QTL Associated with Maize Kernel Traits among Illinois High Oil X B73 Backcross-Derived Lines. (C01-wassom160554-Oral)

Authors:

- J.J.Wassom* - *University of Illinois*
- J.C.Wong - *University of Illinois*
- T.R.Rocheford - *University of Illinois*

Abstract:

Illinois long-term selection strains have extremes for kernel traits and have been used to identify genomic regions controlling kernel composition, but don't represent modern hybrids. To identify kernel trait QTL in a relevant background, 150 BC1:S1 families were created with Illinois High Oil and recurrent parent B73. Oil, starch, and protein content were tested in BC1:S1 and Mo17 test crosses (TC). Kernel weight (kwt) in BC1:S1 and yield in TC were tested. There were positive correlations between starch and kwt or yield and negative correlations between oil and starch, kwt, or yield. Regression models developed with QTL detected by composite interval mapping explain 47, 45, 44, and 18% of phenotypic variance for oil, protein, starch, and kwt, respectively, in BC1:S1 and 17, 23, 40, 24% for oil, protein starch, and yield, respectively, in TC. TC QTL mapped to similar intervals as QTL in BC1:S1. Most QTL were within one of 15 common 20-cM regions. QTL for oil, starch, and protein were mapped to chromosome 6, positions 50-74. This interval includes a BC1:S1 QTL explaining 37% of oil variation. There was no yield QTL in this region, implying the oil QTL's value in selection.

Corresponding Author Information:

James Wassom
University of Illinois
A108 Turner Hall, 1101 S. Goodwin Ave.
Urbana, IL 61801
USA

phone: 217-244-3388
fax: 217-333-9817
e-mail: j-wasso@uiuc.edu

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