An alfalfa bioinformatic database for future discovery of important genes in alfalfa.

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Genomic projects generate a lot of datas. It is imperative to get bioinformatic tools to manage these datas and extract important informations. We have built a searchable bioinformatic database that contains the sequence and description of 10 000 alfalfa cDNA, their homology with the GENBANK database and their expression level during cold acclimation. This database is the first step toward the identification of genes potentially involved in cold tolerance, protein quality and fiber digestibility in alfalfa.

Cold regulated genes : Our database contains the gene expression level for five cold acclimation treatments. The five most up-regulated genes (putatives description) are CAS 18, CAR (1 and 2), MsaciC, an homolog of the drought M. truncatula cDNA clone NF079A08DT and an homolog of a developing leaf M. truncatula cDNA clone NF097E04LF. The five most down-regulate genes are ADR6 / Sali3-2, Beta-amylase (1,4-alpha-D-glucan maltohydrolase), High molecular weight root vegetative storage protein precursor, Transcription factor homolog BTF3-like protein and UDP-glycose:flavonoid glycosyltransferase.

Genes related to the protein quality : Rapid degradation of alfalfa protein limits the efficiency of protein utilization in ruminant animals. The post-harvest proteolysis of alfalfa protein is done by alfalfa proteases. So, we searched in our database all kind of genes related to proteolysis. Some of them are the 26S protease regulatory subunit, an ubiquitin-specific protease , an aspartic protease, a serine protease and a trypsin inhibitor precursor.

Genes involved in fiber digestibility : Genes involved in lignin biosynthetic pathways affect fiber digestibility. We found in our database some important genes from this pathway : a Caffeoyl-CoA O-methyltransferase 1, a Cinnamoyl-CoA reductase, a Trans-cinnamate-4-monooxygenase, a Cinnamyl-alcohol dehydrogenase and a Laccase (diphenol oxidase).

Finally, our database could be use for other projects of interest. We found genes encoding for transcription factors, associated with disease resistance, biostress resistance and dormancy. Genomic projets require sound and good bioinformatic tools. These tools will help us to progress in our future endeavours in alfalfa research.