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Extensive proteome characterization of *L. mutabilis* using a combined approach based on 2D-electrophoresis and mass spectrometry

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State of art and aim. In legumes, seed storage proteins are important for developing seedling and are a relevant source of nutrients for humans and animals. Being a source of low-cost proteins with high nutritional value, lupin is considered more attractive than other protein-rich plants (Holden *et al.*, 2005). Current breeding efforts focus mostly on *Lupinus albus*, L. (white lupin), *L. angustifolius*, L. (narrow-leaved lupin) and *L. luteus*, L. (yellow lupin), but also *L. mutabilis*, L. (pearl lupin) was recently included. Cultivated since more than 2000 years in the South American Andes region, Andean lupin (*L. mutabilis* Sweet) is now regarded as a potential crop for central European and Mediterranean climates. Its seeds possess the highest protein levels among all domesticated lupin species. Indeed, the value of this species is mainly due to the high protein content (40-50%) of its seeds (Santos *et al.*, 1997). The seed protein of *L. mutabilis* is also richer in lysine (Lys) and cysteine (Cys) in comparison to that of the Old World *Lupinus* species (Salmanowicz, 1999). Nevertheless, very little is known concerning the protein structure and proteins composition of *L. mutabilis* seeds, when compared with the seeds of *L. albus*, and *L. angustifolius*. In order to obtain extensive and novel information, a proteome analysis has been conducted in our laboratory using a combined approach based on 2D-electrophoresis and mass spectrometry.

Results and discussion: A species-specific proteome profile of *L. mutabilis* is reported, after a comparative study of the seed protein composition of *L. mutabilis* and *L. angustifolius* through bidimensional electrophoresis. In details, two-dimensional mapping has revealed substantial difference in proteome expression and has shown extensive microheterogeneity of *L. mutabilis*. The proteomic analysis, performed using HPLC-Chip-MS/MS, has shown considerable differences in the structure and composition of α and β conglutins from *L. mutabilis*, when compared with *L. angustifolius* conglutins. Moreover, an overexpression of small subunit of γ -conglutin seems to characterize *L. mutabilis* seeds. From this preliminary screening, new and interesting results has emerged and have helped to improve understanding on the complexity of the protein families present in lupin seeds.

References:

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