

Genetics of Flooding Tolerance in an F2 *Miscanthus sacchariflorus* ssp. *lutarioriparius* × *M. sinensis* population

Background/Objective

Miscanthus is a warm-season, perennial grass cultivated as a feedstock for chemicals, products, and fuels. *M. sacchariflorus* ssp. *lutarioriparius* has high yield potential and is well-adapted to seasonal flooding, but little is known about the genetics of this adaptation. Our long-term goal is to identify both the in-common and distinct molecular mechanisms underpinning flooding tolerance in different grass species, so that we can use the lessons of evolution to optimize crop adaptation to this important abiotic stress. The study's primary objectives were to (1) identify QTL for flooding tolerance in *Miscanthus*, (2) identify candidate genes and (3) compare ethylene response factors in *Miscanthus* with those in rice and *Arabidopsis*, sorghum and maize for binding site sequence homology and synteny, especially those associated with flooding tolerance.

Approach

We conducted a quantitative trait locus (QTL) analysis on a population of 332 diploid *Miscanthus* × *giganteus* (Mxg) F2s derived from an initial cross between diploid *M. sacchariflorus* ssp. *lutarioriparius* ‘PF30022’ and diploid *M. sinensis* ‘PMS-014’, followed by intermating 50 F1s. Using tanks in a greenhouse to assess the effects of partial submergence on actively growing plants, we compared an aerobic soil control to a 6-week flood treatment.

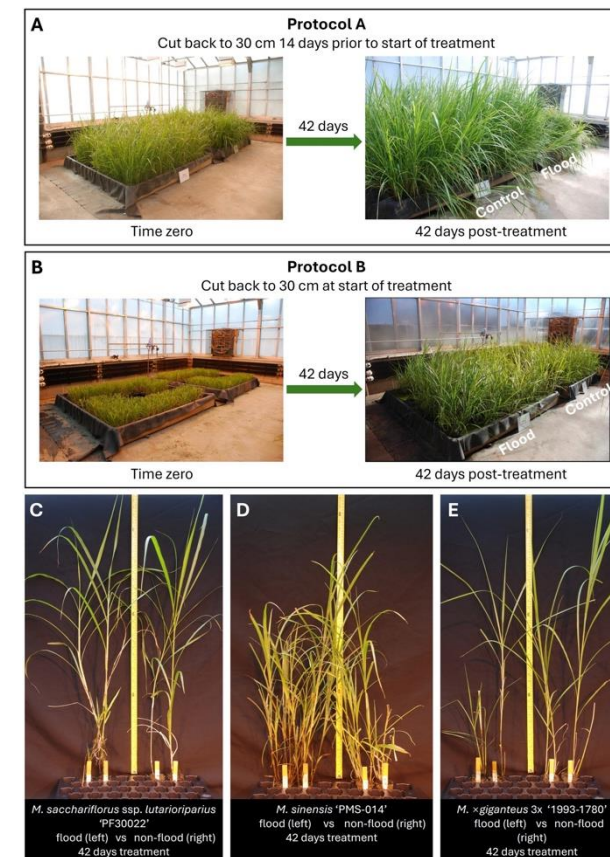
Results

In total, 10 QTL and 66 candidate genes for partial submergence tolerance were identified (including many for ethylene signaling), a first report for *Miscanthus*. Notably, none of the *Miscanthus* candidates were orthologs of rice Sub1A, SK1 or SK2, yet the ‘PF30022’ parent exhibited a snorkeling phenotype, indicating convergent evolution.

Significance/Impacts

To the best of our knowledge, no QTL mapping studies of flooding tolerance in *Miscanthus* have been previously published. There is an opportunity to learn from the lessons of evolution and apply these to the improvement of crops for tolerance to flooding. Additionally, our results show that there is substantial potential to further improve flooding tolerance of *Miscanthus* via selection. The identification and selection of dominant or heterotic alleles for flooding tolerance will be an important strategy for delivering flooding-tolerant biomass cultivars to growers.

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An experiment to study tolerance to partial submergence of actively growing plants in an F2 *Miscanthus sacchariflorus* ssp. *lutarioriparius* ‘PF30022’ × *M. sinensis* ‘PMS-014’ population (n = 363).