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QTL ANALYSES FOR NITROGEN USE AND GRAIN PROTEIN IN BREAD WHEAT

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The cost of nitrogen fertilization and growing environmental concerns tend to limit nitrogen application in a context of expanding world demand for cereal production and quality. Higher nitrogen use efficiency for grain yield, protein concentration and composition is then becoming an important objective for breeders. Phenotyping for these traits are however time and money consuming. Genetic progress may then depend on the development of accurate phenotyping methods and identification of molecular markers associated to chromosomal regions of interest.

To this purpose, different panels of bread wheats were used to assess the genetic diversity, the genetic progress and detect QTL. The first panel is composed of about 200 accessions representing the worldwide variability. It was both phenotyped for adaptation to N stress and for grain protein concentration and composition in multi-environment trials as a combination of different site x season and two nitrogen levels. Association genetics using about 1000 markers enable to detect regions associated to the N allocation to the different seed storage proteins (quantity of gliadin and glutenin) in different environments. One of the main result indicates that the genetic regions controlling the glutenin and gliadin compositions are mostly distinct from each other. The second panel that contains about 225 wheat elite varieties registered during the last 25 years was also experimented in multi-environment trials. Measurements involved grain yield, yield components and nitrogen contents at harvest. The genetic progress was assessed on genotypic additive value revealing significant progresses on grain yield, remobilization and nitrogen use efficiency. The nitrogen level x genotype interaction was significant, with a higher genetic progress for nitrogen use efficiency at low nitrogen attesting an improvement in yield stability. This phenotyping results were then used in a genome wide association study using more than 23k mapped SNP revealing several associated regions. The third panel that partly overlaps the second one was genotyped using a 420k Axiom array (TaBW420k) developed within the BreedWheat project. Genome wide association analysis is ongoing to identify genomic areas linked to nitrogen use efficiency. The comparison of regions identified in the different association studies will enable the identification of robust regions of interest. These results will be used to identify potential target regions for fine mapping and to develop informative markers to facilitate the selection for higher nitrogen use efficiency for grain yield and proteins.