

Next-Generation proteomics suggests a higher antioxidative tolerance to drought in *Coffea arabica* than in *Coffea canephora* genotypes

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Introduction

Drought is a major threat to coffee, compromising the quality and quantity of its production. Understanding the role of proteins in the plant response to drought is crucial to unveil the acclimation mechanisms and to contribute to assist breeding programs to obtain tolerant cultivars.

Materials/Methods

A label-free proteomic approach was used to deepen the knowledge regarding the underlying mechanisms by which two cropped *Coffea* sp. genotypes (*C. canephora* cv. Conilon Clone 153, CL153; *C. arabica* L. cv. Icatu Vermelho) respond to moderate (MWD) and severe (SWD) water deficits, as compared with well-watered plants (WW) [1].

Conclusion/Perspectives

Drought triggered a similar number of DAPs in both genotypes, but with the enrollment of different proteins in each genotype. Results showed that the impact of MWD was almost absent in the proteome, in agreement with the physiological tolerance previously reported at this drought level for CL153 and Icatu. However, the response to drought was dependent on the severity of the applied stress, with SWD having a much greater impact than MWD. An extensive proteomic response was found under SWD, with *C. arabica* having a greater potential for acclimation/resilience than *C. canephora* (as regards these genotypes), associated with antioxidant defenses.

References: [1] Marques I. et al. Next-Generation Proteomics Reveals a Greater Antioxidative Response to Drought in *Coffea arabica* Than in *Coffea canephora*. *Agronomy*. 2022; 12(1):148. <https://doi.org/10.3390/agronomy12010148>

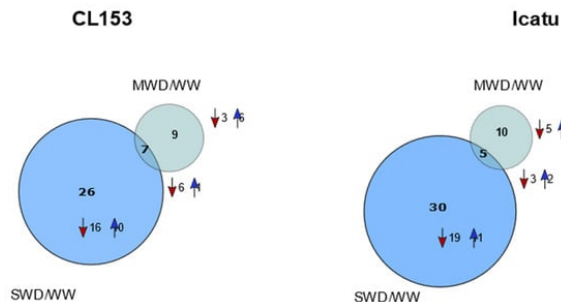


Figure 1: Proportional Venn diagrams showing the patterns of significant differentially abundant proteins (DAPs) found between moderate water deficit (MWD) and well-watered (WW) plants (MWD/WW) or between severe water deficit (SWD) and WW plants (SWD/WW) in *Coffea canephora* cv. Conilon Clone 153 (CL153) (left) and *C. arabica* cv. Icatu (right) genotypes. Arrows indicate the number of DAPs with decreased (red) or increased abundance (blue).

Results/Discussion

Proteomic changes clearly depend on the drought severity level, with greater numbers under SWD, and with an enrolment of different proteins, functions, and pathways than under MWD. SWD triplicated the number of DAPs (26 in CL153; 30 in Icatu), being the majority down-regulated (Figure 1).

The two genotypes displayed stress-responsive proteins under SWD, but, notably, only *C. arabica* showed a higher abundance of proteins involved in antioxidant detoxification activities.