

## COMPARATIVE PROTEOMIC ANALYSIS OF DROUGHT STRESS RESPONSE IN *Coffea*

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Water deficit is an important environmental factor that decreases the productivity of coffee in Brazil and several other producing countries. Knowledge on coffee drought tolerance at the molecular, biochemical and genetic levels may permit to design strategies for the development of tolerant cultivars. To study drought stress response in *Coffea*, a proteomic research network (PROTEOPAR - Paraná Proteome Program) constituted of eight laboratories was established. Four *Coffea* genotypes with differential physiological response to drought were used: *C. canephora* (Clone 14, drought-tolerant and Clone 109A, drought-sensitive) and *C. arabica* (BA10, drought-tolerant and Geisha, drought-sensitive). Proteins were extracted from leaves and roots of eighteen-months greenhouse grown plants using a modified SDS-Phenol method. The treatments were: unstressed, submitted to a severe water deficit (-4.0 MPa water pressure potential) and recovered (36 hours after water stress). The protein extracts were distributed to the laboratories of the PROTEOPAR for comparative 2D analyses to identify protein spots differently expressed. Peptide mass fingerprint (PMF) was used for the identification of these proteins using MALDI-TOF mass spectrometry (MS) of tryptic peptides and comparison with EST-based database of coffee.

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