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Legumes for a Sustainable World

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A protein quantity loci approach combined with a genome-wide association study revealed regulators of protein accumulation in legume seeds

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The seeds of grain legumes provide proteins (20-40% protein content depending on species) for human nutrition and animal feed. The nutritional and technological quality of legume seeds is mainly determined by the composition and functional properties of the seed protein fractions. By accounting for up to 70% of total proteins in mature seeds, the globulins are major determinants of seed quality. In pea, which is one of the grain legumes most cultivated in Europe, the variability in the abundance of globulin polypeptides across lines is significant, which might enable a wide range of food application. To provide knowledge about the molecular determinants underlying differences in seed protein composition, we have used the model legume species *M. truncatula* for which extensive genetics and genomics resources were available (Young and Bharti, 2012), along with comprehensive transcriptomics data related to seed development (Benedito et al., 2008; Thompson et al., 2009). A PQL approach identified the genomic regions controlling variations in seed protein composition, and a translational approach exploiting the resources developed for *M. truncatula* and pea provided a set of candidate genes underlying PQLs conserved between the two species. The candidate gene selection was then refined by genome-wide association studies (GWAS), which enabled the identification of nucleotide variations associated with variations in globulin synthesis and/or maturation.