

Field-Based Proteomic Insights into the Environmental Acclimation of Arabica Coffee Cultivars in the Cerrado Mineiro Region, Brazil

Jéfyne Campos Carréra¹, Leonor Guerra-Guimarães^{2*}, Mário Lúcio Vilela Resende¹, Céline Leclercq³, Jenny Renault³, Paulo Henrique Sales Guimarães¹, John Charles D'Auria⁴, Carla Pinheiro^{5,6}, Luana de Jesus Sartori¹, Vânia Aparecida Silva⁷, Margarete Lordelo Volpato⁷, Christiano de Sousa Machado de Matos⁷, Gladyston Rodrigues Carvalho⁷, Fabio Akira Mori¹

*leonorguimaraes@edu.ulisboa.pt

¹UFPA - Universidade Federal de Lavras, Lavras, Minas Gerais, Brasil; ²CIFC - Centro de Investigação das Ferrugens do Cafeeiro, LEAF - Linking Landscape, Environment, Agriculture and Food Research Centre and TERRA Associated Laboratory, Instituto Superior de Agronomia, Universidade de Lisboa, Lisboa, Portugal; ³Luxembourg Institute of Science and Technology, Hautharange, Luxembourg; ⁴Research Group Metabolic Diversity, Department of Molecular Genetics, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK Gatersleben), Germany; ⁵UCIBIO Applied Molecular Biosciences Unit, Department of Life Sciences, NOVA School of Science and Technology, Universidade NOVA de Lisboa, Caparica, Portugal; ⁶Associate Laboratory i4HB Institute for Health and Bioeconomy, NOVA School of Science and Technology, Universidade NOVA de Lisboa, Caparica, Portugal; ⁷EPAMIG - Empresa de Pesquisa Agropecuária de Minas Gerais, Lavras, Minas Gerais, Brasil.

AIM

The Cerrado Mineiro is one of the main coffee-growing regions in Minas Gerais, Brazil's leading producer of *Coffea arabica*. This study aimed to characterize the proteome of five *C. arabica* cultivars grown at two experimental sites in Cerrado Mineiro - Patrocínio (PT) and Monte Carmelo (MC) - which differ in their water management practices (rainfed vs. irrigated) (Fig 1).

RESULTS

Among the 422 proteins identified in the studied *C. arabica* cultivars, 116 showed differential expression between the two experimental sites, MC and PT (data not shown). Paraíso 2, Catuaí, and Catiguá MG2 exhibited more differentially expressed proteins than Sarchimor and Catiguá MG3, possibly reflecting that the latter were less affected by environmental conditions (Fig. 2). Functional annotation of these proteins revealed changes in several biological processes, particularly photosynthesis, protein metabolism, redox and stress (Fig. 3). Signal peptide analysis showed that, irrespective of the cultivar, most proteins with defined localization were predicted to be in the chloroplasts or the extracellular space (Fig. 4)

APPROACH

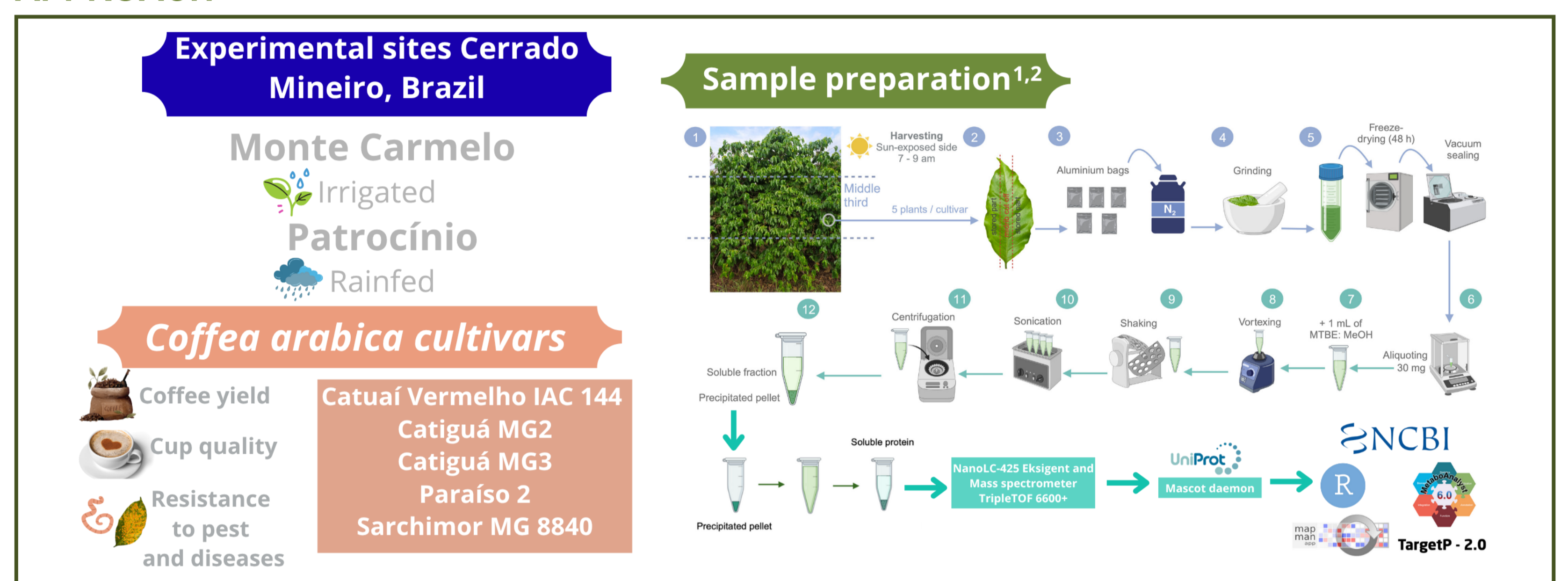


Fig. 1. Experimental design

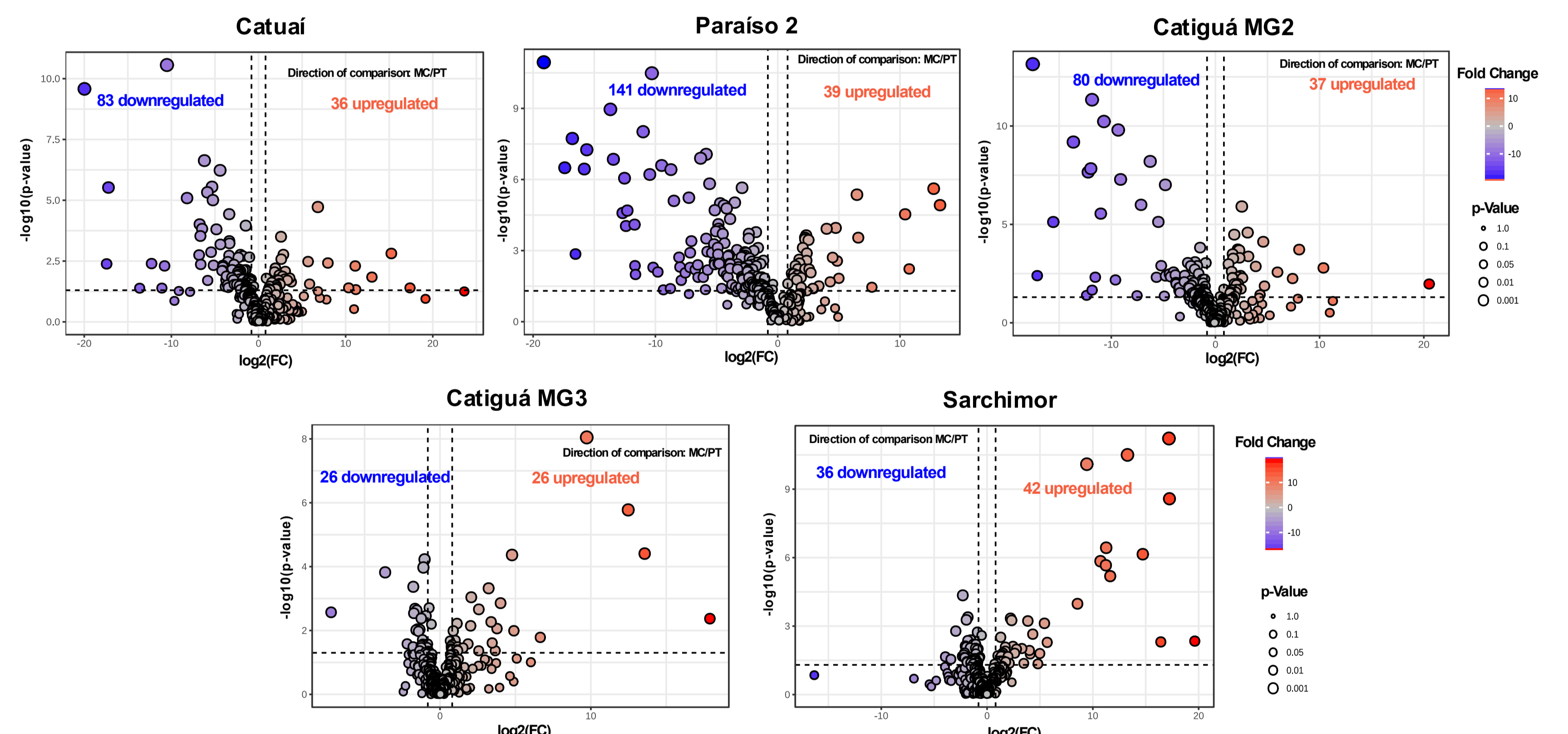


Fig. 2. Volcano plot analysis of the differentially expressed proteins, when comparing Monte Carmelo (MC and Patrocínio (PT)

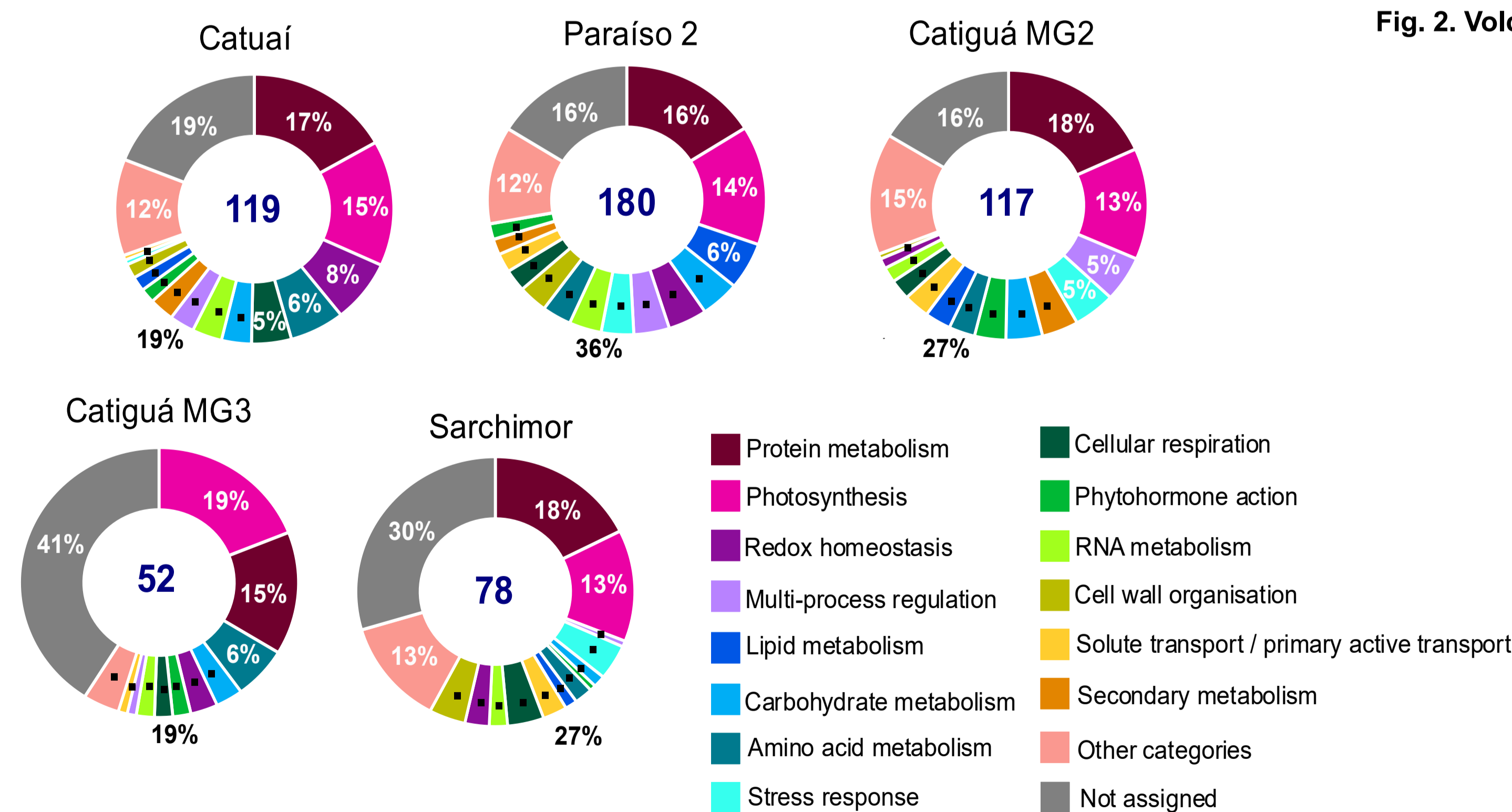


Fig. 3. Biological process annotation of differentially expressed proteins of *C. arabica* cultivars, based on the MapMan "Bin" and GO ontology. (AP) annotated proteins.

CONCLUSIONS & PERSPECTIVES

This first field-based proteomic profiling of *C. arabica* in the Cerrado Mineiro reveals cultivar-specific responses to environmental conditions. Key pathways in photosynthesis and protein metabolism, with most proteins in chloroplasts and extracellular space, highlight mechanisms of adaptation and resilience. These insights can guide targeted breeding and management strategies to improve coffee performance under climate variability.

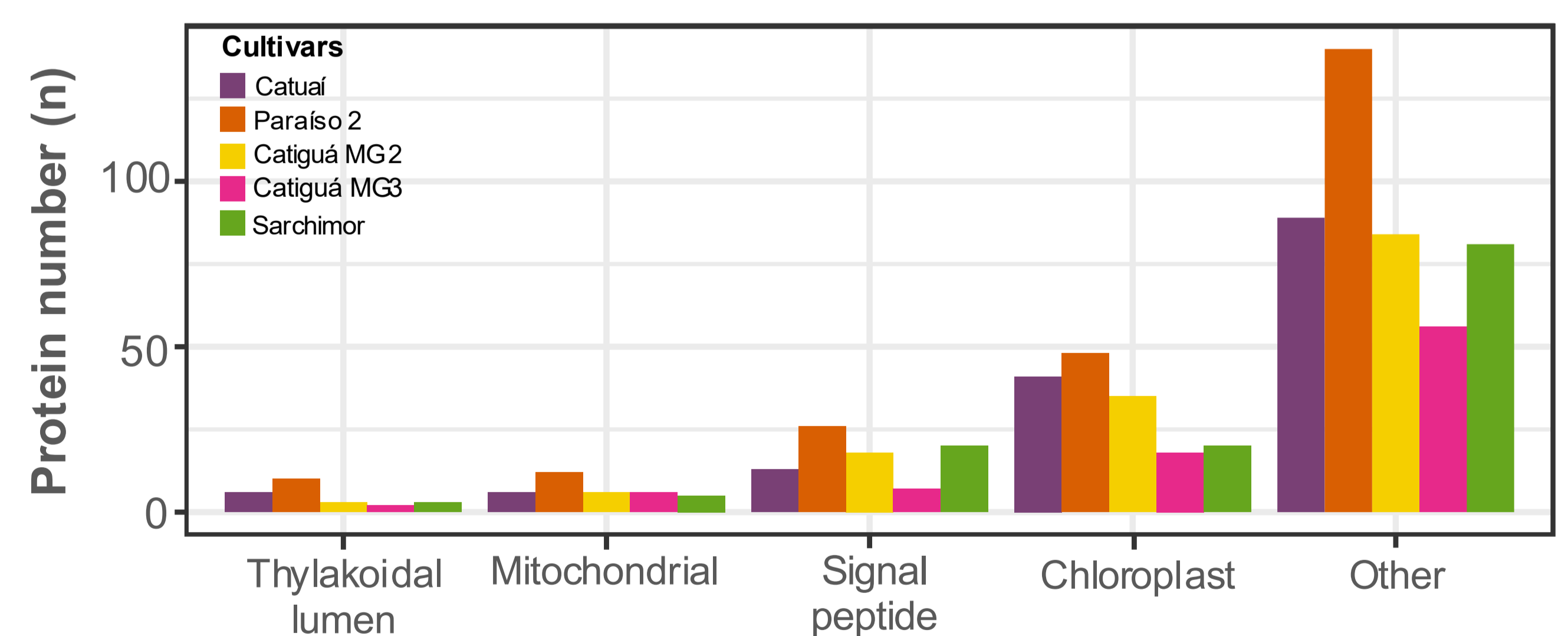


Fig. 4. Subcellular localization of the differentially expressed proteins of *C. arabica* cultivars, based on TargetP 2.0.

ACKNOWLEDGEMENTS

Financial support was provided by Brazilian agencies: CNPq, INCT Café/CNPq, CAPES, FAPEMIG and Consórcios Pesquisa Café - CP&D Café. European Union: Horizon2020 and EPPN2020 (Grant Agreement 731013). FCT, Portuguese funds: UIDP/04378/2020 (DOI: 10.54499/UIDP/04378/2020) and UIDB/04378/2020 (DOI: 10.54499/UIDB/04378/2020) of UCIBIO and i4HB LA/P/0140/2020 (DOI: 10.54499/LA/P/0140/2020); LEAF- UIDB/04129/2020 (DOI: 10.54499/UIDB/04129/2020) and UIDP/04129/2020 (DOI: 10.54499/UIDP/04129/2020); TERRA LA/P/0092/2020 (DOI:10.54499/LA/P/0092/2020).

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