SUNLIBB

Sustainable Liquid Biofuels from Biomass Biorefining

Grant Agreement no. 251132

Collaborative Project
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ENERGY

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Deliverable 1.11

"Markers for Miscanthus biomass digestibility identified"

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Workpackage: **1**
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Dissemination Level: **PU**

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SUNLIBB deliverables

Del No: 1.11	**Deliverable Name: Markers for Miscanthus biomass digestibility identified**			
WP: 1	**Lead partner: P13**	**Dissemination level:** PU	**Delivery date (project month): 28**	**Actual delivery date: 30 (31/03/13)**

Objective:

To identify markers for Miscanthus biomass digestibility.

Results:

A *Miscanthus sinensis* mapping population, named BIOMIS, was phenotyped for different lignocellulosic biomass quality traits. These included quantification of the major classes of polymer; cellulose, hemicellulose and lignin by P13, and saccharification efficiency by P1. As P13 had a preliminary (old) map available for this population, Map-QTL was performed on this population in the attempt to find genetic markers for relevant cell wall traits (Deliverable D1.11 - M28). No QTLs with LOD above 3 were identified, but for all traits peaks were observed (Figure 1), suggesting that with additional data such QTLs could be identified. Given the anonymous nature and the small number of the molecular markers (AFLP) used to genotype the BIOMIS population and the fact that all phenotypic measurements were performed on 1 single plant, we have decided to continue this analysis in a different population, the SUNLIBB mapping population.

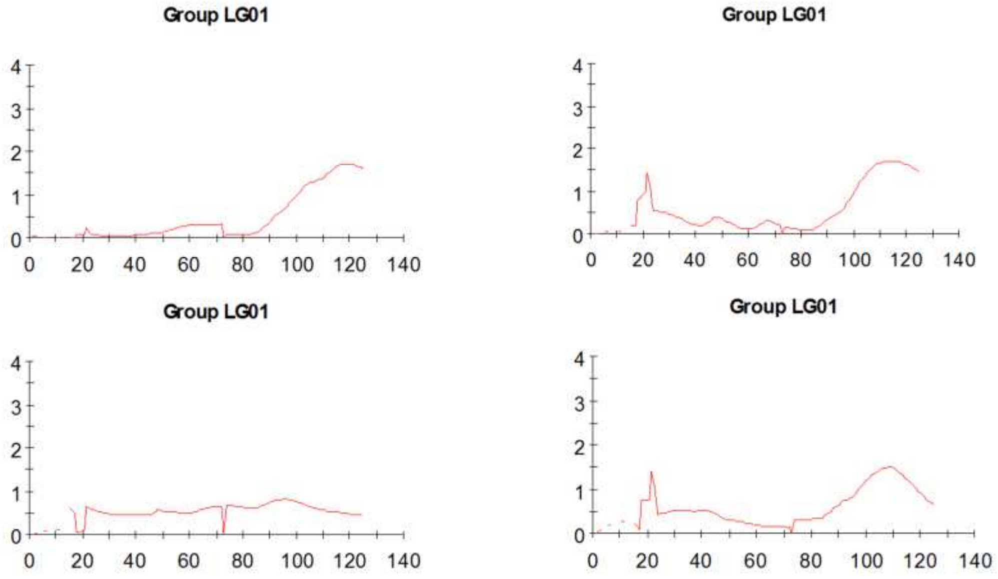

Figure 1: BIOMIS population LOD traces of QTL detection.

The SUNLIBB dedicated mapping population, originated from parents showing contrasting differences in cell wall composition, was prepared and approximately 200 individual plants were transplanted in a field trial with three replicates randomized plots in May 2012 (M20 - delivered month 30).

Discussion /Conclusion:

Genotyping by Sequencing has been performed for the SUNLIBB population by BGI. The obtained raw sequencing data have been processed into a genotype table, which is currently being used to generate a *Miscanthus sinensis* genetic map. This map will form the basis for further QTL analyses.