

Dissecting native and induced root trait variation in barley via GWAS and TILLING

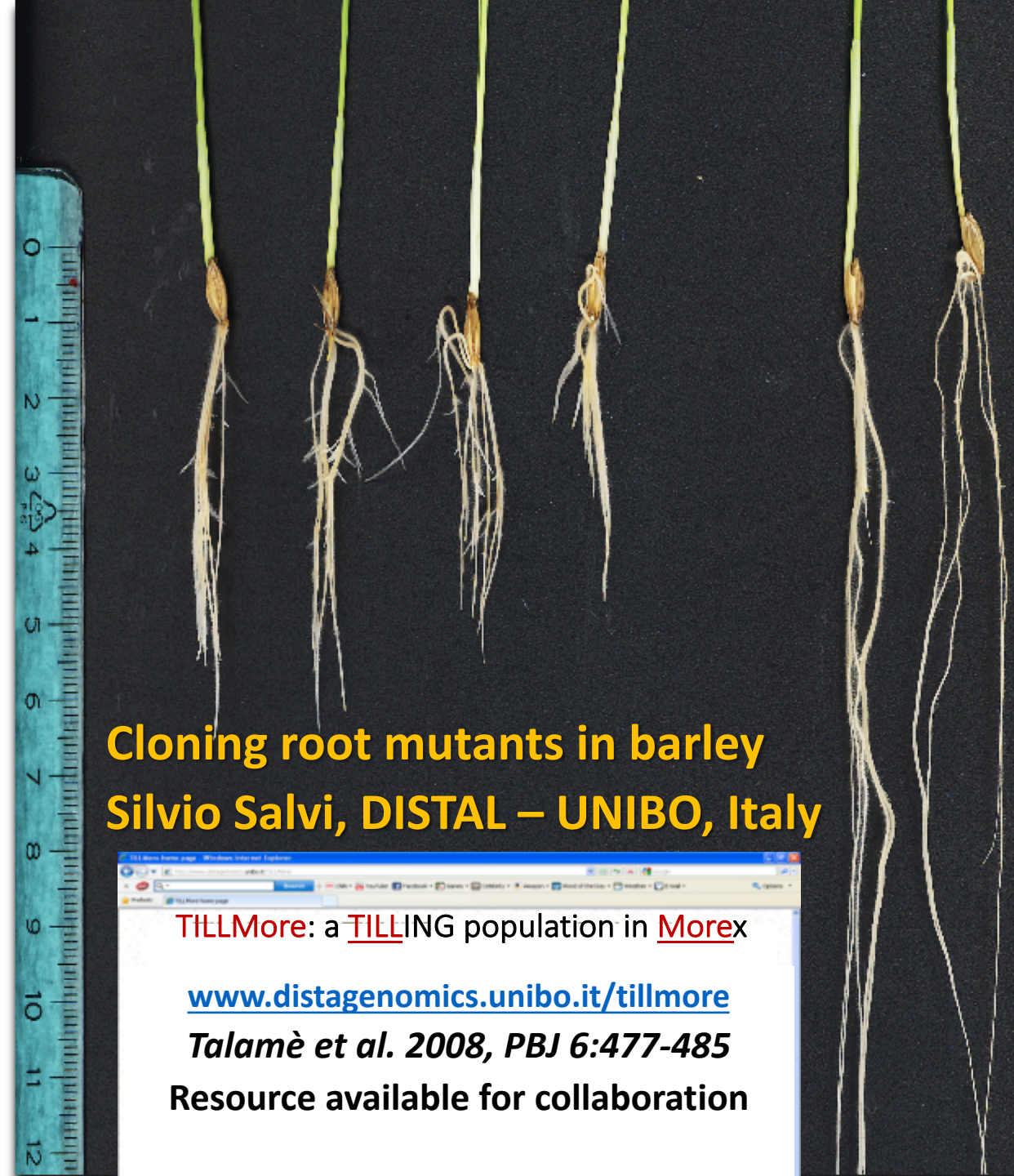
Silvio Salvi, Roberto Tuberosa – DISTAL, UNIBO, Italy

Introduction

- Limited information on the root system architecture (RSA) QTLome in Triticeae.
- No collection of RSA mutants available.

Objectives

- Dissect the barley root QTLome.
- Assemble a large barley collection of root architecture mutants.
- Set up a forward-genetics protocol for fast cloning of barley root mutants.



Cloning root mutants in barley
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TILLMore: a TILLING population in Morex

www.distagenomics.unibo.it/tillmore

Talamè et al. 2008, PBJ 6:477-485

Resource available for collaboration

GWAS for root traits in barley



Partnership with WHEALBI EU project
CREA- Fiorenzuola (IT) – Luigi Cattivelli

Collection of > 400 barley accessions

- Exome sequence and SNP profiling
- Population structure fully resolved

Traits

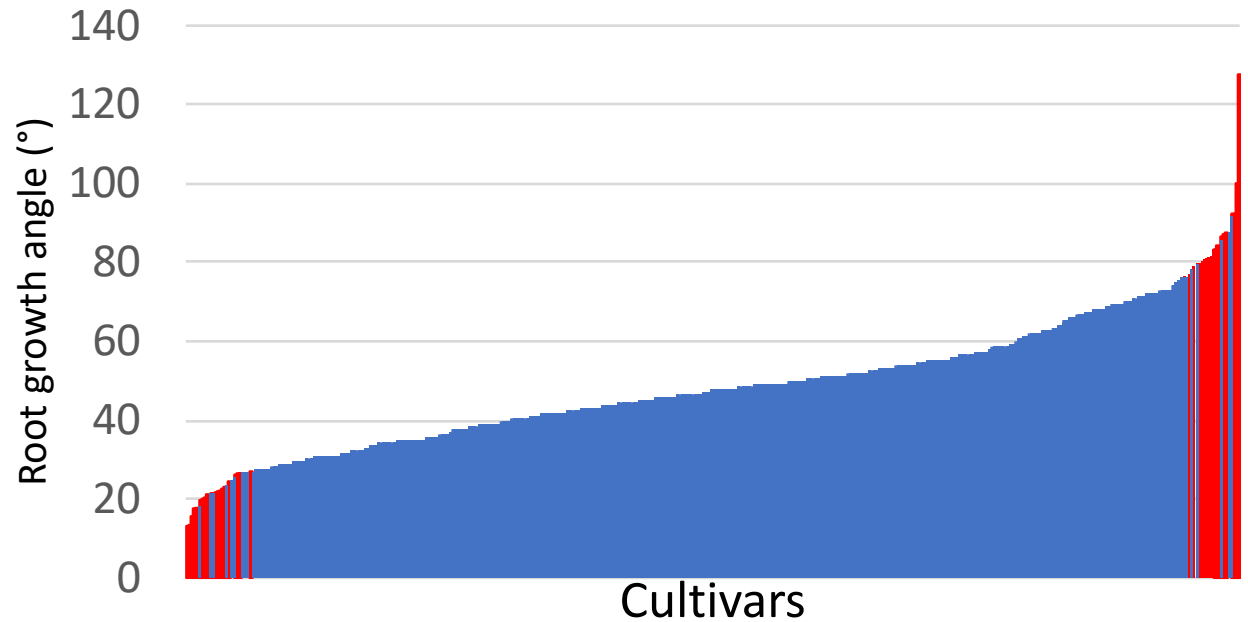
- Number of seminal roots
- Root growth angle
- Root dry weight
- Root diameter
- Number of lateral roots



<http://www.whealbi.eu>



Mean = 49.1° (range 21.0 – 128.9), $H_b^2 = 0.69$



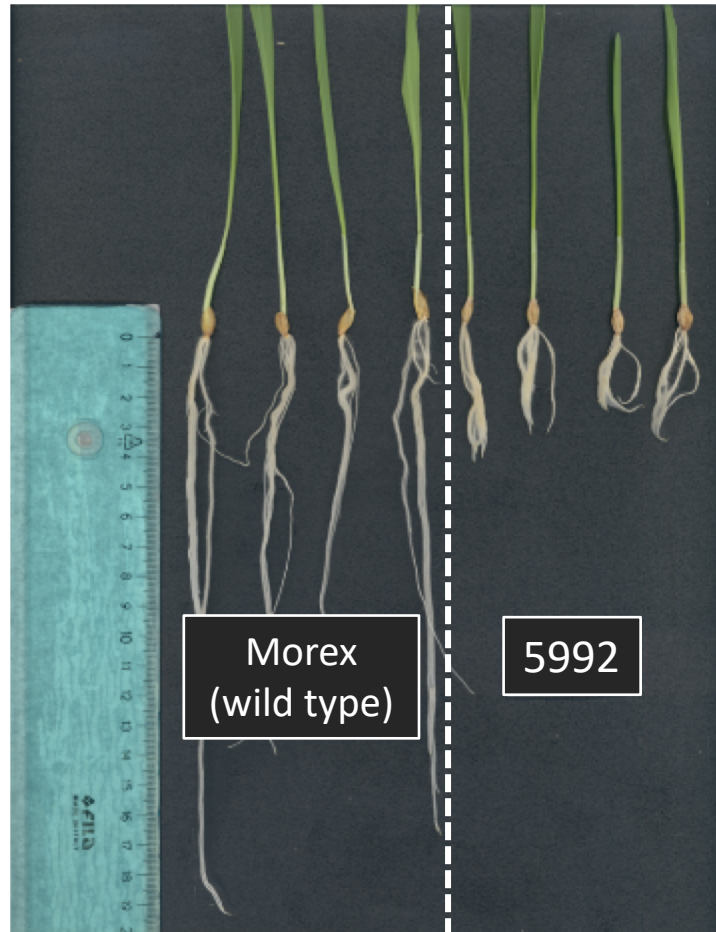
Root mutants in the TILLMore collection



How to clone a TILLMore mutant

Coarse genetic mapping by bulk segregant analysis (BSA) using an F_2 of Morex x 5992 followed by sequencing the coding space of the mutant line.

Mapping SR#5992 by SNP-based BSA



Chr 7H



Shortroot5992 approx 70 cM

Conclusions and perspectives

GWAS for native RSA diversity

- Three major QTLs for root growth angle at the seedling stage have been identified in the Whealbi panel.
- Next, root phenotyping with 50 cm-long rhizotrons will be used for the dissection of the QTLome governing root system architecture (RSA) with particular emphasis for root depth and other traits at the jointing stage.

Characterization and cloning of RSA mutants from TILLMore collection

- 63 lines showed a clear root phenotypes. ***Largest collection of root mutants.***
- Short root mutants #5141 and #5992 were cloned and turned out to be alleles of root-expressed, auxin related gene. Two independent enhanced gravitropic loci are being targeted for cloning.
- Sequencing the whole collection will pave the way to *in silico* TILLING in barley.

Acknowledgements



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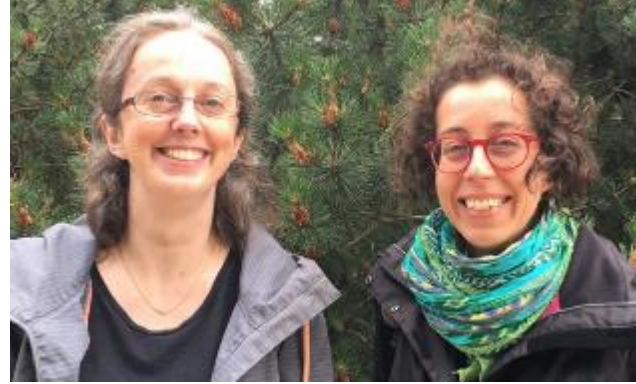
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