



University of
Nottingham

UK | CHINA | MALAYSIA

DeepGenes:

Functional
characterization of genes
enhancing
soil exploration in maize

Riccardo Fusi
MGA meeting
Nottingham
February 2020



UNIVERSITY OF
GEORGIA



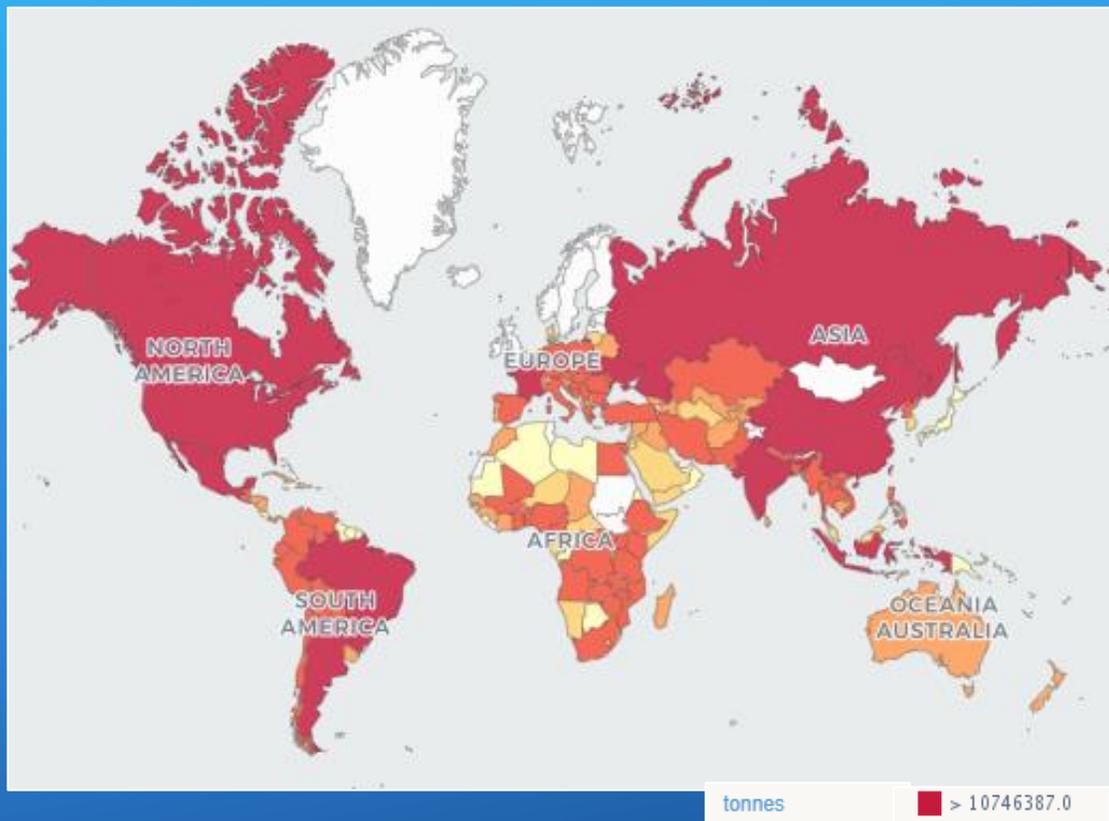
WISCONSIN
UNIVERSITY OF WISCONSIN-MADISON



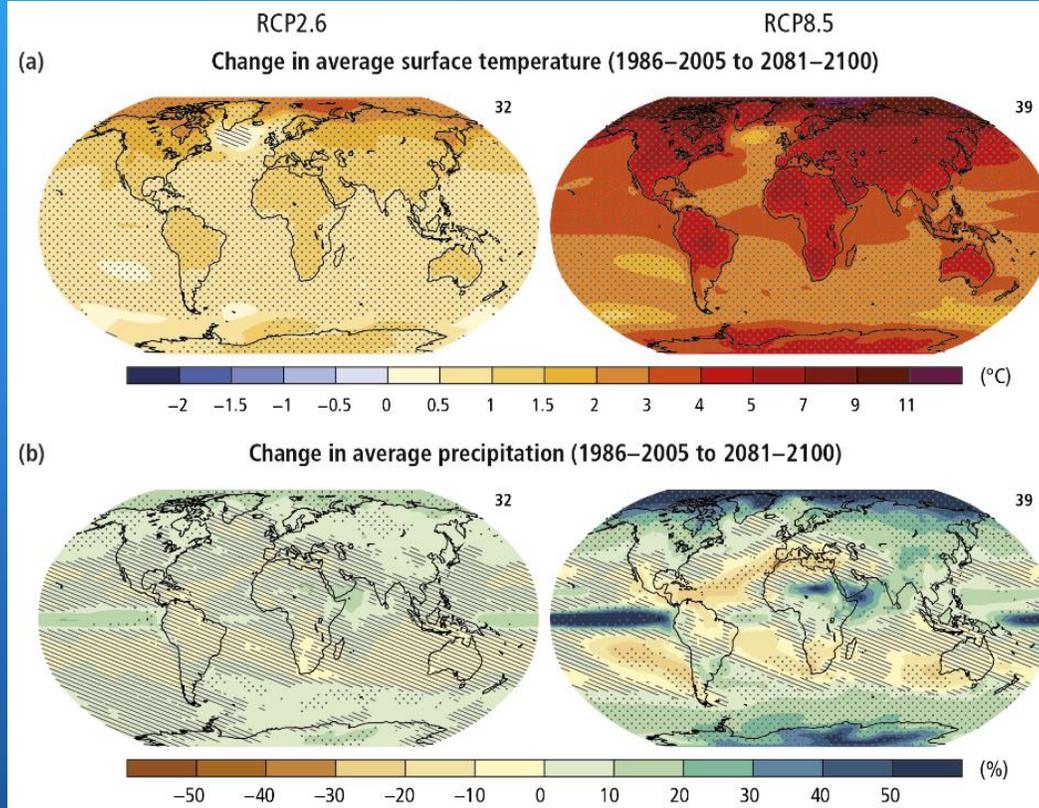
PennState



Why maize?



Maize production. FAOSTAT, 2016



Climate change prediction. IPCC, 2014

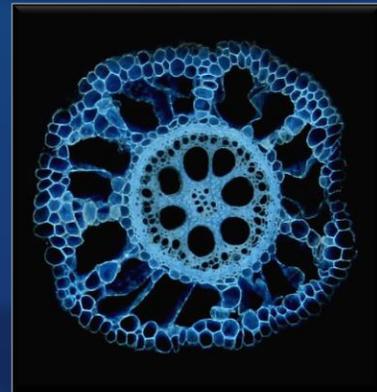
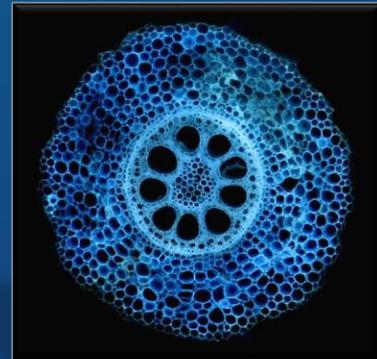


Jonathan Lynch

DEEPER: AN INTEGRATED PLATFORM FOR DEEPER ROOTS *Led by Penn State with Wisconsin, Georgia & Nottingham*

Technology Summary

Development of platform for breeding maize with deeper roots that sequester more carbon and are more efficient in utilization of nitrogen and water.





Overview on DEEPER platform

DEEPER

LEADER

OpenSimRoot

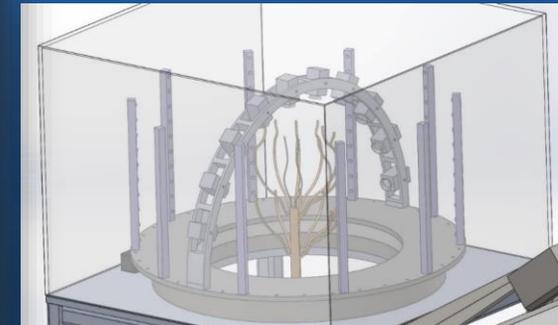
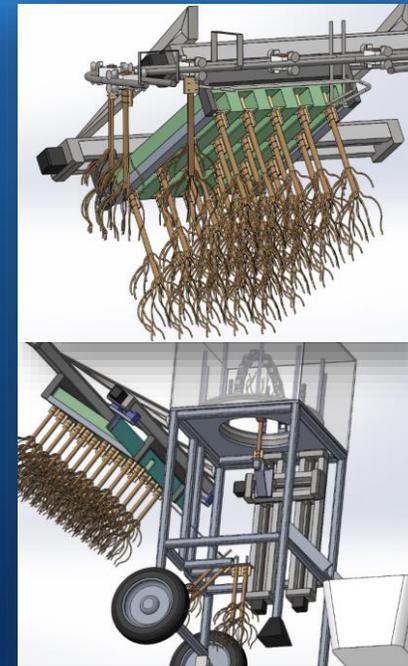
Root Robot

Dirt 3D

Anatomics

Deep Learning

Deepgenes





Overview on DEEPER platform

DEEPER

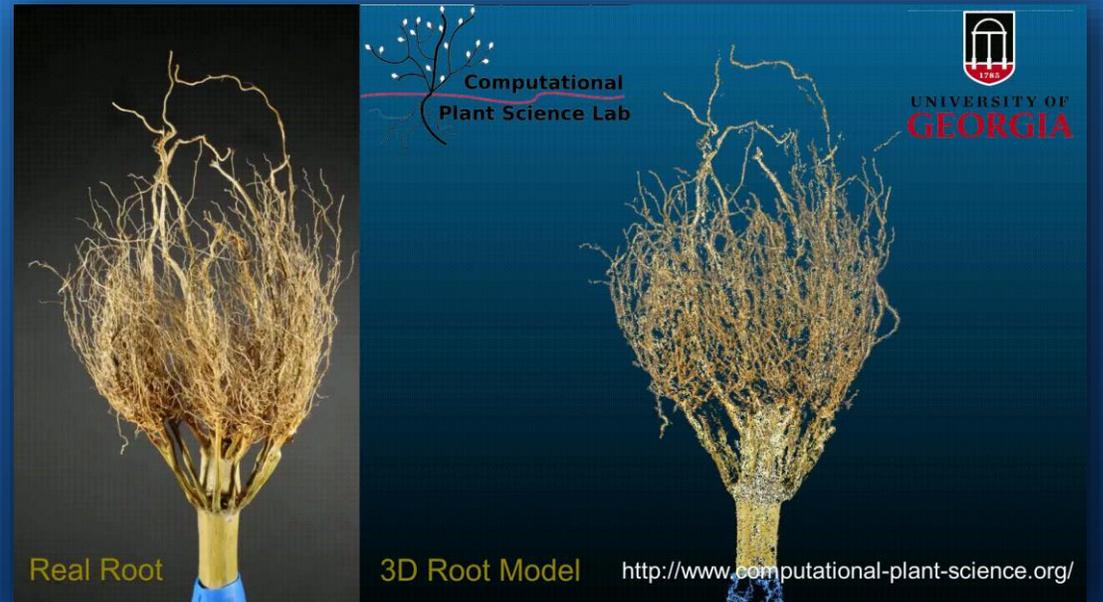
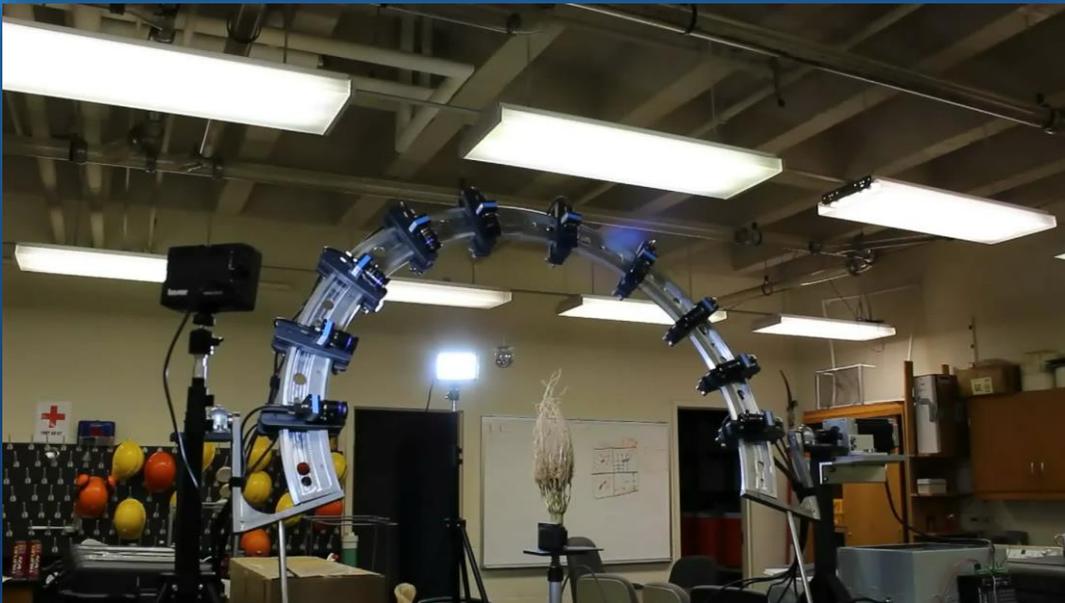
Root
Robot

Dirt 3D

Anatomics

Deep
Learning

Deepgenes





Overview on DEEPER platform

DEEPER

Root Robot

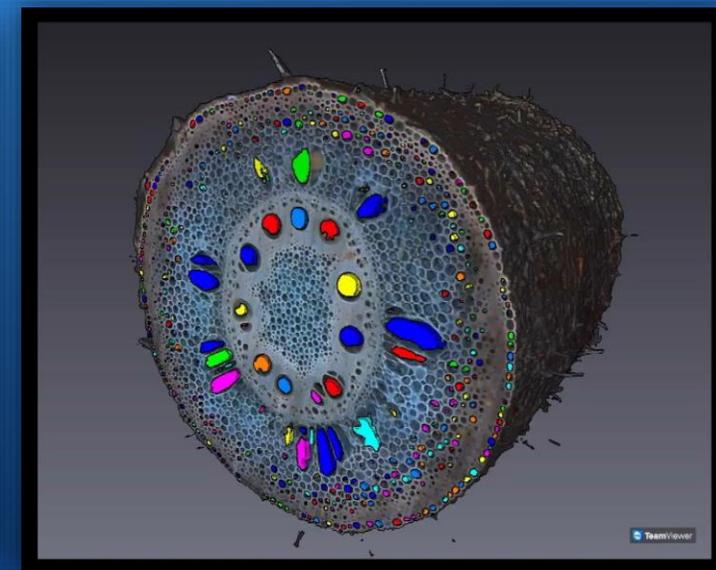
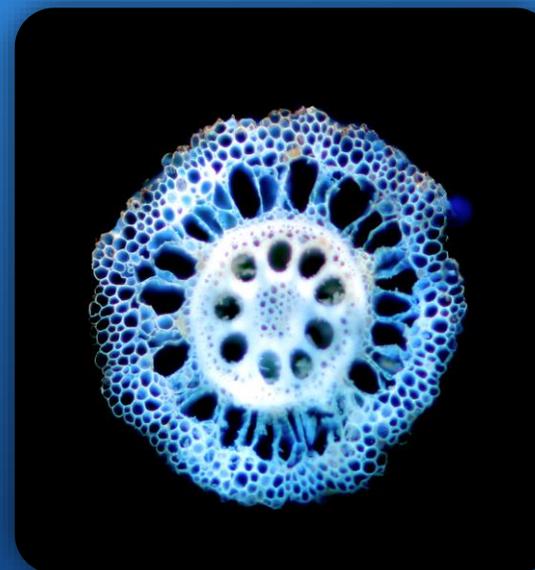
Dirt 3D

Anatomics

Deep Learning

Deepgenes

LAT 2.0



DEEPER

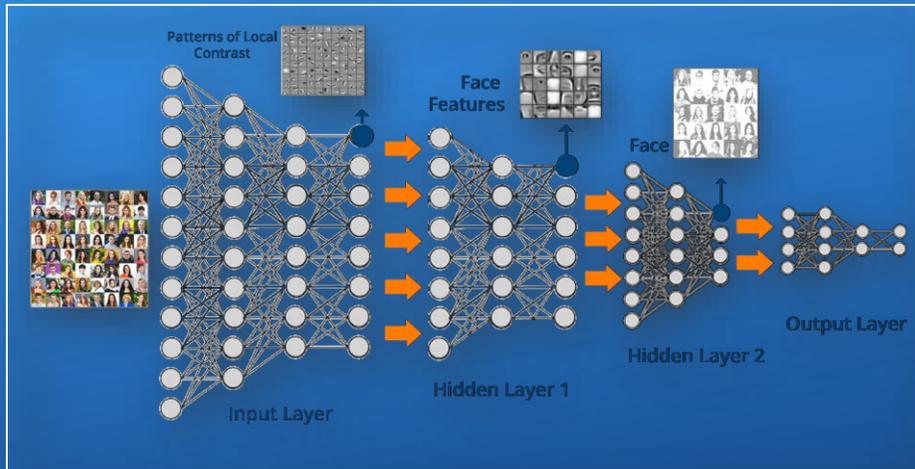
Root Robot

Dirt 3D

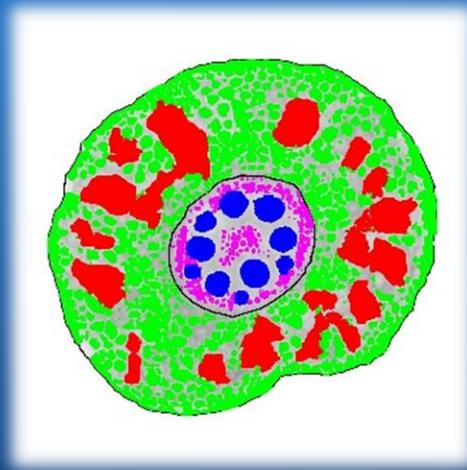
Anatomics

Deep Learning

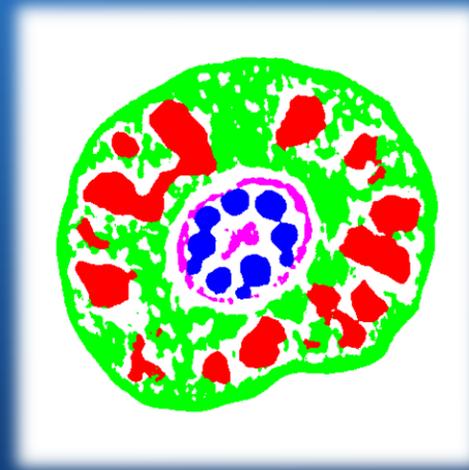
Deepgenes



Input image



Ground truth



Output





DEEPER

Root
Robot

Dirt 3D

Anatomics

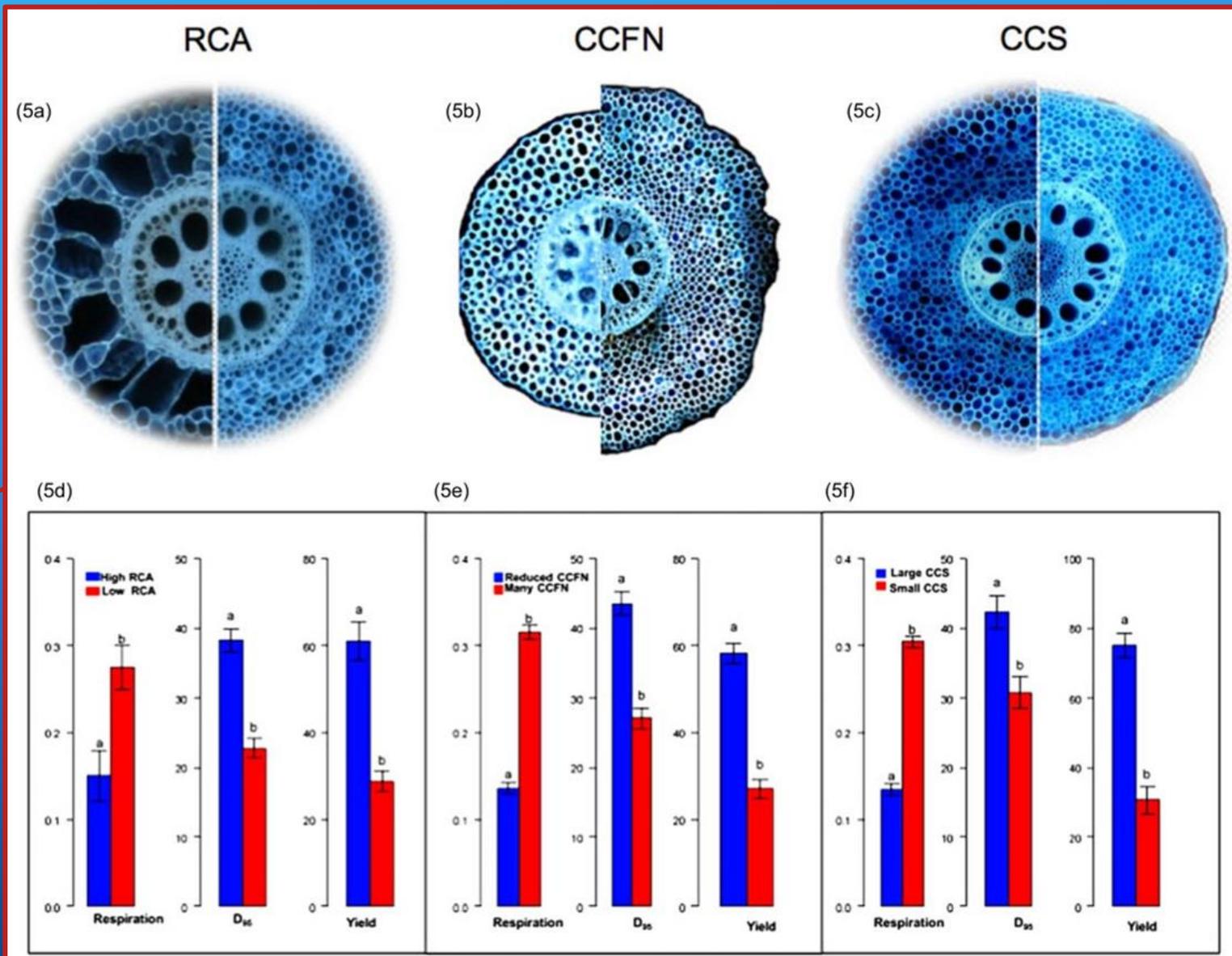
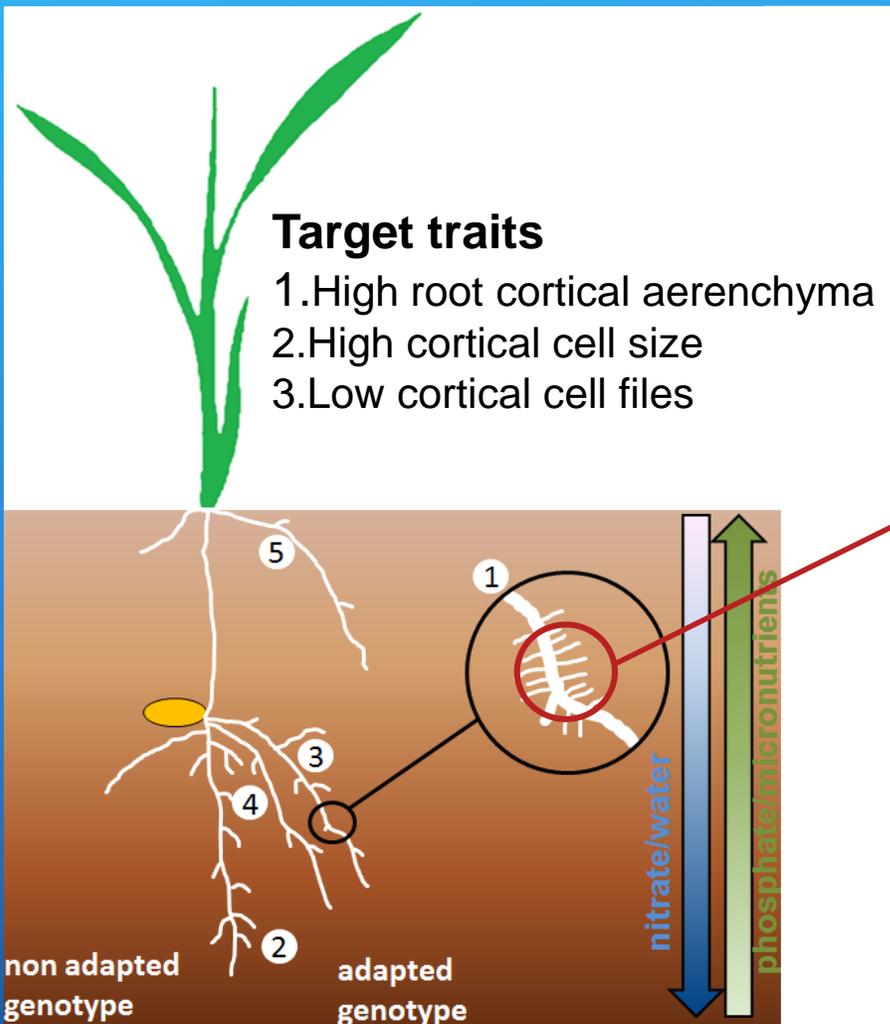
Deep
Learning

Deepgenes

Identify germplasm, genes, and genetic models to develop hybrids with increased root mass at depth while maintaining grain and productivity

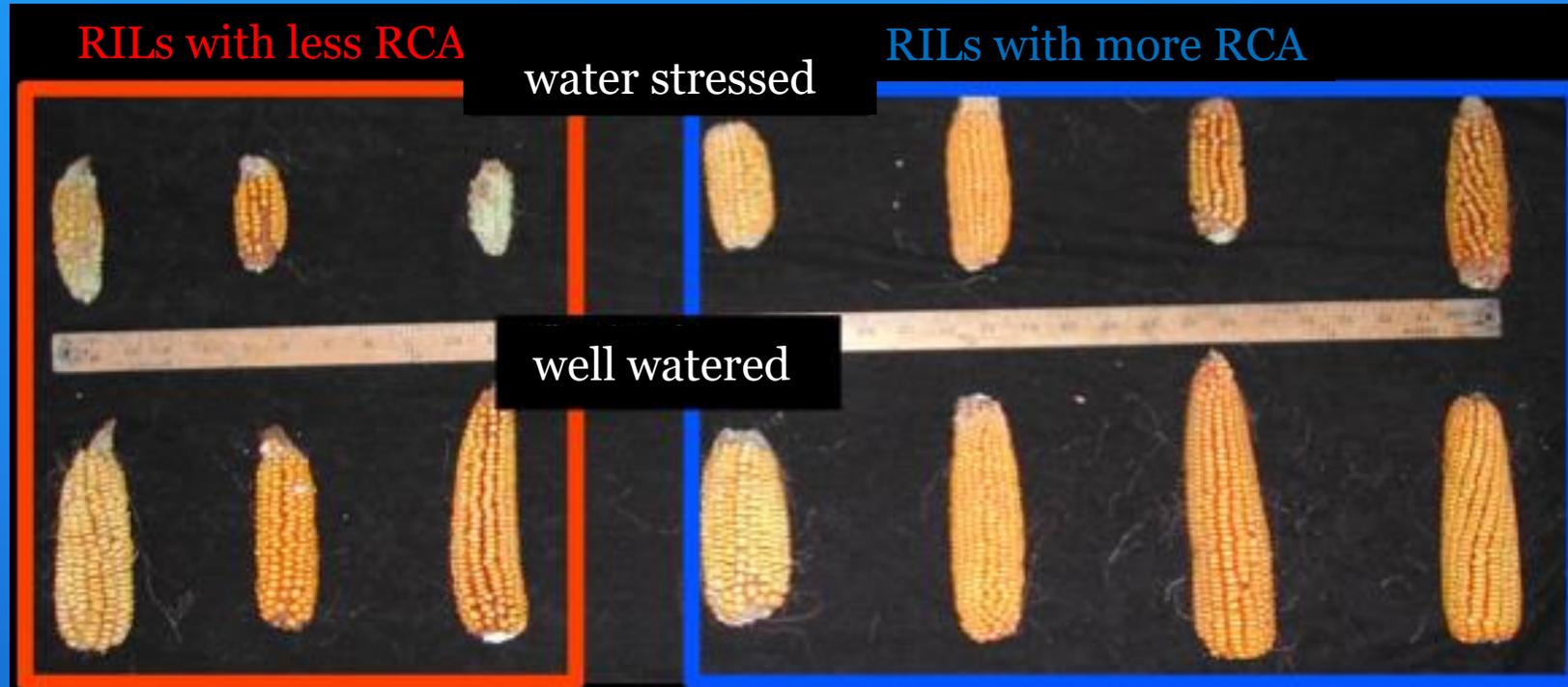


Deepgenes background: Redesigning root anatomy

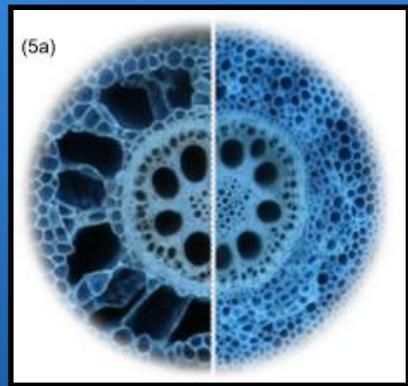
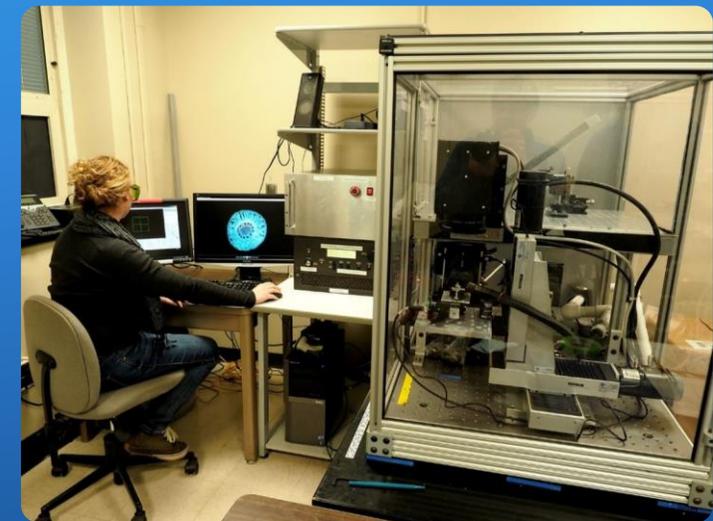
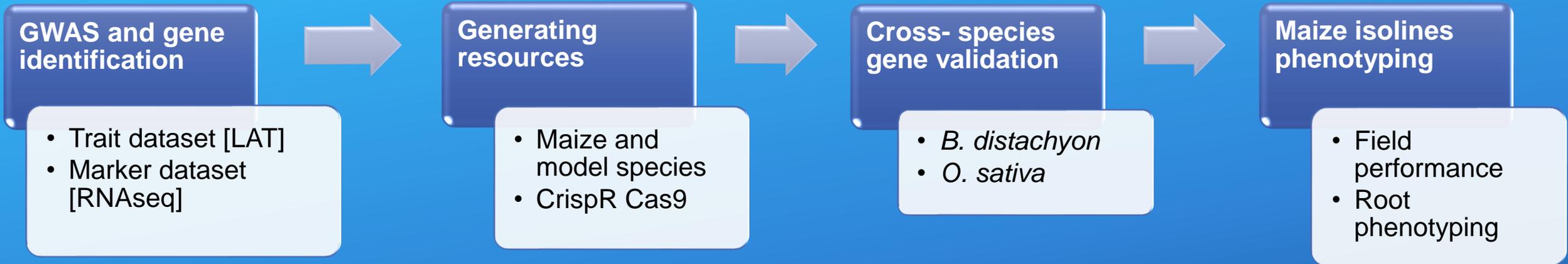




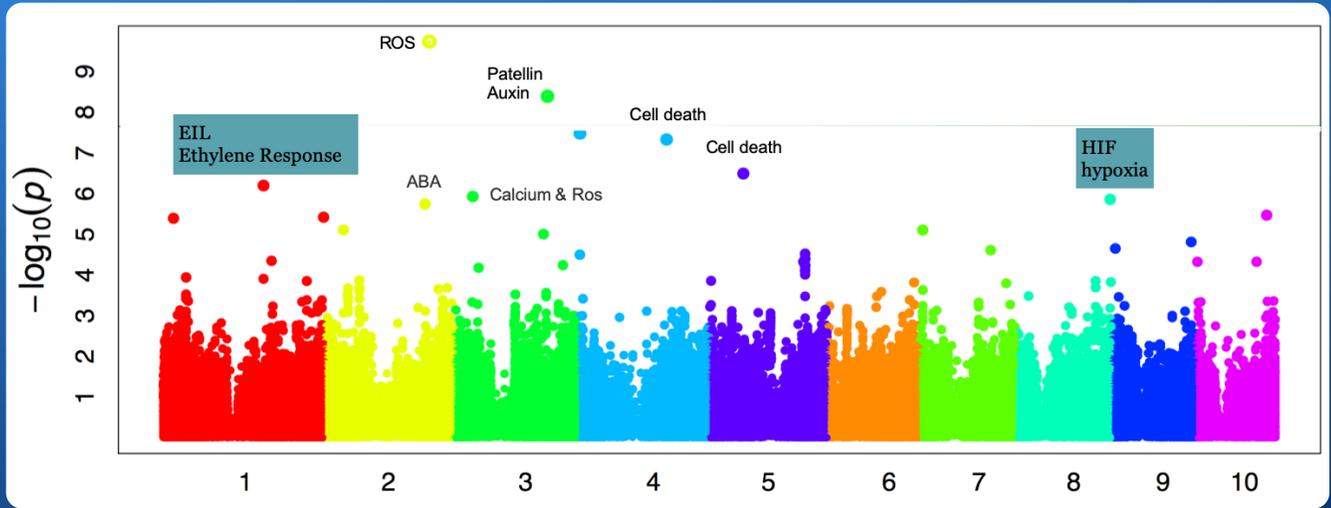
High RCA lines show better yield stability under drought stress



DeepGenes Workflow



900K SNP dataset
>450 maize genotypes

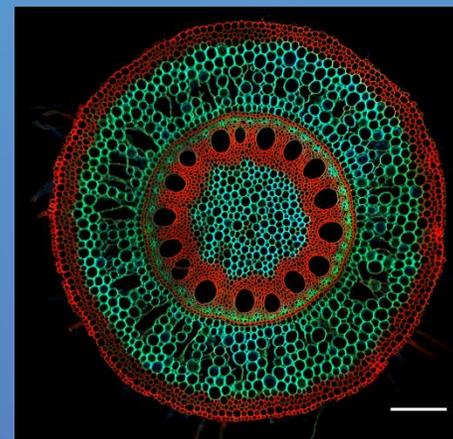




From Maize to model crops



Zea mays sp.



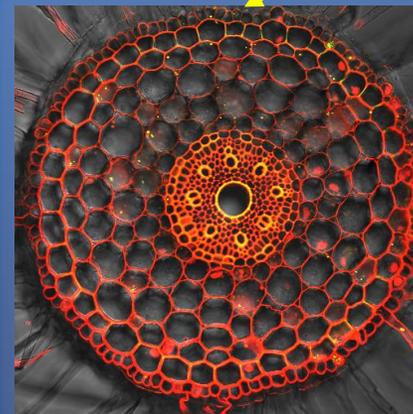
Zea mays sp.



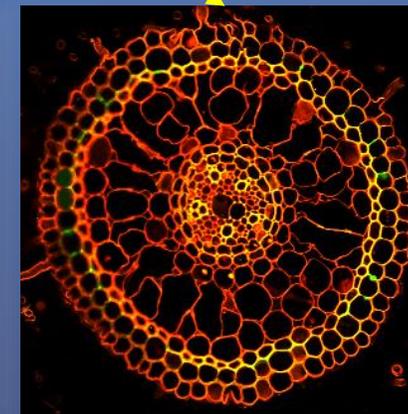
Brachypodium Dystachion sp.



Oryza sativa sp.

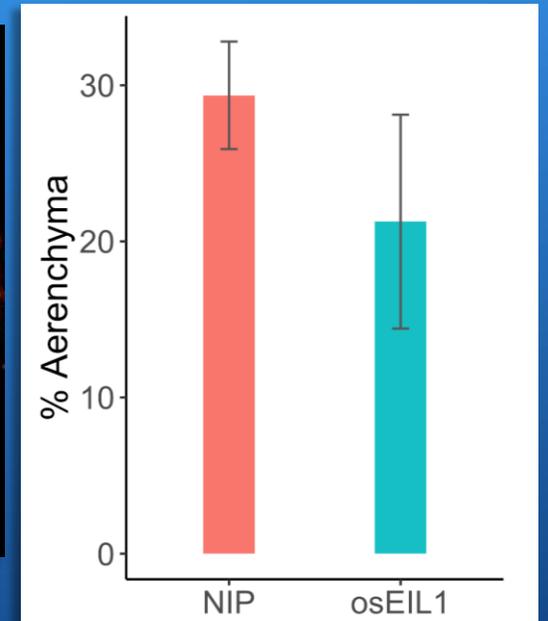
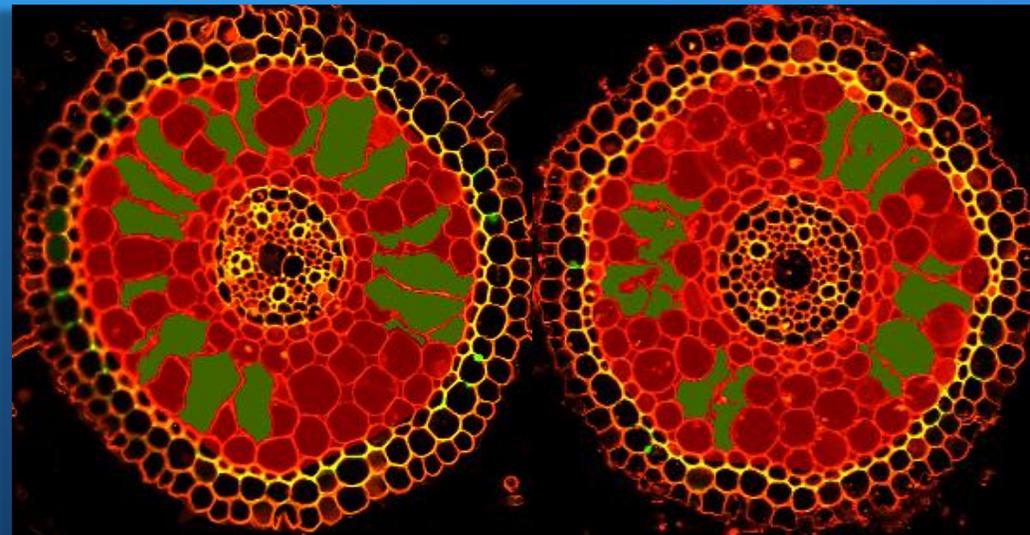
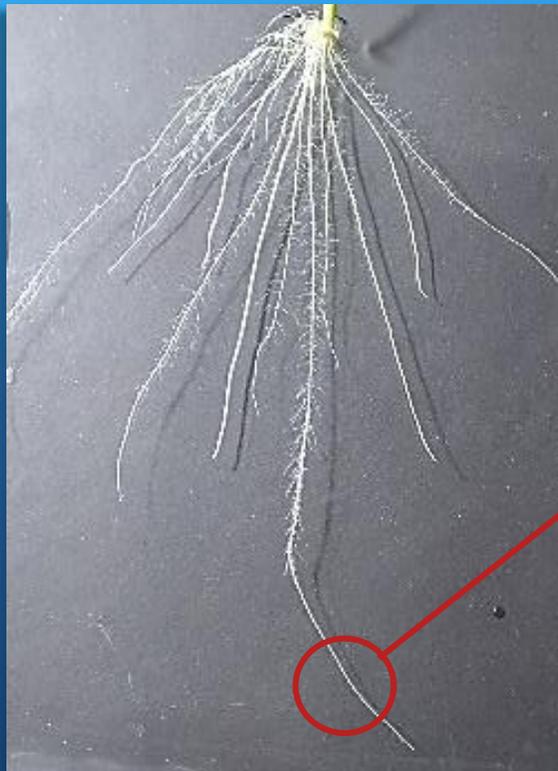


Brachypodium Dystachion sp.
7 days

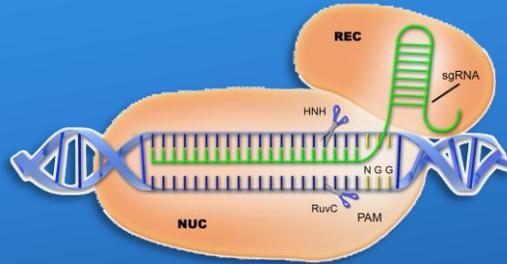
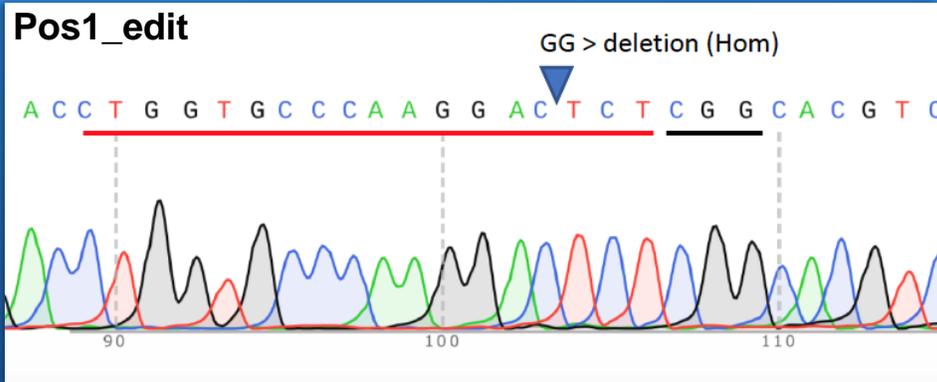
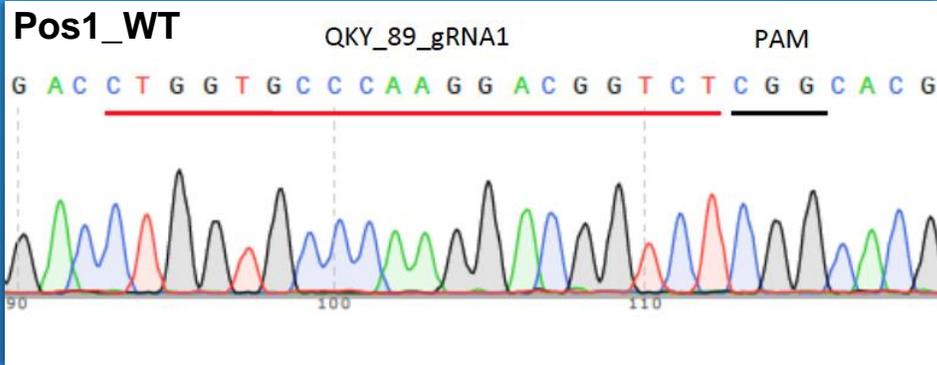


Oryza sativa sp.
12 days

Validating root cortical aerenchyma formation is ethylene dependent



Validating Atr1 is important for Root Cortical Area using CrispR

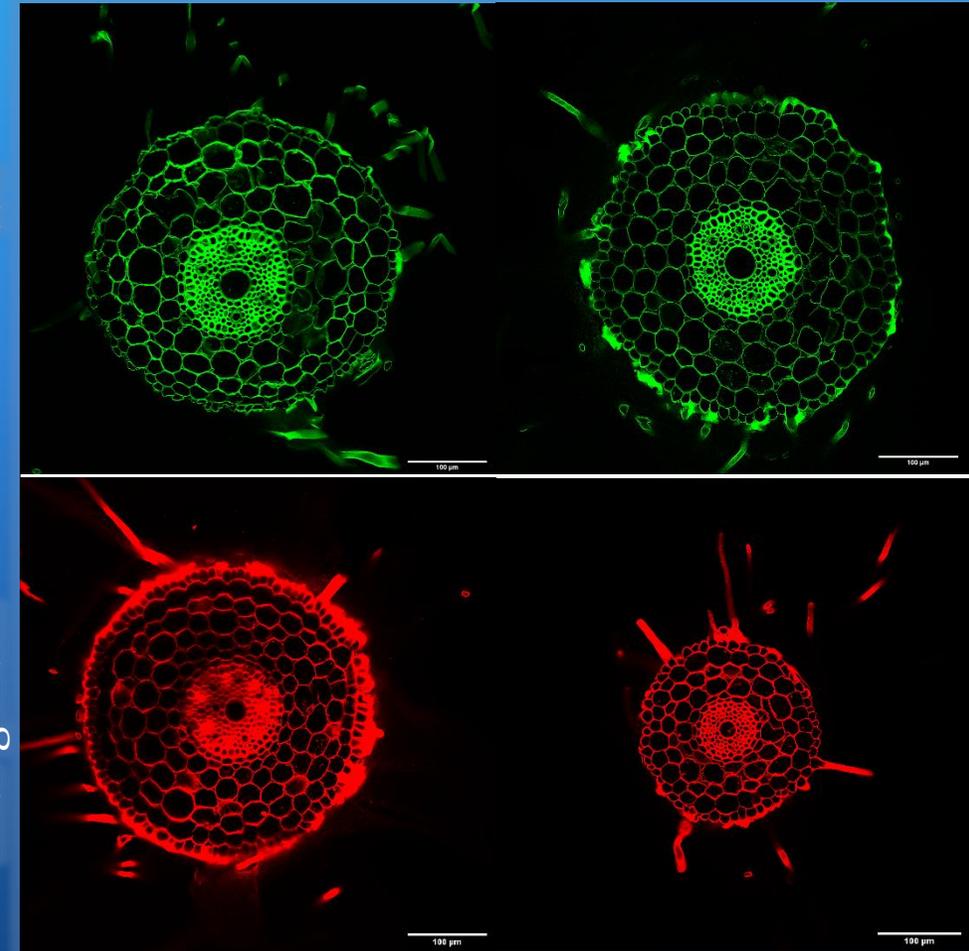


WT

Atr1-gRNA1

Primary

Crown





Conclusions:

- Anatomical traits are important for plant fitness;
- New generation of anatomical phenotyping technologies are available (L.A.T.);
- Anatomical Data can be used to identified key candidate genes;
- Plant model can be used to develop mechanistic insights into anatomical traits.

Future works:

- Characterising candidate genes regulating anatomical (and architectural) root traits;
- Explore natural variation for such genes to be integrated in genomic selection breeding plans



Acknowledgements

Penn State University:

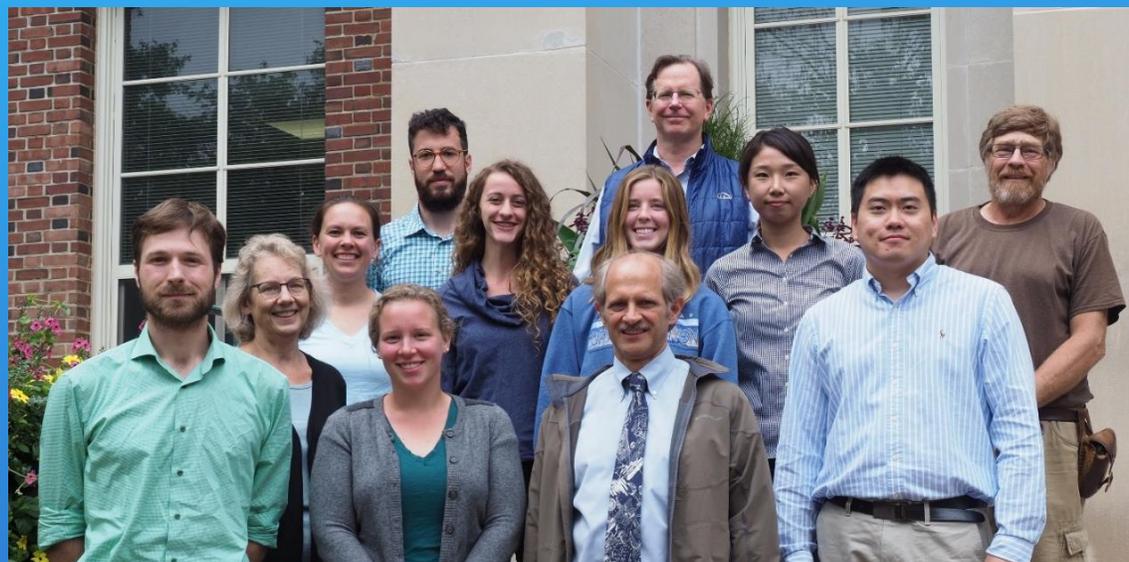
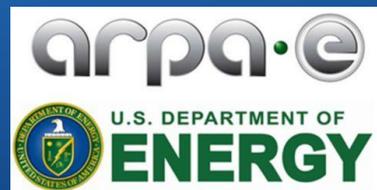
- Prof. Jonathan Lynch
- Prof. Kathleen Brown
- Dr. Hannah Schneider
- Dr. Molly Hanlon

University of Nottingham:

- Prof. Malcolm Bennett
- Dr. Rahul Bhosale
- Dr. Anthony Bishopp

University of Winsconsin:

- Prof. Shawn Kaeppler
- Dr. Vai Lee Nor
- Dr. Ray Collier





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Hounsfield Facility
3D X-ray imaging

THANK YOU!

The Hidden Half

www.nottingham.ac.uk/hiddenhalf/



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YouTube

https://www.youtube.com/watch?v=3eH931N1Rd3I&list=PLpRE0ZU_K-BXLU3FT0DF1QU0wUv1psgDPf

