

Sylvie COURSOL

P5: Water deficit responsive QTLs for cell wall degradability and composition in maize at silage stage

Laëtitia Virlovet¹, Fadi El Hage¹, Yves Griveau¹, Marie-Pierre Jacquemot¹, Emilie Gineau¹, Aurélie Baldy¹, Sylvain Legay¹, Christine Horlow¹, Valérie Combes², Cyril Bauland², Carine Palafre³, Matthieu Falque², Laurence Moreau², Valérie Méchin¹, Matthieu Reymond¹

¹ Institut Jean-Pierre Bourgin, INRA, AgroParisTech, CNRS, Université Paris-Saclay, 78000, Versailles, France

² Génétique Quantitative et Evolution - Le Moulon, INRA, Université Paris-Sud, CNRS, AgroParisTech, Université Paris-Saclay, 91190, Gif-Sur-Yvette, France

³ Unité Expérimentale du Maïs, INRA, 40390, Saint Martin de Hinx, France

The use of lignocellulosic biomass for animal feed or biorefinery requires the optimization of its degradability. Moreover, biomass crops need to be better adapted to the changing climate and in particular to periods of drought. Although the negative impact of water deficit on biomass yield has often been mentioned, its impact on biomass quality has only been recently reported in a few species. In the present study, we combined the mapping power of a maize recombinant inbred line population with robust near infrared spectroscopy predictive equations to track the response to water deficit of traits associated with biomass quality. The population was cultivated under two contrasted water regimes over three consecutive years in the south of France and harvested at silage stage. We showed that cell wall degradability and α -O-4-linked H lignin subunits were increased in response to water deficit, while lignin and p-coumaric acid contents were reduced. A mixed linear model was fitted to map quantitative trait loci (QTLs) for agronomical and cell wall-related traits. These QTLs were categorized as 'constitutive' (QTL with an effect whatever the irrigation condition) or 'responsive' (QTL involved in the response to water deficit) QTLs. Fifteen clusters of QTLs encompassed more than two third of the 213 constitutive QTLs and 13 clusters encompassed more than 60% of the 149 responsive QTLs. Interestingly, we showed that only half of the responsive QTLs co-localized with constitutive and yield QTLs, suggesting that specific genetic factors support biomass quality response to water deficit. Overall, our results demonstrate that water deficit favors cell wall degradability and that breeding of varieties that reconcile improved drought-tolerance and biomass degradability is possible.

This study was supported by LabEx Saclay Plant Sciences-SPS, Grants ANR-10-LABX- 0040-SPS and ANR-11-BTBR-0006 BIOMASS FOR THE FUTURE. The authors benefited from the IJPB "Plant Observatory" facilities.