***Making Genetic Maps More Accurate***

Researchers working on ways to select for improved plant traits for cellulosic biofuels applications use DNA sequence variation (markers) to create genetic linkage maps and apply genomic approaches to identify and improve bioenergy cultivars. Linkage maps provide the relative distance and ordering of locations in the genome, and linkage information from these maps allows researchers to infer characteristics of the genome surrounding the DNA markers. Linkage allows markers associated with bioenergy traits to be identified and selected for to improve bioenergy cultivars, as well as to improve genome assembly which also facilitates crop improvement. Thus, it is critically important that linkage is calculated accurately.

For many plant species, including the cellulosic biofuel crops sorghum, switchgrass, and maize, the typical genetic model used for estimating linkage does not account for phenomena that commonly occur in breeding and research populations. This ultimately results in the frequency of recombination events often being overestimated, which makes linkage maps larger than expected based on the Mendelian model of genetic segregation. While the mechanisms underlying this non-Mendelian segregation are not fully understood, it is believed to be associated with a selective advantage of heterozygote genotypes such that genetic loci containing both parental alleles outperform homozygote loci that contain two copies of only one parental allele.

GLBRC researcher John E. Mullet and colleagues sought to correct linkage estimates in Sorghum, a promising bioenergy grass, by modifying the existing Mendelian genetic model to account for different amounts of heterozygosity maintained per generation in a type of plant research population known as a recombinant inbred line (RIL) population. Researchers then tested their revised model on a simulated RIL population and a sorghum RIL population, and they showed that the model allows for more accurate linkage calculations and retention of more genetic information. This will ultimately benefit applications that use linkage information, including marker assisted selection, QTL mapping, and map-based cloning.

**Reference: Truong SK, McCormick RF, Morishige DT, Mullet JE** (2014) Resolution of genetic map expansion caused by excess heterozygosity in plant recombinant inbred populations. G3 (Bethesda) 4: 1963-1969

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