



Comparative proteomic analysis between early developmental stages of the *Coffea arabica* fruits

G.B. Bandil¹, R.M. Etto², C.W. Galvão², H.J.O. Ramos³, E.M. Souza⁴, F.O. Pedrosa⁴, D.F.S. Chaves⁴, L.F. Huergo⁴ and R.A. Ayub¹

¹Laboratório de Biotecnologia Vegetal,
Departamento de Fitotecnia e Fitossanidade,
Universidade Estadual de Ponta Grossa, Ponta Grossa, PR, Brasil

²Laboratório de Biologia Molecular Microbiana,
Departamento de Biologia Estrutural, Molecular e Genética,
Universidade Estadual de Ponta Grossa, Ponta Grossa, PR, Brasil

³Laboratório de Biologia Molecular de Plantas - Bioagro,
Departamento de Bioquímica e Biologia Molecular,
Universidade Federal de Viçosa, Viçosa, MG, Brasil

⁴Laboratório de Fixação Biológica de Nitrogênio,
Departamento de Bioquímica e Biologia Molecular,
Universidade Federal do Paraná, Curitiba, PR, Brasil

Corresponding author: R.A. Ayub
E-mail: rayub@uepg.br

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ABSTRACT. Coffee is one of the most valuable agricultural commodities. There is much agronomic research on coffee, but molecular knowledge of its fruit development and ripening is limited. This study reports a comparative proteomic investigation of immature coffee fruits in two early developmental stages: stage 1, cell division and elongation of the perisperm; and stage 2, early growth of the endosperm progressively replacing the perisperm. Proteins were extracted using a modified SDS-phenol method and two-dimensional electrophoresis gels stained with

Coomassie blue revealed about 300 well-resolved polypeptide spots in the pH range of 3 to 10. The differentially expressed polypeptides spots were excised, trypsin-digested, and analyzed by MALDI-TOF mass spectrometry. Peptide MS data were searched against the coffee EST database. Most of the identified protein spots are involved in the glycolytic pathway and energy reserve, and are more highly expressed at stage 2.

Key words: Coffee; Growth; Immature fruit; Proteome