

Global Diversity of Source-Sink Senescence in Maize

Mark Gee¹ and Mitchell Tuinstra¹

¹Affiliation not available

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Abstract

Source-Sink Regulated Senescence (SSRS) in maize is a complex trait involving sugar sensing and carbohydrate partitioning. While the yield effects of SSRS are still under investigation, mapping work in Midwest commercial germplasm has found evidence for QTL on several chromosomes. In this study, we seek to understand the variation of this trait in global maize germplasm and map the genetic loci linked to this senescence response using the Maize Nested Association Mapping population. Wide variation was seen in expression of the senescence phenotype including several lines that are potentially anti-senescent in response to sink removal. Phenotypes of NAM RIL populations support the possibility of anti-senescent or senescence suppressing genetic factors. Joint linkage mapping identified QTL for the SSRS trait on three chromosomes which are distinct from those previously reported. By understanding and mapping the global diversity of this trait, we can better understand the physiology of maize senescence and integrate insights into breeding programs.

Mark Gee¹ and Mitchell Tuinstra¹

¹Department of Agronomy, Purdue University, West Lafayette, IN, USA

ORCID: 0000-0003-1472-0028

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