

Integrating gene regulatory networks with root development: adding genetic coefficients to crop models

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Why Roots?

- Roots provide
 - Minerals
 - Nutrients
 - Water
 - Mechanical Support
 - Protection from soil-borne pathogens



Putting mechanisms into crop production models

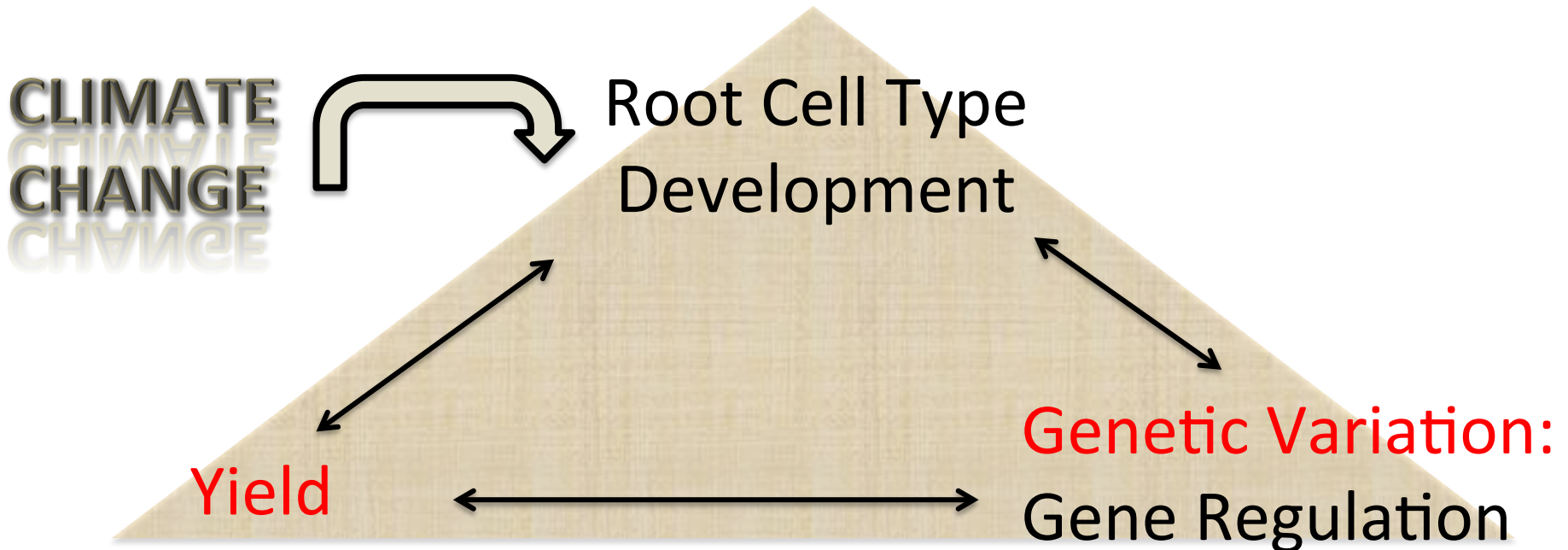
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- Incorporate root growth algorithms to account for static and dynamic soil properties
- Linkage to soil nutrients and soil fertility beyond nitrogen, particularly in the context of climate change.

Grand Challenges

- How completely do gene regulatory networks need to be mapped in order to understand the complex integration of environmental signals and its influence on yield?



Genetic Variation – Root Architecture

- Genetic variation influences yield and other parameters in crop models
- Genetic variation that underlies root architecture both between and within plant species is important

How is root architecture & patterning regulated?



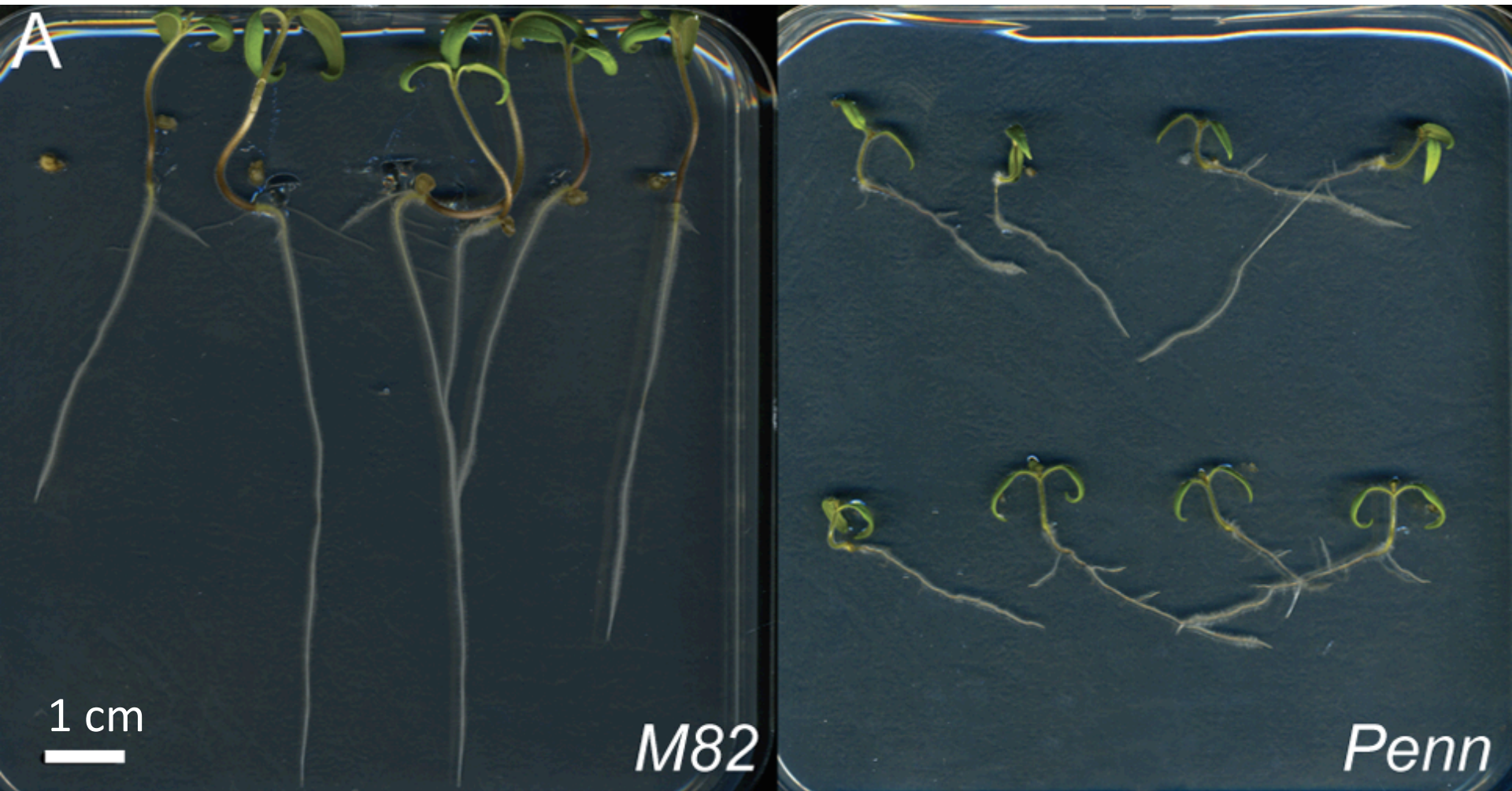
M82



Penn

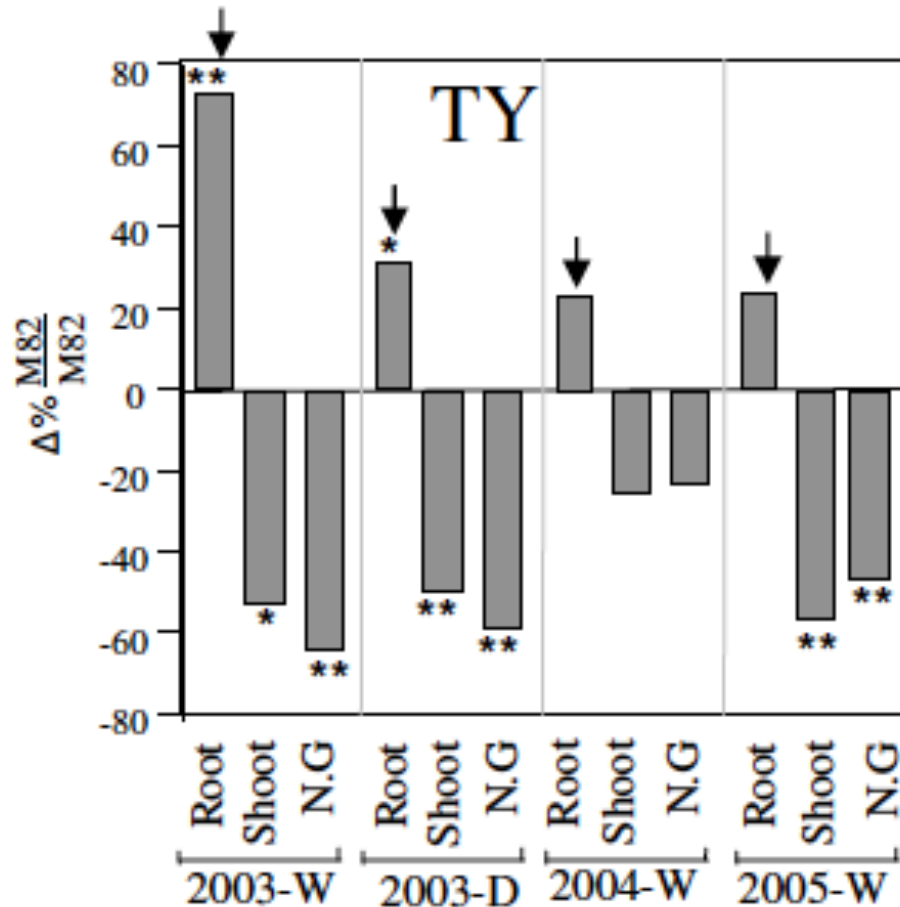


M82 and *Penn* root architecture differ



(Ron et al., Plant Physiology, 2013)

QTL for yield can be derived from the root



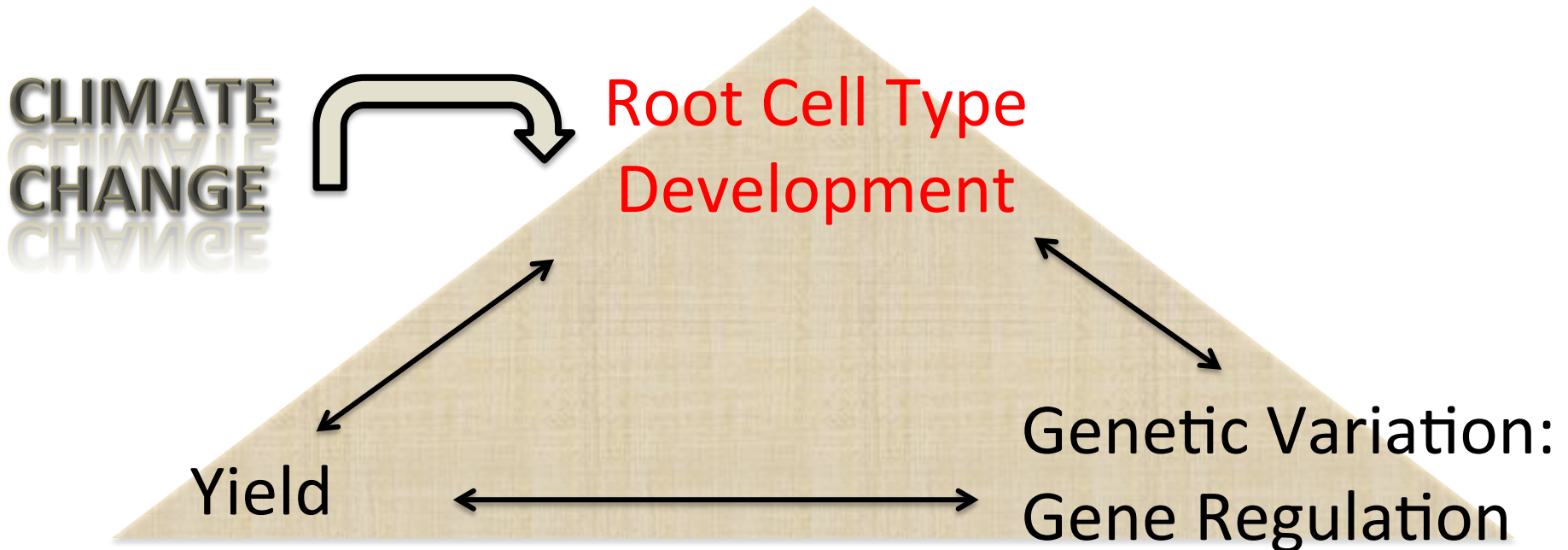
- Gur et al., TAG 2010
- Two field seasons
- Two irrigation treatments
- 13 traits evaluated including Brix and yield
- Grafting to determine root contribution

Bottleneck

- Determination in the field of how the root contributes to yield

Grand Challenges

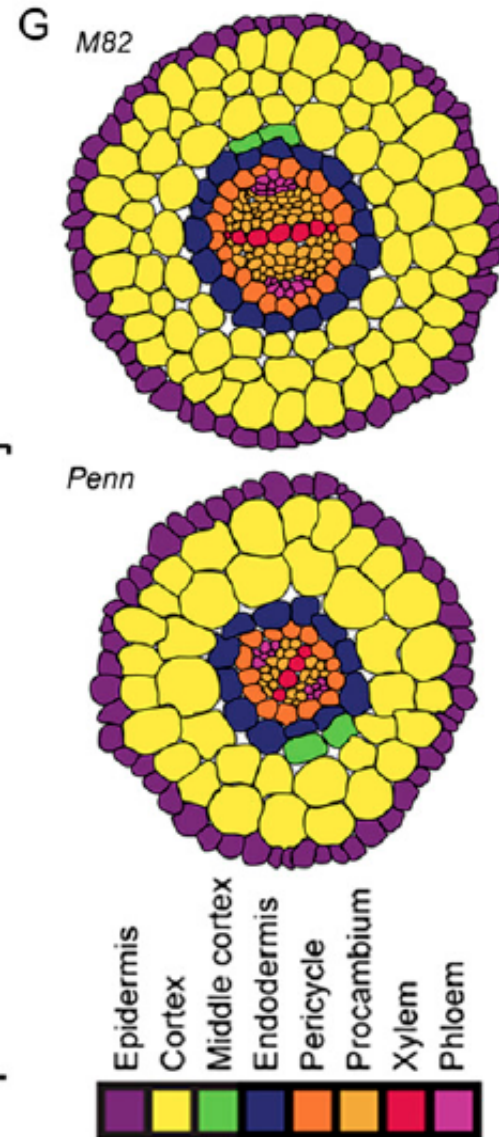
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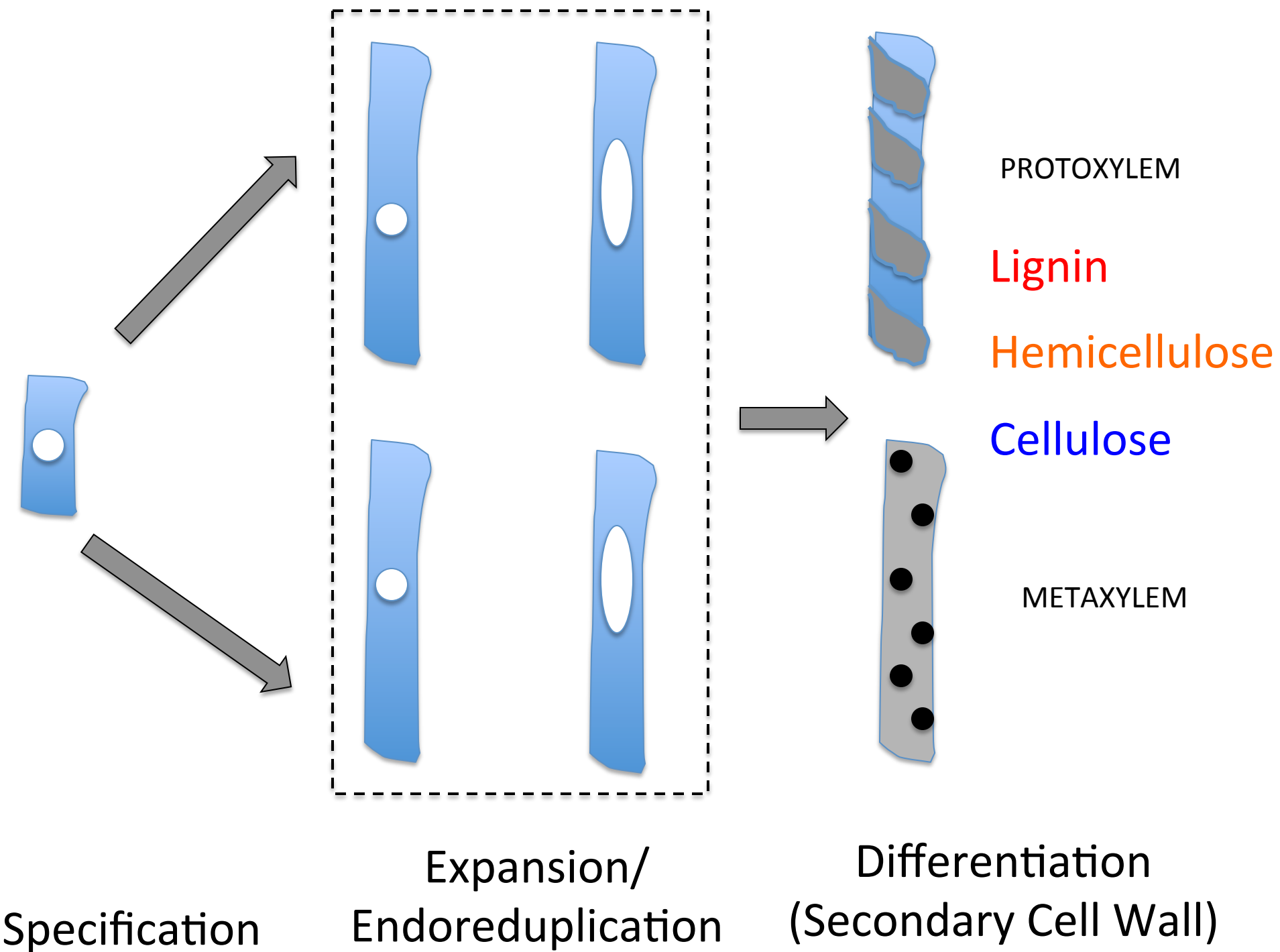
Cell Type Development: Adaptation in Response to the Environment

- Endodermis – salt response (Duan et al. Plant Cell, 2013)
- Light – epidermis (Savaldi-Goldstein et al., Nature 2007)
- Salt transport – cortex – rice (Plett et al., PLoS ONE, 2010)

M82 and Penn differ in root cell patterning

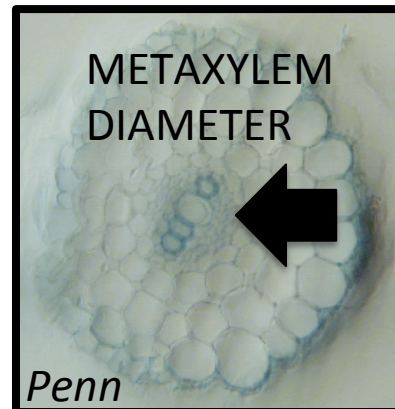
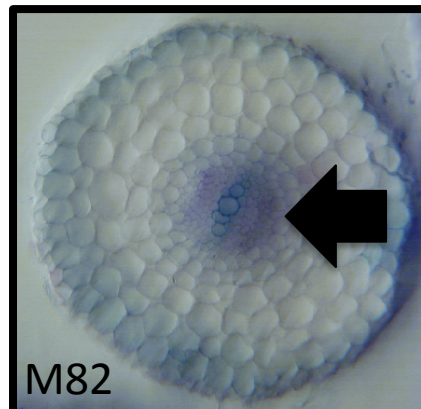
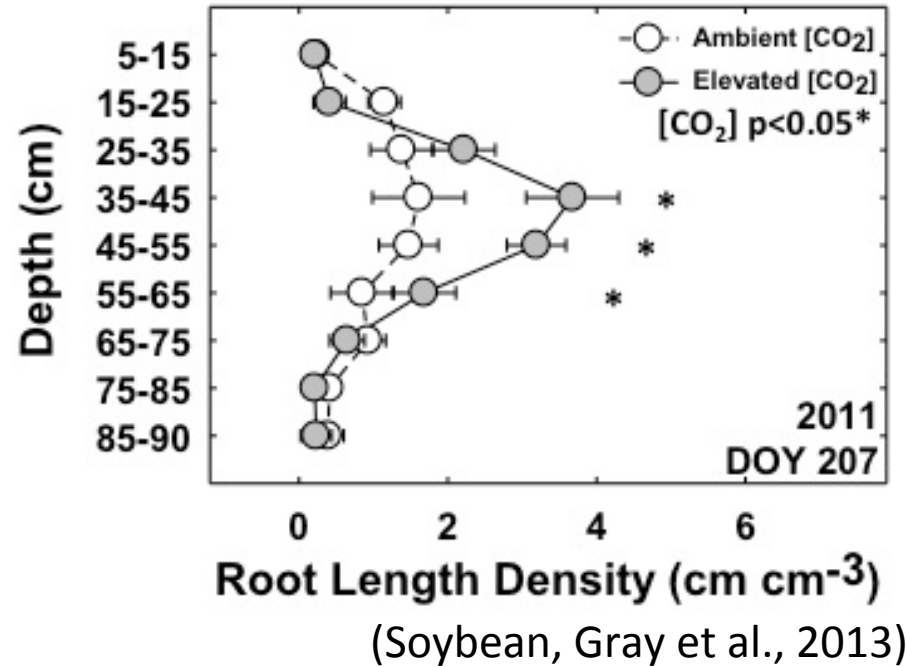
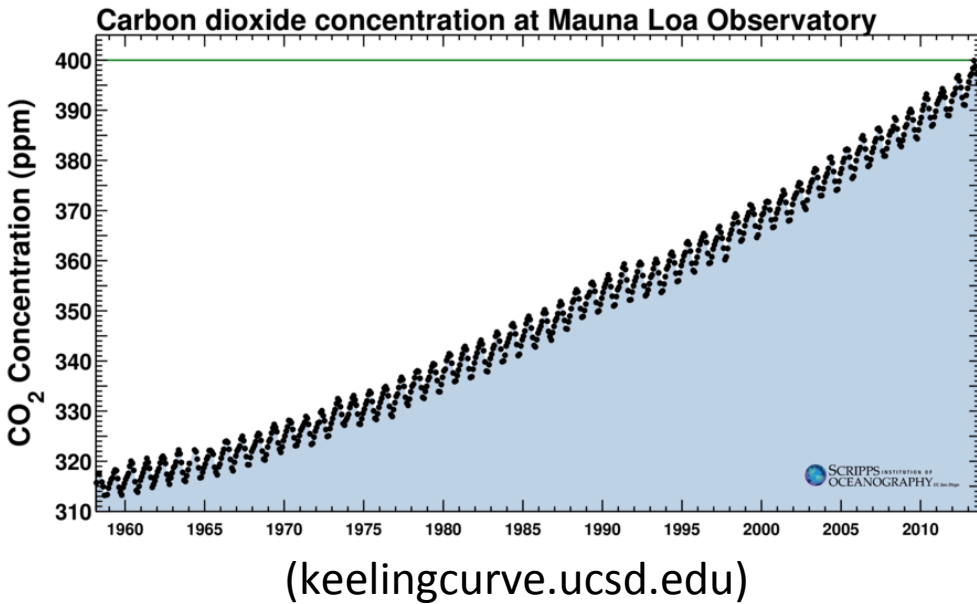


(Ron et al., Plant Phys. 2013)



Is there genetic variation in cell type development in response to a changing environment?

Elevated CO₂ as a Case Study



1100 ppm CO₂

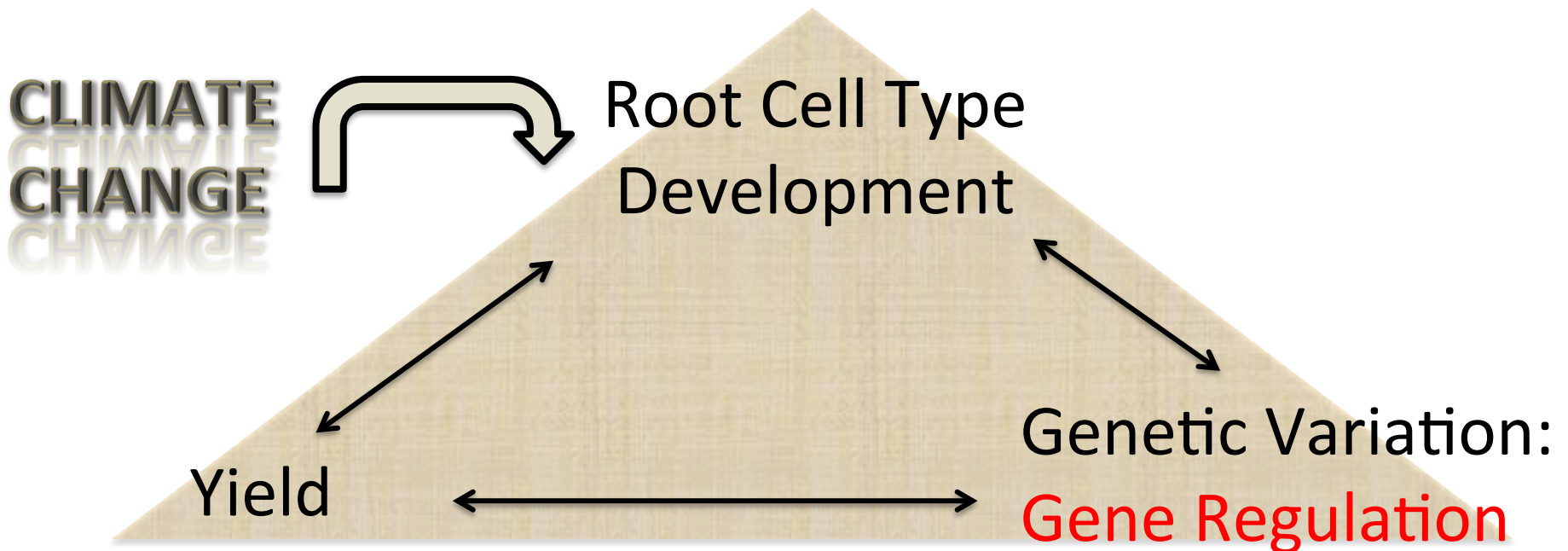


Bottleneck

- Phenotyping at the level of cell type (image recognition, sectioning at high-throughput vs. recalcitrance to imaging with confocal microscopy)
- Interpreting these results with respect to physiology and yield

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Gene Regulation

- Genes are regulated both spatially AND temporally
- This regulation in response to the environment can have different adaptive outcomes

DNA -> RNA -> Protein

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Molecular Signatures in Space and Time

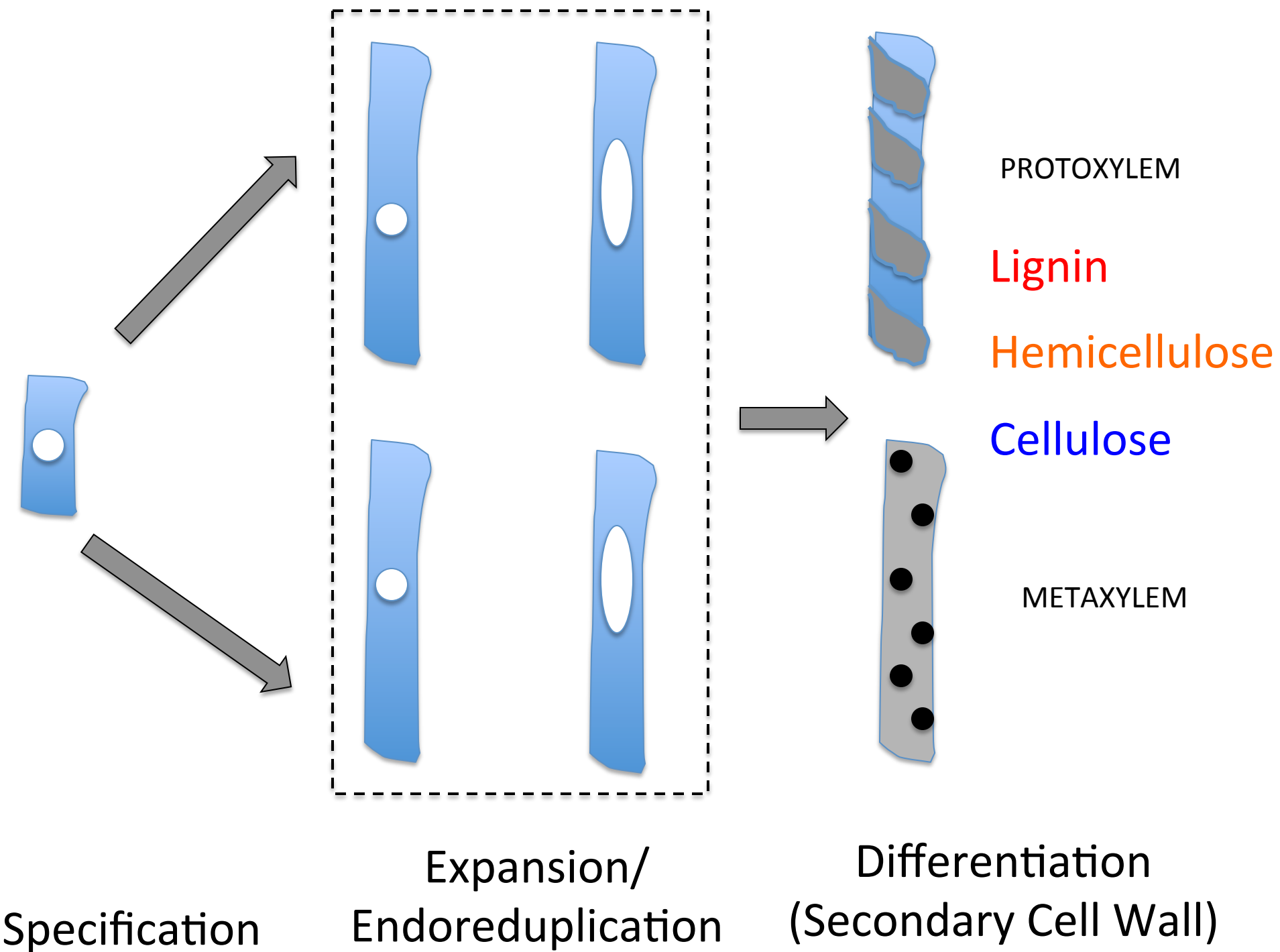
- mRNA (15 cell types)
- miRNA
- TRAP (translating ribosome affinity purification)
- Proteomic
- Metabolomic

(Brady et al., 2007, Mustroph et al. 2009, Petricka et al. 2012, Breakfield et al., 2012, Moussaief et al. 2013)

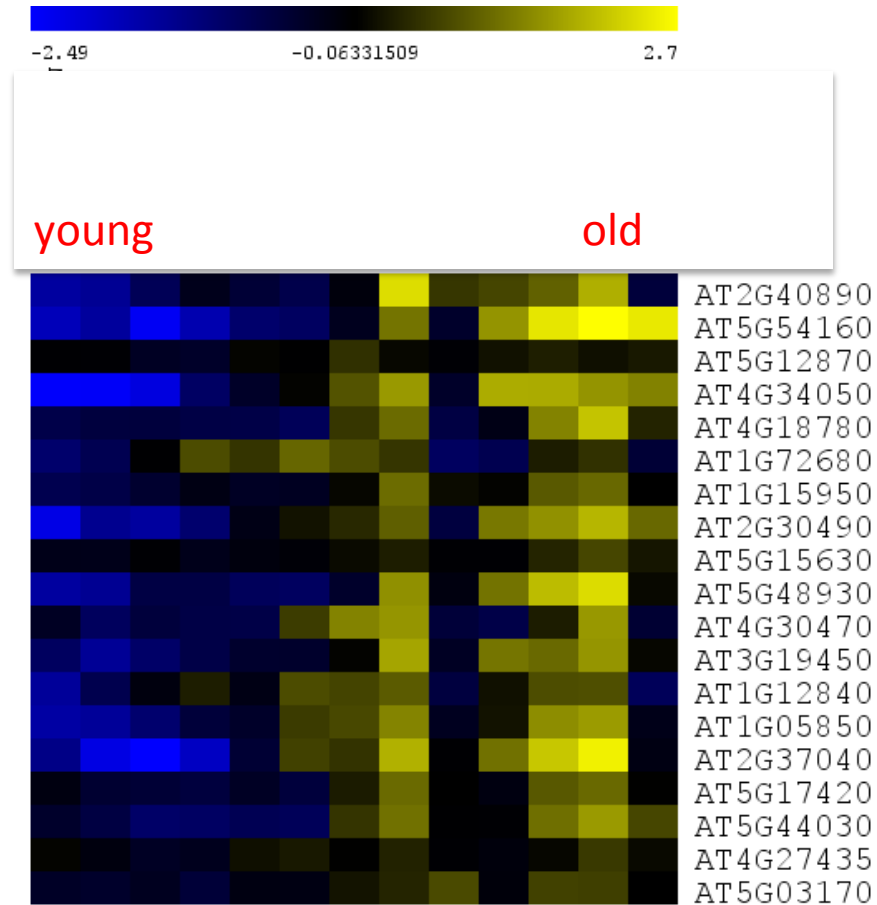
Transcriptional Regulatory Mechanisms



overly simplistic



Secondary wall genes exhibit temporal coexpression



Bottleneck

- Mapping regulation at cell type resolution in crop species is challenging – but surmountable
- Modeling the regulation in response to physiologically relevant stresses and integrating these datasets is even more challenging

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