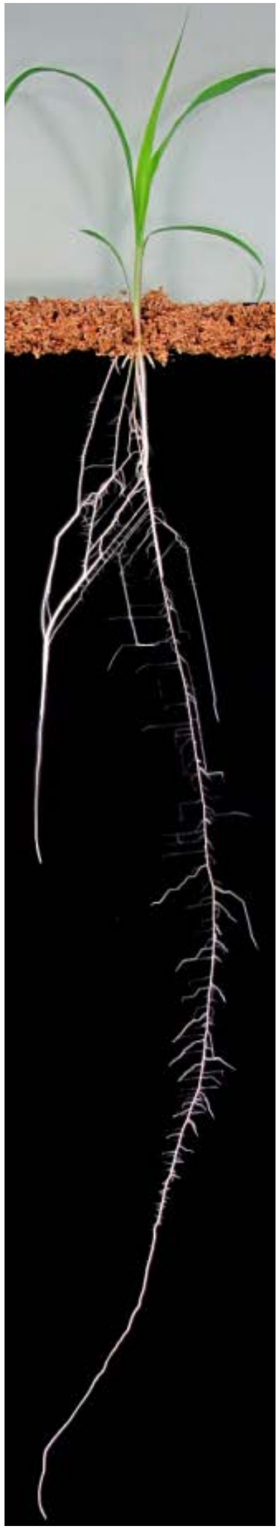


Root traits for improved drought and low soil fertility tolerance in pearl millet (*Pennisetum glaucum* l.)

Laurent Laplaze

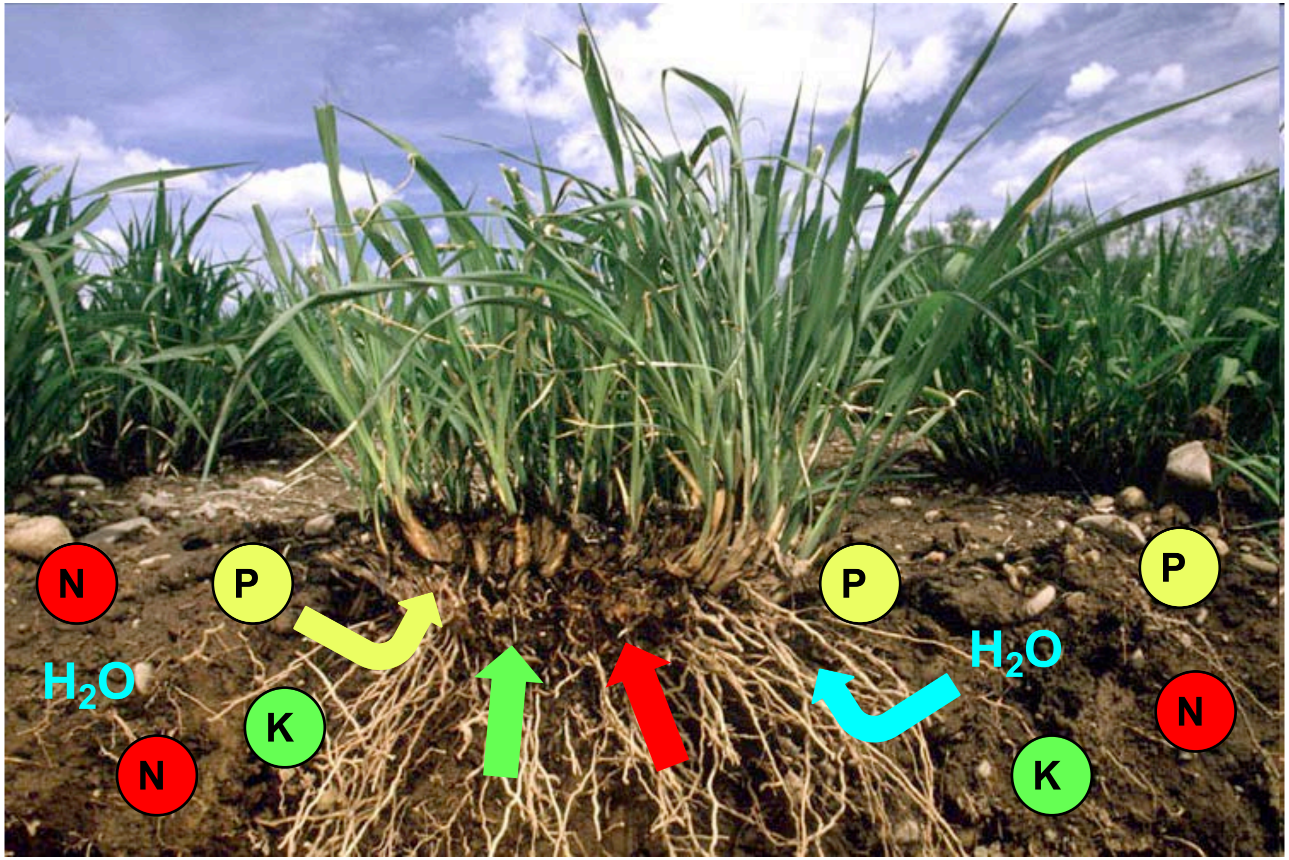
Laboratoire mixte international Adaptation des Plantes et microorganismes associés aux Stress Environnementaux (LAPSE), Dakar, Senegal

Equipe Cereal root systems (CERES), UMR DIADE, Montpellier, France

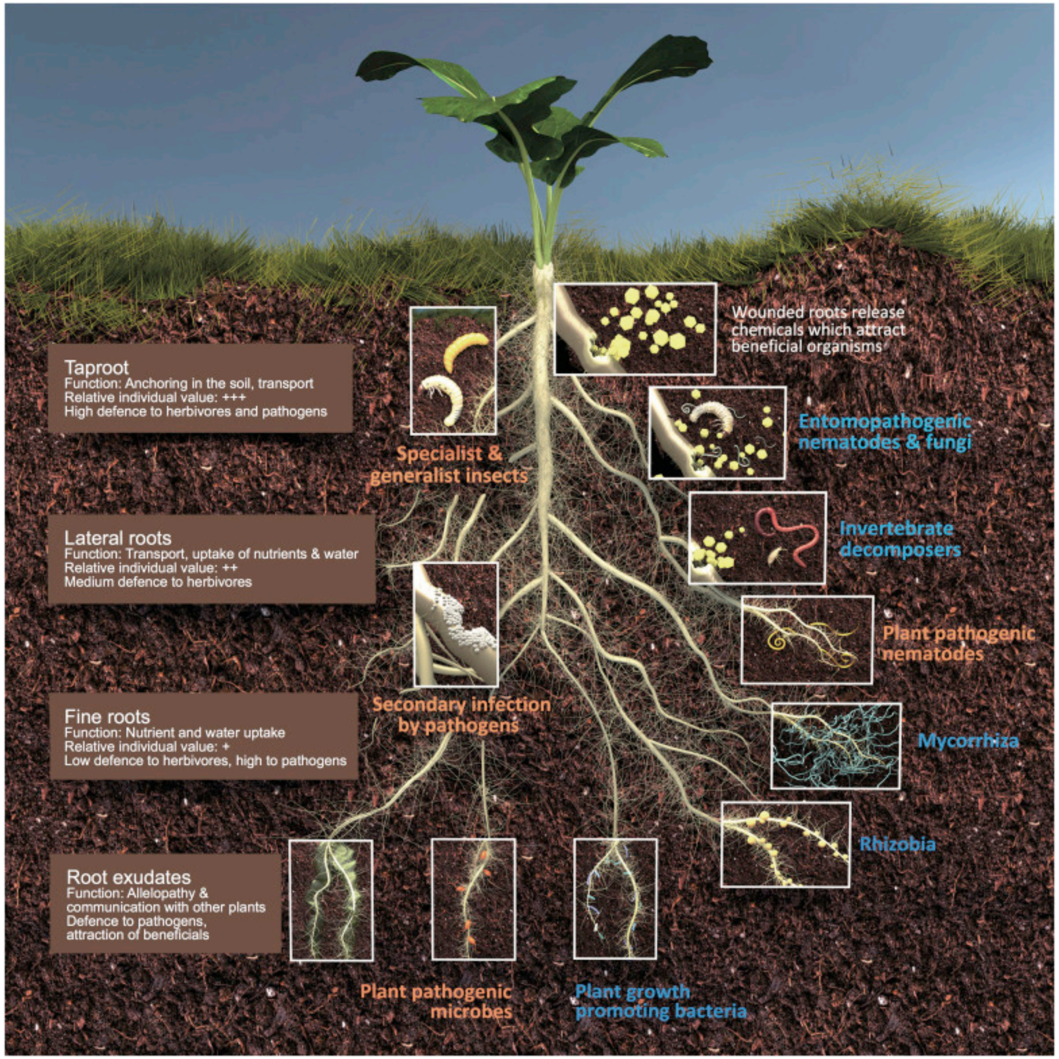
CID2019, Oct 2019

Root systems: the hidden half

Root systems: the hidden half



Root systems: the hidden half



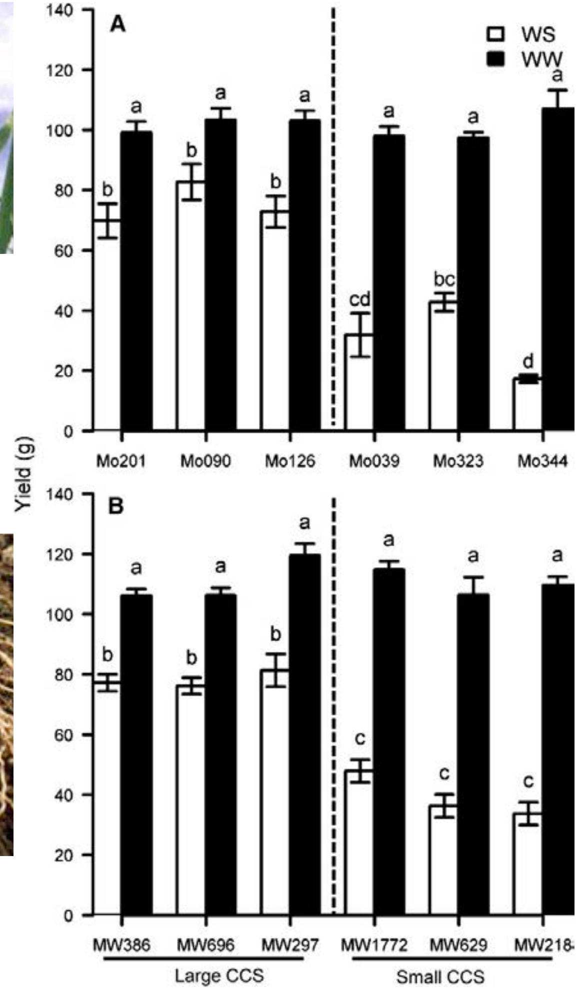
Tsunoda & van Dam, Pedobiologia 2017

Root systems: the hidden half

Large Root Cortical Cell Size Improves Drought Tolerance in Maize[1][C][W][OPEN]

Joseph G. Chimungu, Kathleen M. Brown, and Jonathan P. Lynch*

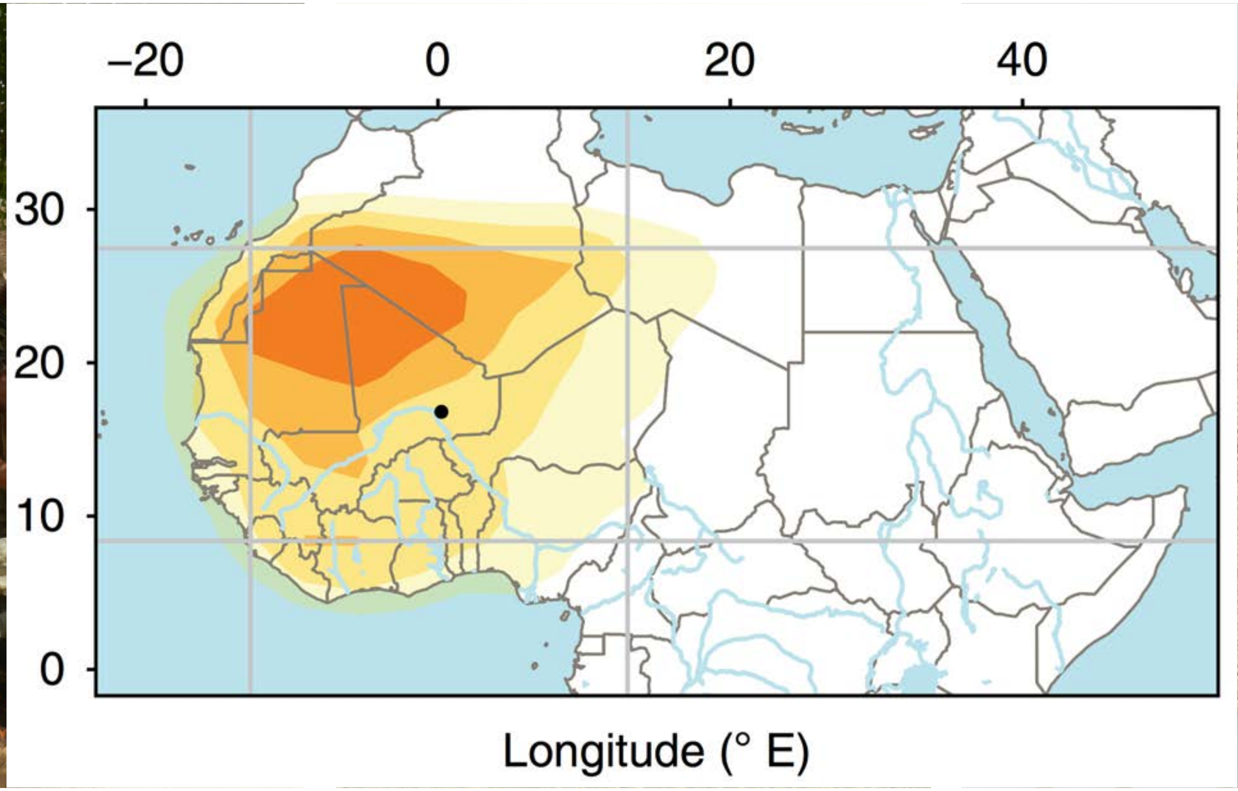
Department of Plant Science, Pennsylvania State University, University Park, Pennsylvania 16802



Chimungu *et al*, Plant Physiol. 2014

Pearl millet

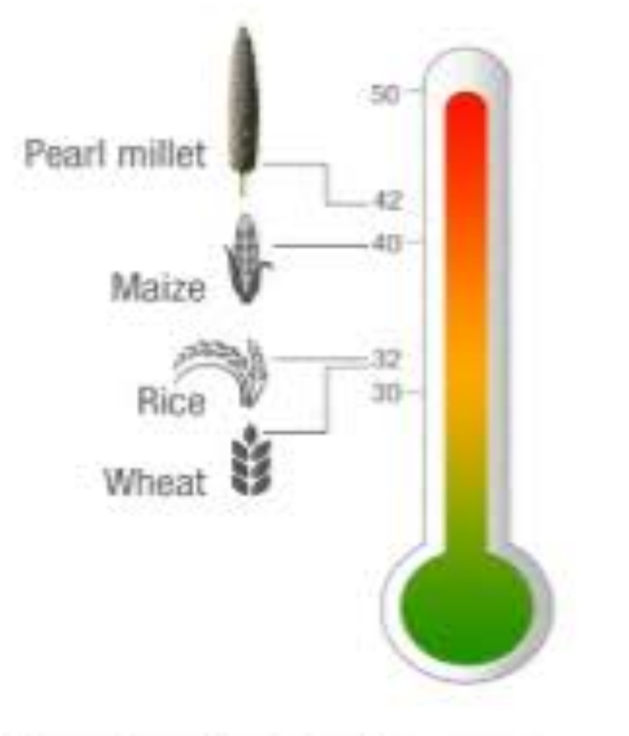
Pennisetum glaucum



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

Pearl millet

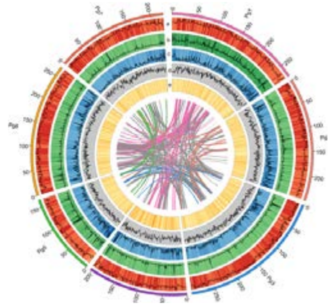
One of the hardiest cereals

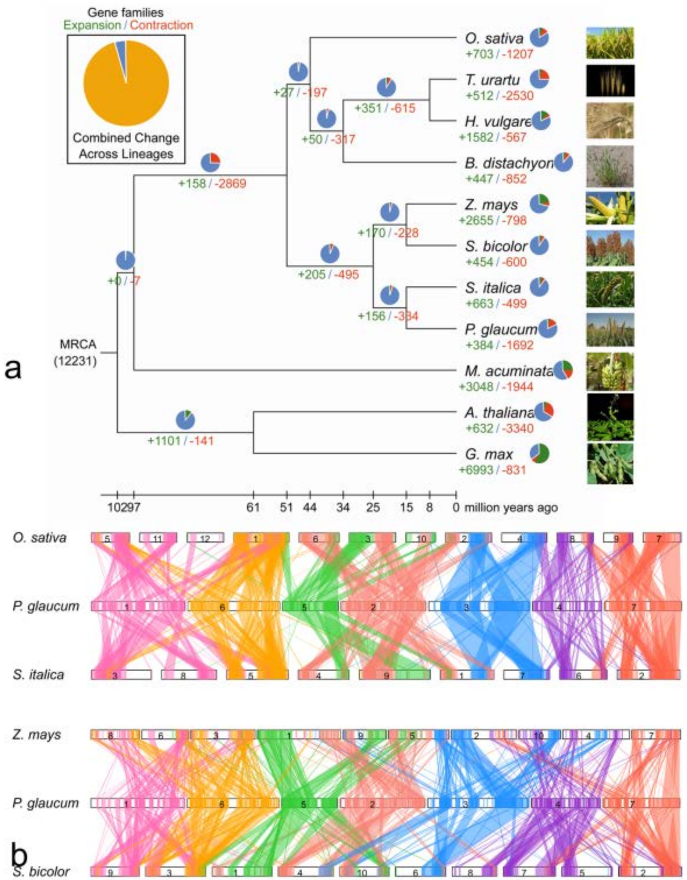


Ref: ICRISAT Newsletter (http://www.icrisat.org/)

Pearl millet

Genomic ressources





Varshney *et al*, Nat. Biotech. 2017

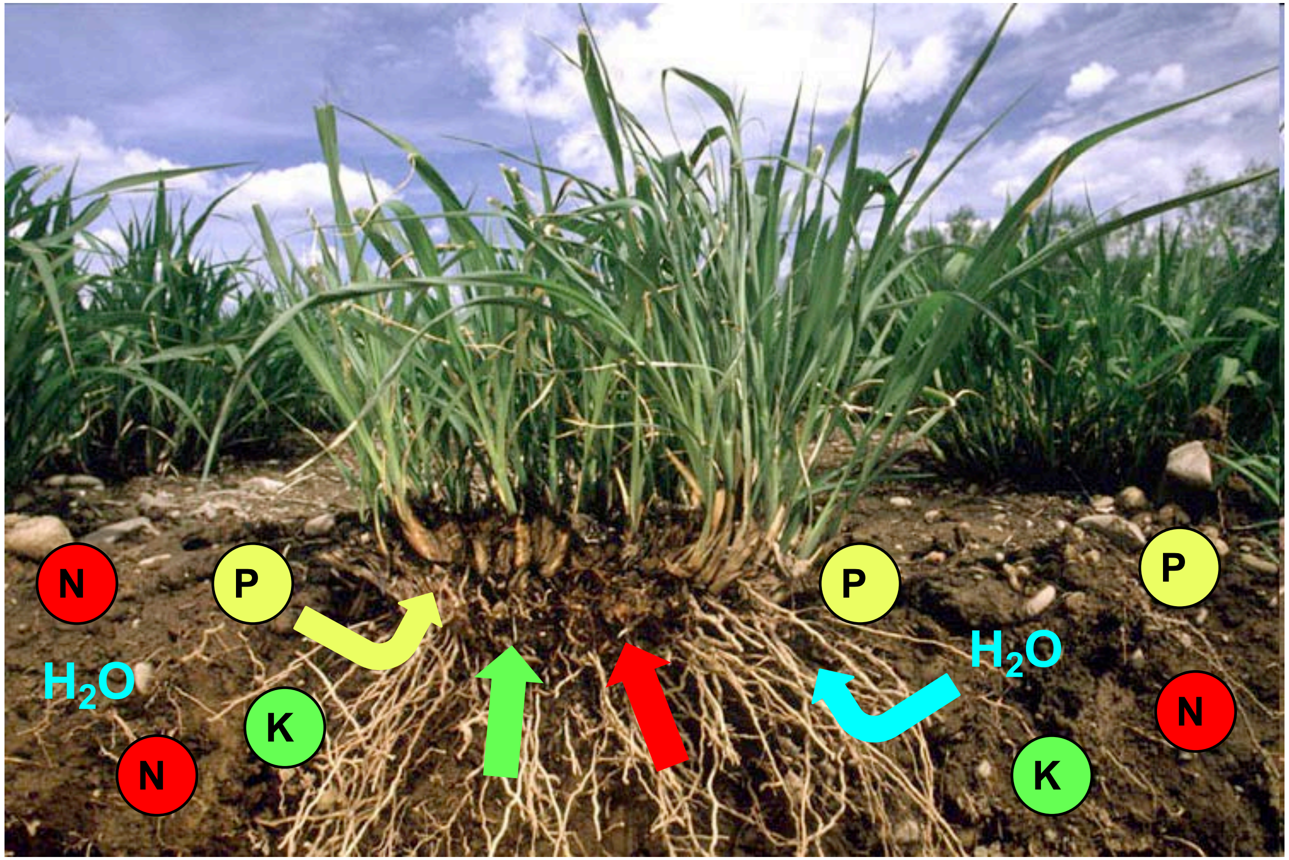
- Consortium ICRISAT/BGI/IRD
- Genome size: 1.79 GB
- 38 579 predicted genes
- High GC (47.9%) and TE (80%) content
- Expansion genes families for cutin/suberin and ABC transporters
- 994 lines fully resequenced

Pearl millet

Main limiting factors

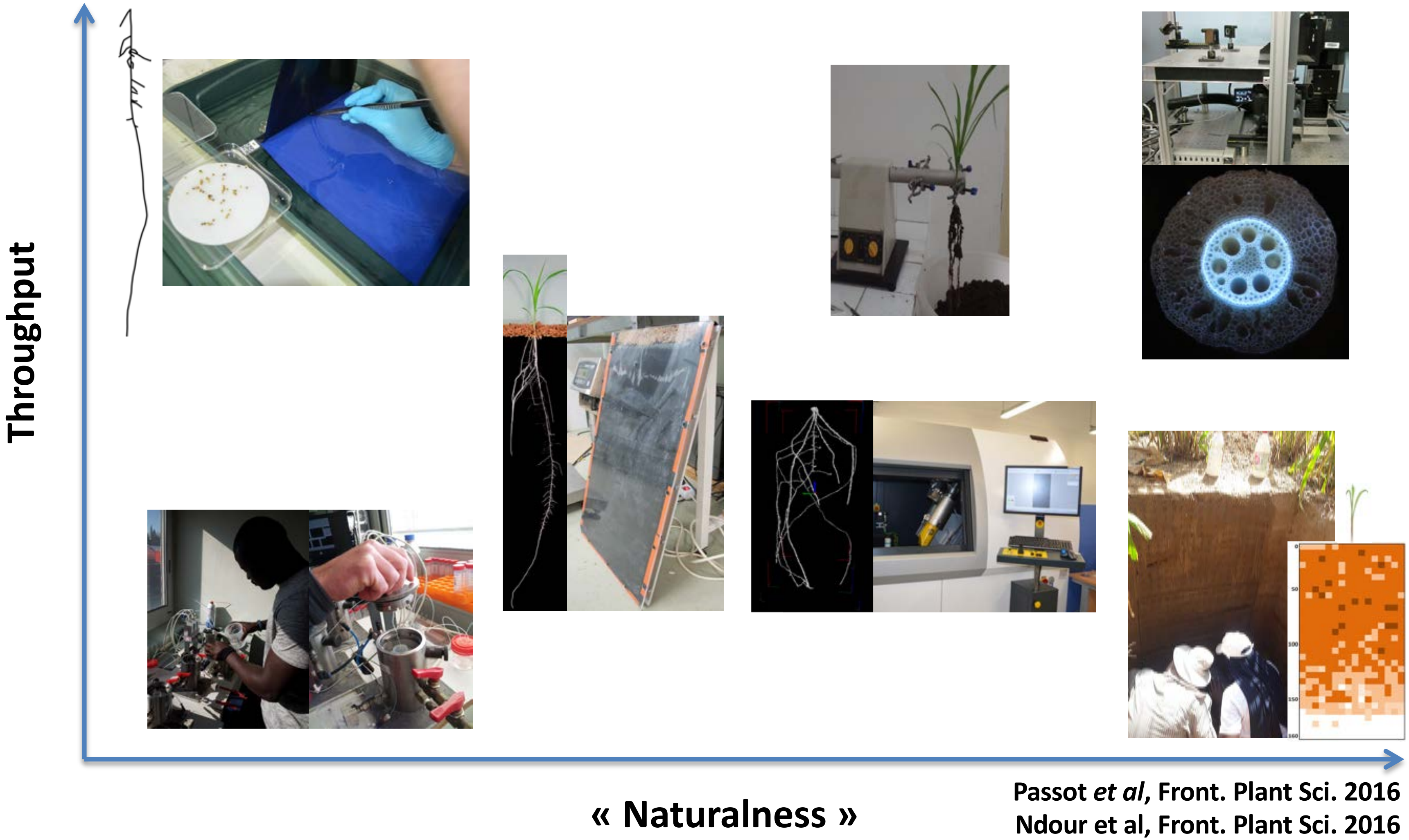
- **Abiotic stresses**
  - Low soil fertility (low P availability)
  - Drought
  - Heat stress
- **Biotic stresses**
  - Striga
  - Fungal pathogens
  - Insects & nematodes
  - Birds

Objectives



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

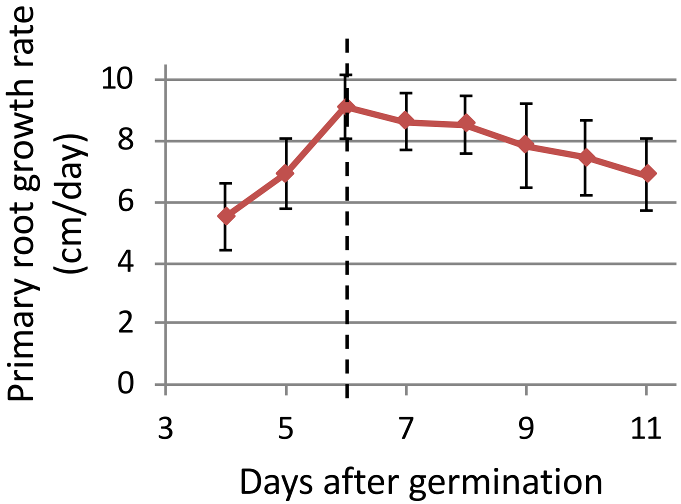
Root phenotyping

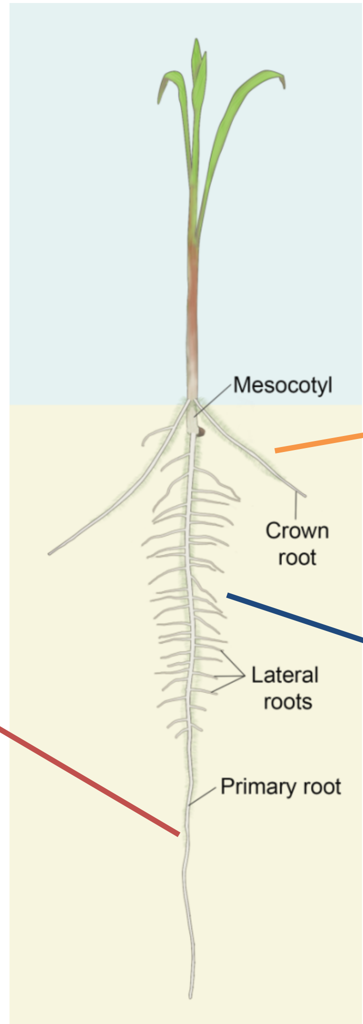


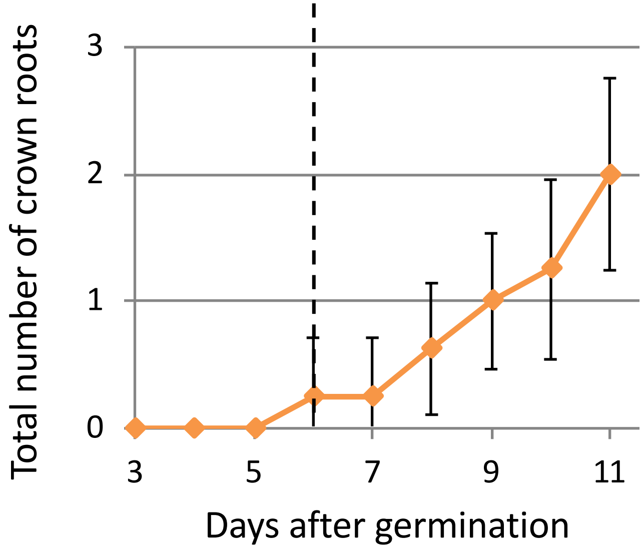
Passot *et al*, Front. Plant Sci. 2016
Ndour et al, Front. Plant Sci. 2016
Passot *et al*, Plant Physiol. 2018
Faye *et al*, PLoS One 2019
Faye *et al*, in preparation

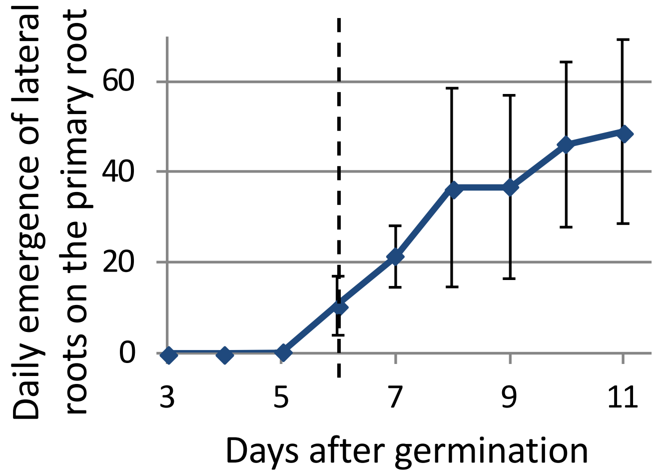
Early developmental dynamics of pearl millet root system

S. Passot









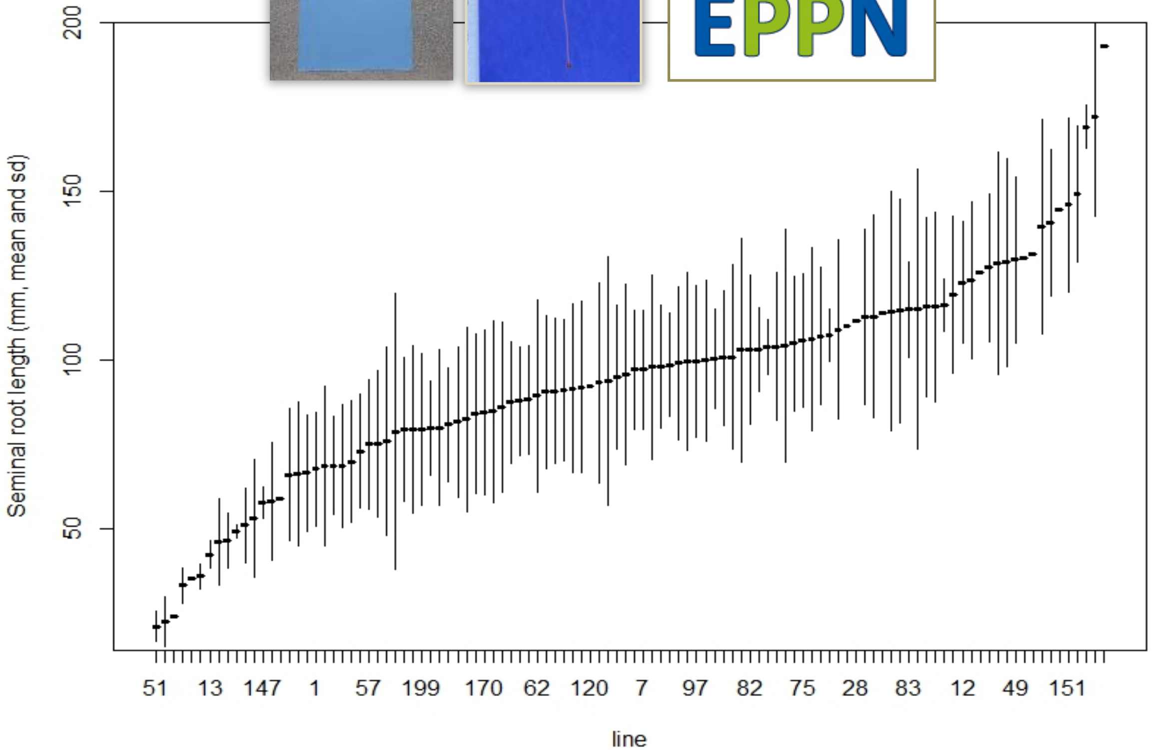
Carbon reallocation to newly born root axes at 6 days

Passot *et al*, Front. Plant Sci. 2016
Passot *et al*, Plant Physiol. 2018

Primary root growth
Available diversity

The University of Nottingham

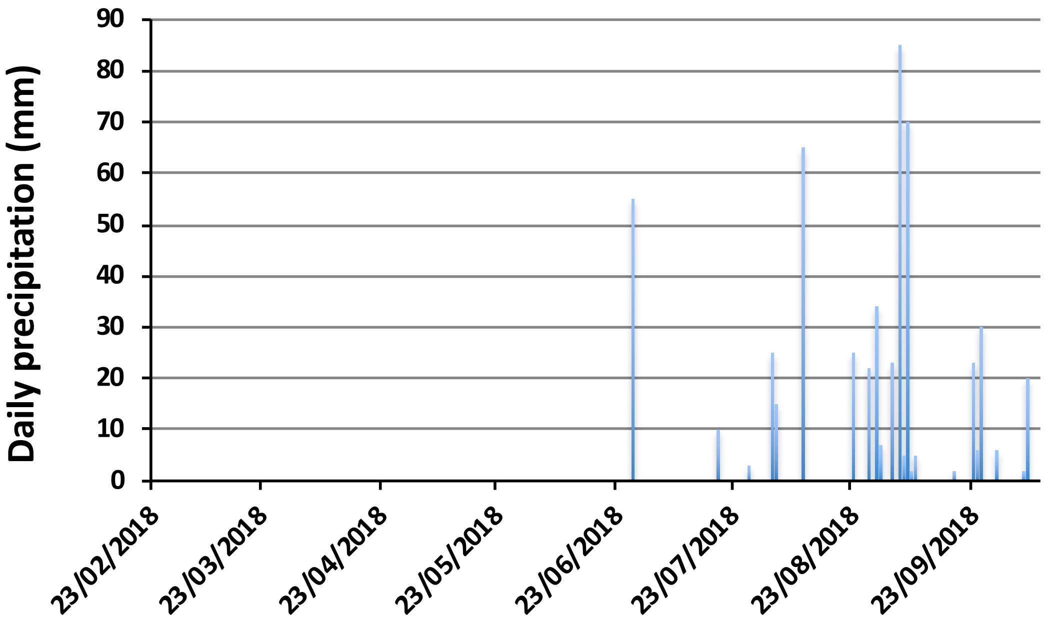
European Plant Phenotyping Network EPPN



Primary root growth

An adaptative trait?

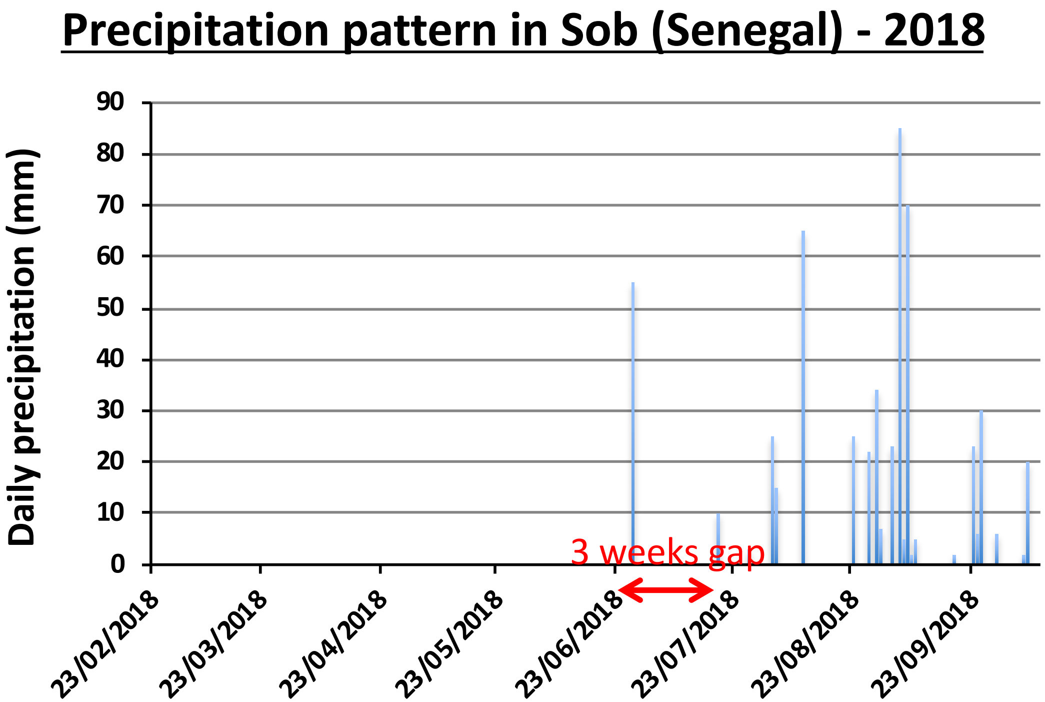
Precipitation pattern in Sob (Senegal) - 2018



Source: OPSE Niakhar

Primary root growth

An adaptative trait?

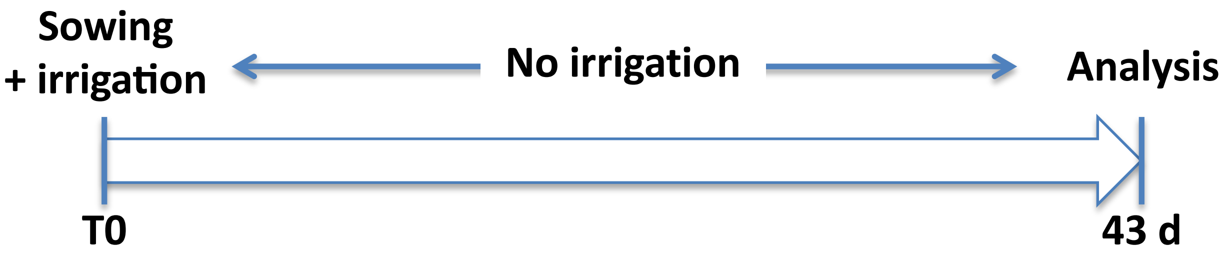


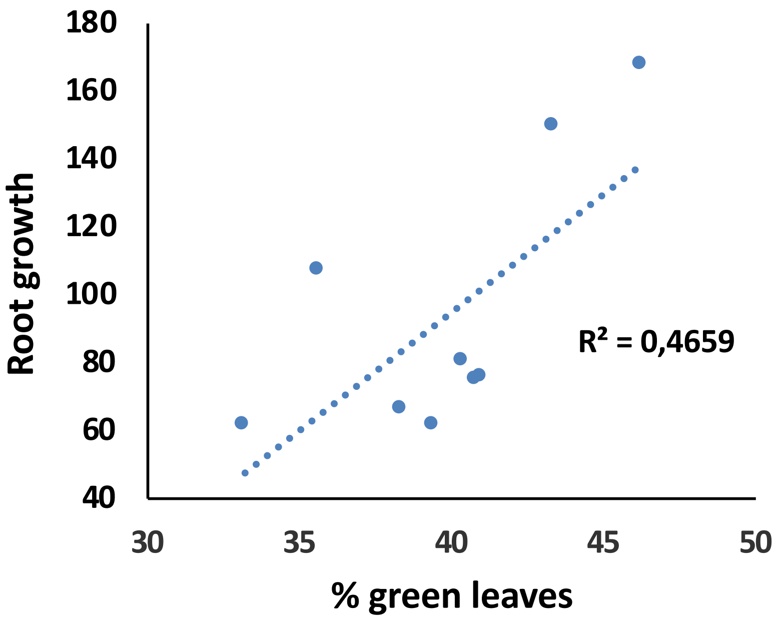
Source: OPSE Niakhar

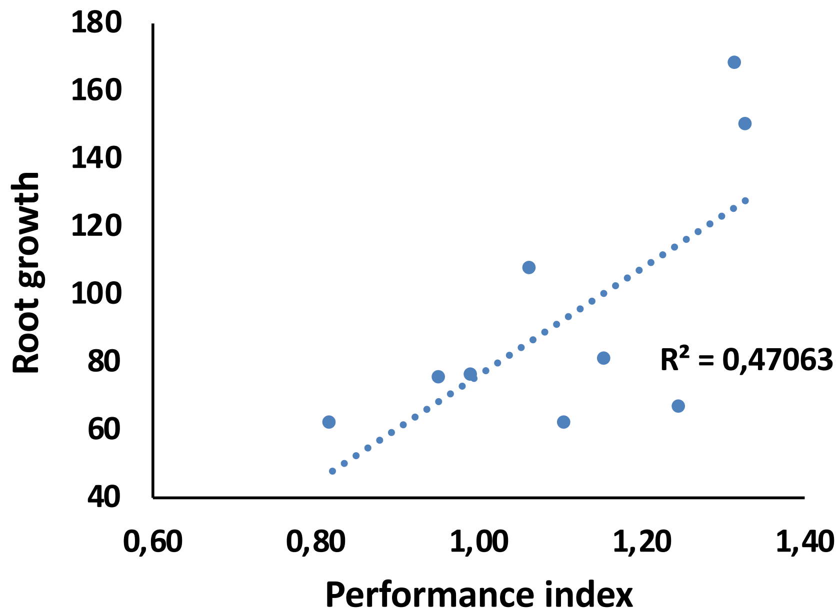
Primary root growth as target trait for crop establishment

B. Sine

A. Grondin





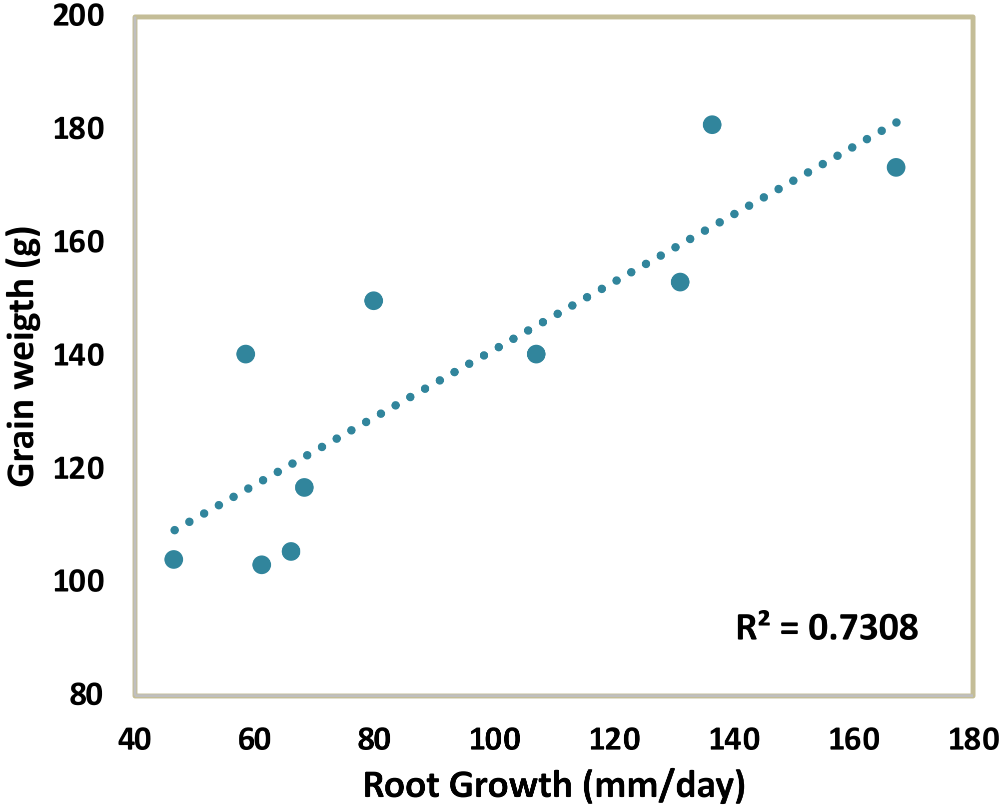


Primary root growth as target trait for crop establishment

B. Sine

A. Grondin

Stress field trials (Bambey, Senegal)
(+/- P, WW/STR1/STR2)



Primary root growth as target trait for crop establishment

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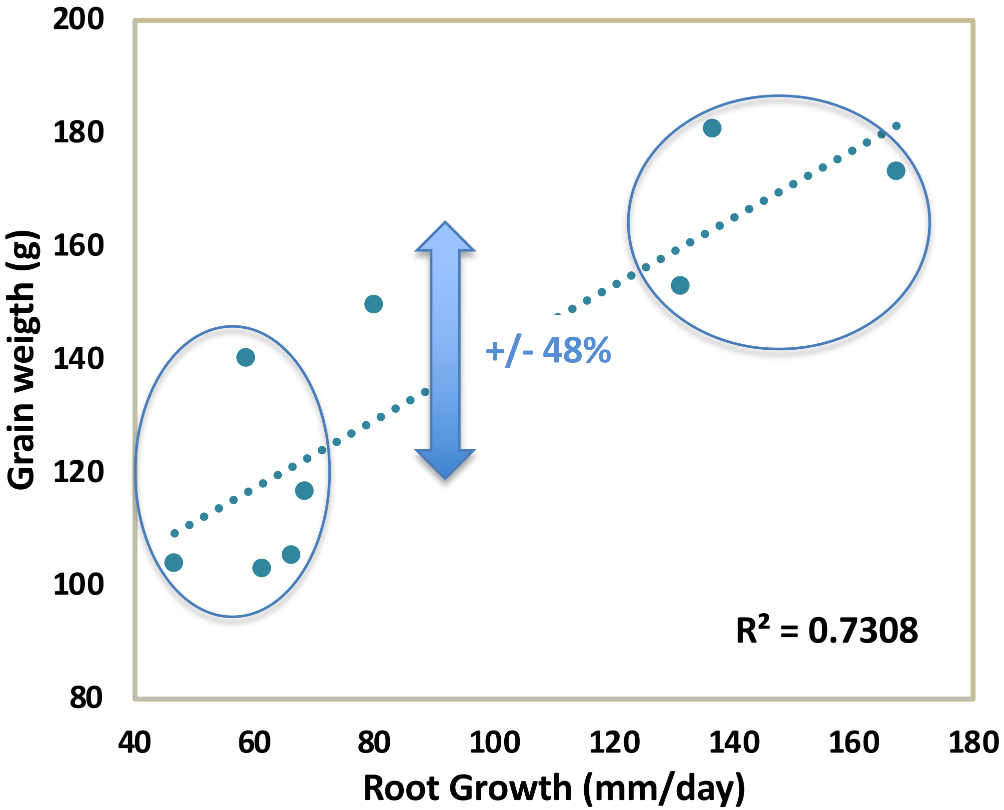
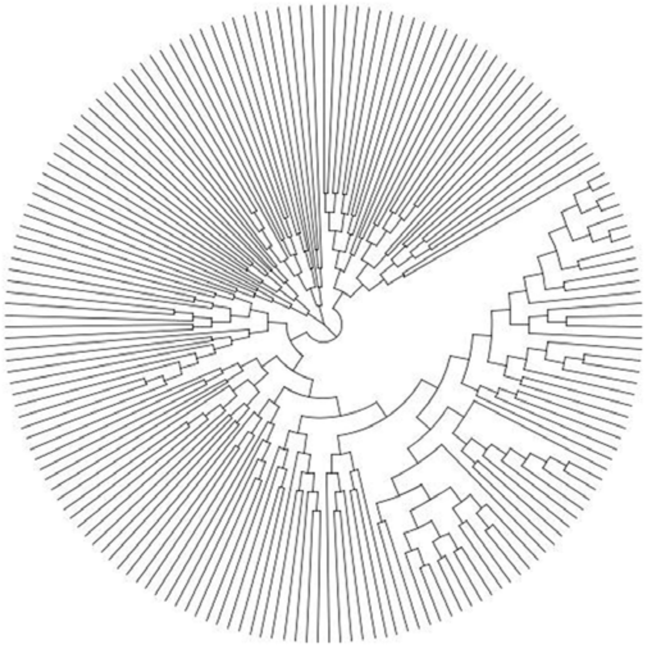
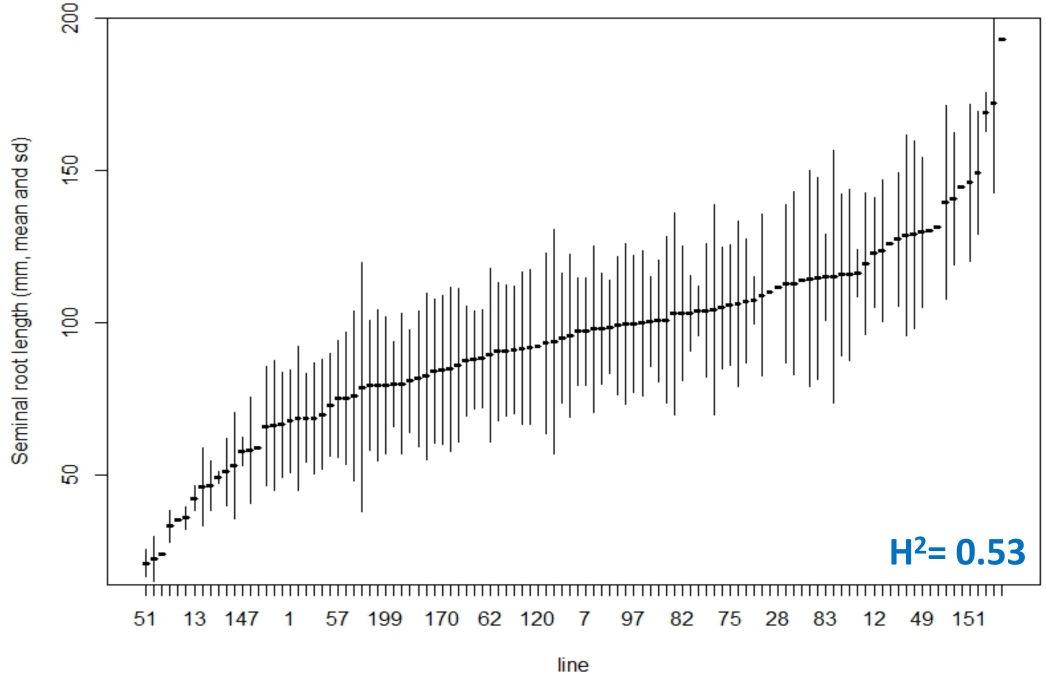


Identification of genomic regions controlling root growth through GWAS

S. Passot

392 493 SNPs identified by GBS

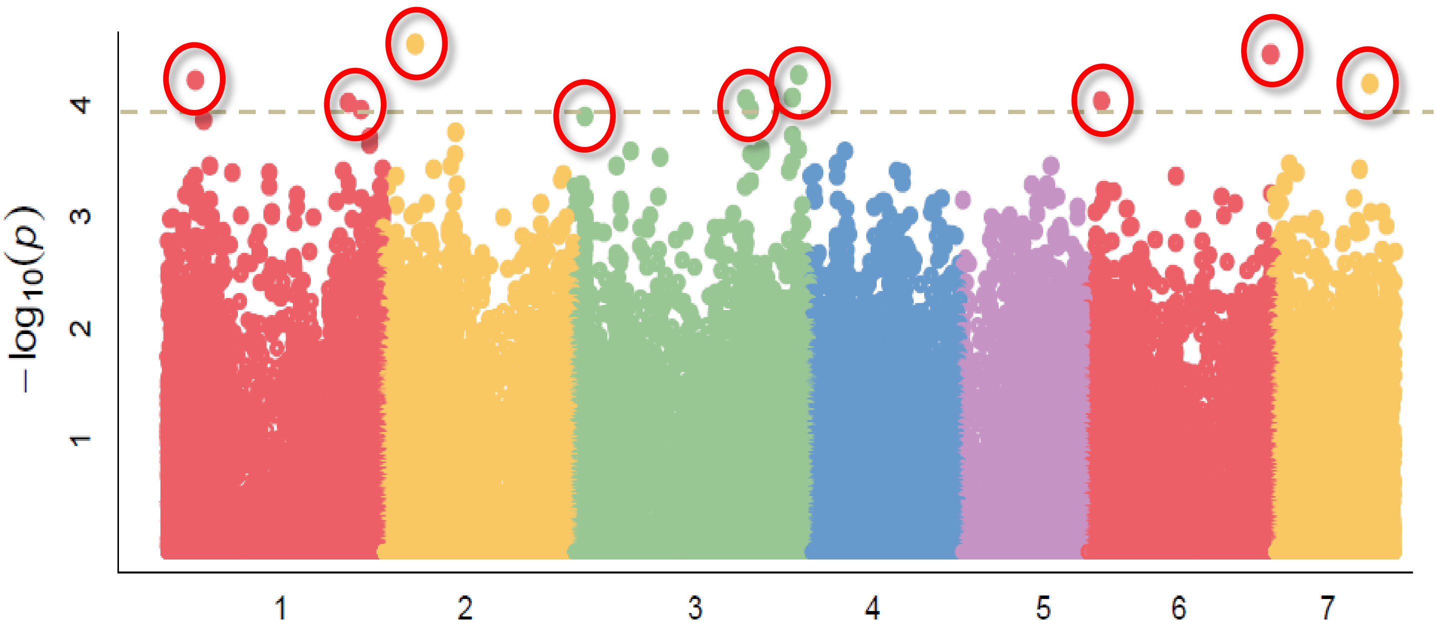




Identification of genomic regions controlling root growth through GWAS

M. Debieu

9 potential QTLs controlling primary root length



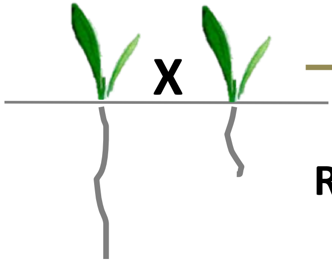
(log10(P)>4)

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

QTL validation using Bulk Segregant Analysis

C. de la Fuente

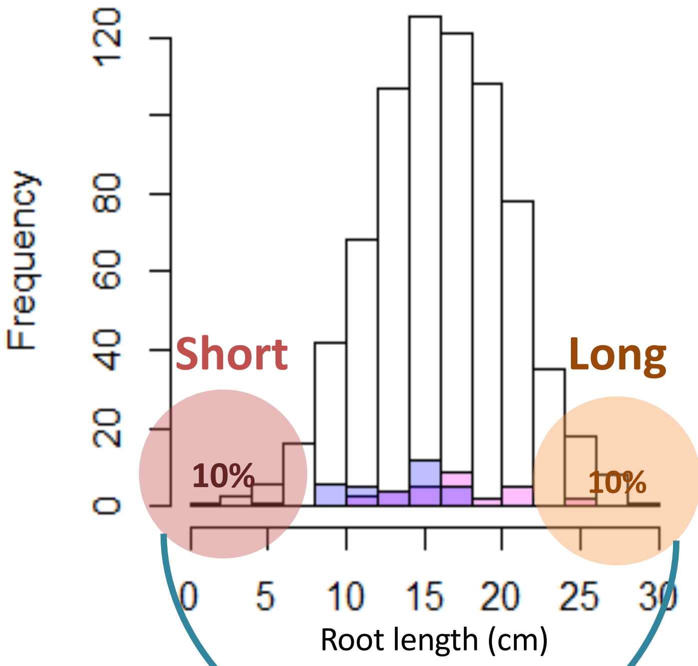
L337 L249



→ F1 → **933 F2 seedlings**

Self pollination

Root length frequency distribution in the 337 x 249 F2 population

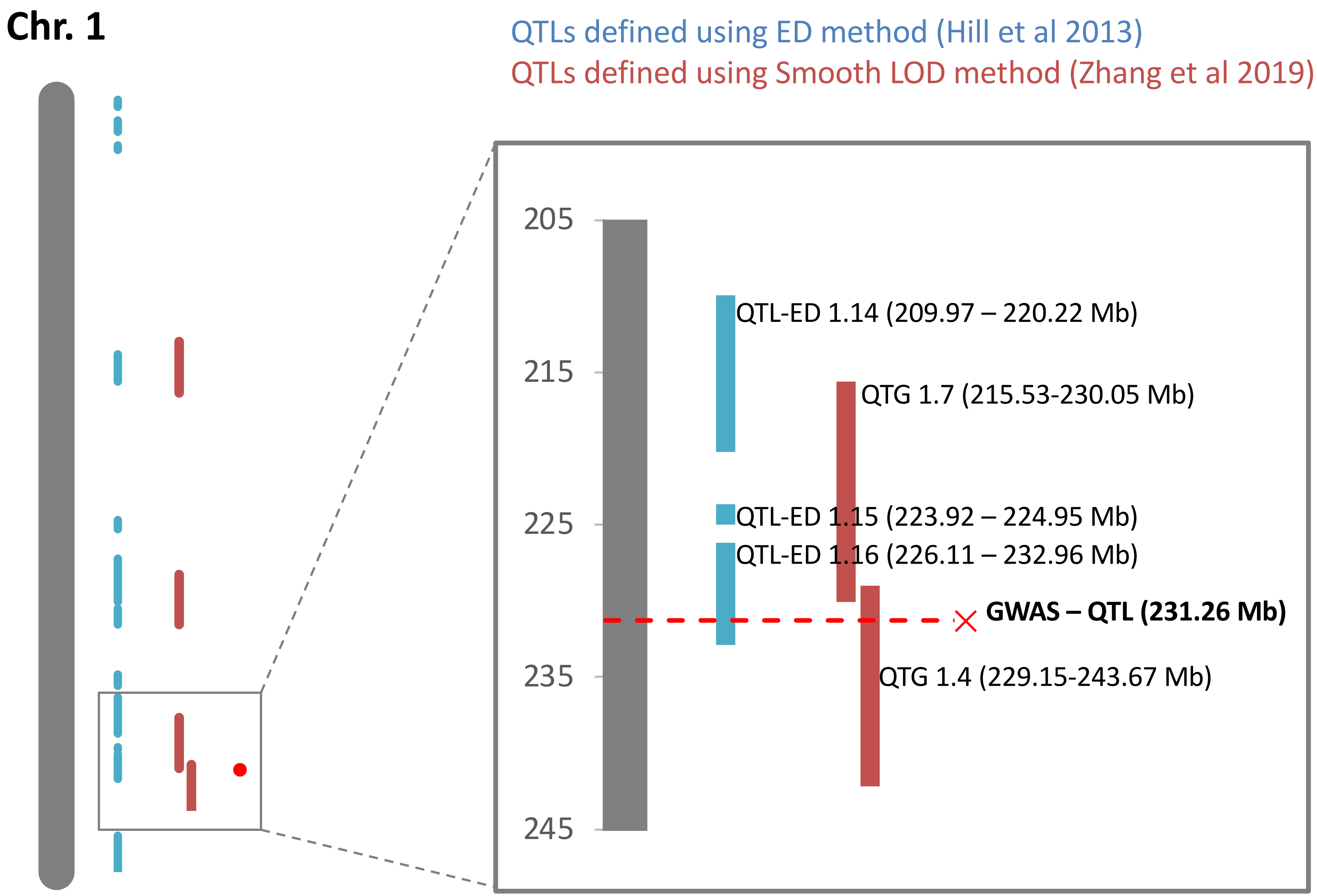


NGS

33 582 SNPs

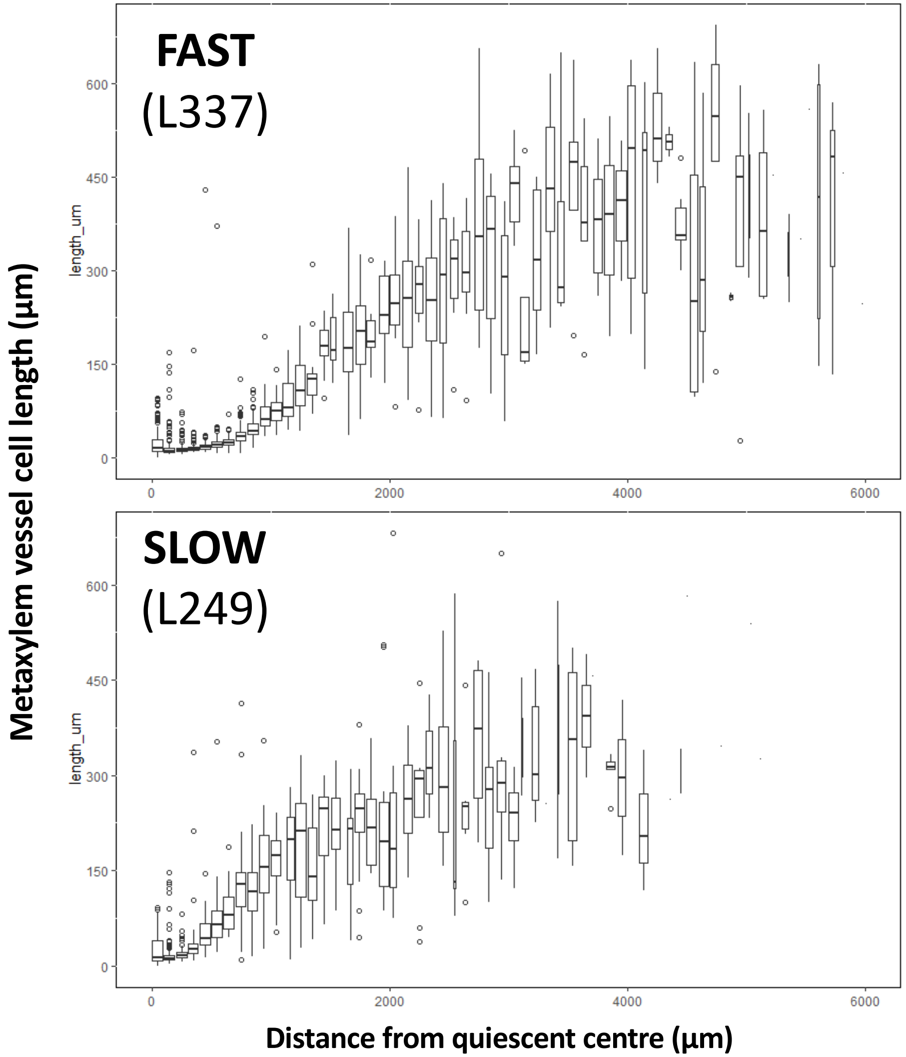
QTL validation using Bulk Segregant Analysis

C. de la Fuente



Comparison of root meristem structure

C. de la Fuente



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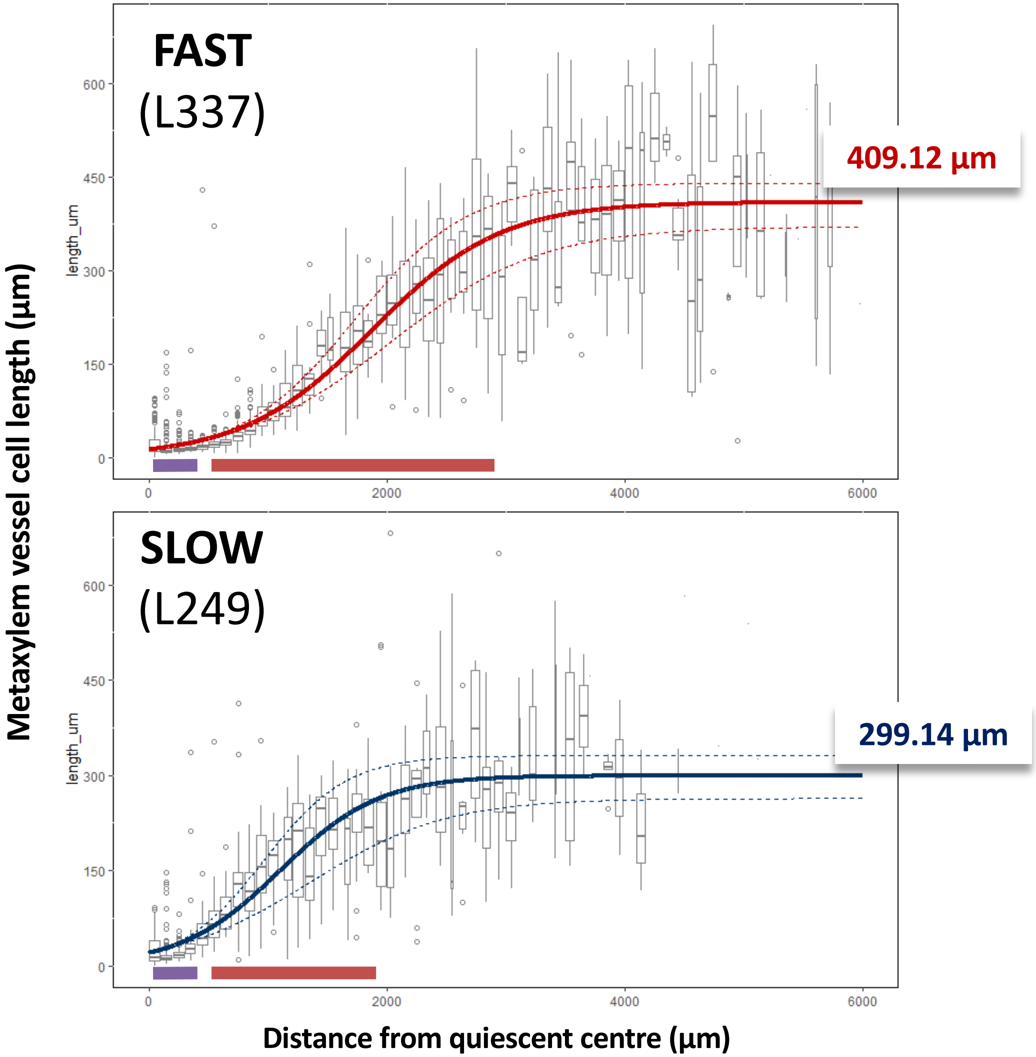
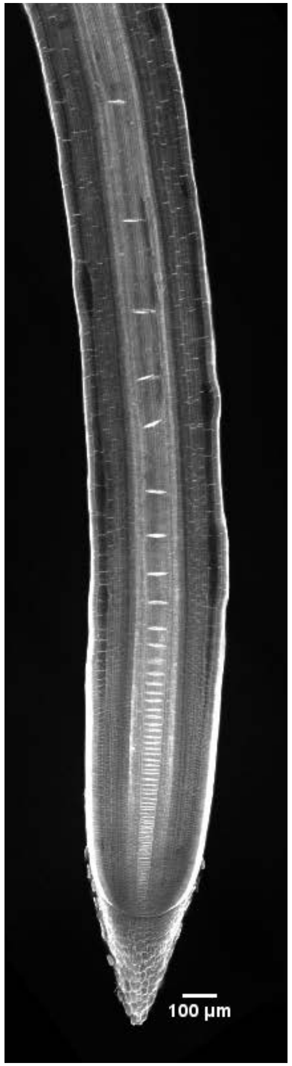


Transcriptomics to target candidate genes at the QTLs

M. Debieu

A. Grondin



RNAseq

Low growth IL 249 VS **High growth IL 337**

Montpellier MGX GenomiX

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

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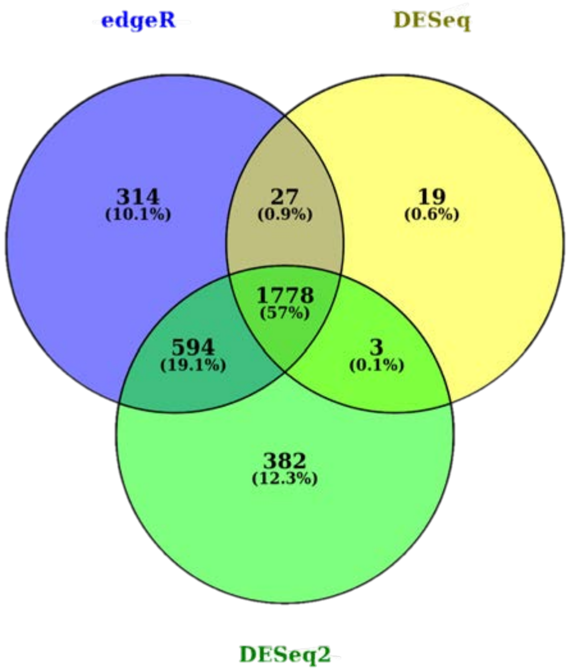

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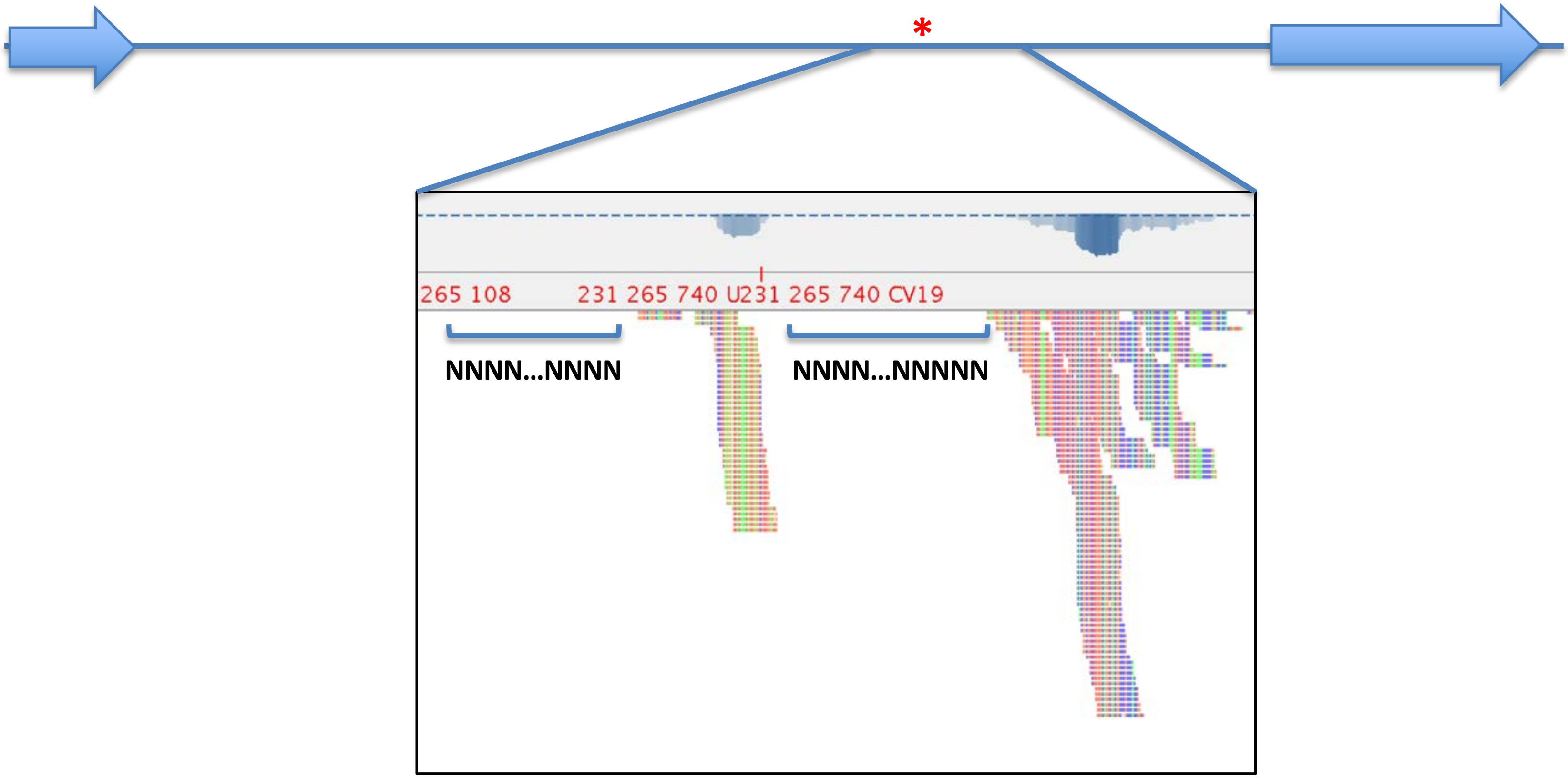
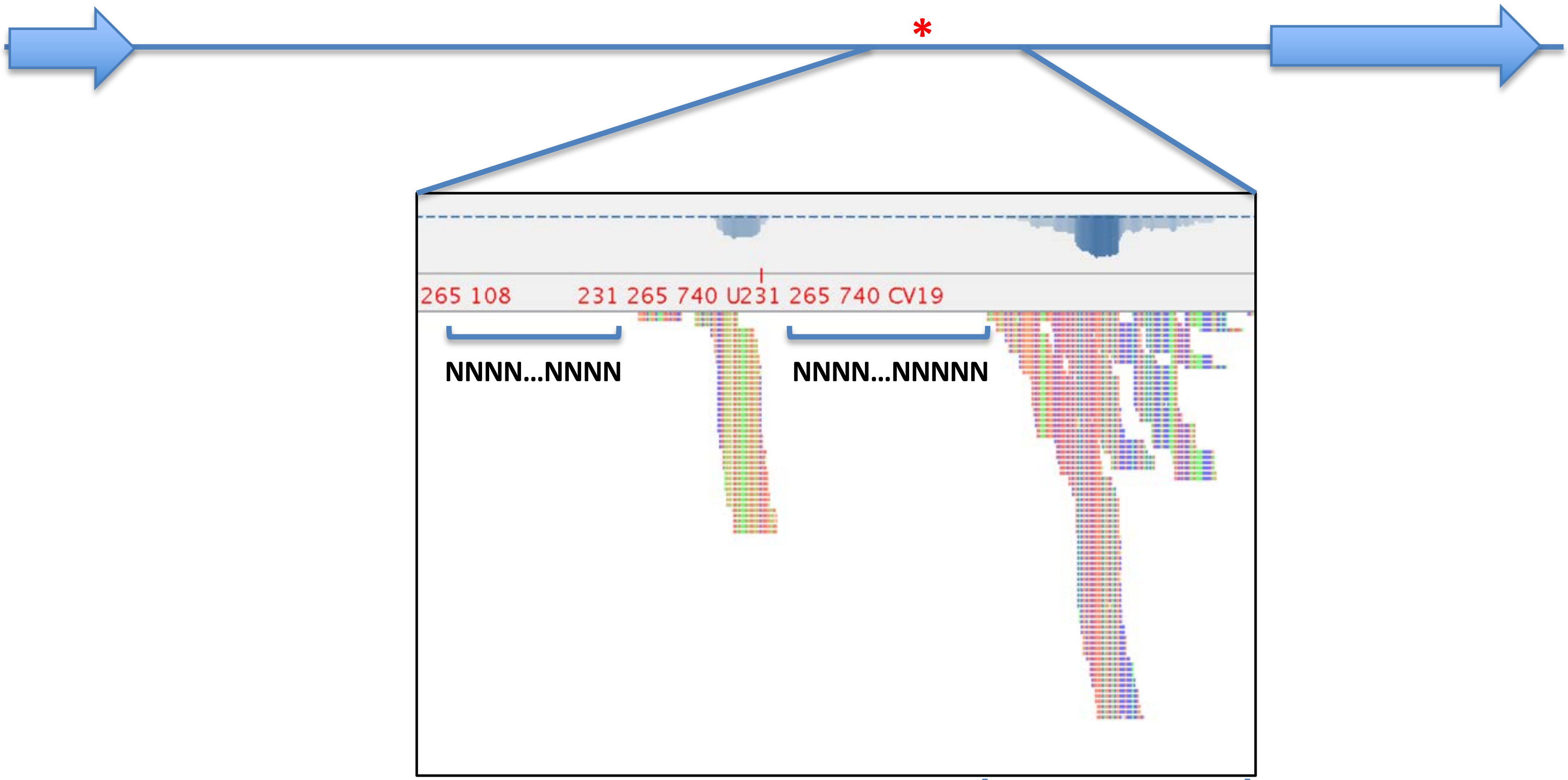
Genetic bases root growth

Genetic bases root growth



Genetic bases root growth



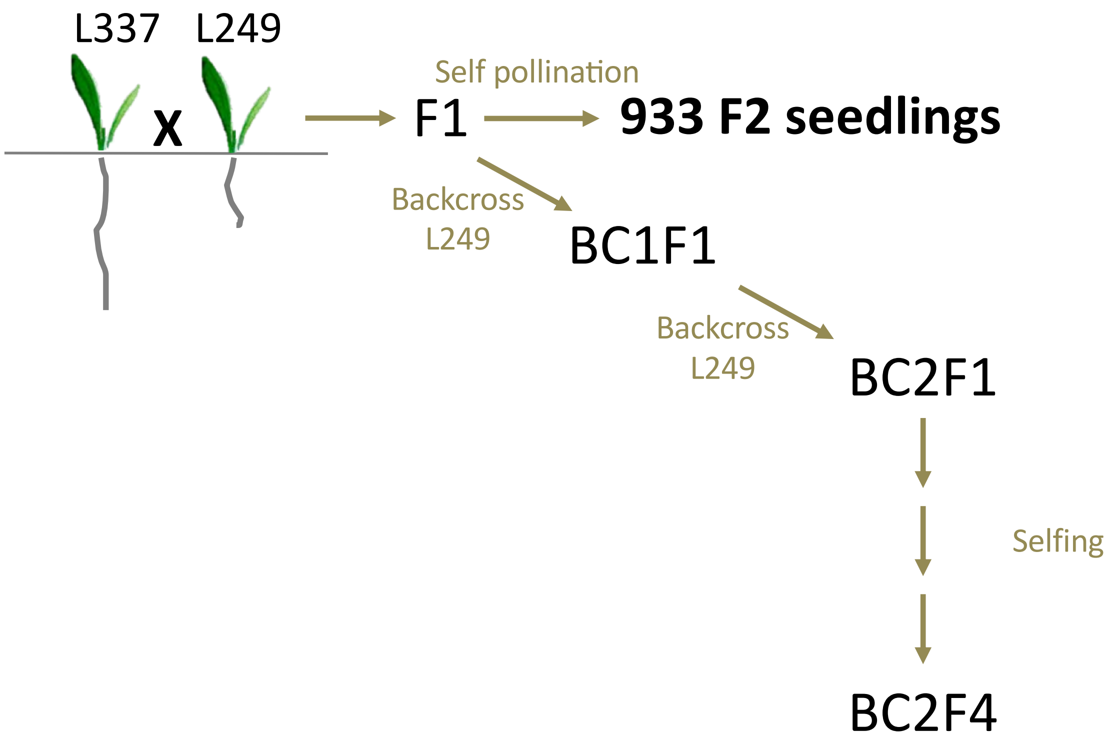
Homologies monothiol glutaredoxine S9

Take home message

- Root traits - potential breeding targets
- Pearl millet - key crop for African agriculture adaptation to future climates
- Seminal root growth – target trait for early drought tolerance
- GWAS/BSA for QTL identification
- Identification of mechanisms will facilitate pyramiding

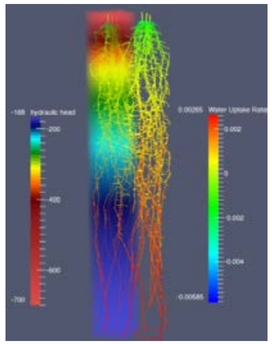
Perspectives

- Validate QTLs using backcross inbred lines (BILs)



Perspectives

- Validate QTLs using backcross inbred lines (BILs)
- Evaluate impact of QTLs on yield using BILs
- Characterization of the genomic regions associated to QTLs
- Validation of candidate genes function using gene editing
- Model of root systems/soil interactions



Acknowledgments

diade

P. Gantet
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M. Debieu
C. de la Fuente-Canto
S. Passot (PhD)

Y. Vigouroux
P. Cubry
L. Zekraoui
M. Couderc

LAPSE
LMI Adaptation des Plantes et microorganismes associés aux Stress Environnementaux

CERAAS (Centre d'étude régional pour l'amélioration de l'adaptation à la sécheresse)

N. Kane
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A. Audebert
A. Ndour (PhD)
A. Grondin

LCM

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A. Faye (PhD)
M.-T. Mofini (PhD)
D. Tchouomo
M. Ngom

CNRA

A. Faye

ICRISAT Science with a human face

P. Gangashetty
C.T. Hash

AgerConsult

J.L. Chopart

Eco&Sols

L. Cournac
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M. Sitor (PhD)
D. Tine
M. Diouf (PhD)

Laboratoire Mixte International iesol
Intensification Ecologique des Sols Cultivés en Afrique de l'Ouest

beb

T. Heulin
W. Achouak
M. Barakat
P. Ortet
A. Alahmad

The University of Nottingham

M. Bennett
D. Wells
J. Atkinson
C. Sturrock
R. Bhosale

PennState

J. Lynch
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Kansas State University

D. Min

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