Structural and functional analysis of genes with potential involvement in resistance to coffee leaf rust: a functional marker based approach

Geleta Dugassa Barka[1], Eveline Teixeira Caixeta[1,2,*], Sávio Siqueira Ferreira[1], Laércio Zambolim[3]

[1]Universidade Federal de Viçosa (UFV), Laboratório de Biotecnologia do Cafeeiro (BIOCAFÉ), BIOAGRO, 36570-000, Viçosa, MG, Brazil
[2]Empresa Brasileira de Pesquisa Agropecuária, Embrapa Café, 70770-901, Brasília, DF, Brazil
[3]Universidade Federal de Viçosa (UFV), Departamento de Fitopatologia, 36570-000, Viçosa, MG, Brazil

Abstract

Physiology based differentiation of S_H genes and *Hemileia vastatrix* races is the principal method being employed in characterizing coffee leaf rust resistance. Though nine major rust resistance genes (S_H1-9) had been proposed based on gene-for-gene theory, none of them were yet molecularly characterized. Consequently, it was indicated that the absence of characteristic candidate rust resistance genes remains one of the bottleneck problems in coffee breeding. To that purpose, we screened a BAC library with resistance gene analogs (RGAs), characterized and explored for any S_H related candidate genes. Here we report the identification and characterization of a gene (gene 11) which shares conserved sequence with other S_H genes and display a characterstic polymorphic allele conferring different resistance phenotypes.. Further comparative analysis of two RGAs belonging to the CC-NBS-LRR gene family revealed an intense diversifying selection while high interaspecies variability was evident between the two genes in related species than in coffee. For the first time, our study unveiled a novel insight into the molecular nature of S_H genes, thereby opening up a new avenue for coffee rust resistance molecular breeding.

Recent Publications:

Andre Freire Cruz, **Geleta Dugassa Barka**, Justine Sylla, Annette Reineke (2018). **Biocontrol of strawberry fruit infected by *Botrytis cinerea*: Effects on the microbial communities on fruit assessed by next-generation sequencing.** *J Phytopath.* DOI: 10.1111/jph.12700

Geleta Dugassa Barka, Eveline Teixeira Caixeta, Robson Ferreira de Almeida, Samuel Mazzinghy Alvarenga, Laércio Zambolim (2017). **Differential expression of molecular rust resistance components have distinctive profiles in *Coffea arabica* - *Hemileia vastatrix* interactions.** *Eur J Plant Pathol*. doi:10.1007/s10658-017-1202-0

Geleta Dugassa and Tileye Feyissa (2011). ***In vitro* production of virus free sweet potato [*Ipoma batatas* (L.) Lam] by meristem culture and thermotherapy.** *SINET*: *Ethiop. J. Sci*., **34** (1): 17-28



Dr. Geleta Dugassa Barka has his expertise in plant molecular genetics applied to crop improvement in disease resistance. He has many years of experiences in plant micropropagation by tissue culture aimed at disease cleaning and rescuing of endangered tree species. His current research area focuses on molecular profiling of resistance components induced during plant-microbe interactions for in-depth understanding of diseases resistance development mechanisms at molecular level.

Email: turadugassa@yahoo.com

Contact number: +251975359969