PROTEOME DYNAMICS OF EARLY SKOTOMORPHOGENESIS DURING REMOTE GERMINATION IN CARNAÚBA (Copernicia prunifera)

Francisco Augusto Santos de Azevedo Carioca[1], Sheheryar[1], Ítalo Antônio Cotta Coutinho[1], Francisco de Assis de Paiva Campos[1], Fábio César Sousa Nogueira[2], Gilberto Barbosa Domont[2], Yara Martins da Silva[2]

[1.] UFC, Universidade Federal do Ceará, Av. da Universidade, 2853 - Benfica, Fortaleza - CE, CEP 60020-181;
[2.] UFRJ, Universidade Federal do Rio de Janeiro, Rua Antônio Barros de Castro, 119 - Cidade Universitária, Rio de Janeiro - RJ, Brasil - CEP 21941-853;

While germinating under the soil, some dicots and monocots seeds attains a developmental program called skotomorphogenesis. In dicots, the seedling’s hypocotyl takes the shape of an embryonic stem and, and as it grows speedily toward the soil surface, it forms an apical hook that protect the fragile cotyledons and the apical meristem from physical damage. After reaching the soil surface, a photomorphogenic developmental program ensues, which is marked by the development of chloroplasts, and leaf development. In monocots such as maize, rice and wheat, the apical hook is substituted by a sheath formed by the coleoptile that has a role equivalent to that of the apical hook in dicots.

Skotomorphogenesis and photomorphogenesis are controlled by a complex network of internal (HY5 genes, hormones, COP/DET/FUS genes, photoreceptors, PIF proteins) and external factors (light, temperature, soil, gravity). In this context, the dicot *Arabidopsis thaliana*, and the monocot *Oryza sativa* (rice) are the two organisms most extensively studied. The understanding of the role of PIF proteins as negative regulators of light responses by inhibiting photomorphogenesis and maintaining the skotomorphogenesis condition under dark has evolved substantially, but the understanding of the proteome dynamics of skotomorphogenesis, photomorphogenesis and the transition between these two states has not been investigated and remains to be established.

Here we set out to establish the proteome changes associated the development of carnauba (*Copernicia prunifera*) seedlings under dark conditions. For that, we separate the embryo into its two components: the haustorium and the cotyledonary petiole (CP) where the embryo axis is located. We proceeded to establish the quantitative proteome of four developmental stages of these tissues isolated from quiescent seeds and from seeds germinated for two, five and ten days. A total of 5205 and 6028 proteins were identified in haustorium and CP, respectively. Of these, 3920 are shared between the two tissues. These proteomes are populated by a vast array of proteins known to maintain the skotomorphogenic state under dark conditions (e.g., Sucrose nonfermenting protein kinase and COP1-interacting protein 7), and a complete set of proteins from pathways involved in cellular respiration and biosynthesis of phenylpropanoids, particularly lignin. A quantitative analysis of the MS data revealed that a total of 583 proteins from the haustorium and 383 proteins from the CP were differentially abundant, with 251 proteins being shared by both datasets. These results reveal that the haustorium is involved in the digestion of food reserves present in the haustorium itself and in the endosperm, functioning as a conduit of nitrogen and carbon sources for the growing embryo axis. Among the differentially abundant protein from the CP we find the presence of proteins from metabolic pathways from the cellular metabolism, and proteins involved in the hydrolysis of food reserves such as starch and proteins, indicating that the CP and not only the endosperm and the haustorium are source of food reserves for the embryo axis.

Agradecimentos: Financial support from CAPES and CNPq are gratefully acknowledged.