GWAS in a sorghum NAM population, a Diversity Panel and an elite breeding population identifies common genomic regions associated with nodal root angle

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Nodal Root Angle

- Changes in nodal root angle are likely to influence water capture in different environments by modifying horizontal and vertical exploration of the soil.

- Modelling with best bet assumptions indicated substantial yield gains in some environments if correct root architecture was deployed in MxE.

- Different architectures are likely to be suited to different soils x management systems.


In terms of growth and development of the root system

- Sorghum produces only one seminal root
- Nodal root starts to appear at 5-6 leaf stage
- Genotypic difference in nodal root angle
- Critical stage for root angle screening, leaf 5-6
- Phenotyping requires chambers of 50cm X 45cm

Singh et al. 2010. Plant and soil 333: 287-299
• potential importance
• understanding the developmental stage

What variation exists in the germplasm pool within the sorghum pre-breeding program in QLD Australia?
Develop a rapid screening methodology for root architecture variation


Develop a rapid screening methodology for root architecture variation

Parental lines of mapping populations, NAM populations and breeding populations screened

(a)

Initial screens revealed considerable variation in nodal root angle in sorghum

Variation in root angle in seedlings is predictive of the amount and timing of water uptake in adult plants grown in large root chambers.

Wide angle tended to extract less water from below the plant line (vertical) but more water at a distance from the plant (horizontal).
High throughput screening methodology developed (500 entries per experiment)

~3000 lines screened in total

Mapping Populations

NAM Population

Breeding Populations

Diversity Panel

n=213

n=1385

n=563

n>900
**Mapping Populations**

In total, the 4 nodal root angle QTL explained 58.2% of the phenotypic variance.

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In total, the 4 nodal root angle QTL explained 58.2% of the phenotypic variance. QTL are colour-coded according to trait; nodal root angle - green; root dry weight - brown; shoot dry weight - dark blue; total leaf area - bright blue.

Only limited genetic linkage was detected between the nodal root angle QTL and the plant size QTL.
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Biplots generated from principal components analysis of traits. Directional vectors represent root and shoot traits and the points are genotype values.

Selection for nodal root angle will not have unforeseen consequences on plant size at this stage of crop growth.

Mapping Populations

n=213
Nested Association Mapping Resource

- >100 exotic parental lines back-crossed to a single elite genotype
- Provides opportunity to evaluate exotic alleles in an elite genetic background
- 23 populations, consisting of 1385 progeny, genotyped with high density SNP markers.
- Whole genome sequence data available for 17 of the 23 parental lines

Mapping Populations

\[ X \]

NAM Population

Breeding Populations

Diversity Panel

\[ n=213 \]

\[ n=1385 \]

\[ n=563 \]

\[ n>900 \]
Elite sorghum breeding trials

- Advanced Yield Testing (multiple environments)
- 342 unique genotypes tested in hybrid combination with multiple females
- 563 hybrid combinations
Diversity panel resource

- >900 genotypes
- Highly diverse genotypes
- Excellent point of entry to explore native variation
- High degree of overlap with S.A.P.

Mapping Populations

\[ n=213 \]

NAM Population

\[ n=1385 \]

Breeding Populations

\[ n=563 \]

Diversity Panel

\[ n>900 \]
Integrated set of germplasm resources
High density genotyping
Multi-trait and multi-environment phenotyping

Powerful tool for trait dissection and high resolution mapping

Mapping Populations

NAM Population

Breeding Populations

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Box-plots of root angle variation in 3 complementary populations

- **Diversity Panel**: Heritability 90.6
- **NAM**: Heritability 86.3
- **Breeding populations**: Heritability 80.1

Root Angle (Degrees)
Mapping Populations

NAM Population

Breeding Populations

Diversity Panel

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GWAS and mapping reveals complex multigenic trait architecture
Mace et al. 2014. BMC Plant Biology 14: 253

Using comparative genomics, common genomic regions associated with root angle can be identified across species.

- Sb Root Angle QTL
- Os Root Angle QTL
Using comparative genomics, common genomic regions associated with root angle can be identified across species.
Using comparative genomics, common genomic regions associated with root angle can be identified across species.
QTL mapping of root angle in F₂ populations from maize 'B73' x teosinte 'Zea luxurians'.

Fame Onwuike and Yoshito Maesh

plantroot.org
Control of root system architecture by DEEPER ROOTING 1 increases rice yield under drought conditions

Yusaku Uga1, Kazuhiko Sagimoto1, Satoshi Ogawa2, Jagadeesh Bote3,4, Manabu Ishitsuki1, Naho Hara1, Yuka Kitomi1,2, Yoshiaki Imokai1, Kazuko Otsuki1, Tatsuro Kann1, Kazuhiko Inoue5, Himako Takehisa1, Ritsuko Motomura1, Yoshiaki Naozuma1, Kazuhiko Inoue1, Takaaki Matsumoto1, Toshiyuki Takai2
Diversity (θπ)
Wild and weedy Landraces
Improved inbreds
Diversity (θπ)

Wild and weedy Landraces
Improved inbreds

NAM
RIL
Breeding populations
Diversity Panel
Further mine resequence data in QTL region:
1) Signatures of selection for domestication and improvement
2) Interrogate particular SNPs in predicted gene models
   - non-synonymous SNPs
   - large effect SNPs

Genes with signatures of selection
Genes with large effect SNPs
Candidate genes from other species
Mapping Populations

Develop a rapid screening methodology for root architecture variation

Identify genomic regions and multiple alleles

Integrate with our multi-layer genome map

Mace & Jordan. 2010. TAG 121: 1339-1356

Mine existing performance data on breeding populations across environments to better understand trait value and impact on yield

Does root angle make a difference?

Integrate with our resequencing resource


Parental lines of mapping populations, NAM populations and breeding populations screened

Gene diversity
Identify causal variants

Sorghum QTL Atlas

Does root angle make a difference?
Does root angle make a difference?

- Identify the allelic state of genotypes and compare with pre-existing performance data across many environments and multiple years
- The genetic regions controlling nodal root angle also have an effect on yield and stay-green
- Yield was increased in the presence of the narrow root angle allele

Using our database of
historical yield data
Impact in elite germplasm

Other types of environment are sampled within our target population of environments.
Crop Simulation Modelling

What if questions
- What type of environments are common in our TPE?
- What root architecture QTL alleles would work best in my current environments and management systems?
- What combination of root angle alleles and row spacing would give the best yields on average at a particular location? What happens if I plant earlier?
- What is the likely variation (risk) associated with growing the best combination?
Whole Genome Marker Scans and Genomic Technologies

Trait Biology
Root angle varies in sorghum germplasm

Genome resources maps, markers, genes

Breeding program
Genotypes and phenotypic data

Questions we can answer
• Are the genes for root architecture segregating in my breeding program?
• Am I selecting for particular root architecture?
• Are there other sources of the trait I should look at?
• What impact does a particular gene for root architecture have in a specific environment?
• Does variation in these genes have different effects in early flowering compared to late flowering genotypes?
Integrated systems approach to complex trait dissection

- Large variation in nodal root angle exists in sorghum
- Associated with temporal and spatial patterns of water use.
- Linked to grain yield under drought.
- Rapidly identify genomic regions and allelic variation significantly associated with nodal root angle across populations and species
- Predict allelic impact on yield through simulation modelling
- Potential to deliver to industry is promising through the use of accessible and relevant genetics
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Background IP and access to germplasm