

PB229

In Silico Description of *Multi Drug and Toxic Compound Extrusion* (MATE) Gene Family in *Coffea canephora*.

- ♣ Pinto, Renan T*, Cardoso, Thiago B*, Andrade, Alan C**, Paiva, Luciano V.*
- *Federal University of Lavras, Lavras, MG, Brazil, **EMBRAPA CAFÉ.

Rationale

In world parameters, coffee is an important commodity, regarding its to economical, medicinal and social relevance. *C. canephora* is beyond the cultivated species related to beverage production and is one parental of the hybrid *Coffea arabica*, which retains the majority of production. For the reasons of genetic improvement, it is important to identify and comprehend key genes on plant metabolic processes and one of the gene families widely studied for this purpose is the *MATE* family, which is composed by membrane transporter proteins and remains unexplored for *Coffea*.

Methods

Forty two members of MATE family from different species, with several described functions were utilized as query to BLASTp algorithm analysis against a proteome database of *C. canephora*. The output redundancies were excluded and the sequences were checked against a RNA-seq database aiming to assess its predictions. From that, the protein sequences of known MATE members and putative *C. canephora* MATE members were aligned by ClustalW algorithm and the phylogenetic relations were estimated by with MEGA 6.0, using the Neighbor-joining method, with substitution mode of p-distance and bootstrap of 10,000 replicates.

Results

Fifty five putative MATE family members were identified on *C. canephora* proteome. The phylogenetic tree of the proteins can be divided in 11 groups with sequences of known MATEs sharing relevant similarity with *C. canephora* putative MATEs. Some of the groups have strong relation to protein functions, like vacuolar alkaloid accumulation, flavonoid transport and citrate exudation for aluminium tolerance, all of them with *C. canephora* putative MATE members.

Conclusions & Perspectives

Candidate genes that were identified are related to several metabolic processes involved on *Coffea* genetic improvement and can be characterized for the application on breeding programs.

References

- 1. TAKANASHI, K.; SHITAN, N.; YAZAKI, K. The multidrug and toxic compound extrusion (MATE) family in plants. **Plant Biotechnology**, v. 31, n. 5, p. 417-430, 2014.
- 2. STEPHEN F. ALTSCHUL, THOMAS L. MADDEN, ALEJANDRO A. SCHÄFFER, JINGHUI ZHANG, ZHENG ZHANG, WEBB MILLER, AND DAVID J. LIPMAN. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. **Nucleic Acids Research**, v. 25, p.3389-3402, 1997.