

Mapping QTL for Freeze Tolerance in Zoysiagrass



Jessica M. Brown¹, McCamy P. Holloway¹, Tan D. Tuong², Xingwang Yu¹, David P. Livingston², Aaron J. Patton³, Consuelo Arellano⁴, Michelle DaCosta⁵, Brian M. Schwartz⁶, and Susana R. Milla-Lewis¹

¹Crop & Soil Sciences, North Carolina State University, Raleigh, NC, ²U.S. Department of Agriculture, Raleigh, NC, ³Agronomy, Purdue University, West Lafayette, IN, ⁴Statistics, North Carolina State University, Raleigh, NC, ⁵University of Massachusetts Amherst, Amherst, MA, ⁶Crop & Soil Sciences, University of Georgia, Tifton, GA

 Background Zoysiagrass (<i>Zoysia</i> spp.) is one of the most freeze-tolerant warm season grasses. However, there is opportunity for improvement → to compete with cool season grasses north of the transition zone. Desirable characteristics: Dense texture, competitive with weeds, low input requirements, general tolerance to drought, shade and salinity stress. Previous research by Holloway et al. (2018) 	 Evaluate 175 individuals from the mapping population plus the two parents. Experimental Design: RCBD with two acclimation (NCA=no acclimation, CA= acclimated 4 wk at 8°C) and two temperature (-8 and -11C °C) treatments. Cold acclimation = critical in development of freeze tolerance. Rate surviving green tissue (SGT) and regrowth (RG) on 0-5 scale for 6
 Generated first high density linkage based map of Z. japonica 	weeks post-freeze
 Conducted winter field trials at three locations. Identified putative QTL: 	QTL Mapping

- Seven regions of interest identified on chromosomes 8, 11, and 13
 - Colocation of QTL for three or more traits

Objective:

> Map QTL for freeze response under controlled environmental conditions in a pseudo- F_2 population of Meyer (freeze tolerant) x Victoria (freeze susceptible).



- Analyze the freeze data with the high density linkage map (Holloway et al., 2018)
- Identify putative regions of interest by way of LS means from freeze data
 - Screened for cofactors and established LOD threshold
- MQM mapping \rightarrow narrow down regions of interest
- Assess co-localization of winter survival QTL (Holloway et al. 2018) with acclimation and freeze-tolerance QTL.



QTL Mapping Results

- Right: Acclimation and freeze tolerance QTL
- Bottom: winter survival QTL (Holloway et al. 2018) QTL identified for multiple traits and environments. Regions of interest for acclimation/freeze tolerance on chromosomes 5, 12, 14 and 19. Regions of interest for winter survival on chromosomes 8, 11, and 13 Overlap between the two studies occurs primarily on chromosomes 8, 12, and 19.



Proteomic Analysis (Brown et al. doi 10.1101/581488v1)

Next steps

- Study of Meyer and Victoria tissues before and after cold acclimation identified several proteins of interest for cold acclimation response:
 - LEA 3, MAPK, SOD, GAST1, Phytochrome A, ATP synthase, AGP, PLD, PSII



starch metabolizing proteins in Meyer, \downarrow photosynthesis related proteins in Victoria \succ Need to determine if these protein coding regions overlap with QTL of interest.

Conclusions

- Overlap between the QTL of interest in the two studies
- occurs primarily on chromosomes 8, 12, and 19.
- Overlapping regions may be of interest for further study into their role in freezing tolerance.
- Further assess similarities between winter survival and acclimation/freeze tolerance QTL and proteomic data.
- Conduct transcriptomic analysis of cold acclimated Meyer and Victoria. Identify genes/proteins at major effect regions for future breeding efforts.