

Alfalfa Breeding with Implementation of Molecular Tools

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Bernadette Julier is Research Director at INRAE (www.inrae.fr), Grasslands and Forage Plants Research Unit (URP3F), in Lusignan, France. Since her PhD, she has been continuously working on legume genetics and mostly on alfalfa, a species now well recognized as the highest protein producer forage species while providing ecosystem services. Her main topic was first to evidence genetic variation for energy value and to combine it to forage production. She has been involved in projects on seed production and protein degradation too. Her research has then focused on the genetic bases of aerial morphogenesis, either in pure stand or in mixtures with forage grasses. More recently, she is investigating how molecular markers could assist alfalfa breeding and speed up the genetic progress. She has coordinated EUCLEG, an European project (H2020, 2017-2021) “Breeding forage and grain legumes to increase EU’s and China’s protein self-sufficiency” that aimed to use more genetic resources and develop molecular tools to be able to create improved legume varieties (www.eucleg.eu) and thus promote protein production. She is a member of the Permanent Technical Committee of Selection (CTPS), in the section “Forage and turf plants” since 1998, in charge of the variety registration in France.

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Genome-wide, high throughput, cost-effective molecular markers have been developed for less than a decade in alfalfa. Their use for breeding this autotetraploid, heterozygous species is not straightforward but highly promising. We propose to browse through their main uses with an emphasis on results from the European project EUCLEG (www.eucleg.eu) and to highlight the interest of using allele frequencies directly estimated on pools of individuals from a population. A first use is the description of genetic resources. With a large set of markers (>100.000), a continuum among the European – American accessions was evidenced but clearly separated from the Chinese accessions. A second domain is the use of markers to identify genes or locus associated to valuable traits and explaining a substantial part of the variation: QTL. Genome wide association studies on a highly diverse panel of alfalfa populations (varieties, landraces, breeding populations) revealed QTL for yield and quality traits such as protein and ADF contents, explaining up to 15% of the variation. Despite the great advantage of dealing with a high level of diversity, a drawback is that the detection of some QTL could be hampered by the genetic structure within the panel. Another possibility to seek QTL is reverse genetic with allele mining in candidate genes. We used this method to find potentially interesting alleles involved in plant growth or digestibility. A third use is genomic selection based on all available markers to predict the phenotype of an individual from its genotype with a calibration set up on a training population. Within a highly diverse panel and a training set of about 270 populations, we obtained predictive ability ranging from 0.50 to 0.66 for yield, protein and ADF contents measured at two locations for two years. These values are relatively high compared to other studies with less diversity and seem promising. The use of genomic selection within breeder plant material has to be demonstrated but the expected genetic gain per year is huge (more than six times compared to phenotypic selection) especially regarding the decrease of selection cycle duration. We conclude that these different uses of molecular markers could renew alfalfa breeding programs for any trait of current and future interest.