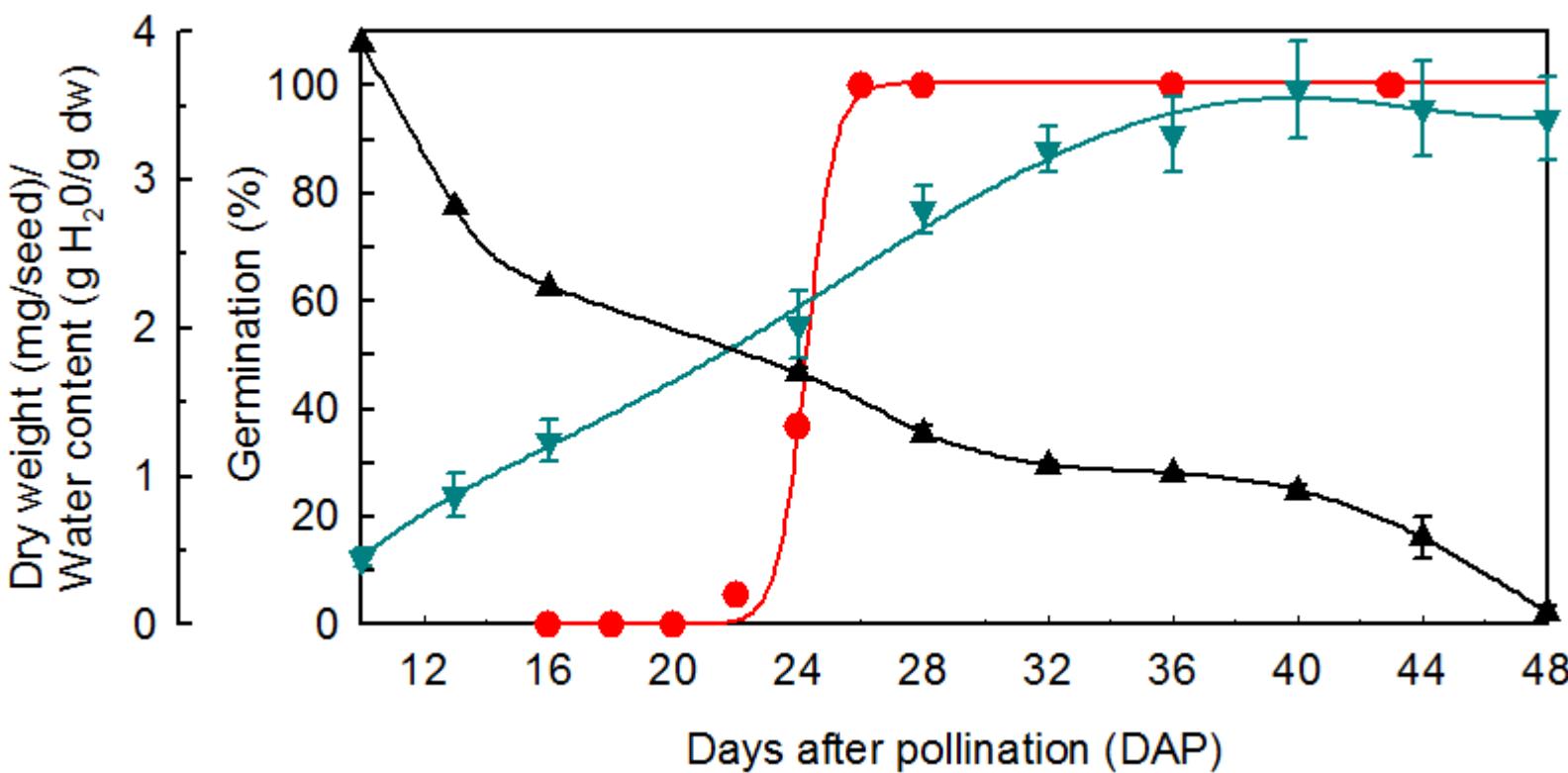
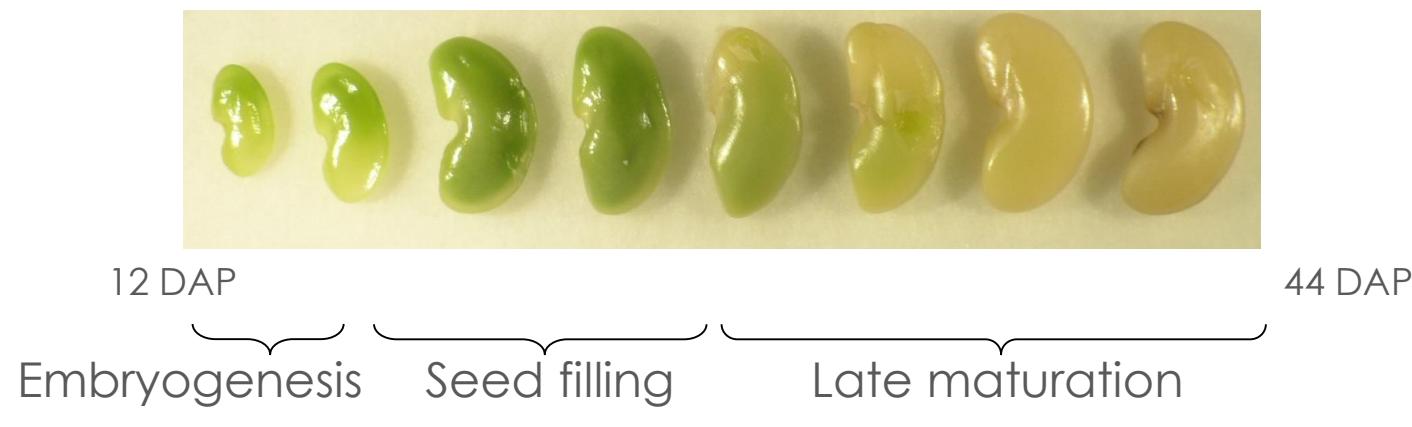


# ABSCISIC ACID INSENSITIVE 5 (ABI5) IS A MAJOR REGULATOR OF LATE SEED MATURATION AND LONGEVITY IN *MEDICAGO* *TRUNCATULA*

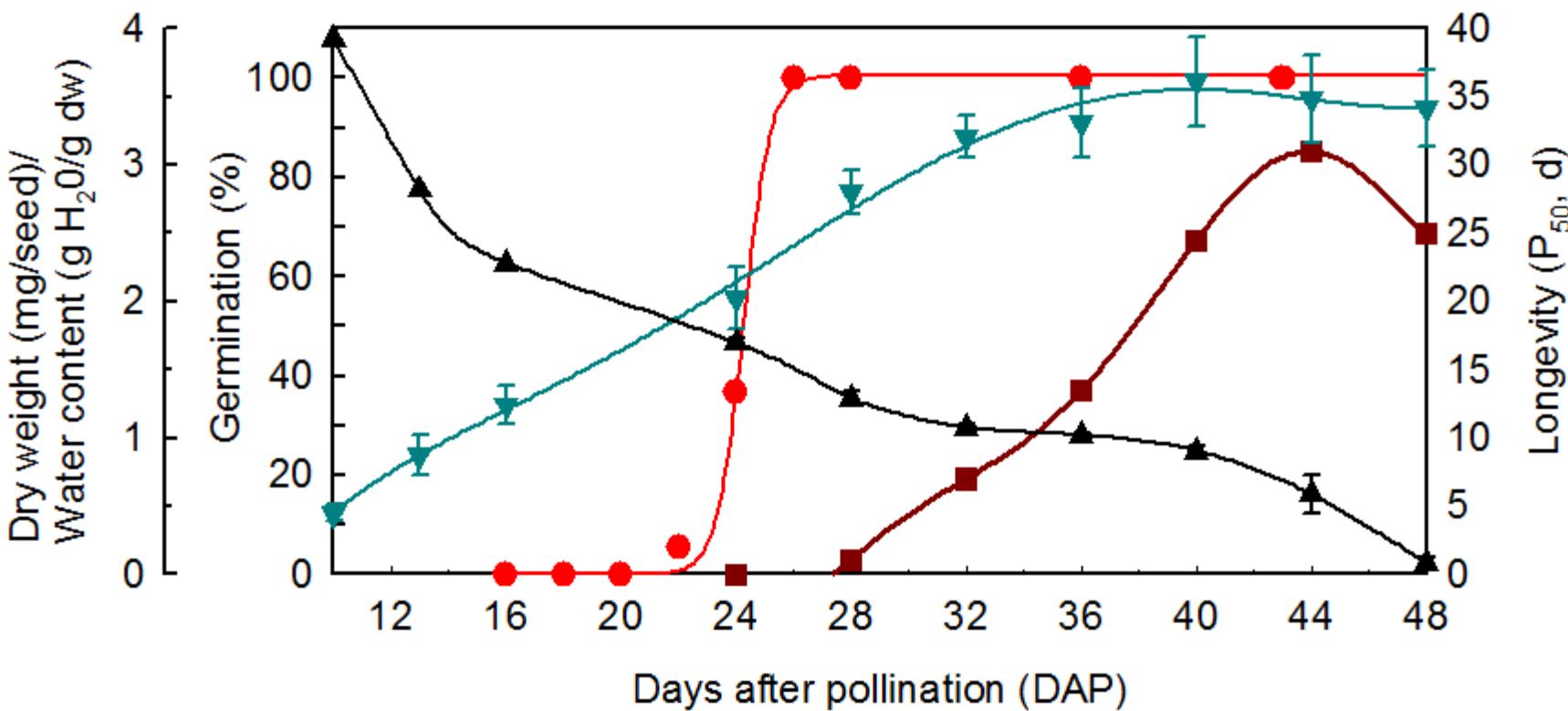
Julia Zinsmeister

Research Institute of Horticulture and Seeds,  
Angers, France

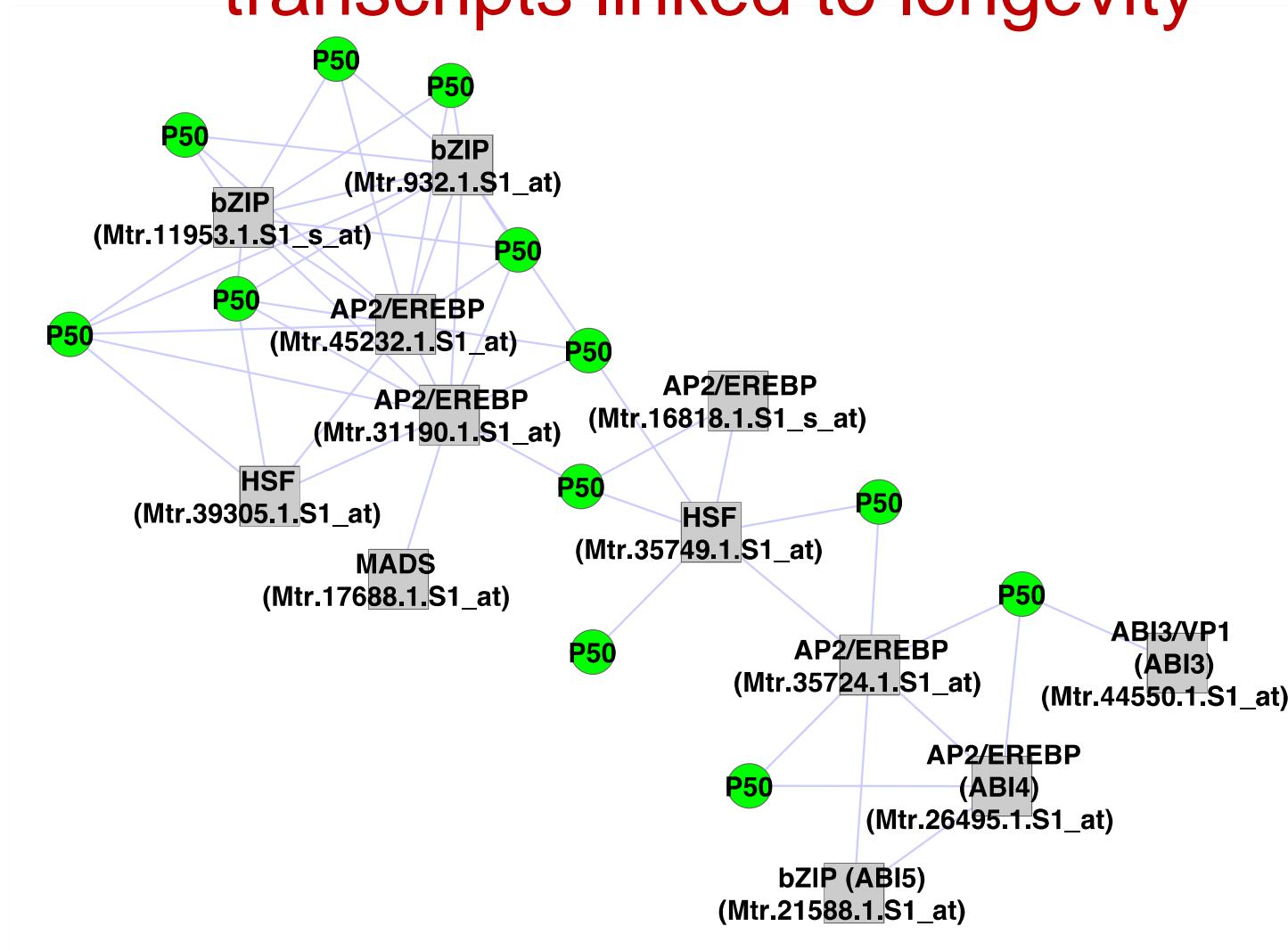
# Seed maturation of *Medicago truncatula*



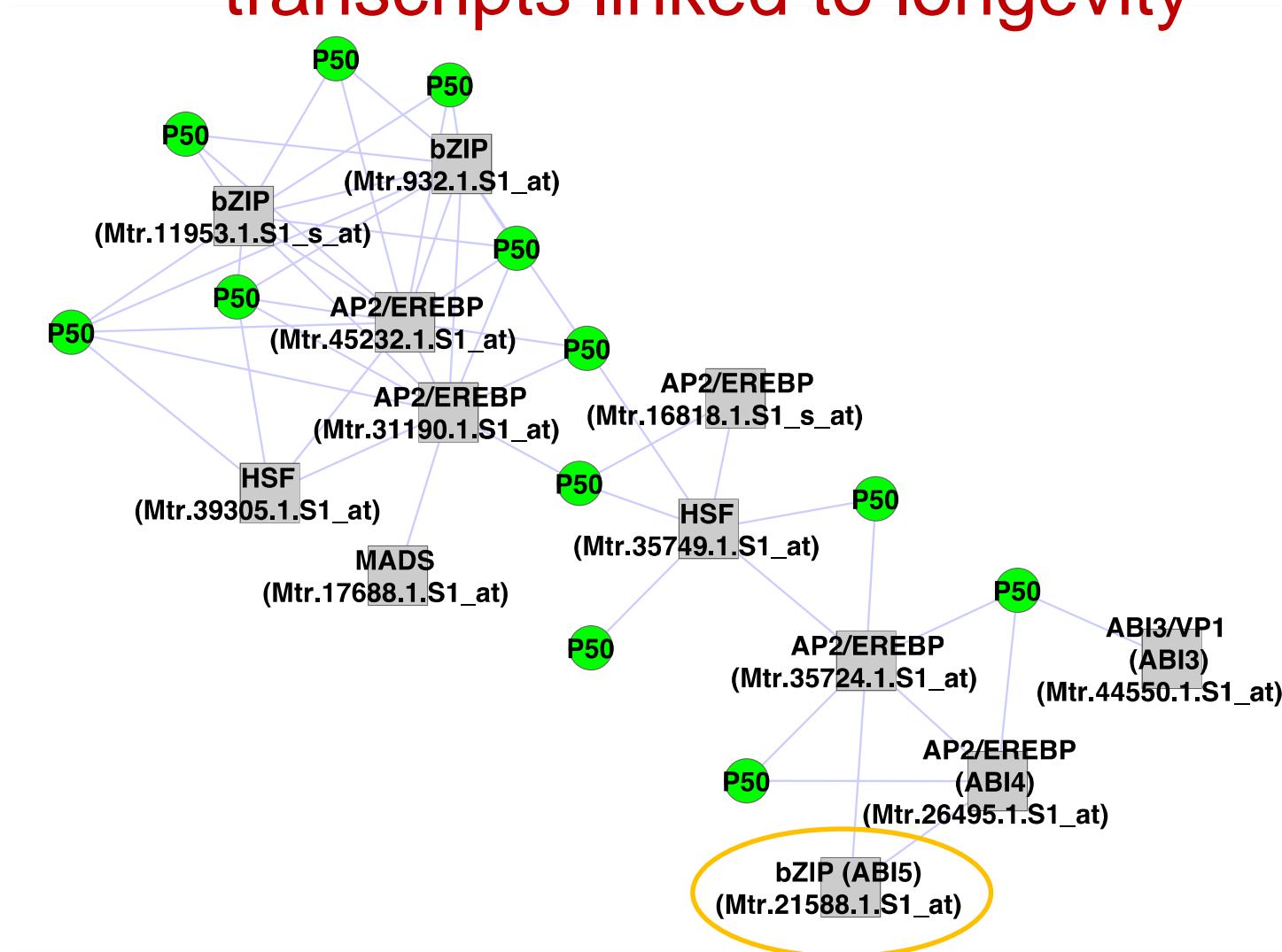
# Seed maturation of *Medicago truncatula*



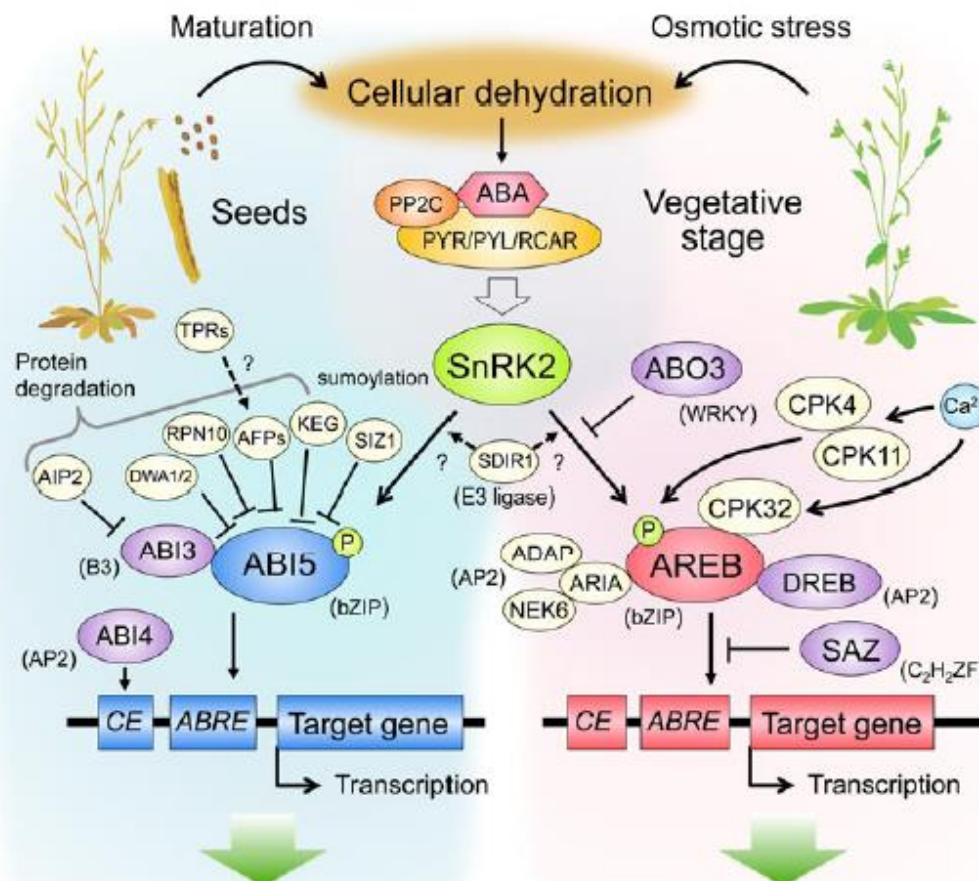
# Co-expression network of seed maturation identifies *MtABI5* as a TF co-expressed with transcripts linked to longevity



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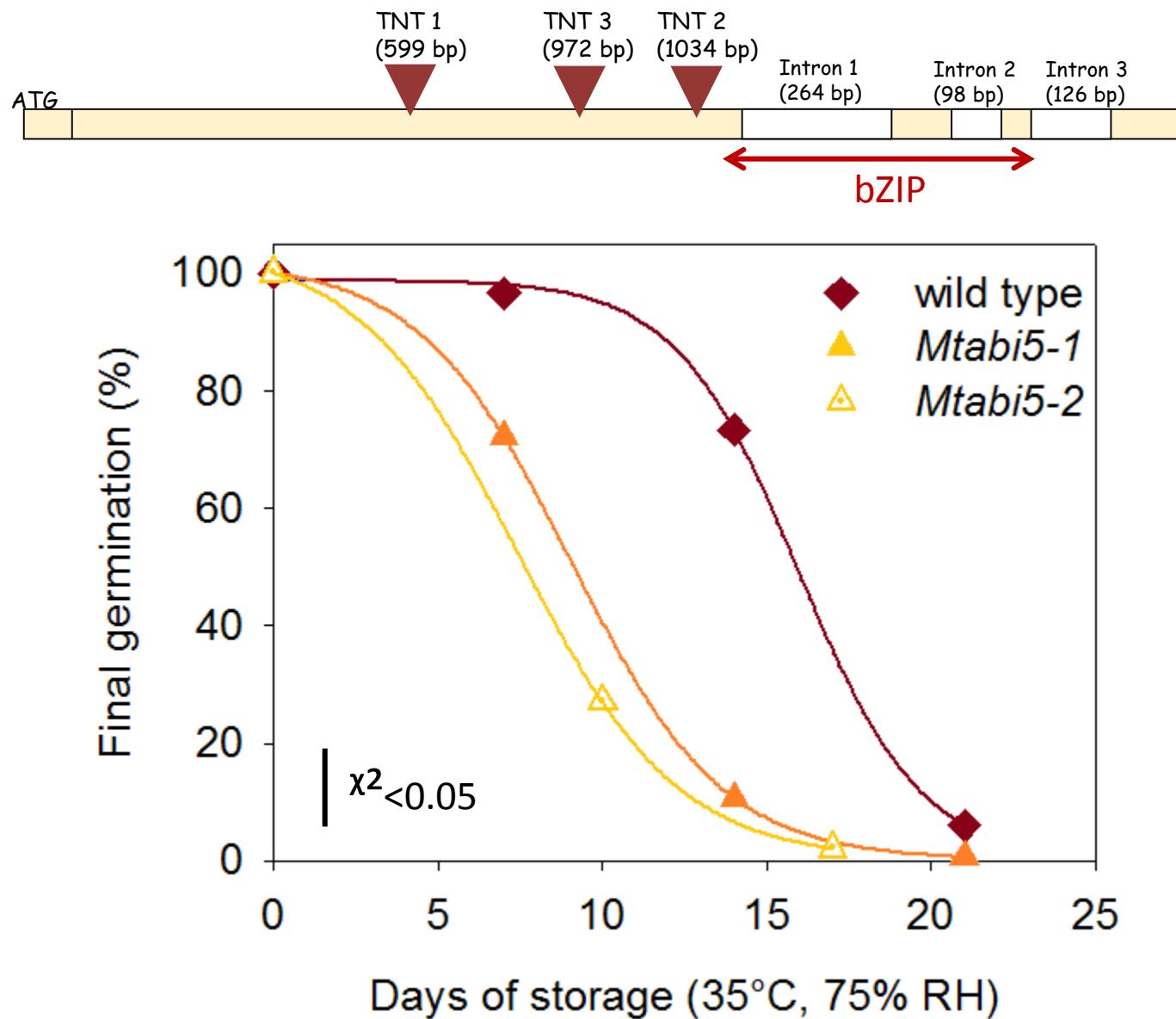


# ABI5: a transcription factor involved in ABA signaling pathway and seed quality

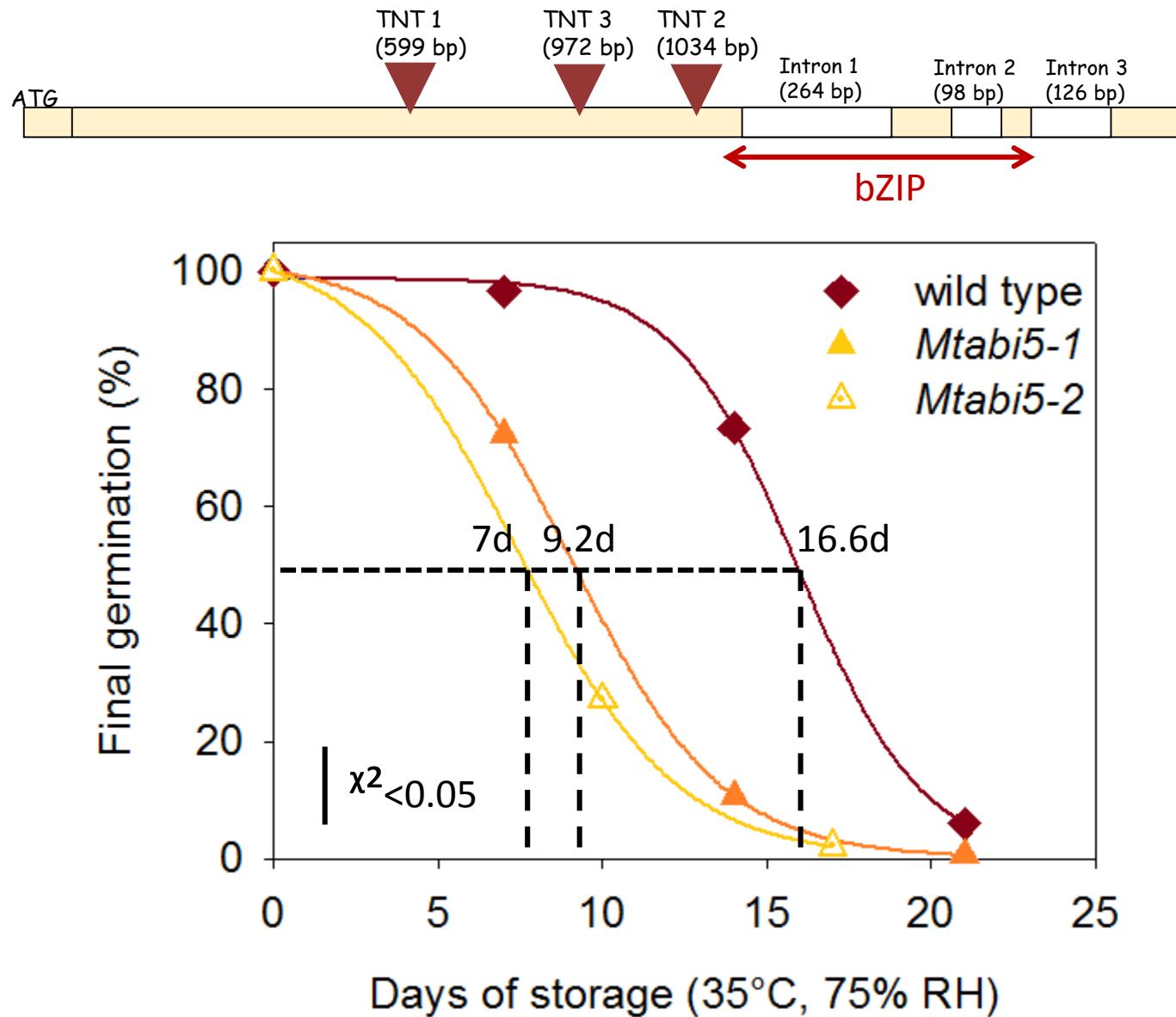


- Seedling growth arrest (Lopez-Molina *et al.*, 2001)
  - Re-establishment of DT in emerged radicles in *Arabidopsis* (Maia *et al.*, 2014) and *Medicago* (Terrasson *et al.*, 2014)
- Stress tolerance  
Growth regulation

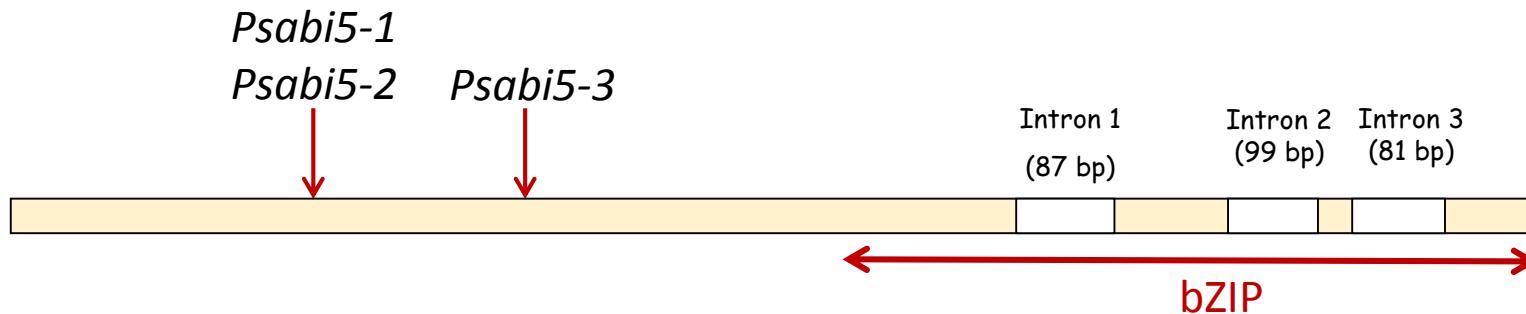
# Seed longevity is affected in *Mtabi5* mutants



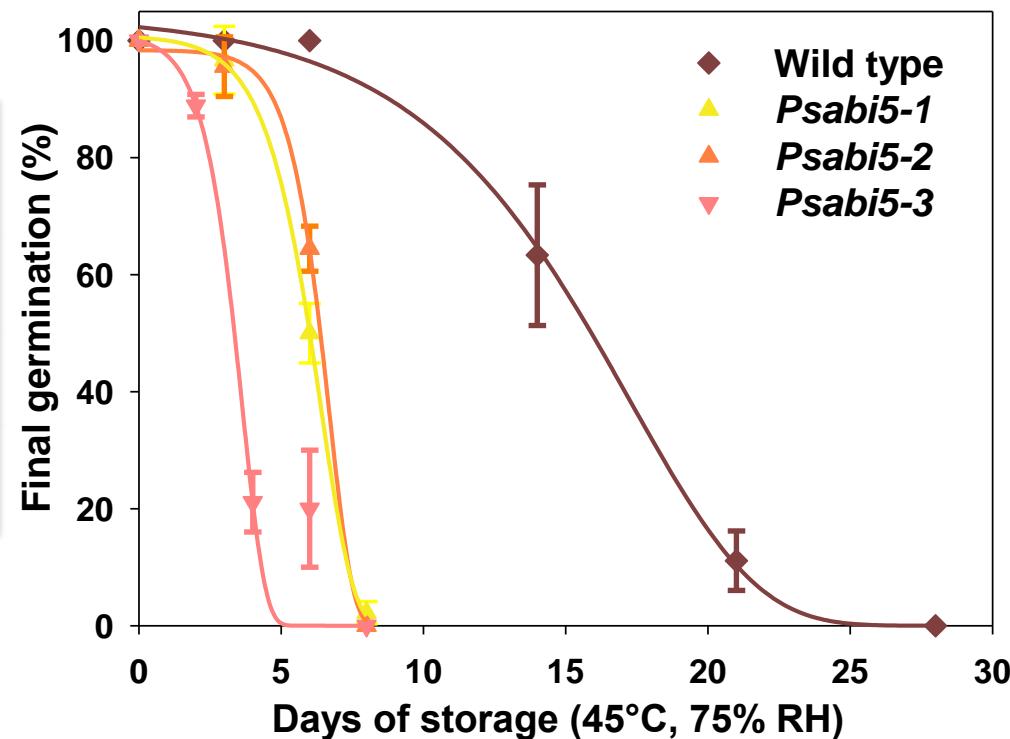
# Seed longevity is affected in *Mtabi5* mutants



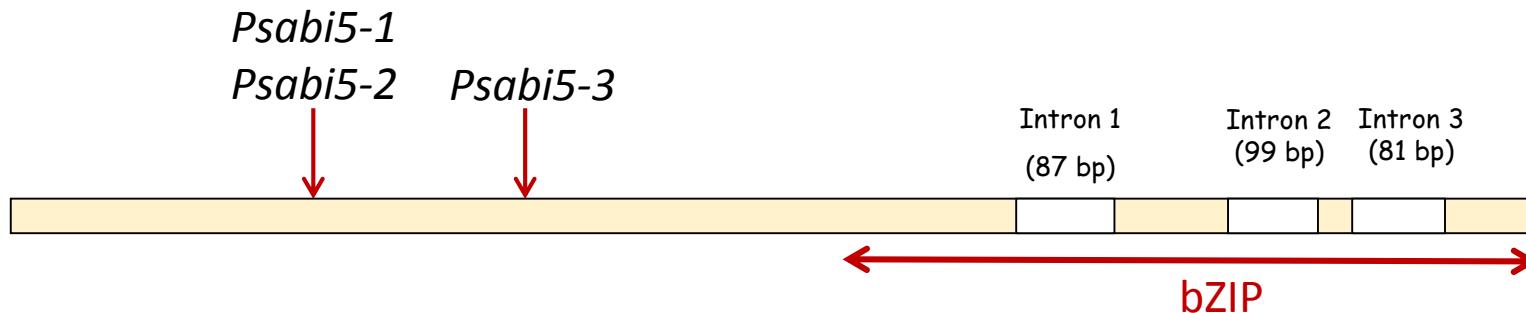
# Characterization of seed longevity in *abi5* EMS mutants of pea



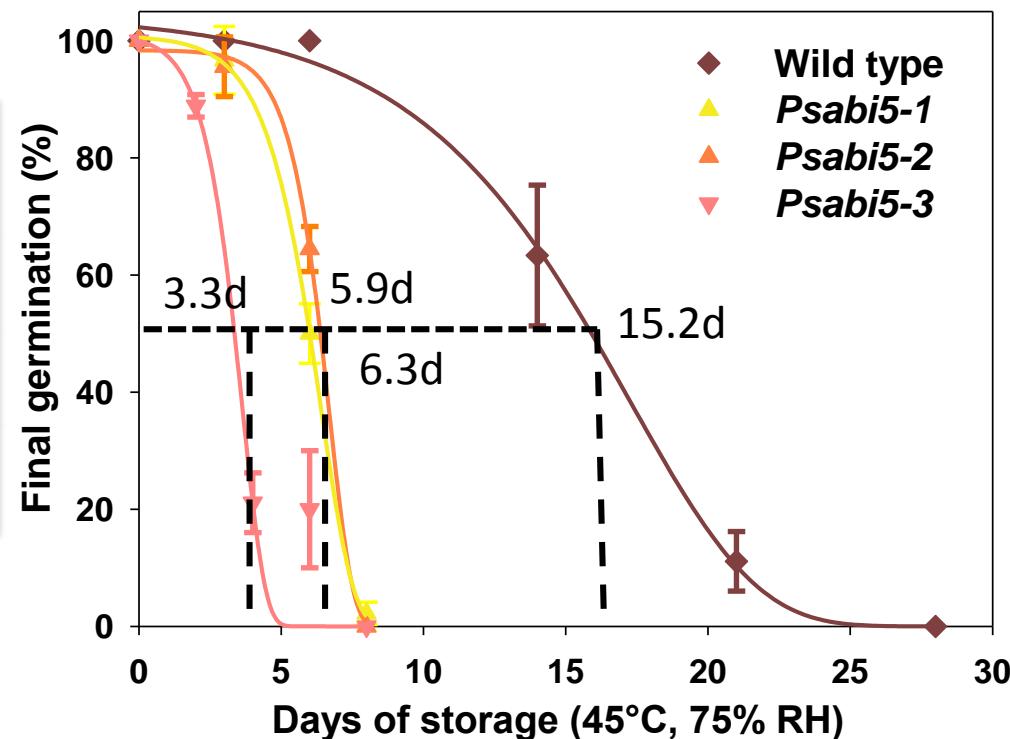
Family	Mutation	Base from ATG	Protein position	Type of mutation
<i>Psabi5-1</i>	7	C266T	Q89amber	Nonsense mutation
<i>Psabi5-2</i>	8	C266T	Q89amber	Nonsense mutation
<i>Psabi5-3</i>	12	G340A	W113opal	Nonsense mutation



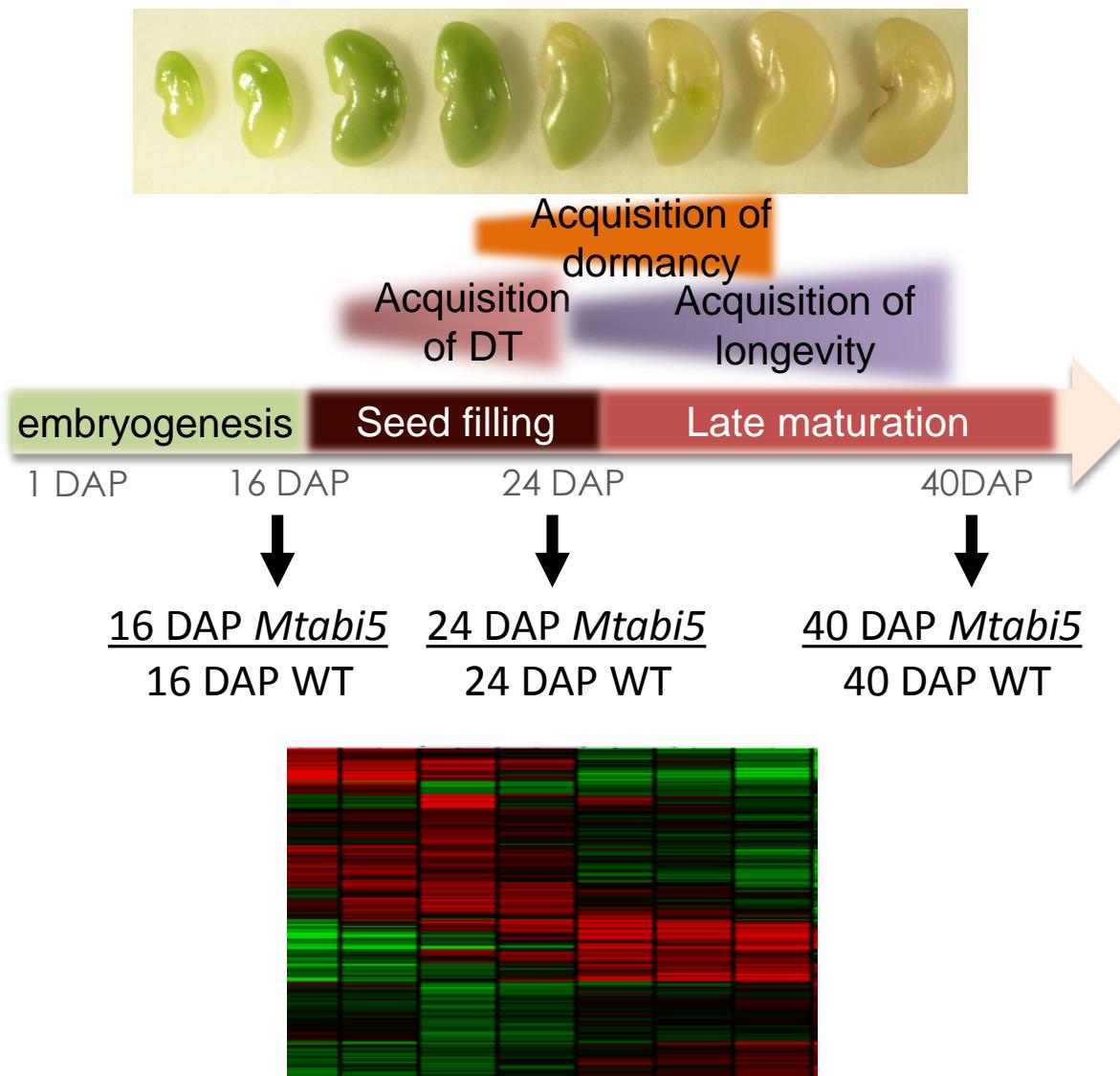
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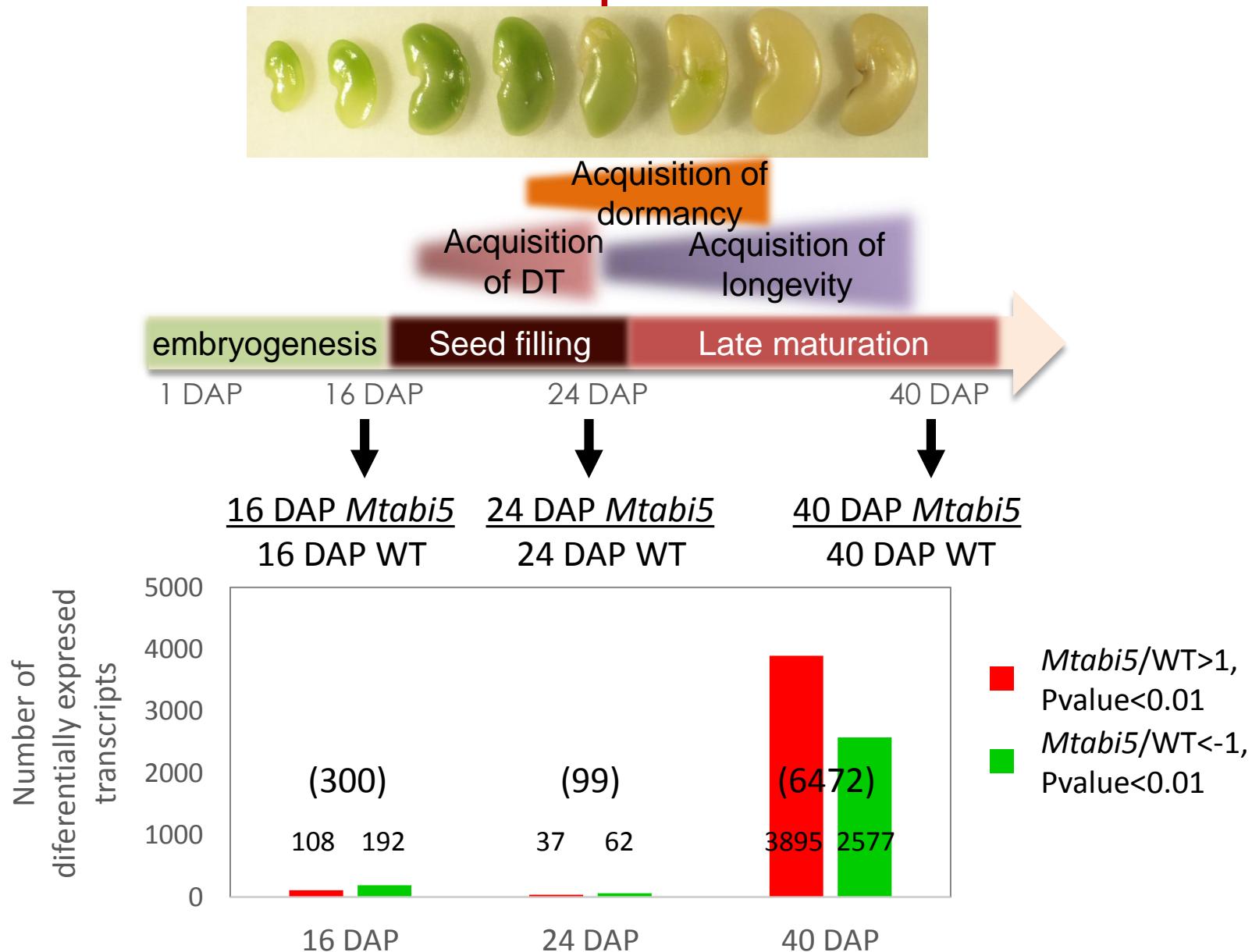
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# Transcriptomic analysis of *Mtabi5* during seed development



# Transcriptomic analysis of *Mtabi5* during seed development



# RFO contents increase during *Medicago* seed maturation



Acquisition of dormancy  
Acquisition of DT      Acquisition of longevity

embryogenesis

Seed filling

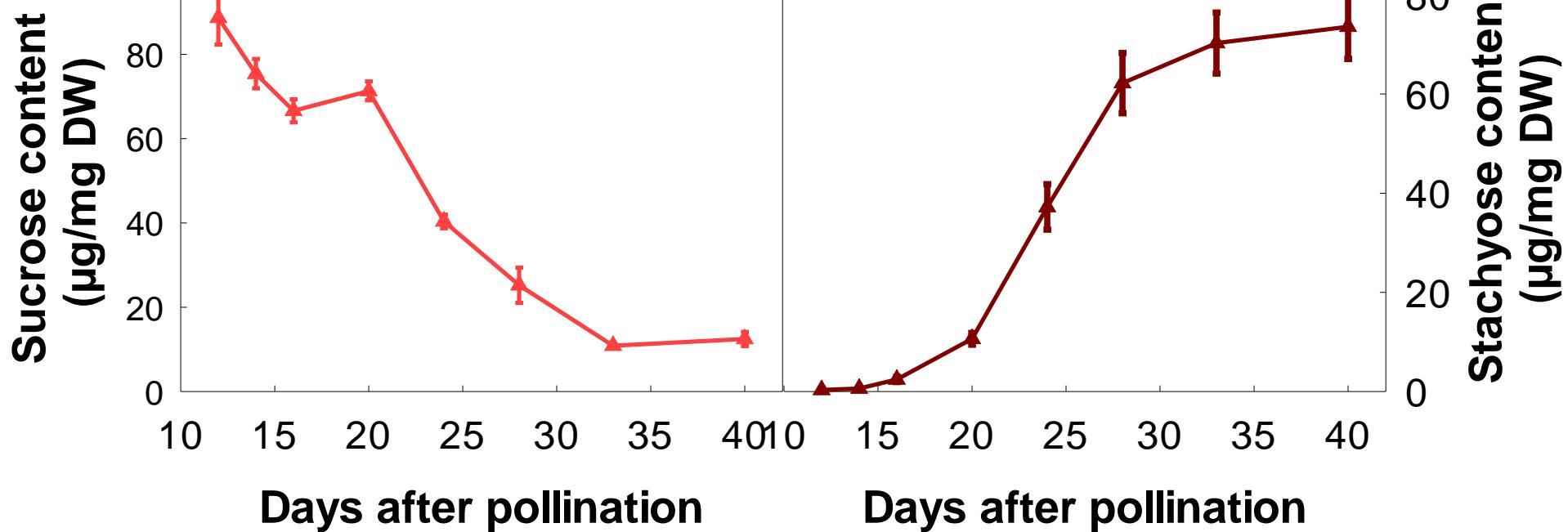
Late maturation

1 DAP

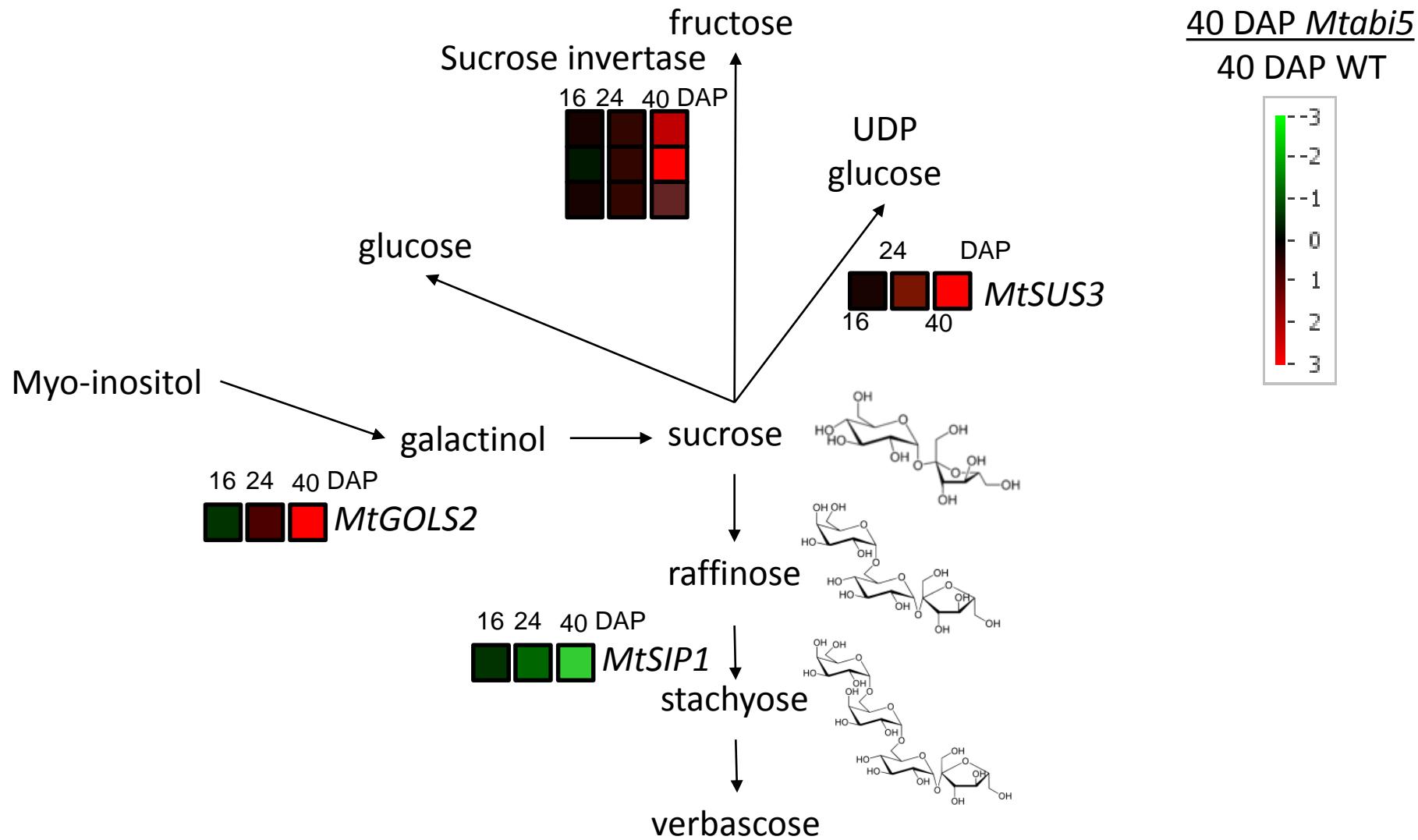
16 DAP

24 DAP

40 DAP

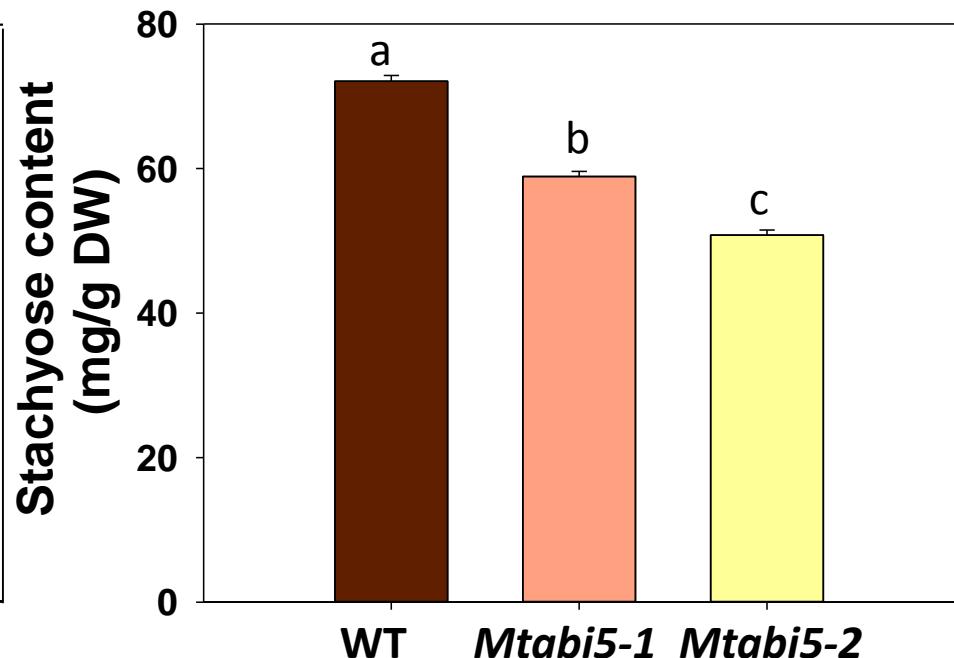
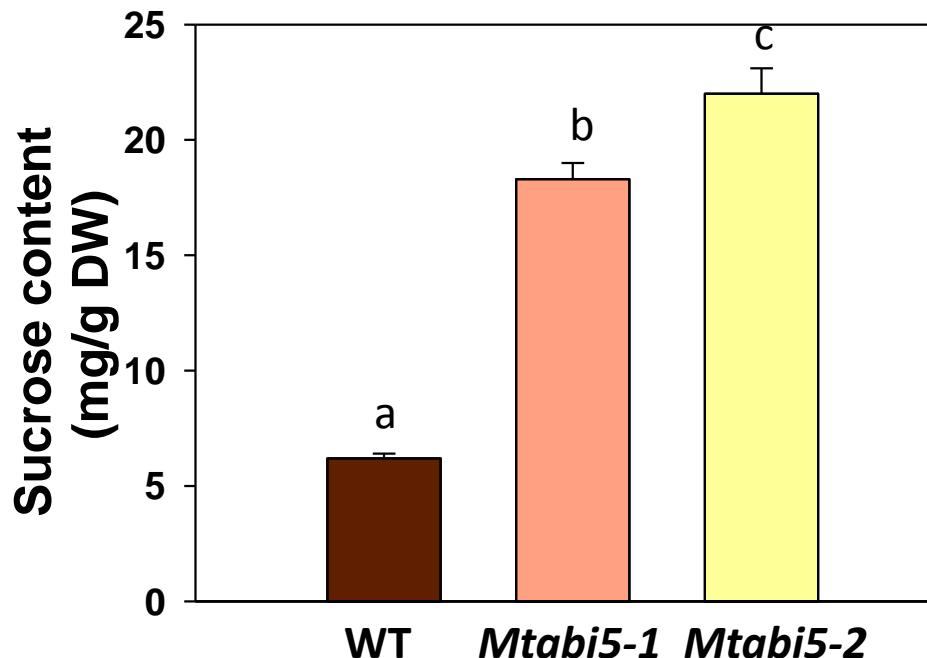


# Genes involved in RFO metabolism are deregulated in *MtABI5*



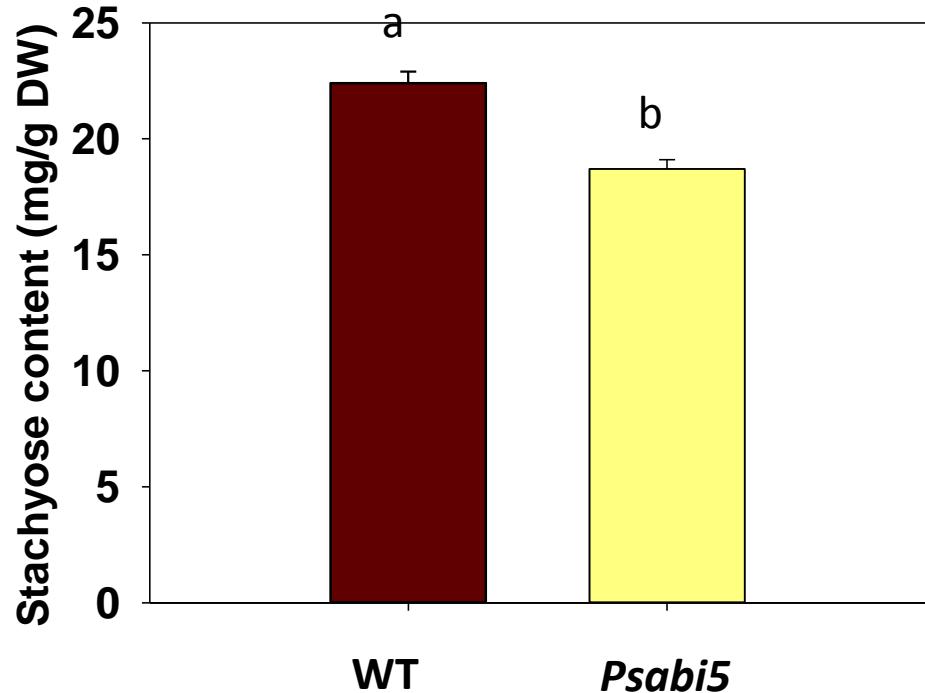
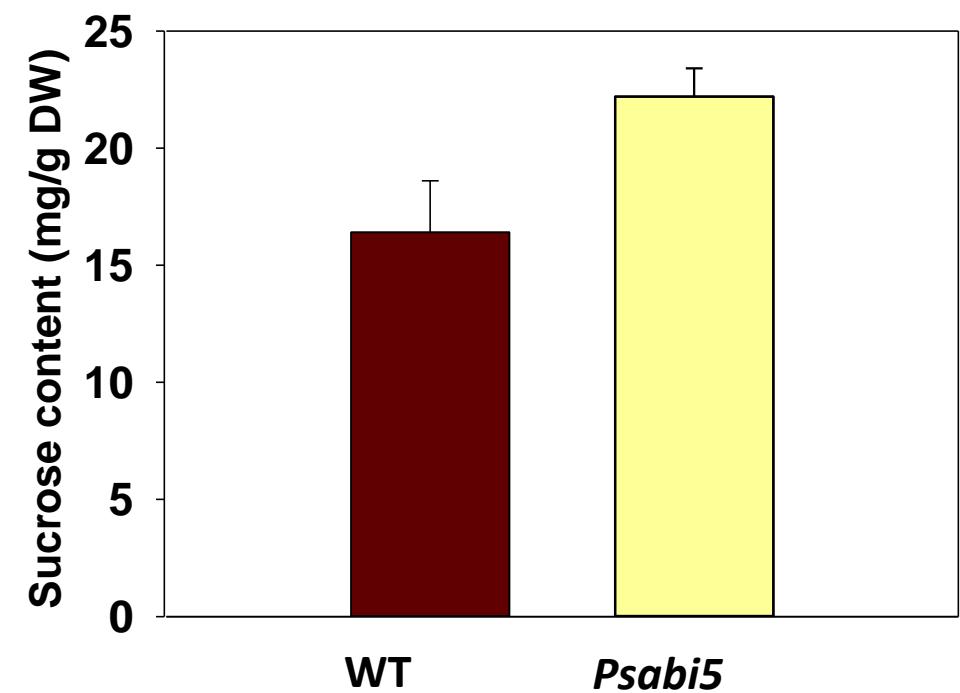
# *MtABI5* is involved in raffinose oligosaccharide family accumulation

Medicago



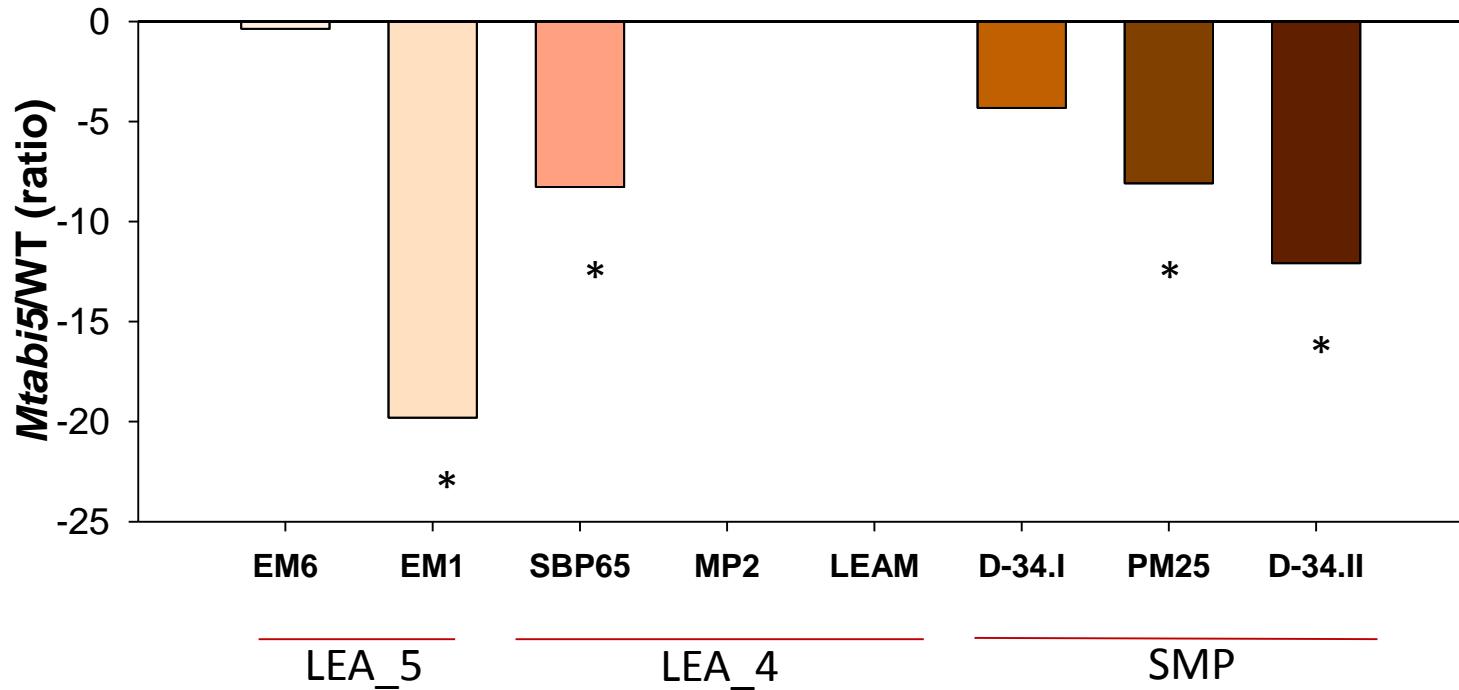
# *PsABI5* is involved in raffinose oligosaccharide family accumulation

Pea



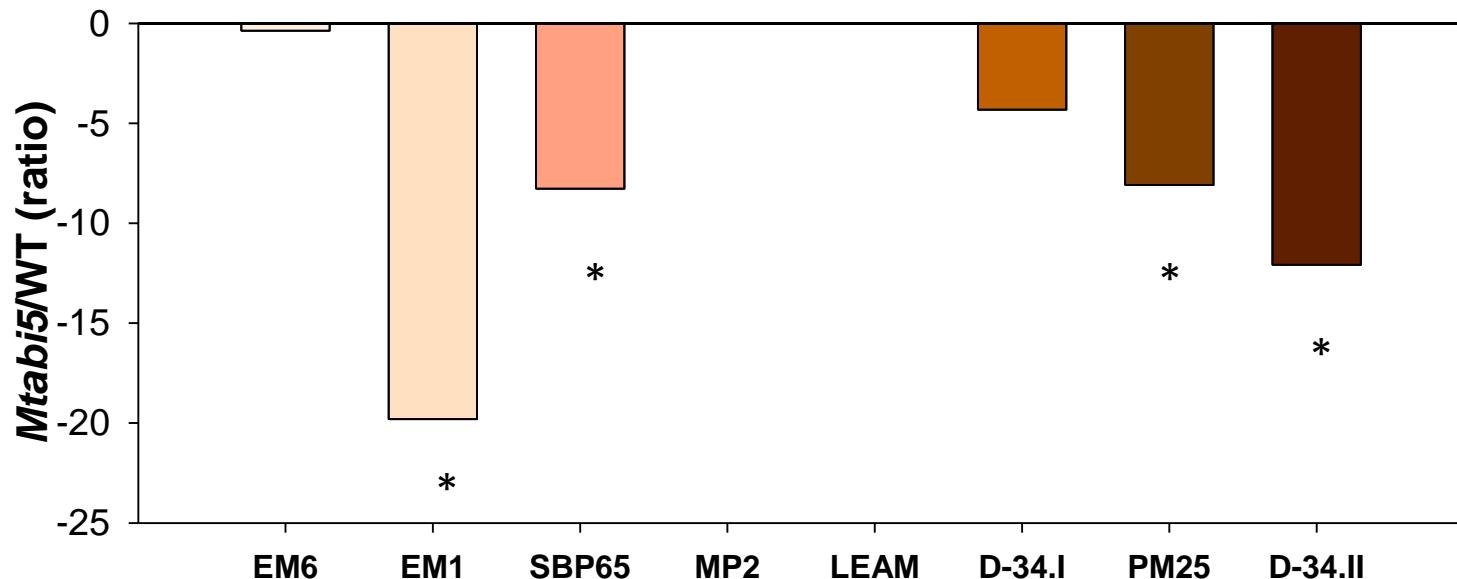
# LEA proteins are deregulated in *Mtabi5*

**Transcriptome**  
(LEA transcript  
ratio between  
*Mtabi5* and WT  
at 40 DAP)

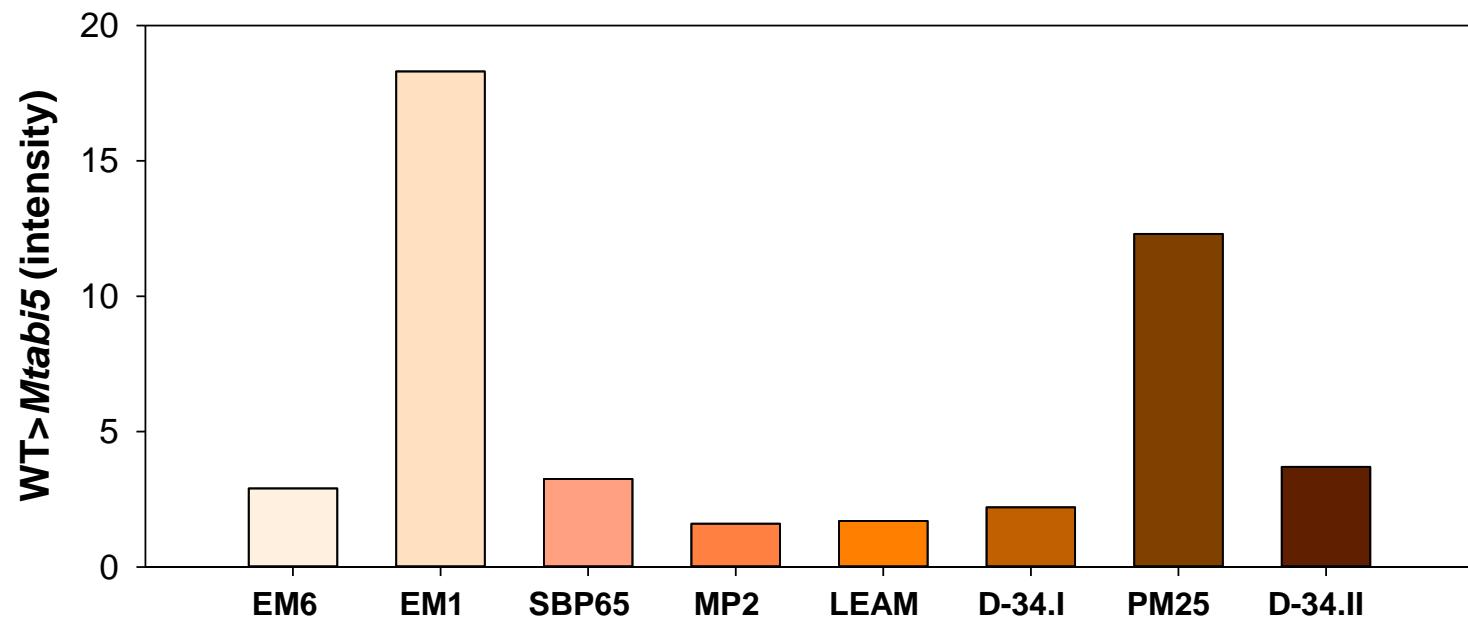


# LEA proteins are deregulated in *Mtabi5*

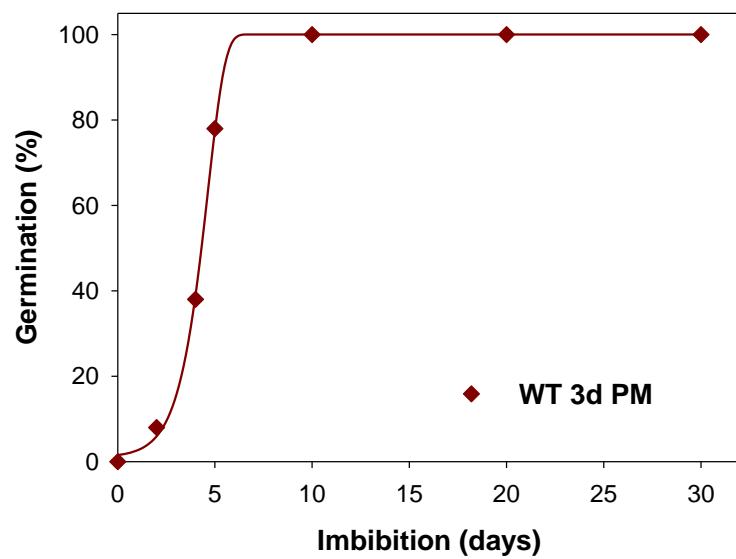
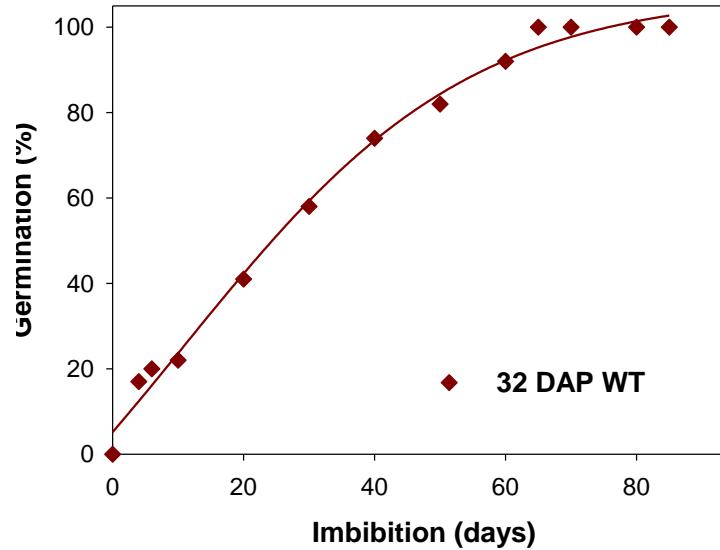
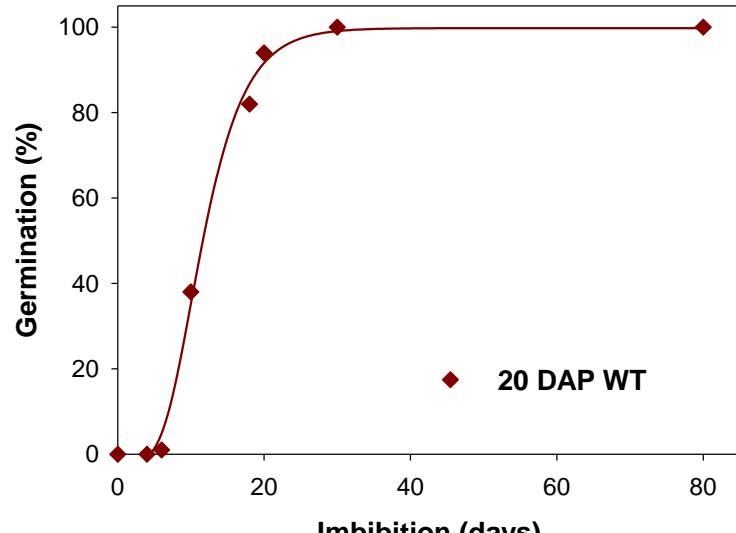
**Transcriptome**  
(LEA transcript ratio between *Mtabi5* and WT at 40 DAP)



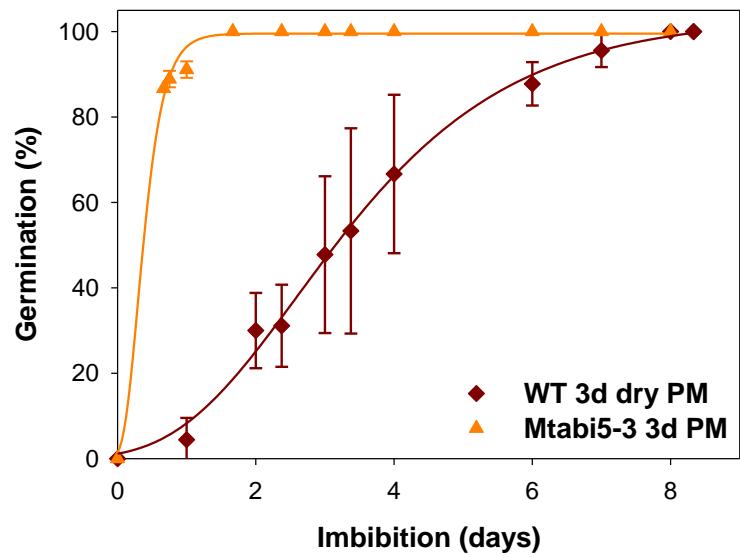
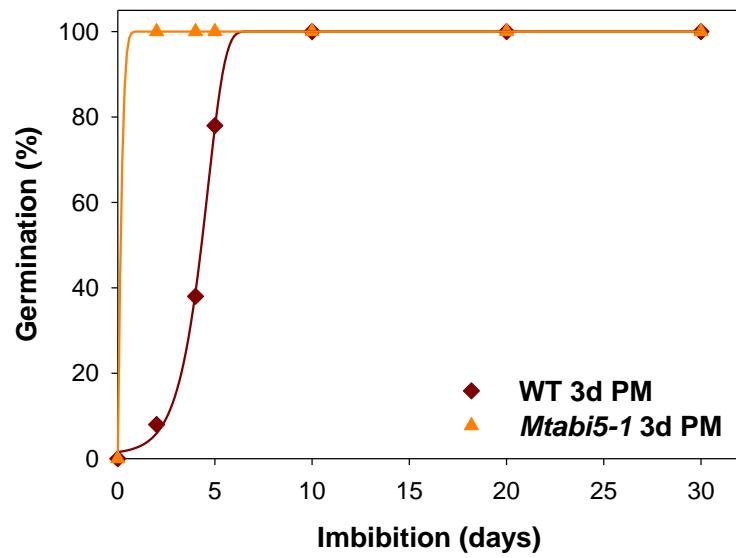
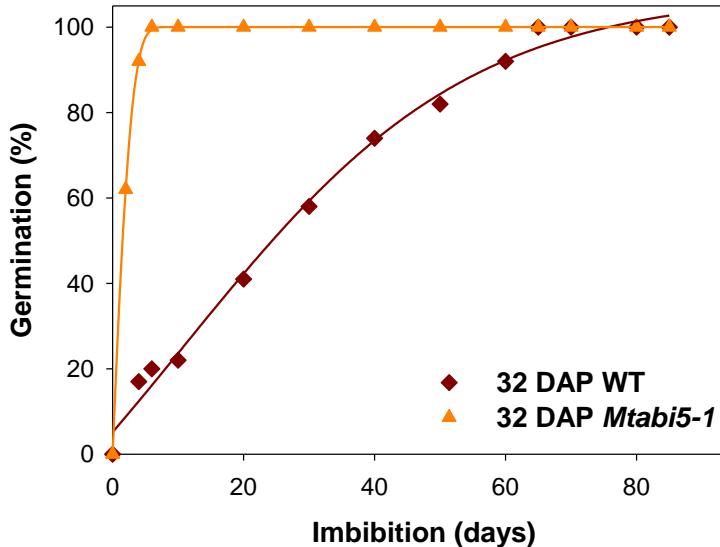
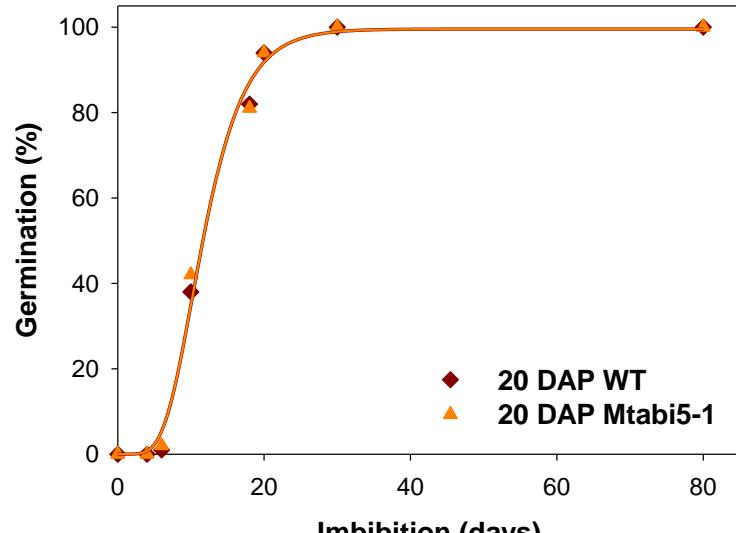
**Proteome**  
(ratio between LEA intensity in mature *Mtabi5* vs WT seeds)



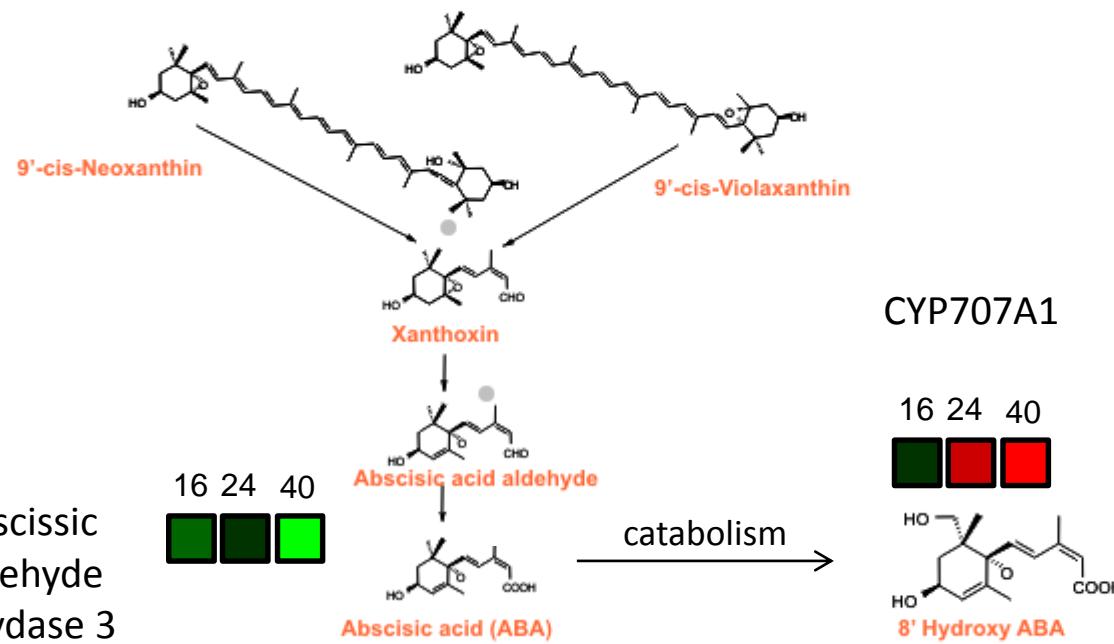
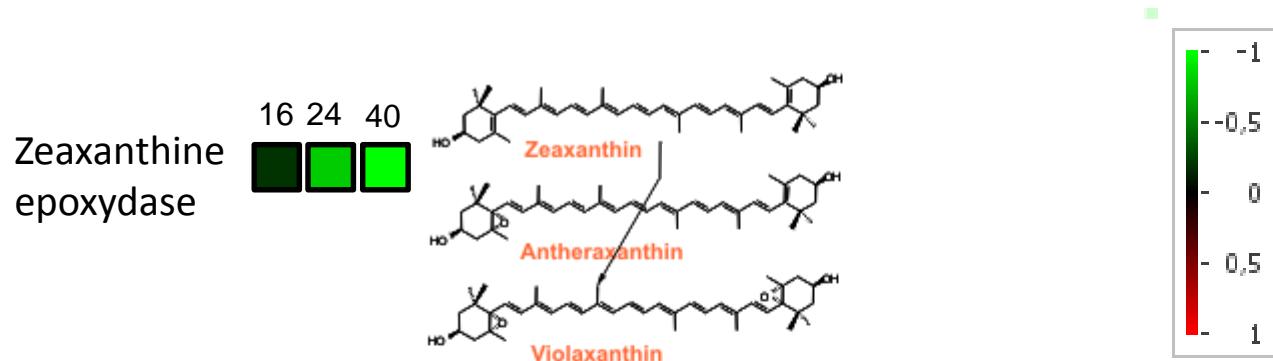
# Seed dormancy is not acquired during *Mtabi5* seed development



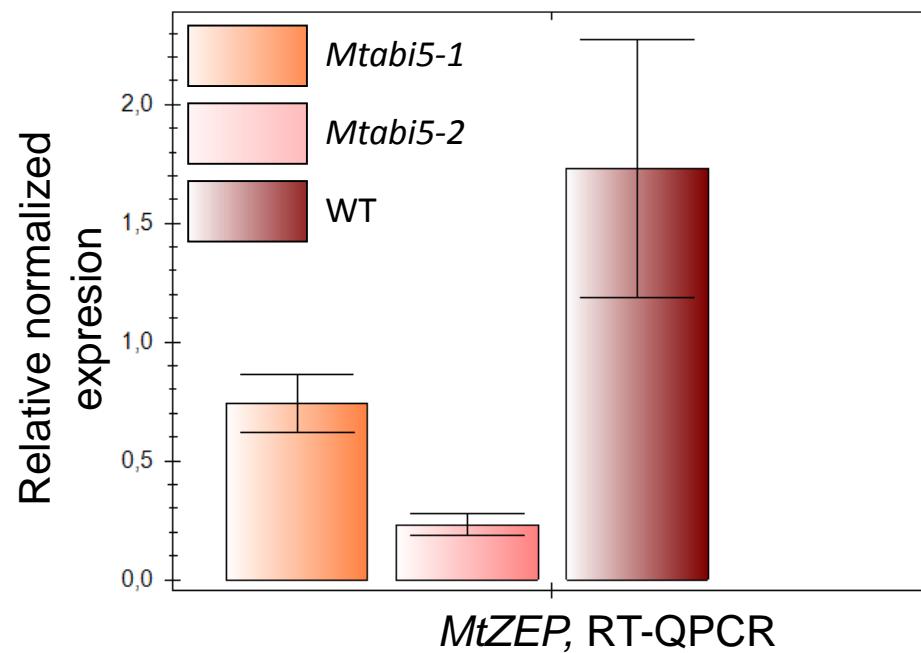
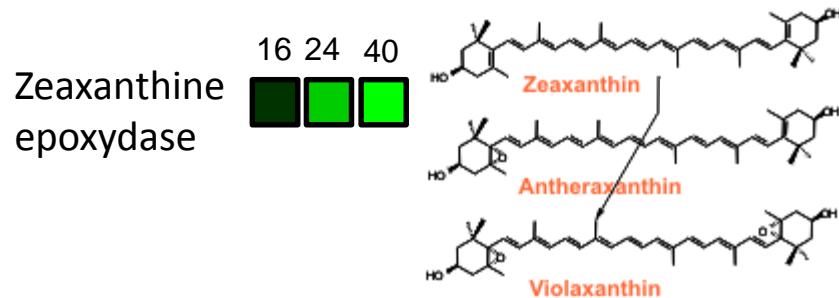
# Seed dormancy is not acquired during *Mtabi5* seed development



# ABA metabolism and catabolism genes are deregulated in *Mtabi5*

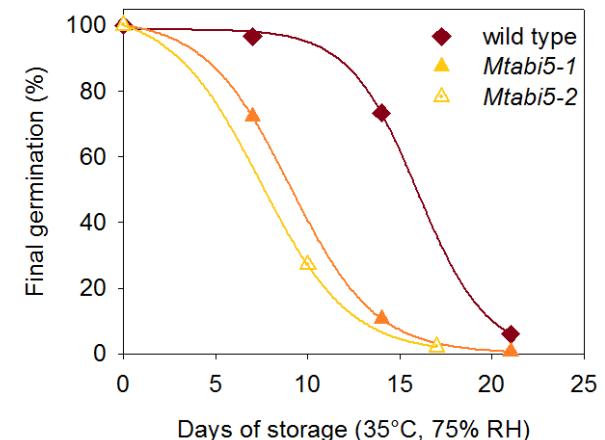
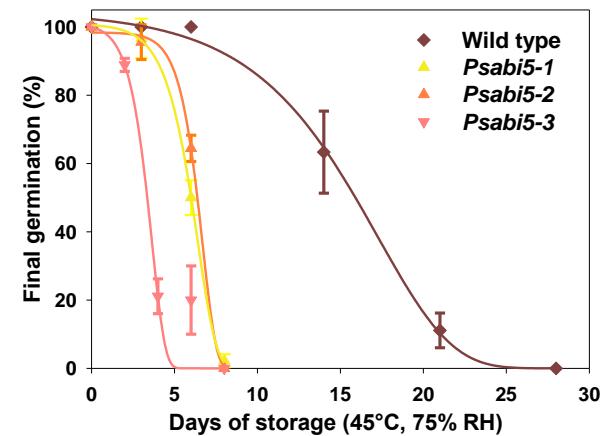
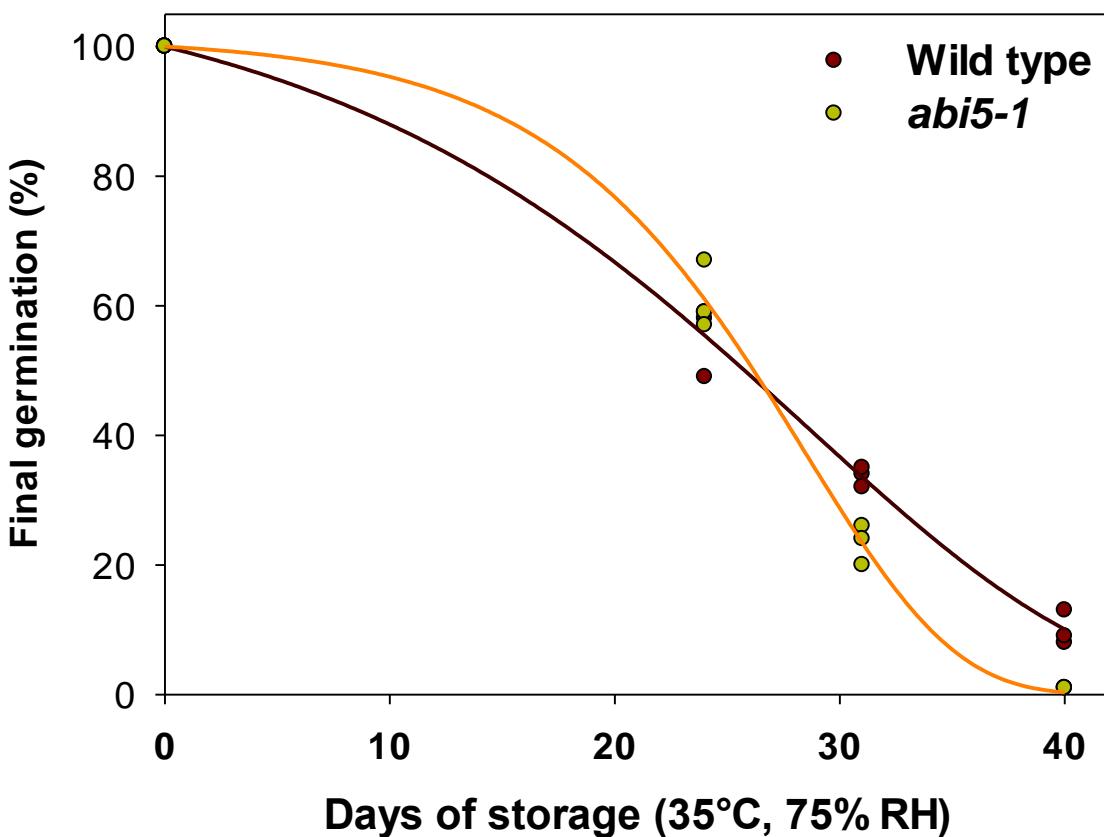


# ABA metabolism and catabolism genes are deregulated in *Mtabi5*



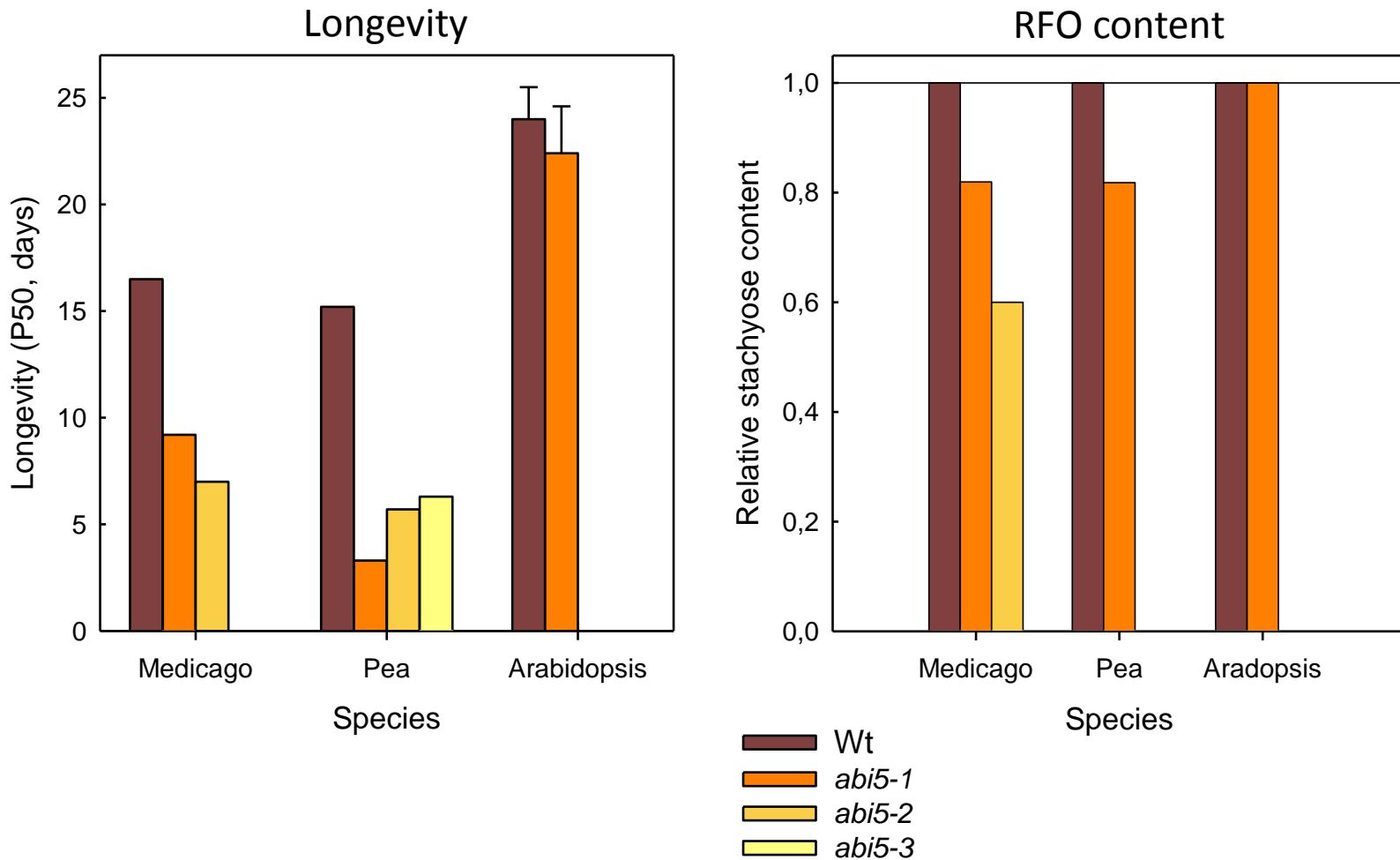
# Characterization of longevity and RFO content in *Arabidopsis abi5-1*

- *abi5-1* mutant (Finkelstein, 1994): Ws background.

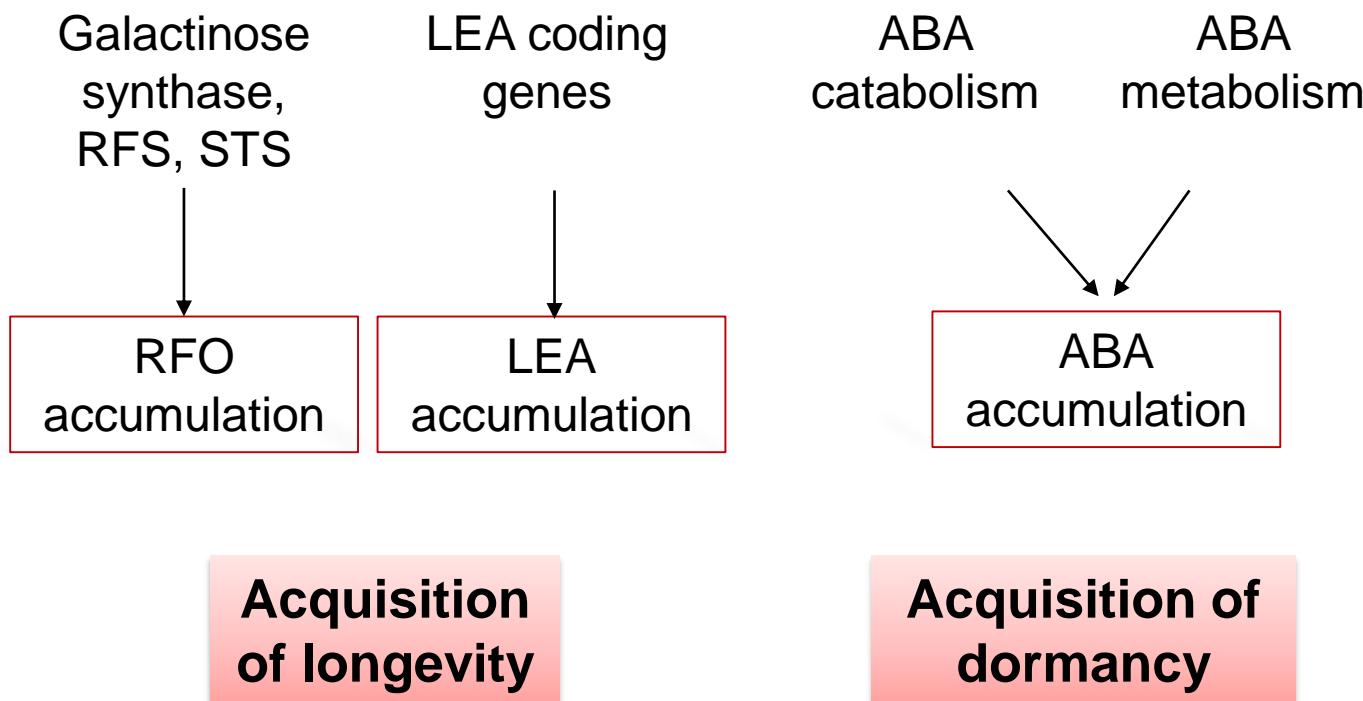
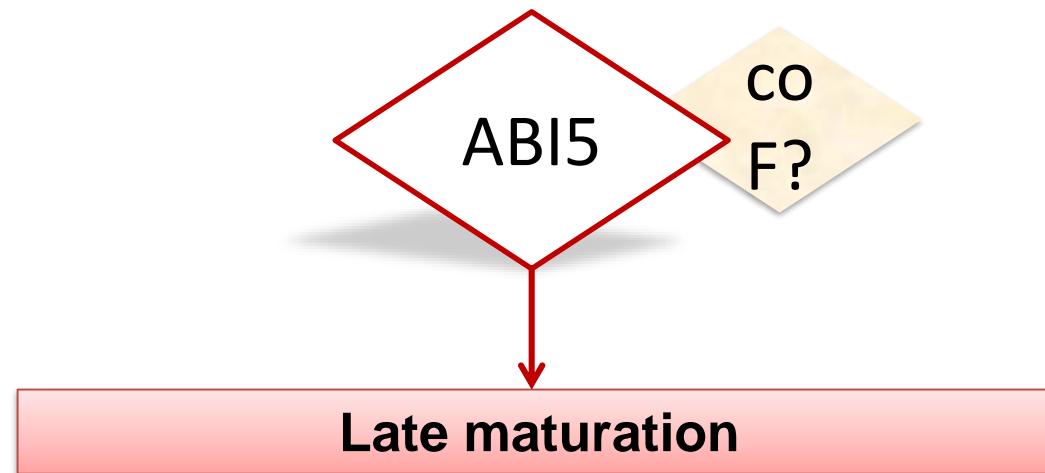


Legume species: Pea  
and Medicago

# Comparative analysis of phenotypes of *Arabidopsis abi5-1* and legume *abi5-1*



# Conclusion: *Medicago* seed maturation



# Acknowledgements

## UMR IRHS, Angers

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## UMR Agroécologie, Dijon

Karine Gallardo

## UMR URGV, Evry

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Samira Elftieh

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Thank you for your attention

Characterization of *MtABI5*. Phylogenetic tree showing the Arabidopsis ABI5 (AT2G36270) amino acid sequence alignment together with nine homologues of *Medicago* identified based on Blast search on Medicago.org (Mt3.5)

