

(P18)

Wild Mexican lupins: proteomic analysis of the seeds of four species

Boschin G¹, Bermudez Torres K², Sirtori E¹, Arnoldi A¹

¹Department of Pharmaceutical Sciences, University of Milan, Milan, Italy. ²Centro de Desarrollo de Productos Bióticos-IPN Departamento de Biotecnología Apdo, Yautepec, Morelos, México.

Corresponding Author's e-mail: anna.arnoldi@unimi.it

State of art and aim: *Lupinus* is a wide genus, comprising between 200 and 500 species, most of them represented in America. Mexico is a secondary distribution center with more than 100 species growing along the highlands (Bermudez Torres *et al.*, 2009). Due to morphological similarities, the taxonomy of wild *Lupinus* species is still incomplete. It is therefore useful to collect morphological, chemical, and molecular data for a correct differentiation of these plants. The aim of this work is the characterization of seed proteins of four wild Mexican *Lupinus* species.

Results and discussion: The seeds of four species were collected: *Lupinus aschenbornii* Schauer, *Lupinus campestris* Cham and Schlecht, *Lupinus bintonii* C.P. Smith, and *Lupinus montanus* Kunth. Plants grown in the Mexican National Park Iztaccihuatl-Popocatepetl at different altitudes.

Total protein extracts (TPEs) were obtained from seeds and single proteins were purified from TPEs by chromatographic procedures (Brambilla *et al.*, 2009). Both TPEs and single proteins were analyzed by electrophoretic techniques, either SDS-PAGE or 2D-electrophoresis.

With these techniques, a detailed characterization of the major seed proteins of *L. aschenbornii*, *L. campestris*, *L. bintonii*, and *L. montanus*, were obtained. Experimental data were compared with those of domesticated species (*L. albus* and *L. angustifolius*) whose proteome has been already described in literature (Wait *et al.*, 2005). SDS-PAGE analyses revealed that mature proteins, i.e. α -, β -, γ - and δ -conglutins, are composed of numerous polypeptides showing a large heterogeneity both in terms of MW and pI values. Furthermore, these proteins undergo a similar fate, in terms of proteolytic processing and post-translational modifications such as phosphorylation and glycosylation.

References:

- Bermudez Torres K *et al.* (2009) *BioControl*, 54, 459
Brambilla F *et al.* (2009) *Proteomics*, 9, 272
Wait R *et al.* (2005) *J. Agric Food Chem*, 53, 4599

Tags: 2D-electrophoresis, seed protein purification, wild Mexican *Lupinus*