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Inventons
les céréales
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USE OF TRANSLATIONAL GENOMICS TO IDENTIFY GENES IMPORTANT FOR PEA SEED DEVELOPMENT AND COMPOSITION

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We have been using genomics approaches with *Medicago truncatula* as a tool to identify key genes determining seed yield and composition in closely related legumes of agricultural importance including pea. By separating the developing seed tissues we have shown extensive compartmentalization of gene expression and metabolic activities at different stages of development (Gallardo et al, 2007). Putative regulatory genes specific for each seed tissue have been identified using a TF (Transcription Factor) qRT-PCR platform (Verdier et al., 2008), the Affymetrix Gene Chip (Benedito et al, 2008), and more recently, Nimblegen arrays (Buitink et al. submitted). By cluster analysis, putative target genes of selected TFs could also be identified. The genetic map positions of genes of interest have been compared with QTLs in *M. truncatula* for protein quantities and other seed phenotypes, and a number of the loci fell within QTL intervals. In several cases, similar QTLs have been mapped at syntenic positions in pea. Using this approach, putative roles were assigned to two genes, both specifically expressed in the developing endosperms of *M. truncatula* and pea. One encodes a DOF class transcription factor, whose mutant phenotype severely affects endosperm development (Noguero et al, 2015). The second gene encodes an endosperm-specific subtilase (SBT1.1), which affects final seed weight in both *M. truncatula* and pea (D'Erfurth et al, 2012). The analysis of further genes affecting seed composition is ongoing, using the same strategy.

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