**Proteomic approaches for engineering the protein composition of lupin grain**

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Narrow-leafed lupin (NLL, *Lupinus angustifolius*) is the principal pulse crop grown in Western Australia. Due to its unique adoption to nutrient-poor soils and nitrogen fixing ability, it serves as a key rotation crop for sustainable farming systems. Currently, NLL seeds are mainly used as animal feed, but there is a growing interest in them as a human food, owing to their excellent nutritive value determined by high protein and fibre content.

The previous proteomics evaluation of NLL genotypes revealed distinct differences in the protein composition of the domesticated NLL cultivars compared to wild accessions. It also detected lower levels of allergenic seed storage proteins in a subset of Australian NLL cultivars, which instead contained higher levels of bioactive proteins. The observed diversity of proteome provides opportunities to improve the protein composition of lupin grain as a human food [1].

In this study proteome measurements were implemented to examine the protein profiles of a larger number of domesticated cultivars, aiming to understand how they related to the available pedigree information of these varieties. Furthermore, these assays were employed to study the changes in the protein composition of lupin grain caused by the environment. These enabled the identification of the breeding line which introduced divergence in the protein profiles of Australian NLL cultivars and revealed environmental influence in the protein pattens of the studied genotypes. The knowledge established from this study generates prospects to enhance the protein quality of lupin grain and encourage its utilisation as a complementary plant-based protein source.

***References:***

[1] Tahmasian A. et al, 2022, Front Nutr, 9, p. 842168