

## Coffea nutriome: minding the gap among genomics, biotechnology and fertilization practices

Domingues, DS<sup>1</sup>; Meda, AR<sup>1</sup>; Santos, TB<sup>1</sup>; Vespero, EB<sup>1</sup>; Sitta, RB<sup>1</sup>; Pereira, LFP<sup>1,2</sup>; Vieira, LGE<sup>1</sup>

<sup>1</sup> Laboratório de Biotecnologia Vegetal, Instituto Agrônomo do Paraná

<sup>2</sup> Embrapa Café

**Keywords:** coffee, genomics, plant nutrition, nitrogen, boron

Since the Green Revolution, productivity in agriculture has largely increased by improving management practices, including fertilization. Due to its fundamental importance in agriculture, fertilizers consumption is growing in a much faster pace than food production, with great impact in environment and in agricultural costs. This impact is clearly observed in coffee production, with Brazil as the world's largest producer and exporter, by the fact that fertilizers represent a great share in the total production cost and coffee breeding programs are not focused in plant nutrient efficiency. In order to reduce management costs and environmental impact, genotypic variation in mineral nutrient requirements must now be considered in *Coffea* breeding. In this context, this work presents the initial steps to understand *Coffea* nutriome based in two approaches: evaluation of *Coffea* genotypes from IAPAR germplasm collection for the accumulation of mineral nutrients in leaves and fruits, as well as the characterization of candidate genes involved in mineral nutrient uptake and transport, with a focus in nitrogen and boron, two important macro and micronutrient for coffee production. The initial evaluation of fifteen genotypes from IAPAR germplasm identified *C. arabica* varieties with differential boron accumulation in leaves, what was strongly correlated with plant vigour. We also identified Expressed Sequence Tags of *C. arabica* and *C. canephora* related to genes involved in nitrogen and boron uptake and transport. *In silico* analysis displayed different expression patterns among these transporters in *Coffea*, depending on the tissue and growth conditions. Other experiments are in progress to understand gene-phenotype association. Taken together, these data will provide the opportunity to help *Coffea* breeding programs in three ways: 1) identification of genotypes more efficient in nitrogen and boron utilization; 2) characterization of molecular targets for genetic engineering in *Coffea*; 3) understand molecular mechanisms involved in nutrient transport and utilization in coffee plants, providing biotechnological tools to support a better management of fertilization practices in this perennial crop. Financial support: Fundação Araucária, CAPES, CNPq and CBP&D/Café.