of different varieties of coffee, encouraging the study and understanding of the molecular mechanisms responsible for resistance to diseases in species of the genus *Coffea*.

Materials/Methods

Using DRAGO2¹ we have identified resistance genes in the reference genomes of C. arabica (GCA_003713225.1), C.eugenioides(GCA_00371320 5.1), and C.canephora(GCA_900059795.1).Homology between proteins was inferred on the basis of reciprocal blast results. Data analysis and graphs were performed using R.

