Differential Proteomic Analysis of *Araucaria angustifolia* Seed Germination

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Germination is a crucial event during plant development. It represents an important transition between a quiescent dry seed state to a highly active metabolic state. Currently, different gene expression tools have been used to understand metabolic changes and to unveil complex biological processes. In the present work, a differential proteomic analysis was carried between mature (0 days after sowing) and germinated (8 days after sowing) *Araucaria angustifolia* embryos through two-dimensional electrophoresis (2-DE) and mass spectrometry. No significant differences were detected between mature and germinated spot distribution patterns. Alignment of the 2-DE gels indicated the presence of 29 stage-specific spots. Aiming the identification of proteins involved in the germination, these spot were *in gel* digested and injected into a nanoHPLC coupled to a LTQ mass spectrometer. Stringent (MASCOT) and sequence similarity (MS BLAST) searches resulted in the identification of multiple proteins involved in different cellular processes. Enzymes involved in the oxidative metabolism, such as glyoxalase I, ascorbate peroxidase and glutathione reductase, and hormonal signaling, such as the auxin-induced aldo/keto reductase, were specifically detected in mature embryos; while RuBisCo subunits were identified only in germinated embryos, indicating a late development of the photosynthetic apparatus. These results suggest a highly active metabolism during *A. angustifolia* seed maturation and corroborates with the recalcitrant behavior in this species..

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