



Genetic bases of early root growth ~~and rhizosheath formation~~ in pearl millet (*Pennisetum glaucum* L.)

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UNIVERSITÉ
DE MONTPELLIER

Laboratoire mixte international Adaptation des Plantes et
microorganismes associés aux Stress Environnementaux (LAPSE),
Dakar, Senegal

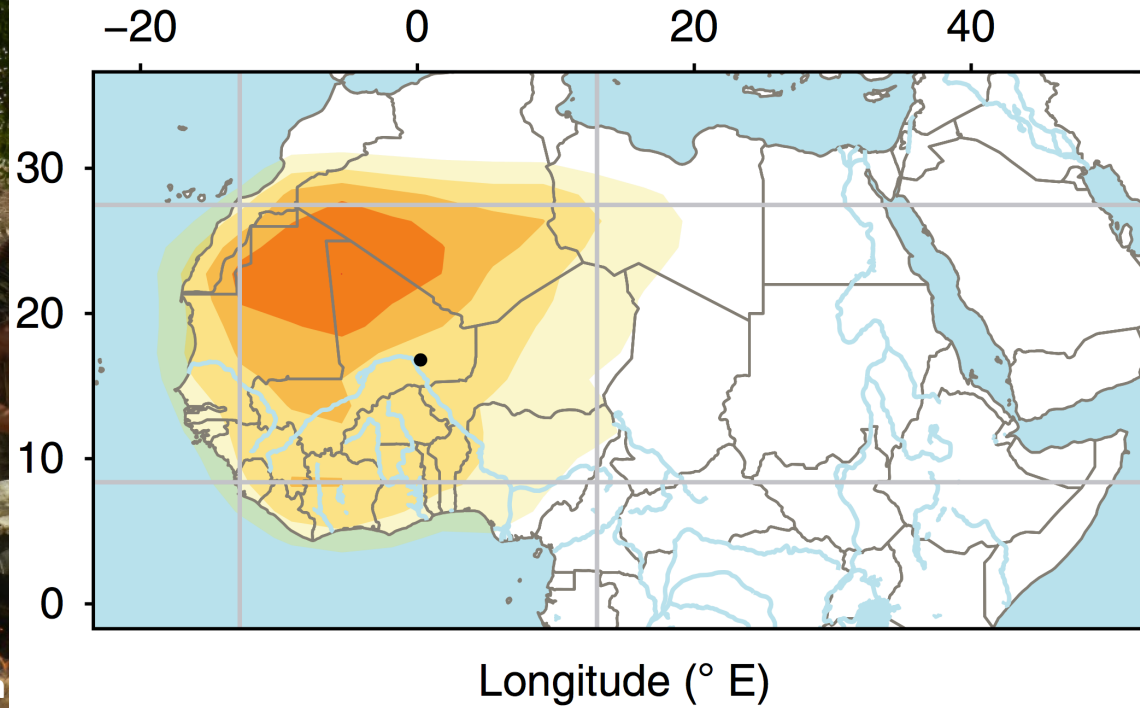
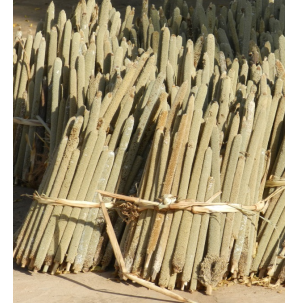


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Pearl millet

Pennisetum glaucum



Burgarella *et al*, Nat. Ecol. Evol. 2018



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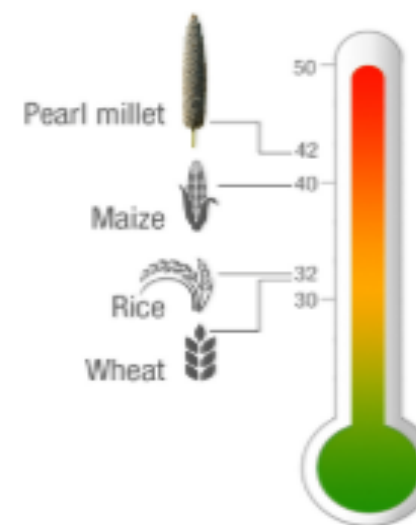


Pearl millet

One of the hardiest cereals



Photos: Y. Vigouroux (IRD)



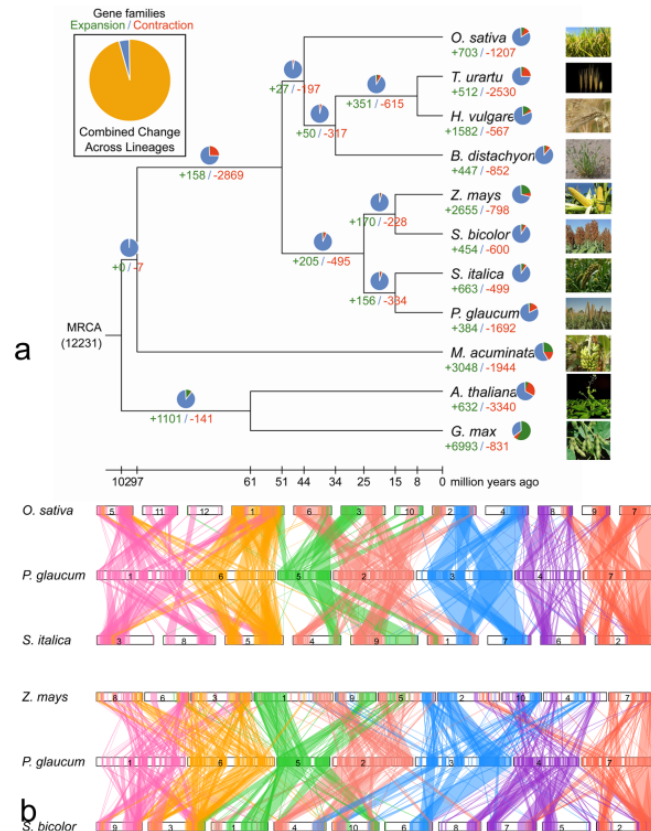
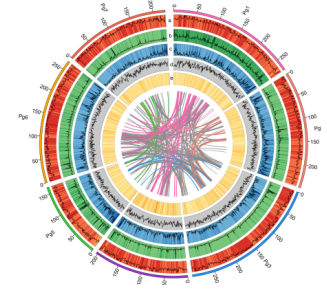
Ref: ICRISAT Newsletter (<http://www.icrisat.org/>)

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Pearl millet

Genome



Varshney *et al*, Nat. Biotech. 2017

- Consortium ICRISAT/BGI/IRD
- Genome size: 1.79 GB
- 38 579 predicted genes
- High GC (47.9%) and TE (80%) content
- Expansion genes families for cutin/suberin and ABC transporters
- 994 lines fully resequenced

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Pearl millet

Main limiting factors



- **Abiotic stresses**
 - Low soil fertility (low P availability)
 - Drought
 - Heat stress
- **Biotic stresses**
 - Striga
 - Fungal pathogens
 - Insects & nematodes
 - Birds



Objectives

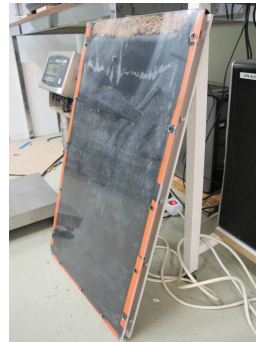
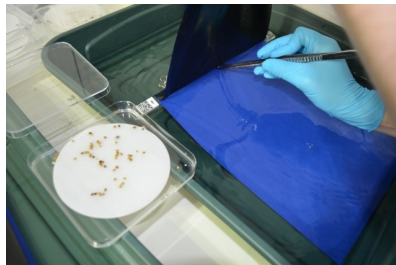
Identify root traits that contribute to pearl millet adaptation to low water and low nutrients conditions

- **Describe/quantify root trait**
 - *root architecture and anatomy*
 - *interactions with beneficial microbes*
- **Identify desirable root traits**
- **Identify genes controlling desirable root traits**



Root phenotyping

Throughput



Passot *et al*, Front. Plant Sci. 2016

Passot *et al*, Plant Physiol. 2018

Faye *et al*, in preparation

« Naturalness »

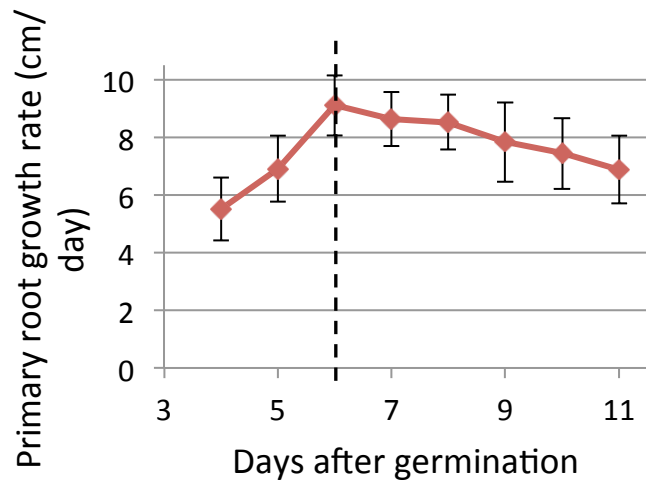
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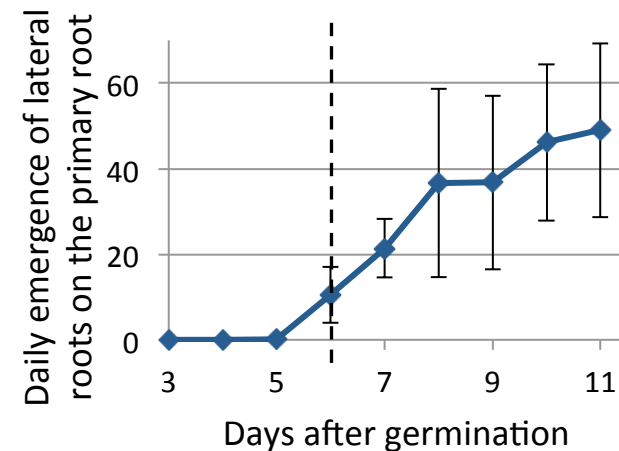
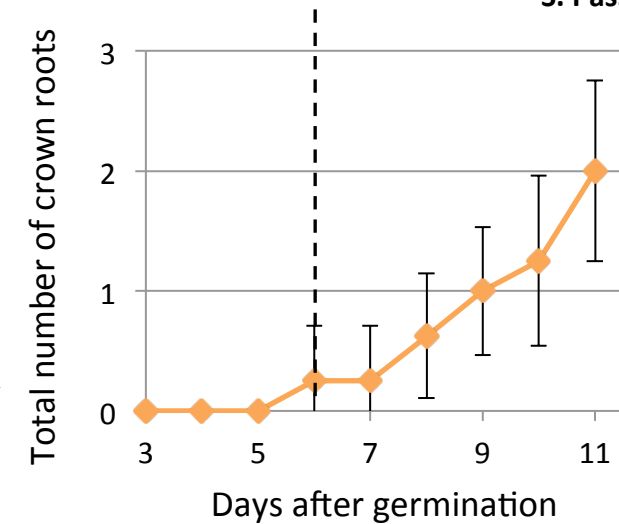
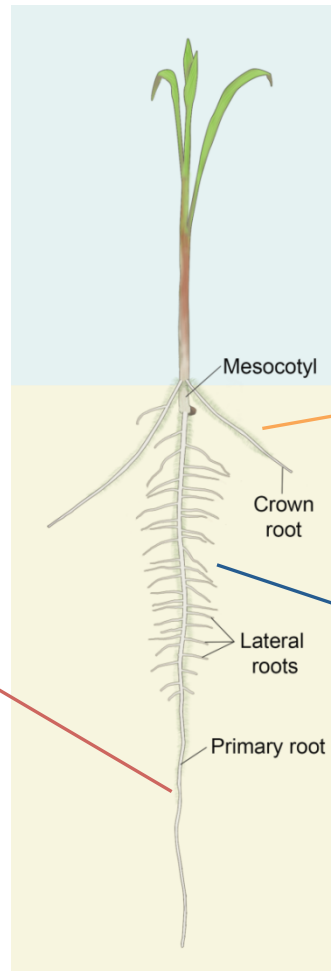
Early developmental dynamics of pearl millet root system



S. Passot



Carbon reallocation to newly born root axes at 6 days



Passot *et al*, Front. Plant Sci. 2016

Passot *et al*, Plant physiol. 2018

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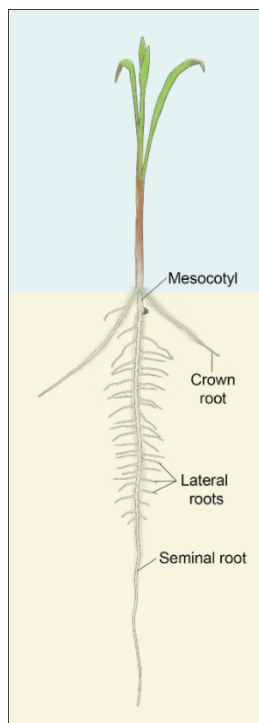
Primary root growth

High-throughput phenotyping



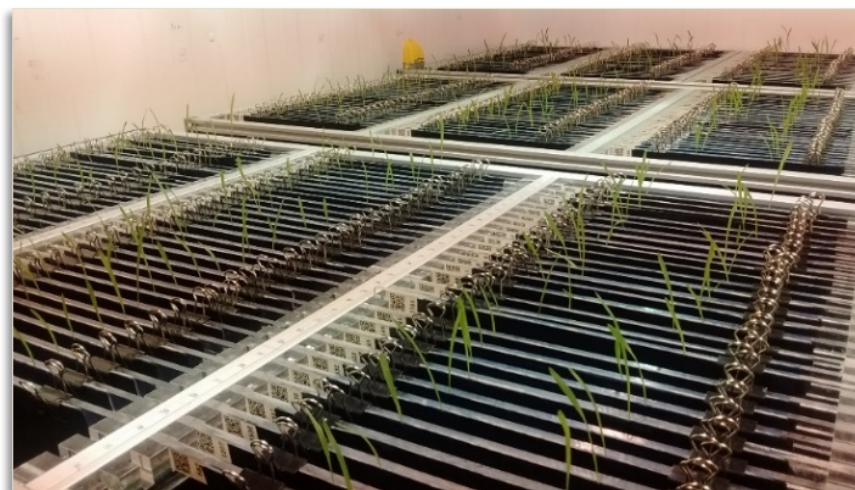
S. Passot

Pearl millet early root system



Very fast growth of seminal root

Hydroponic paper-based phenotyping platform



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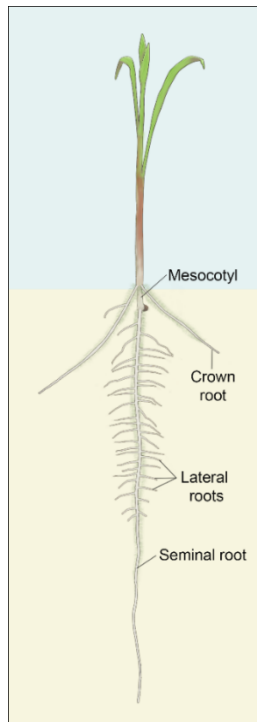
Primary root growth

Genetic diversity



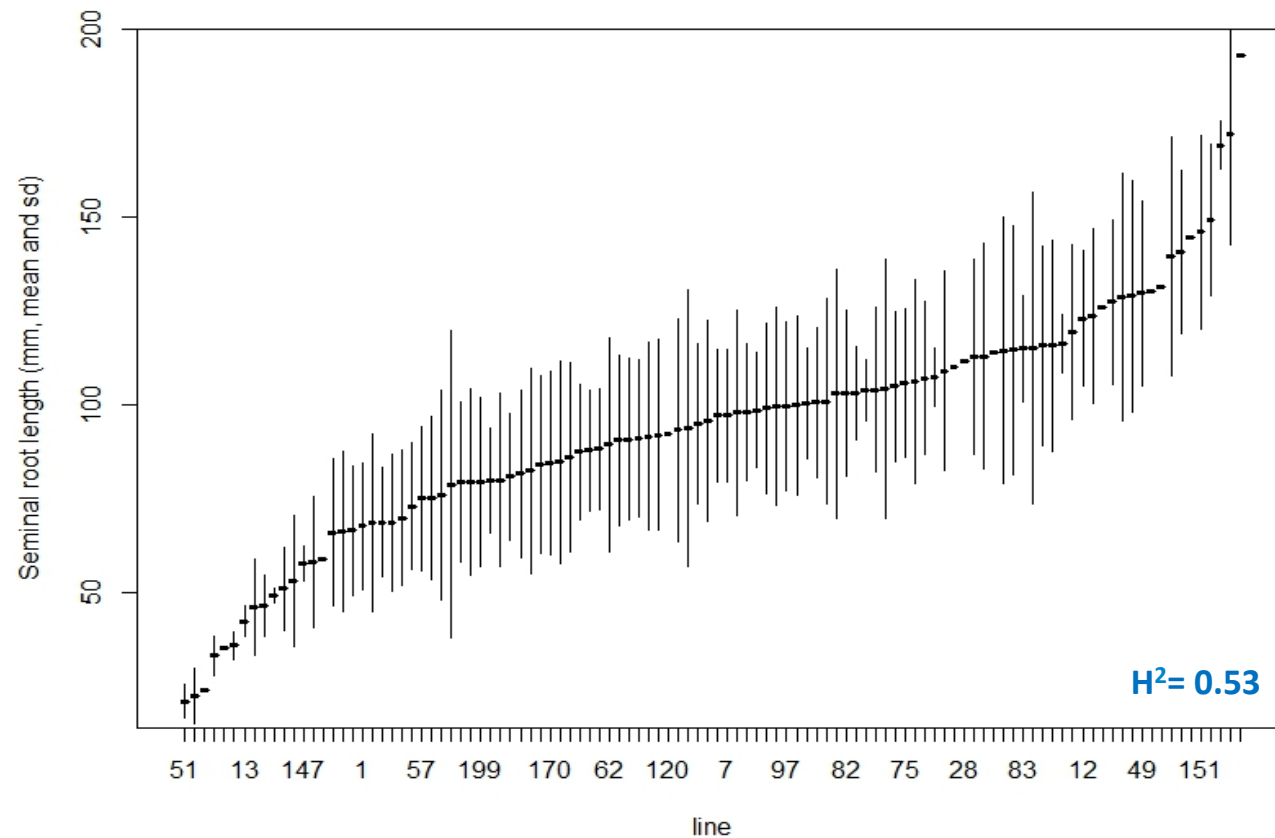
S. Passot

Pearl millet early
root system



Very fast growth
of seminal root

Seminal root length in a panel of 108 inbred lines 6 days after
germination



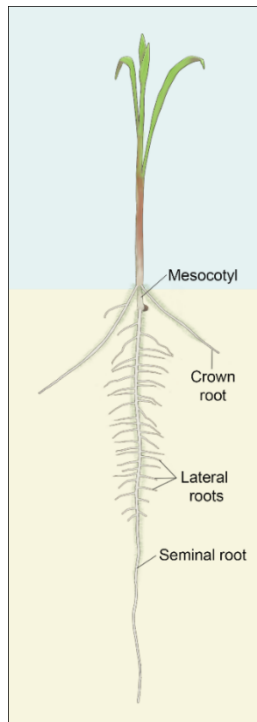
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Primary root growth

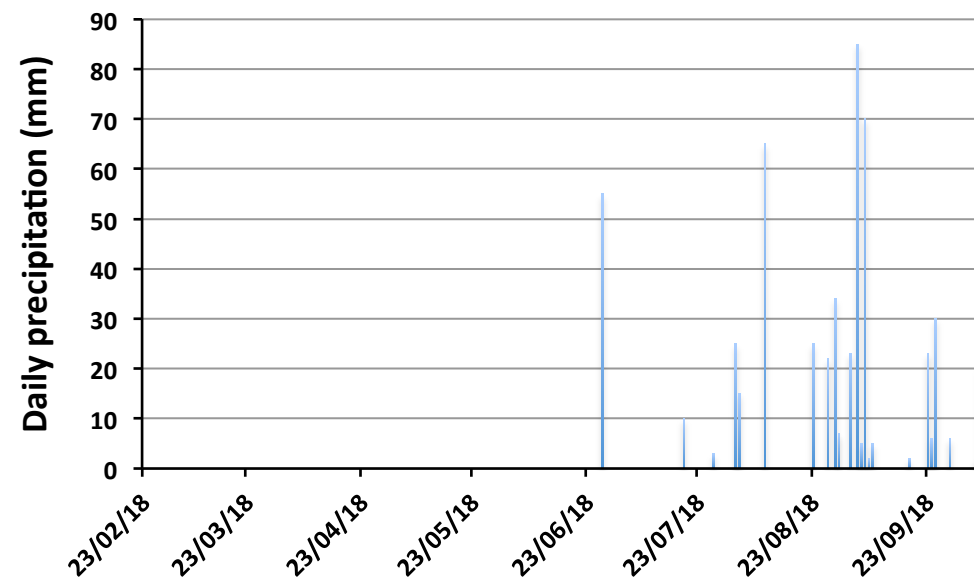
An adaptative trait?

Pearl millet early
root system



Very fast growth
of seminal root

Precipitation pattern in Sob (Senegal) - 2018



Source: OPSE Niakhar



Primary root growth

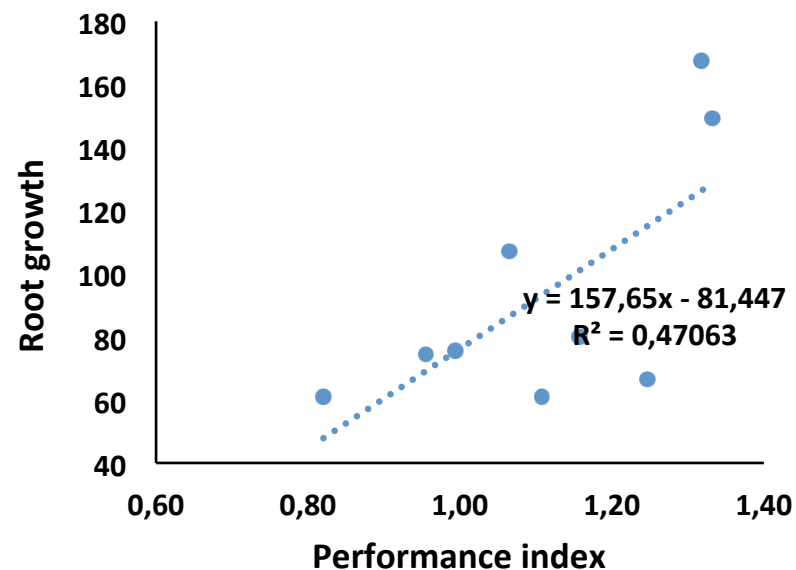
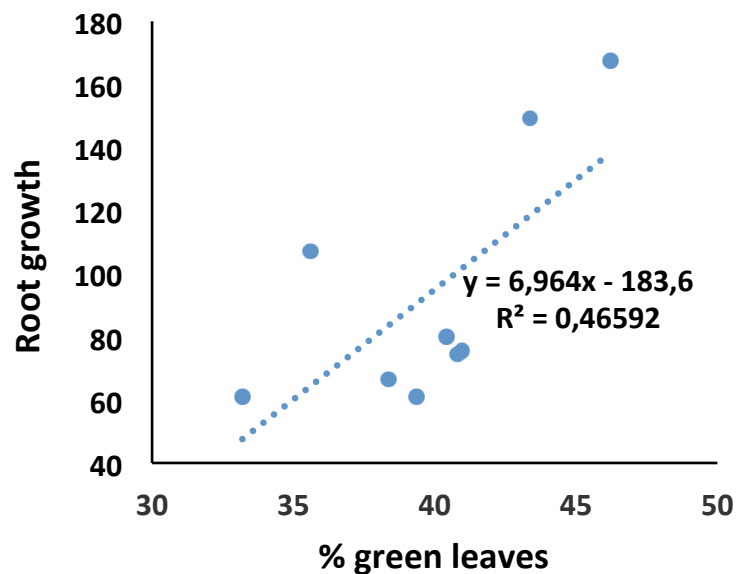
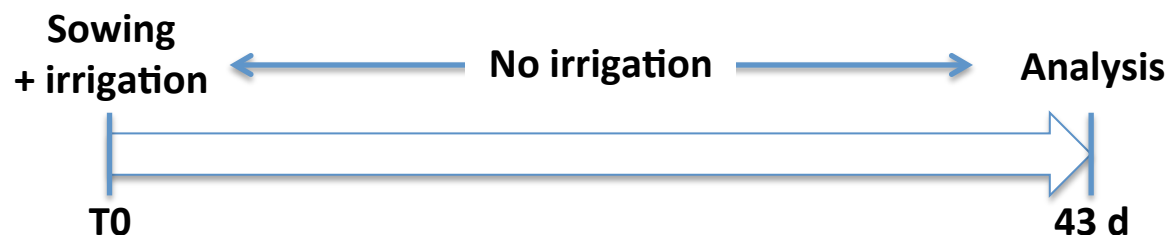
Field trials results



B. Sine



A. Grondin





Primary root growth

Field trials results

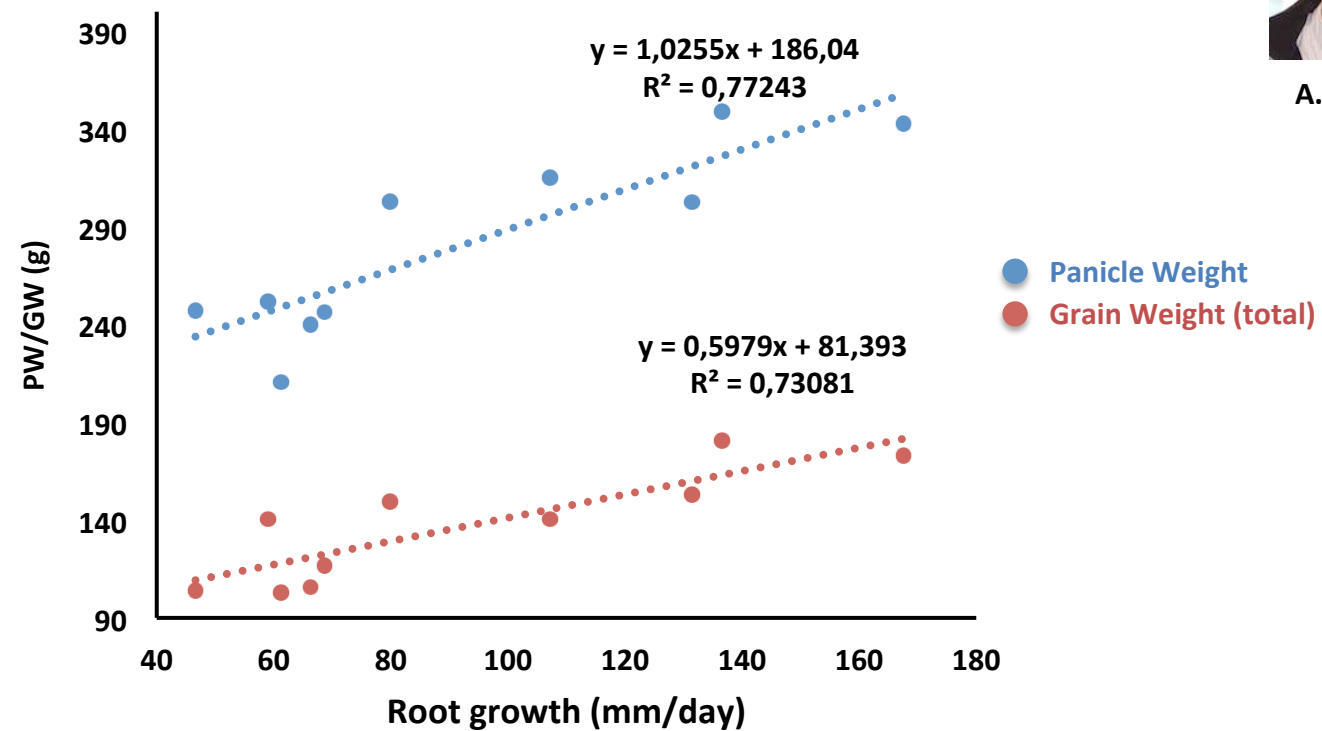


B. Sine



A. Grondin

Field trials (+/- P, WW/STR1/STR2)



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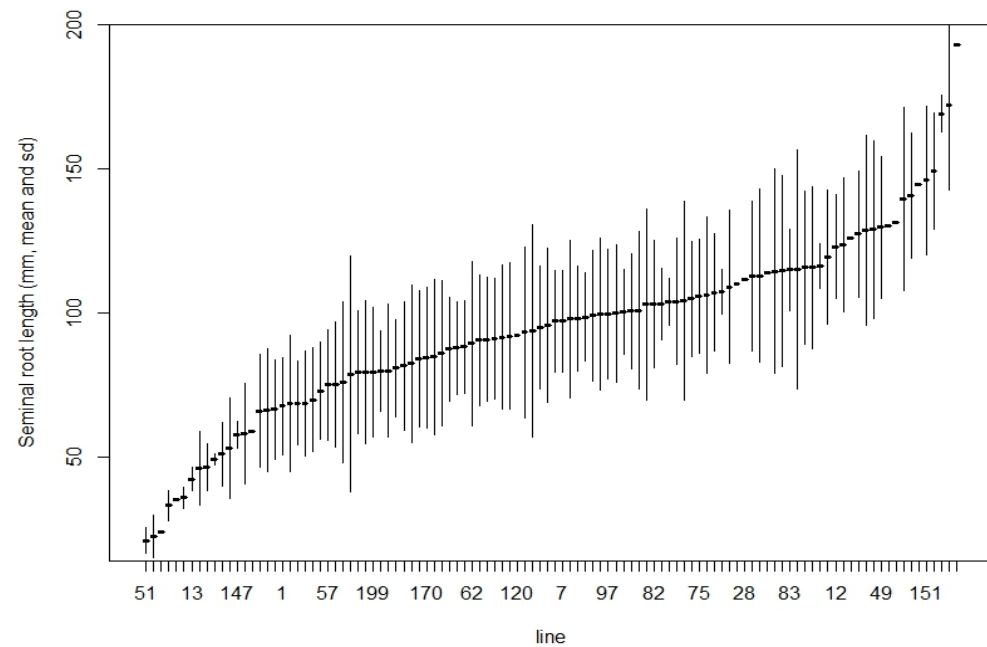
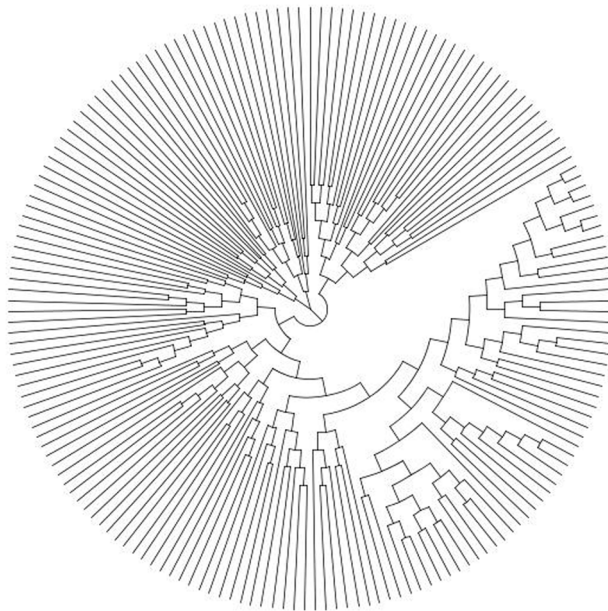


Primary root growth *GWAS*



S. Passot

392 493 SNPs identified by GBS



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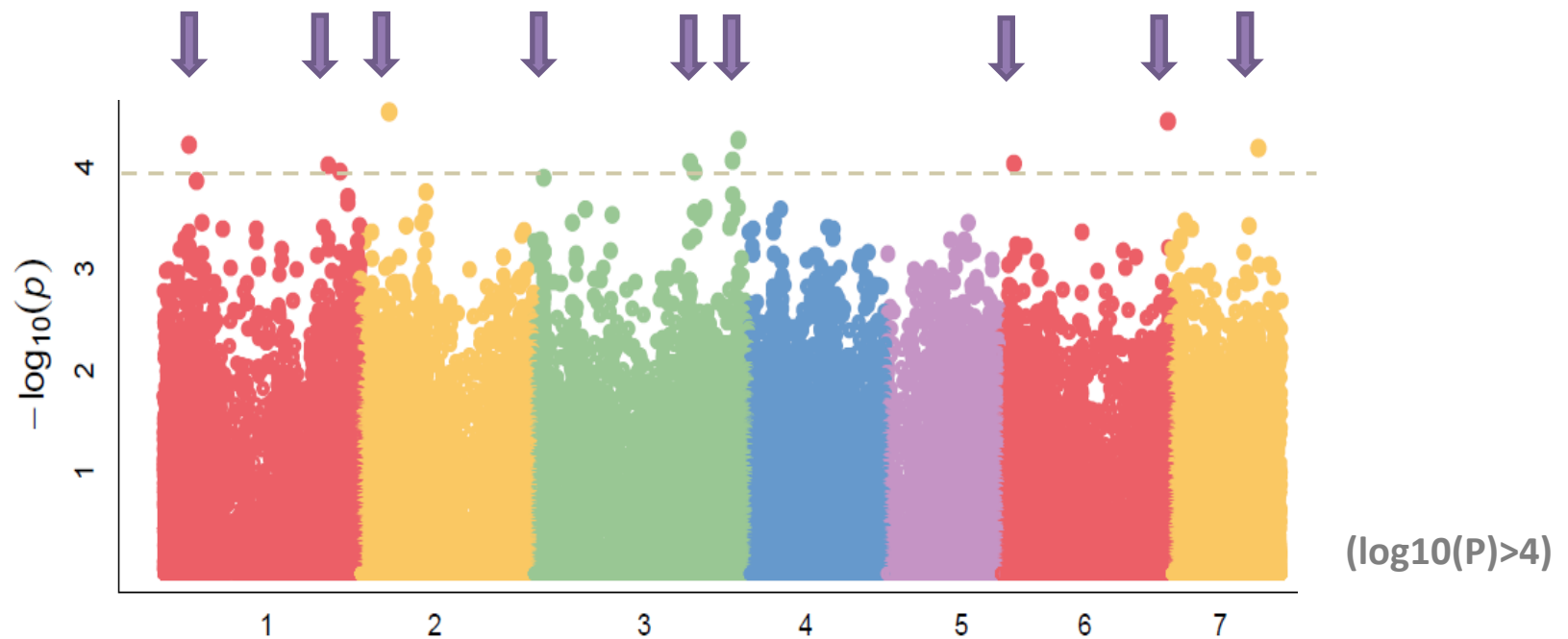


Primary root growth *GWAS*



M. Debieu

9 potential QTLs controlling primary root length

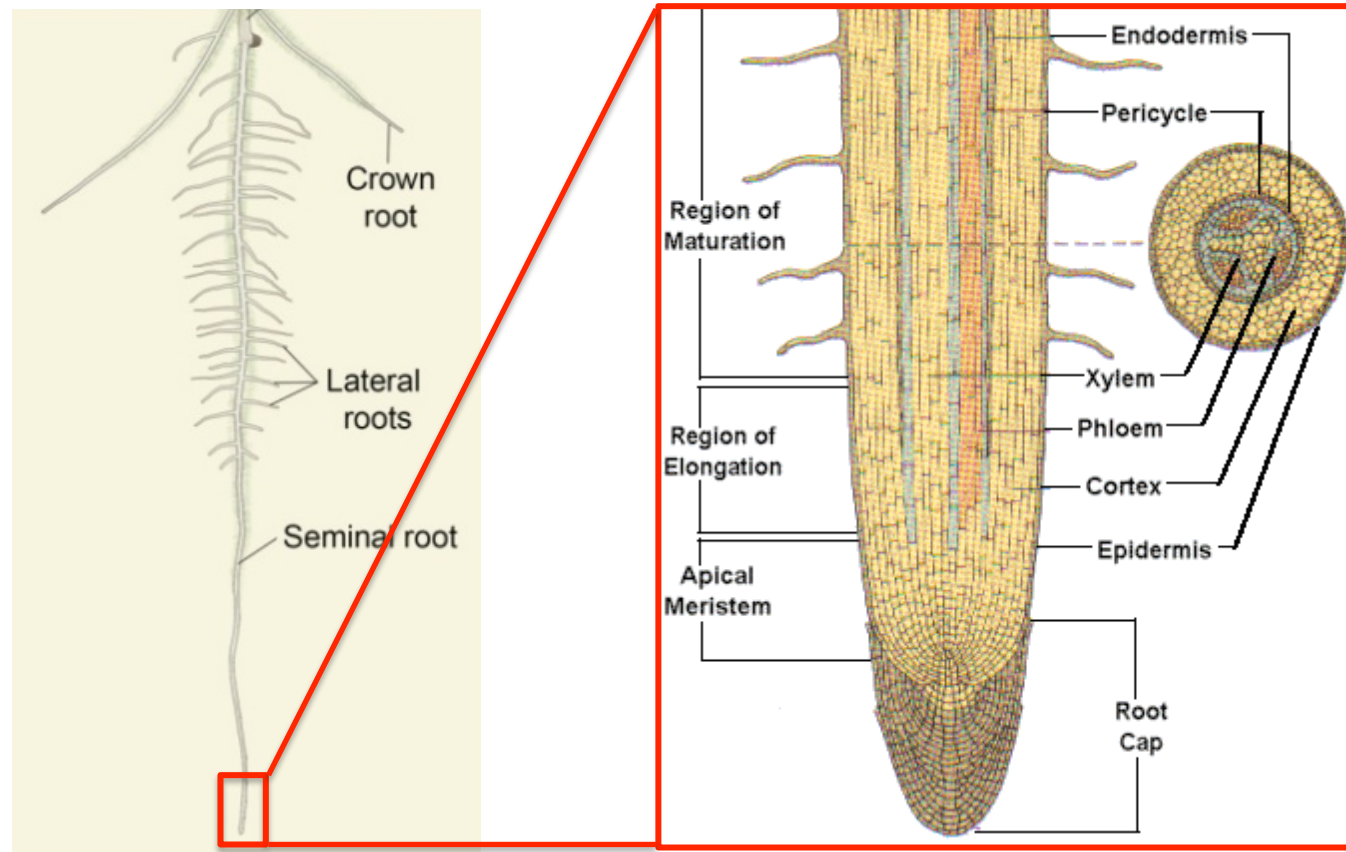


~ 150 genes in QTL regions (500 kb interval around most significant SNP markers)



Primary root growth

Transcriptomics



From <https://www.tes.com/lessons/nHBDO6YooXG09A/plant-anatomy-physiology>

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Primary root growth

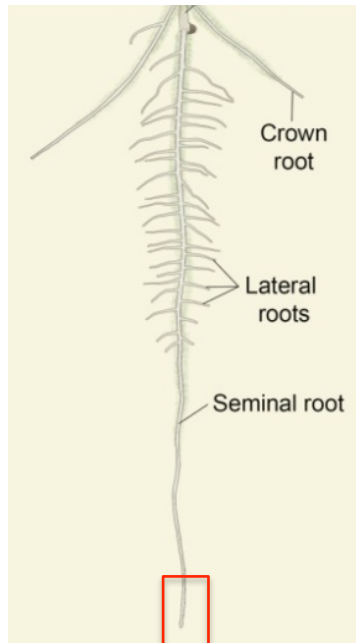
Transcriptomics



M. Debieu



A. Grondin



RNAseq

Low
growth
IL 249

VS

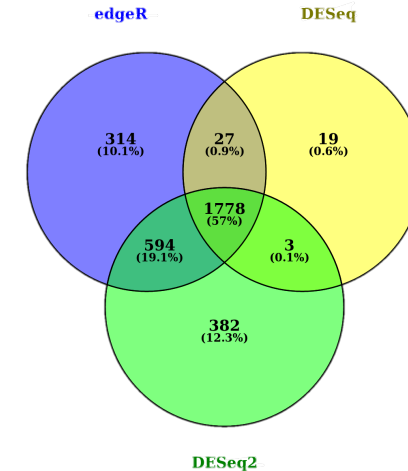
High
growth
IL 337



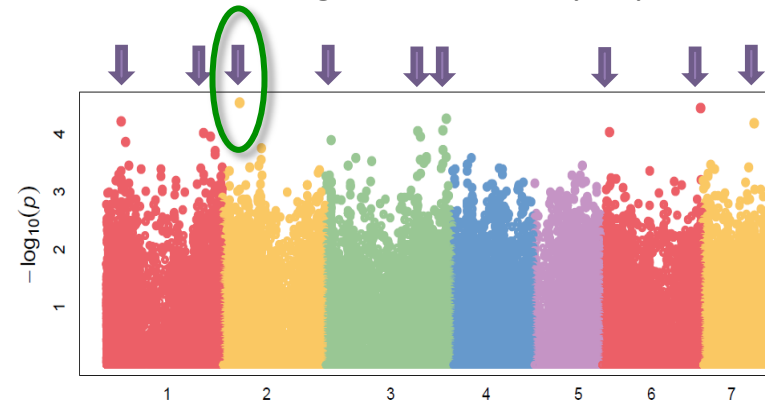
- 3 replicates
- single read 50 nt (Illumina HiSeq 2500)
- 1/3 reads not mapped to predicted CDS
- 3 statistical tests (EdgeR, DESeq & DESeq2)



Genetic bases root growth



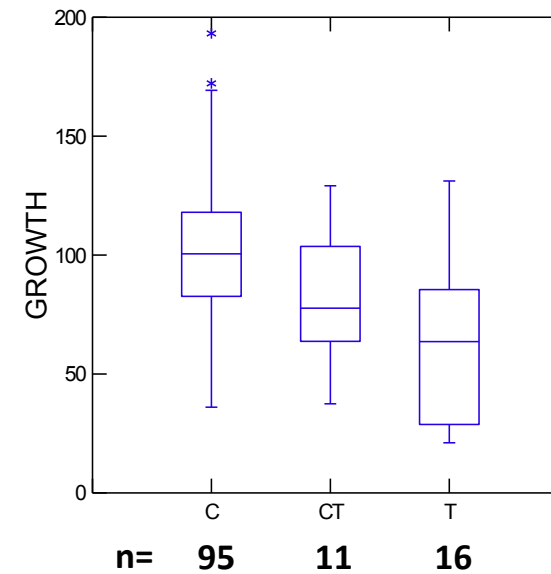
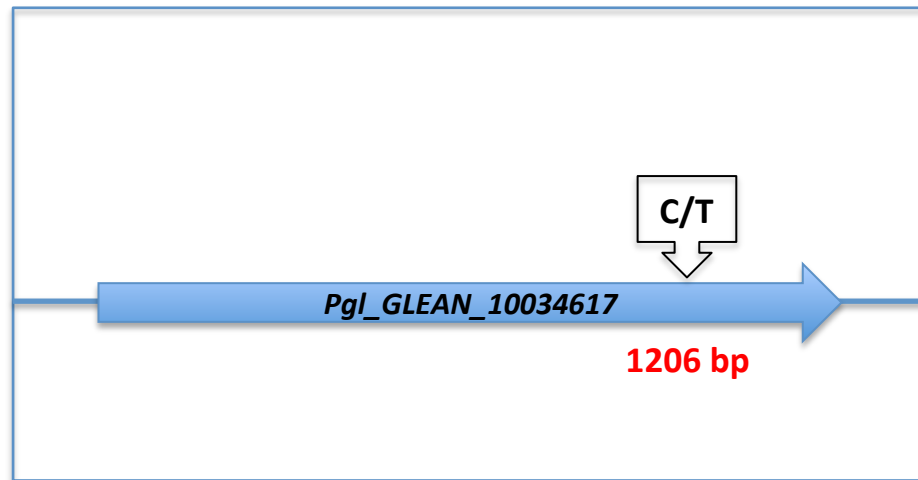
RNAseq data from root tips of two contrasting lines revealed 1778 genes differently expressed



- ~ 100 expressed genes in QTL regions
- 3 SNPs located within genes with predicted functions for root growth



Genetic bases root growth



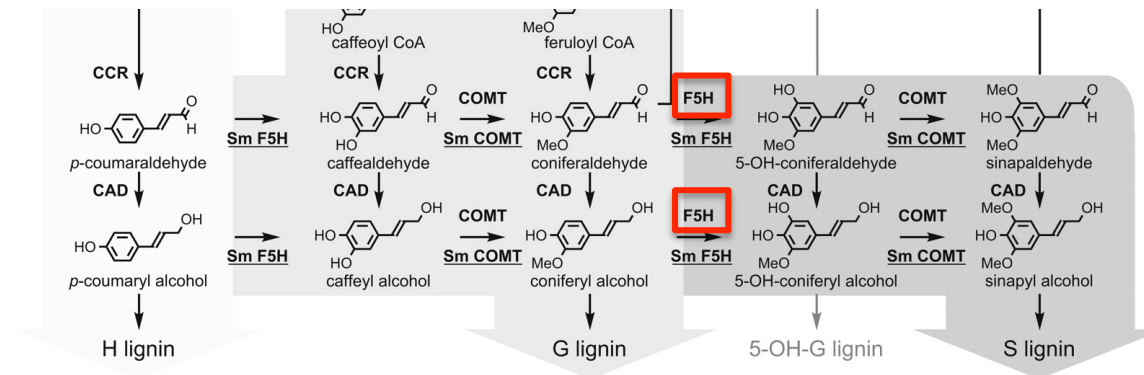


Genetic bases root growth

Progressive Inhibition by Water Deficit of Cell Wall Extensibility and Growth along the Elongation Zone of Maize Roots Is Related to Increased Lignin Metabolism and Progressive Stellar Accumulation of Wall Phenolics¹

Ling Fan, Raphael Linker, Shimon Gepstein, Eiichi Tanimoto, Ryoichi Yamamoto, and Peter M. Neumann*

Plant Physiology Laboratory, Department of Environmental, Water, and Agricultural Engineering, Faculty of Civil and Environmental Engineering (L.F., R.L., P.M.N.) and Faculty of Biology (S.G.), Technion-Israel Institute of Technology, Haifa 32000, Israel; Plant Physiology Laboratory, Department of Information and Biological Sciences, Graduate School of Natural Sciences, Nagoya City University, Nagoya 467-8501, Japan (E.T.); and Biology and Chemistry Laboratory, Tezukayama University, Nara 631-8585, Japan (R.Y.)

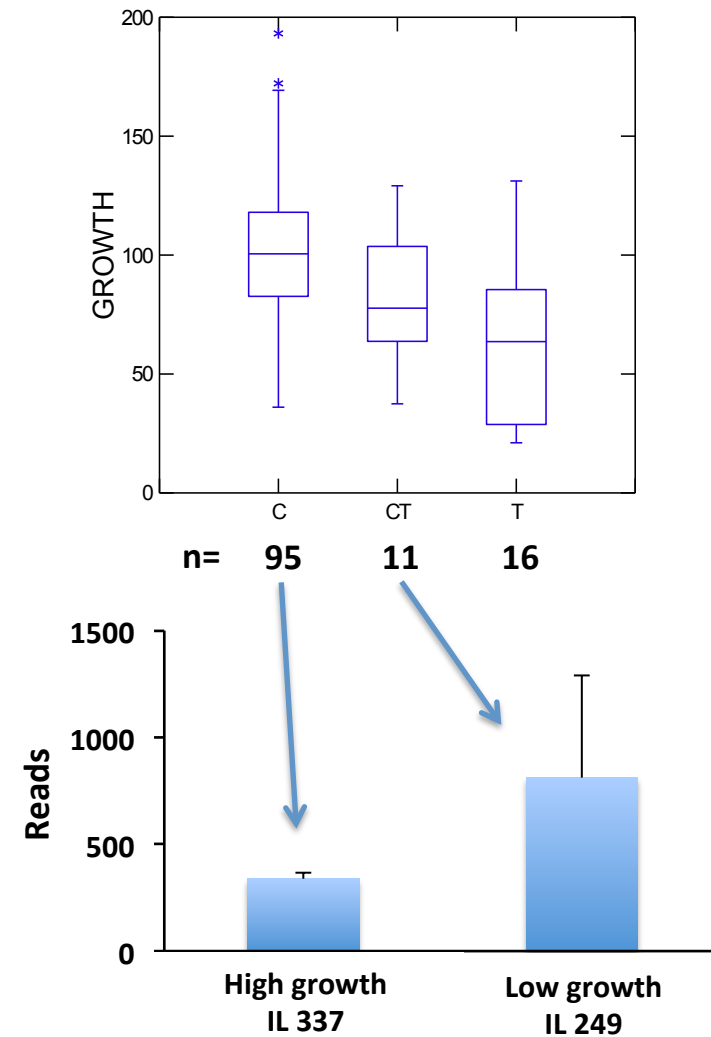
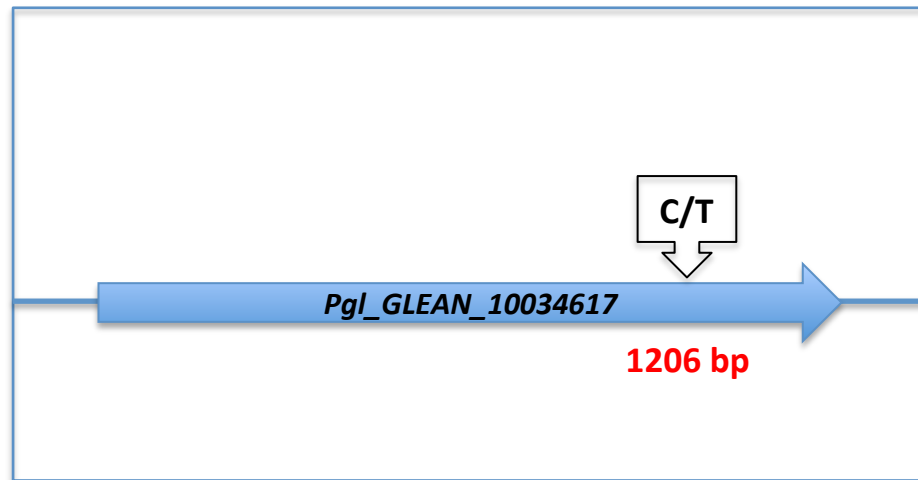


Jing-Ke Weng et al. Plant Cell 2011;23:2708-2724

Hangzhou, November 2018

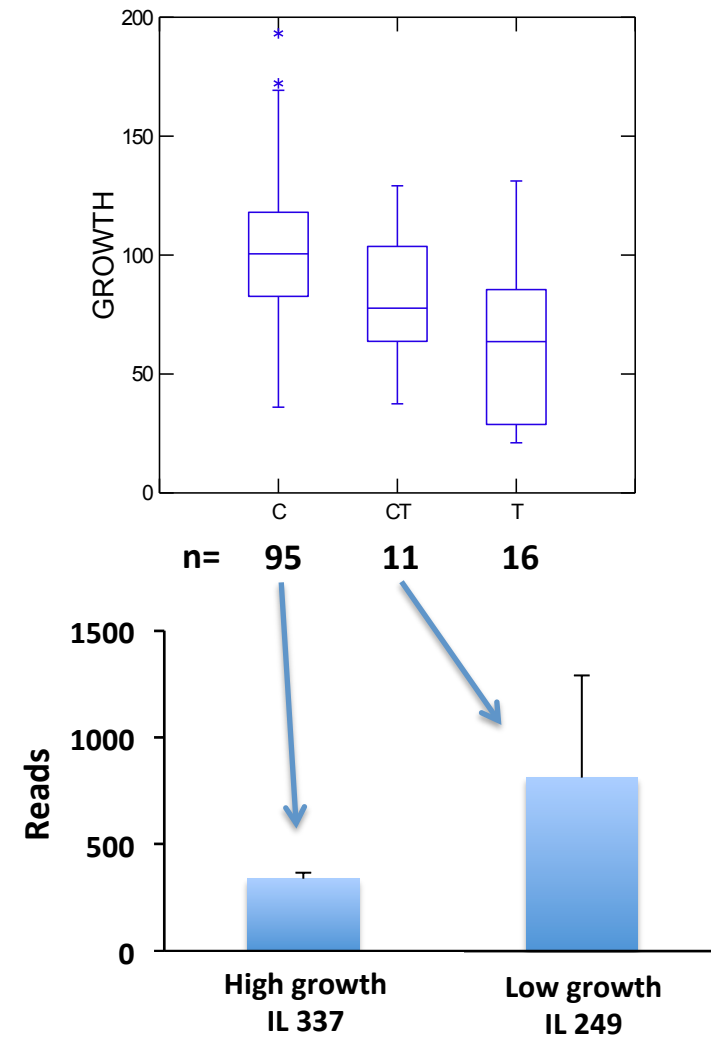
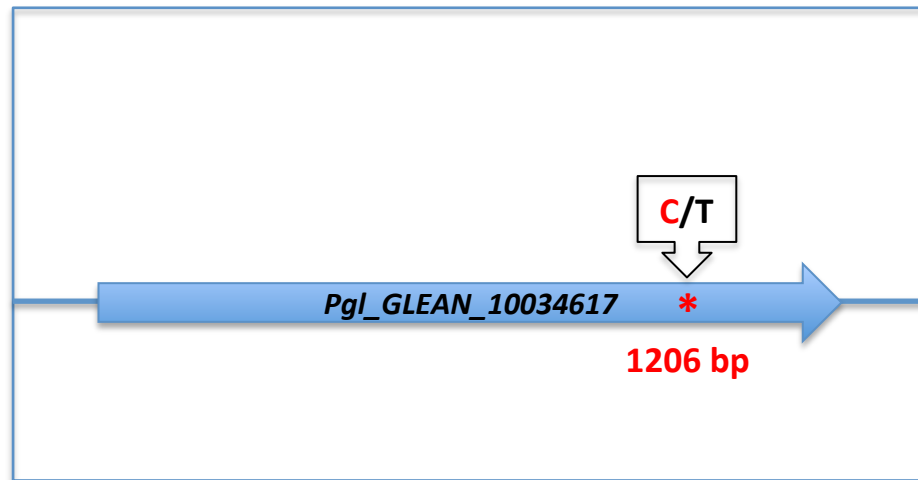


Genetic bases root growth





Genetic bases root growth





Genetic bases root growth

249 (short root) = 337 (long root)

Plant-Specific Histone Deacetylases HDT1/2 Regulate *GIBBERELLIN 2-OXIDASE2* Expression to Control Arabidopsis Root Meristem Cell Number^{OPEN}

Huchen Li,^a Jesus Torres-Garcia,^a David Latrasse,^{b,c} Moussa Benhamed,^{c,d} Stefan Schilderink,^a Wenkun Zhou,^a Olga Kulikova,^a Heribert Hirt,^{b,d} and Ton Bisseling^{a,1}

^aDepartment of Plant Sciences, Laboratory of Molecular Biology, Wageningen University, 6708 PB Wageningen, The Netherlands
^bUnité de Recherche en Génomique Végétale, UMR INRA 1165, Université d'Evry Val d'Essonne, ERL CNRS 8196, Saclay Plant Sciences, 91057 Evry, France

^cInstitut de Biologie des Plantes, CNRS-Université Paris-Sud 11, UMR 8618, 91405 Orsay cedex, France

^dKing Abdullah University of Sciences and Technology, Thuwal 23955, Saudi Arabia

¹Department of Plant Sciences, Plant Developmental Biology, Wageningen University, 6708 PB Wageningen, The Netherlands

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249 (short root) >>> 337 (long root)

The Plant Cell, Vol. 23: 1107–1123, March 2011, www.plantcell.org © 2011 American Society of Plant Biologists

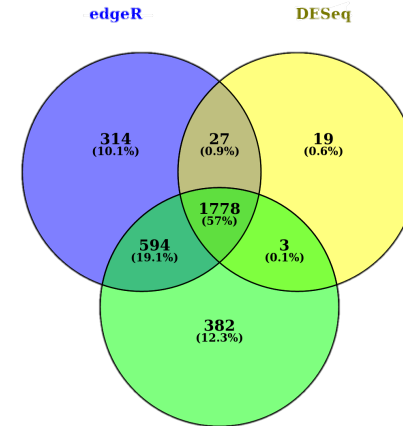
Patatin-Related Phospholipase pPLAIIβ-Induced Changes in Lipid Metabolism Alter Cellulose Content and Cell Elongation in *Arabidopsis*^{©/W}

Maoyin Li,^{a,b} Sung Chul Bahn,^{a,b} Liang Guo,^{a,b} William Musgrave,^b Howard Berg,^b Ruth Welti,^c and Xuemin Wang^{a,b,1}

^aDepartment of Biology, University of Missouri, St. Louis, Missouri 63121

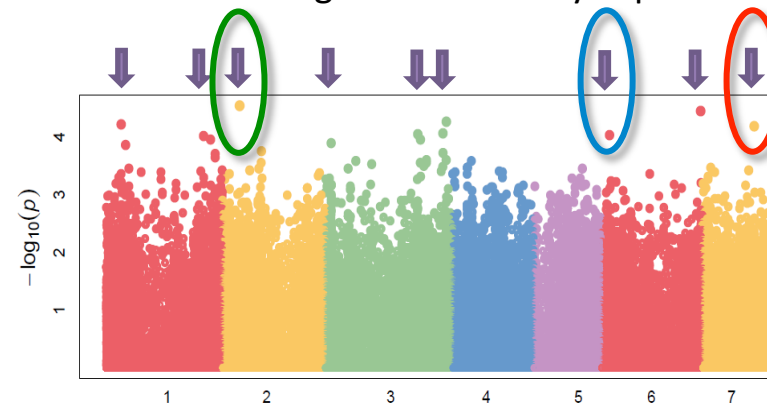
^bDonald Danforth Plant Science Center, St. Louis, Missouri 63132

^cKansas Lipidomics Research Center, Division of Biology, Kansas State University, Manhattan, Kansas 66506



DESeq2

RNAseq data from root tips of two contrasting lines revealed 1778 genes differently expressed



- ~ 100 expressed genes in QTL regions
- 3 SNPs located within genes with predicted functions for root growth

Hangzhou, November 2018



Summary

- Pearl millet – crop for African agriculture adaptation to future climates
- Root growth - adaptative trait for abiotic stresses tolerance in pearl millet
- GWAS - QTLs for root growth (9) & rhizosheath formation (5)
- RNAseq on root tip of contrasted lines



Perspectives



C. de la Fuente

➤ Validate/refine QTLs

Slow growth parent

X

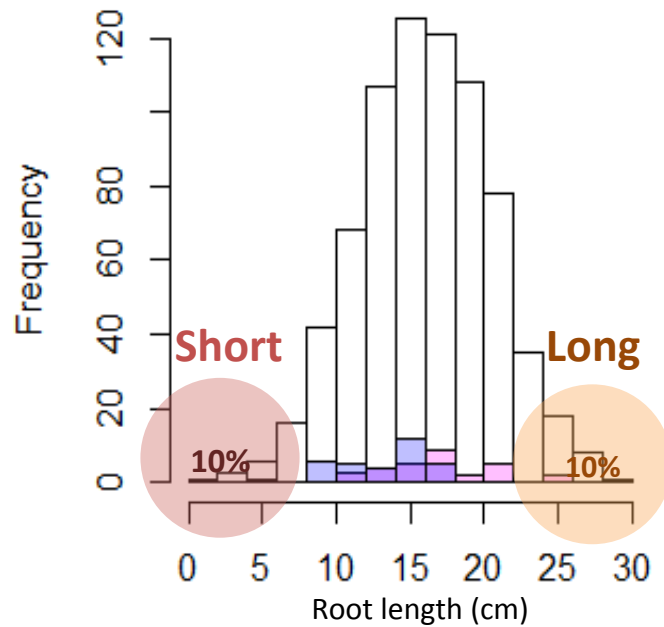
Fast growth parent

→ F1

Self pollination

→ F2

- 933 F2 seedlings 337x249 cross →
- 1116 F2 seedlings 109x57 cross →



Bulks Mean root length values ($\pm$ SD) in cm

Cross	Short seminal	Long seminal
337 x 249	8.15 $\pm$ 1.84 cm	23.70 $\pm$ 1.73 cm
109 x 57	6.86 $\pm$ 1.75 cm	22.50 $\pm$ 1.63 cm



NGS (Illumina HiSeq)



Perspectives



C. de la Fuente

➤ Validate/refine QTLs

Slow growth parent

X

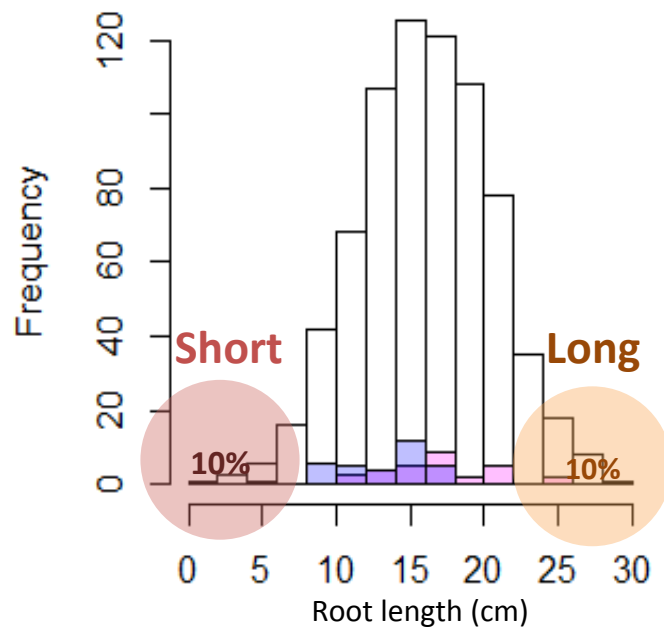
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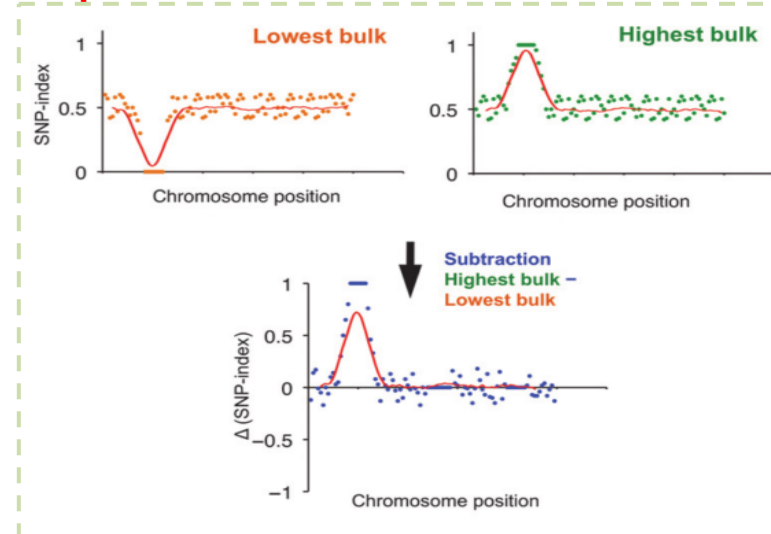
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Expected results...



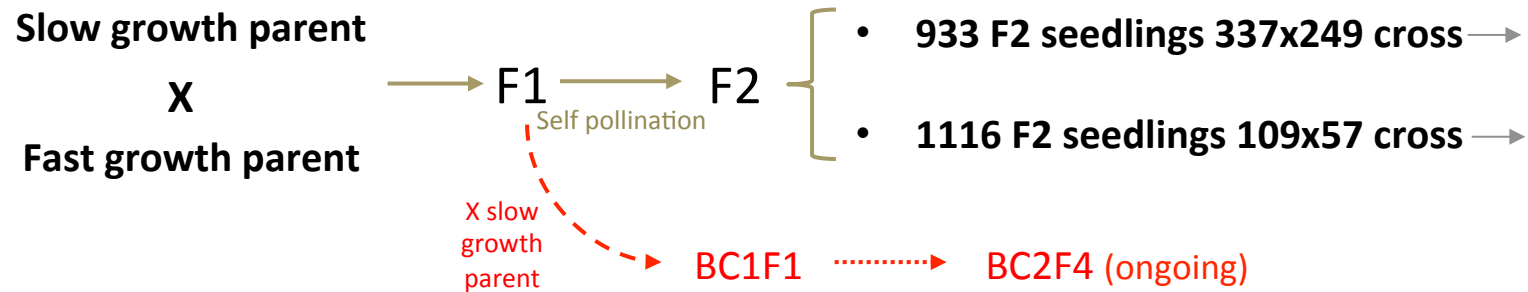
Adapted from: Takagi et al. (2013) The Plant Journal, 74: 174-183

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Perspectives

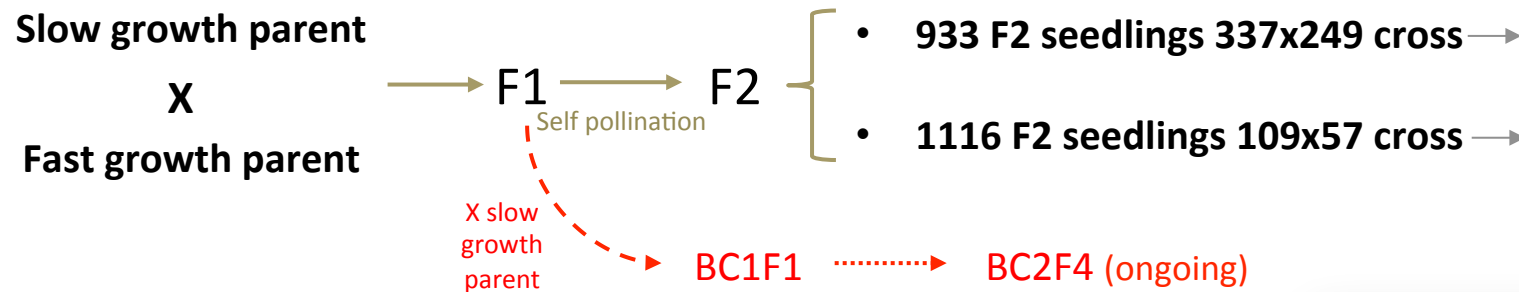
➤ Validate/refine QTLs





Perspectives

➤ Validate/refine QTLs



➤ Refine gene annotation in QTL regions

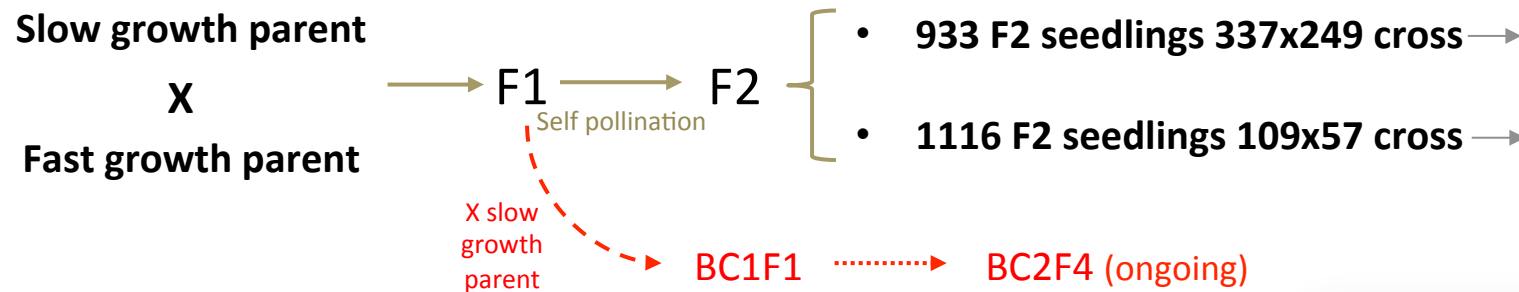
- RNAseq Data
- smallRNAseq





Perspectives

➤ Validate/refine QTLs



➤ Refine gene annotation in QTL regions

- RNAseq Data
- smallRNAseq

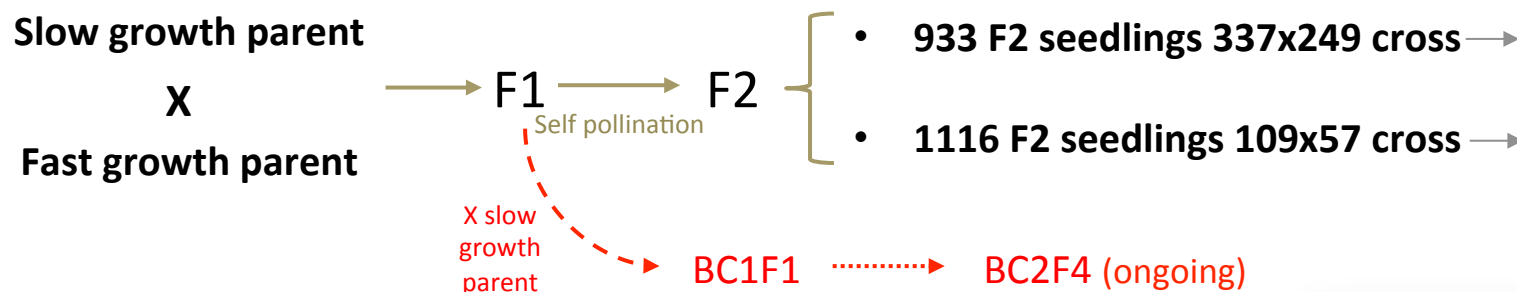
➤ Functional analysis of candidate genes





Perspectives

➤ Validate/refine QTLs



➤ Refine gene annotation in QTL regions

- RNAseq Data
- smallRNAseq



➤ Functional analysis of candidate genes

➤ Measure impact validated QTL in field conditions



Acknowledgments



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D. Moukouanga
M. Debieu
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A. Diedhiou



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