

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

## 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<sub>1</sub> 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.

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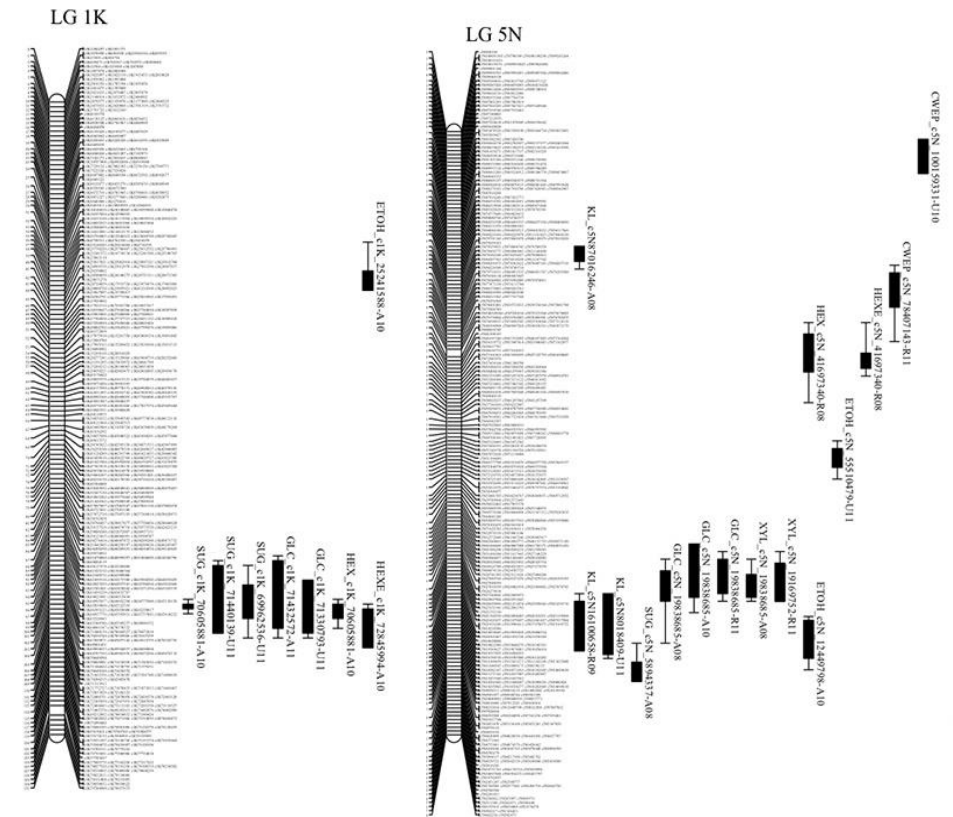


Figure shows the major biofuel trait QTL mapped on chromosomes 1K and 5N. Several candidate genes involved in lignin biosynthesis and transcription regulation were identified in these genomic regions.