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Transcriptomic effects of drought and the positive effect of elevated CO_2 in promoting tolerance in two *Coffea* sp. genotypes

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Introduction

Drought is a major constraint to plant growth and productivity worldwide and will aggravate with predicted climate changes. We hypothesized that elevated air [CO_2] (eCO_2) interacts at the transcriptomic level to promote metabolic performance, and acclimation mechanisms.

Materials/Methods

The impact of drought at the transcriptomic level was assessed on the leaves of two cropped *Coffea* sp. genotypes (*C. canephora* cv. Conilon Clone 153, CL153; *C. arabica* L. cv. Icatu Vermelho), which were grown under ambient (aCO_2; 380 ppm) or elevated (eCO_2: 700 ppm) air [CO_2], and well-watered (WW), and moderate (MWD) or severe (SWD) water deficit [1].

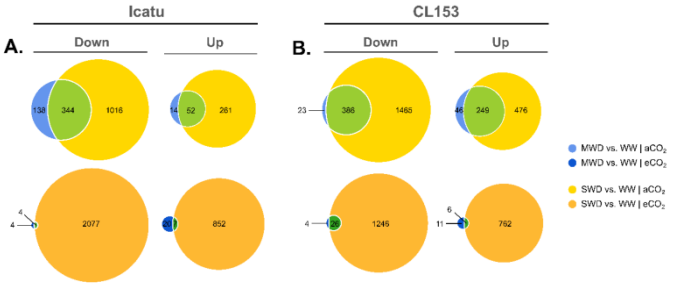

Figure 1: *Patterns of differentially expressed genes (DEGs) at MWD or SWD in comparison with WW in (A) Icatu and (B) CL153 plants grown under either aCO_2 (lighter colors) or eCO_2 (darker colors), at 25/20 ºC (day/night). DEGs specifically found under MWD (Blue) or SWD (Yellow), or expressed by both water conditions (Green).*

Results/Discussion

Expression levels were barely affected by MWD, while the SWD condition led to a down-regulation of most differentially expressed genes (Figure 1). eCO_2 attenuated the drought impact in the transcripts of both genotypes, mostly in Icatu.

Under MWD and aCO_2, DEGs were mostly down-regulated in the two genotypes, but they were substantially reduced under eCO_2. The positive effect of eCO_2 was even more relevant under SWD in Icatu plants, which showed an increase in up-regulated DEGs.

Conclusion/Perspectives

Icatu and CL153 plants showed different leaf transcriptomic mechanisms in response to drought, with minor effects of MWD and the positive action of eCO_2. However, the photosynthetic pathway was affected, namely under SWD and eCO_2, contrary to previous physiological and biochemical studies. Results suggest the existence of a complex post-transcriptional regulatory mechanism in *Coffea*, explaining some apparent discrepancies between transcriptomic and physiological (and proteomic) data in these genotypes, thus highlighting the need for integrated studies to a full understanding of plant responses to drought and/or eCO_2.

References: *[1] Marques I. et al. Overexpression of Water-Responsive Genes Promoted by Elevated CO_2 Reduces ROS and Enhances Drought Tolerance in Coffea Species. International Journal of Molecular Sciences. 2023; 24(4): 3210. https://doi.org/10.3390/ijms24043210*