Genome-wide QTL detection for biofuel traits in switchgrass (*Panicum virgatum* L.)

U.S. DEPARTMENT OF ENERGY | Office of Science

Background

- Exploitation of natural genetic variation for feedstock composition can play an important role in improving cell wall recalcitrance in switchgrass.
- Identification of quantitative trait loci (QTL) and markers associated with feedstock quality traits can expedite genetic improvement of recalcitrance traits through marker-assisted breeding.

Approach

- An inter-ecotype mapping population generated from a bi-parental cross, AP13 x VS16, consists of 349 pseudo-F_1 testcross progenies were evaluated at multiple environments. QTL mapping was performed on eight important biofuel traits obtained from NIRS prediction equations. Candidate genes flanking 50 kb up- and down-stream of the major QTL peak markers were identified.

Outcome

- A total of 327 QTLs, distributed in 111 regions in switchgrass genome, were found associated with the eight feedstock quality traits evaluated in this study.
- Forty-five candidate genes, involved in lignin biosynthesis, carbohydrate and sugar metabolism, and other biological and cellular functions, were identified in the QTL regions.

Significance

- We have identified QTL associated with important feedstock quality traits in switchgrass. A number of additional candidate genes were identified in this study that falls outside the gene list currently targeted for manipulation through RNAi or genome editing technologies.

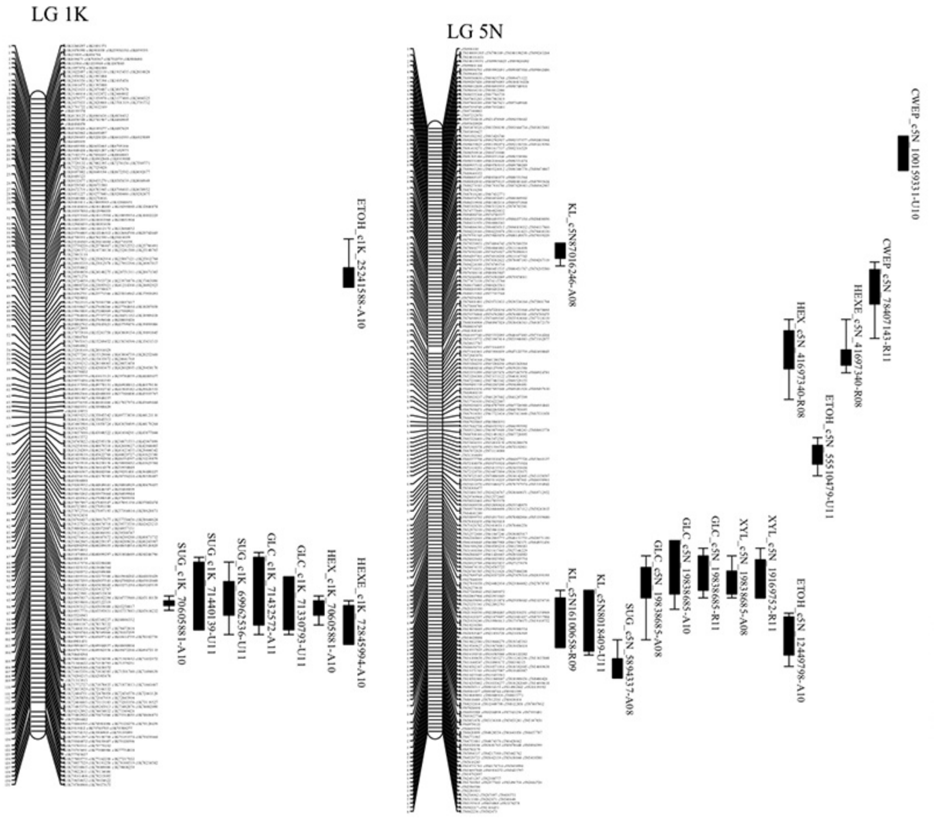

Figure shows the major biofuel trait QTL mapped on chromosomes 1K and 5N. Several candidate genes involved in lignin biosynthesis and transcription regulation were identified in these genomic regions.

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