



**COLLEGE of
BIOLOGICAL SCIENCE**

DEPARTMENT OF MOLECULAR
AND CELLULAR BIOLOGY

Announcement:

*All interested members of the university community are invited to attend the Final Oral Examination for the degree of **Doctor of Philosophy** of*

MARK MINOW

on Thursday, November 12, 2020 at 1:30 pm (online)

Thesis Title: **Molecular genetic investigation into the processes underlying transitions in plant gene expression**

Examination Committee:

Dr. Annette Nassuth, Molecular and Cellular Biology (Exam Chair)
Dr. Joseph Colasanti, Dept. of Molecular and Cellular Biology
Dr. Lewis Lukens, Dept. of Plant Agriculture
Dr. John Vessey, Dept. of Molecular and Cellular Biology
Dr. Yuhai Cui, Agriculture and Agri-Food Canada (External Examiner)

Advisory Committee:

Dr. Joseph Colasanti (Adv)
Dr. Lewis Lukens
Dr. Joseph Yankulov
Dr. Nina Jones

Abstract: This thesis investigates several unanswered questions about how plant transcription factors and small RNA (sRNA) mediate transitions in gene expression. Specifically, this thesis addresses three goals: i) to better understand the maize autonomous flowering pathway and to what extent it overlaps with the ancestral photoperiod flowering pathway, ii) to providing insights into how sRNA transcriptomes change during the creation of maize recombinant inbred lines (RILs) and near isogenic lines (NILs), and iii) to determine if Arabidopsis phloem derived sRNA signals can influence gene expression in the shoot apical meristem (SAM). The first research goal addresses the floral transition, a critical change in SAM gene expression, that initiates reproductive growth. In maize, the transition to reproductive growth is driven by an autonomous pathway controlled by the transcription factor INDETERMINATE1 (ID1). Our RNA-sequencing revealed that *ID1* influences the floral transition through a pathway distinct from that used by ancestral maize, teosinte. In pursuit of the second goal, next generation sequencing was used to examine the sRNA transcriptome of maize RILs and NILs. Genome wide, most sRNA expression were found to be co-inherited with the parental DNA. However, RIL non-parental sRNA expression patterns were also observed. These non-parental sRNA expression patterns often resembled the expression state found at the same locus in the other parent. In the NIL, many sRNA expression differences were observed over the introgressed DNA and the homologous region from

the recurrent parent. However, the introgressed region had low 24nt sRNA expression, perhaps related to poor genome wide homology and past breeding history. The third goal used two synthetic systems to test phloem-to-SAM sRNA trafficking. Both systems provide evidence of phloem-to-SAM sRNA movement. Since the SAM gives rise to plant gametes, phloem-to-SAM sRNA transport provides a route for somatic sRNA to initiate heritable epigenetic transitions. Understanding the mechanisms behind these various transitions in plant gene expression will ultimately allow for the precise manipulation of traits that improve plant productivity to meet the challenges of climate change in the coming century.

Curriculum Vitae: Mark completed his Bachelor of Science (Honours) at the University of Guelph in 2013, and then entered directly into the Ph.D. program in the lab of Dr. Joseph Colasanti in May of the same year.

Awards: Dr. Donald Robert Phillips Molecular and Cellular Biology Scholarship (2020)
Honorable Mention for the Best Oral Presentation at the Annual Meeting of the CSPB (2019)
CSPB Eastern Regional Meeting Student Presentation Honorable Mention (2018)
Class of OAC '60 Award for Outstanding Teaching Assistant (2018)
Alexander Graham Bell Canada Graduate Scholarship Doctoral (CGS D) (2017-2018)
NSERC PGS-D (2015-2017)
Dean's Tri-Council Scholarship (2015-2018)
OGS Scholarship (2013-2014)

Publications: **Minow, M. A. A.** and Colasanti, J. (2020). Does variable epigenetic inheritance fuel plant evolution? *Genome*. 63:253-262.

Minow, M. A. A., Ávila, L. M., Turner, K., Ponzoni, E., Mascheretti, I., Dussault, F. M., Lukens, L., Rossi, V. and Colasanti J. (2018). Distinct gene networks modulate floral induction of autonomous maize and photoperiod-dependent teosinte. *Journal of Experimental Botany*. 69:2937-2952.

MacNeill*, G. J., Mehrpouyan*, S., **Minow***, **M. A. A.**, Patterson*, J. A., Tetlow I. J. and Emes, M. J. (2017). Starch as a source, starch as a sink: the bifunctional role of starch in carbon allocation. *Journal of Experimental Botany*. 68:4433–4453.

*Authors contributed equally to the manuscript

Coelho, C. P., **Minow, M. A. A.**, Chalfun-Júnior, A. and Colasanti, J. (2014). Putative sugarcane *FT/TFL1* genes delay flowering time and alter reproductive architecture in *Arabidopsis*. *Frontiers in Plant Science*. 5: doi: 10.3389/fpls.2014.00221