Construction of linkage map in alfalfa and assessment of colinearity with *Medicago truncatula*. Possible uses in QTL detection and gene mapping

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Alfalfa (*Medicago sativa*) is a major forage crop but the genetic structure (autotetraploidy) of this species makes difficult the construction of saturated genetic maps. The synteny of alfalfa with the model species *M. truncatula* is supposed to be high but needs to be demonstrated. To build a genetic map of alfalfa and to compare it to *M. truncatula* map, we used the available codominant microsatellite markers (SSRs), most of them being identified and mapped in the model legume *Medicago truncatula* from EST database. Mapping procedures in alfalfa were based on specific procedures for autotetraploids (1), using TetraploidMap software (ftp://ftp.bioss.sari.ac.uk/pub/cah/). The genetic map of alfalfa was obtained for a F1 mapping population composed of 168 individuals produced from the cross of 2 heterozygous parental plants. Based on 107 SSR loci, the map comprised 8 linkage groups and covered 709 cM (2). Compared to a saturated diploid alfalfa map (3), this map covers 94% of the genome and is considered as saturated. A fully tetrasomic inheritance of the markers was assessed, and the double reduction events seemed to be rare. Except for 2 out of 107 SSR markers, we found a similar order of markers on the chromosomes between the tetraploid alfalfa and *M. truncatula* genomes indicating a high level of colinearity between these two species, as found between diploid alfalfa and *M. truncatula* (4). This synteny justifies the use of knowledge on *M. truncatula* genetics and genomics for understanding alfalfa genetics. Indeed, QTL identification is now possible on the cultivated species, in which the range of variation used in breeding programs can be observed. Mapping of candidate genes is easier on the model species, because of its diploidy, the available EST database and the progress in genome sequencing, but is also feasible on alfalfa. Colocation between QTLs and candidate genes will be a major indication for a future use of molecular markers in breeding programs. Association studies will be needed to relate allelic variability of candidate genes to phenotypic variation. We are focussing on aerial morphogenesis, because it contributes to forage production and quality but also to the ability of the plants to compete and survive in dense canopies.

Literature cited

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