

Genetic and phenotypic characterization of global *Lupinus albus* genetic resources for the development of a CORE collection

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ABSTRACT:

Lupinus albus is a food grain legume recognized for its high levels of seed protein (30–40%) and oil (6–13%), and its adaptability to different climatic and soil conditions. To develop the next generation of *L. albus* cultivars, we need access to well-characterized, genetically and phenotypically diverse germplasm. Here we evaluated more than 2000 *L. albus* accessions with passport data based on 35 agro-morphological traits to develop Intelligent CORE Collections. The reference CORE (R-CORE), representing global diversity, exemplified the genotypic variation of cultivars, breeding/research materials, landraces and wild relatives. A subset of 300 R-CORE accessions was selected as a training CORE (T-CORE), representing the diversity in the entire collection. We divided the *L. albus* R-CORE into four phenotypic groups (A1, A2, A3 and B) based on principal component analysis, with groups A3 and B distinguished by pod shattering and seed ornamentation, respectively. The coefficient of additive genetic variation differed across morphological traits, phenotypic groups, geographic regions, and according to biological status. These CORE collections will facilitate agricultural research by identifying the genes responsible for desirable traits in crop improvement programs, and by shedding light on the use of orphan genetic resources for origin and domestication studies in *L. albus*. Understanding the variation in these genetic resources will allow us to develop sustainable tools and technologies that address global challenges such as providing healthy and sustainable diets for all, and contrasting the current climate change crisis.