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Exploring the genetic basis of cell wall traits upon contrasted water regimes in maize

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Cell wall digestibility and composition are the major targets for improving both feeding value and industrial valorizations (such as bioethanol) from lignocellulosic biomass. Biomass production should also reach expected yields under environmental-friendly practices. It was brought back that the variations of the biomass quality and composition are not only impacted by genetic, but also by environmental factors, such as water stress episodes. To guide breeding of maize and other dedicated C4 species for biomass production, we evaluated a F271 x Cm484 recombinant inbred population under non-irrigated and irrigated conditions during three consecutive years near in Montpellier (South of France). We quantified over 1,300 harvested stover samples using dedicated near-infrared spectroscopy equations established with calibrated samples harvested under both water regime conditions. We showed that biomass digestibility and composition varied between irrigated and non-irrigated scenarios. Using a genotyping-by-sequencing approach, we then built a dense genetic map with 1,000 single nucleotide polymorphism (SNP) markers and performed single-marker analyses to identify constitutive quantitative trait loci (QTLs) across years and conditions, and responsive QTLs using the interaction effect between the marker and the treatment. Overall, we identified 16 clusters of constitutive QTLs and 5 clusters of responsive QTLs, of which only one did not co-localized with constitutive QTLs. These results showed that co-localization between traits were different depending on the QTLs, underlying different strategies for breeding.

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