Genetic Control of Natural Variation in Maize Shoot Apical Meristem Architecture

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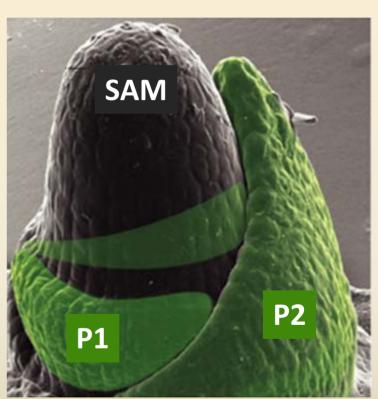
The Shoot Apical Meristem (SAM)

Contains undifferentiated cells

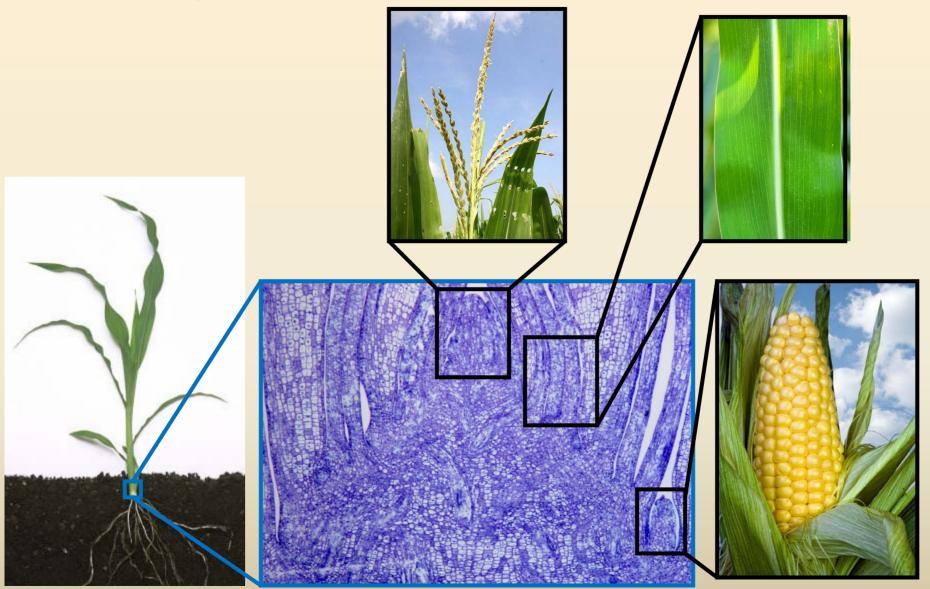
Forms above-ground organs

Leaves initiated in plastochron intervals

 Balance between stem cell maintenance and organogenesis



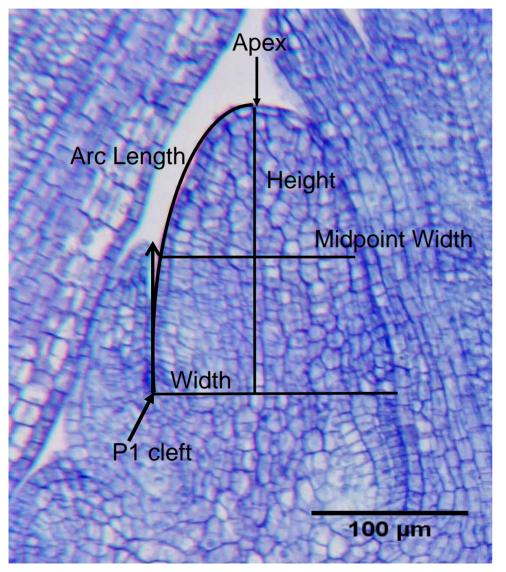
Importance of the Meristem

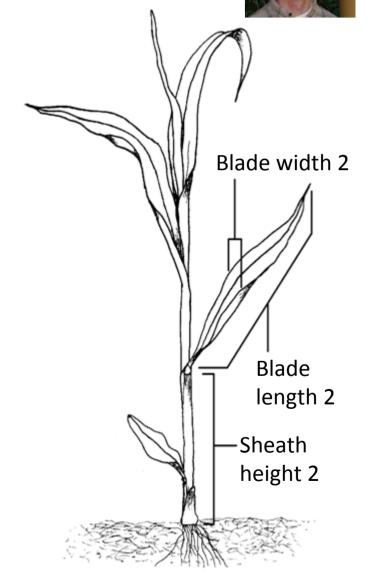


Objectives

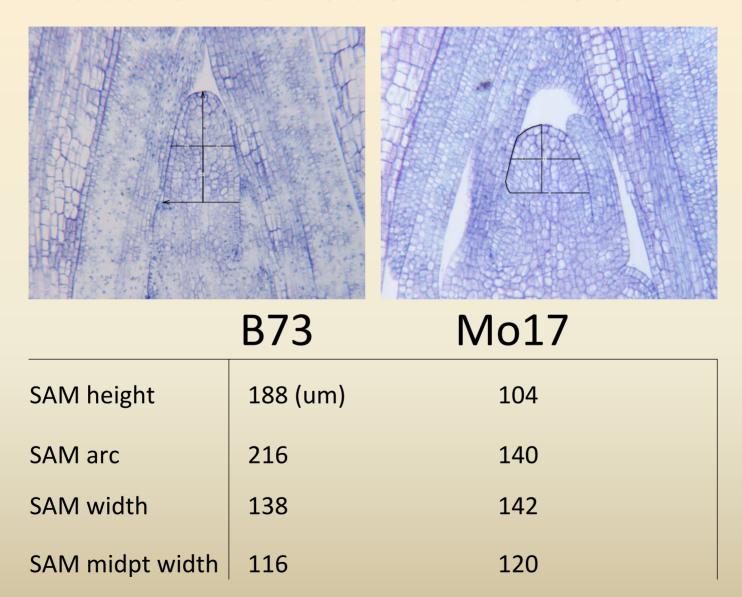
- Determine the relationship of SAM architecture with whole-plant traits
- Map QTL to determine genetic architecture of SAM morphology
- Compare genetic architecture of SAM traits and morphological traits
- Identify potential regulatory genes using expression-QTL analysis

Seedling Measurements

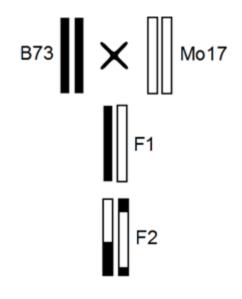




Natural Variation in the SAM

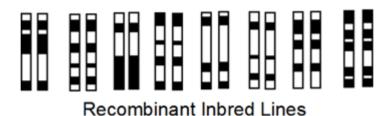


Population: Intermated B73 x Mo17 Recombinant Inbred Lines



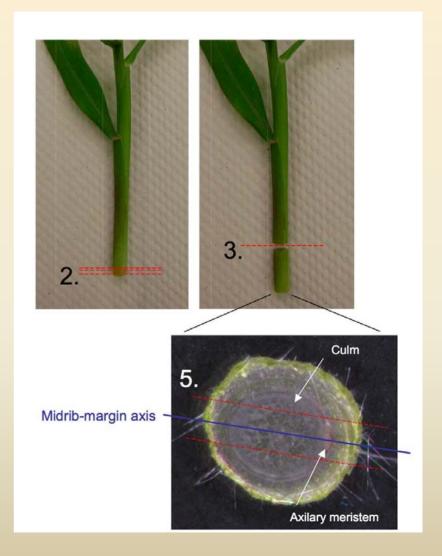
Intermating and recombination

Selfing



Experimental Design

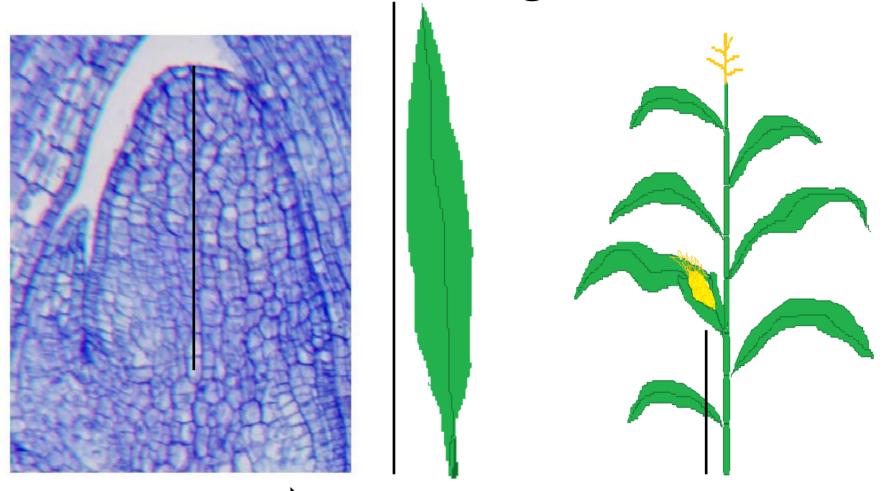
- 2 environments, 2 reps each
- 94 lines + 3 B73 + 3 Mo17
- 10 plants per line
- 2 x 2 x 100 x 10 = 4000 total plants
- Meristematic region dissected by hand, embedded in paraffin and sectioned longitudinally



Additional Trait Datasets

- Plant morphology
 - Stem diameter
 - Internode length
 - Node number
 - Plant height
 - Height of ear on plant
- Adult leaf traits
 - Length, width for leaves 9, 11, 13, 15, maximum, and average
 - Leaf angle
 - Total number of leaves and number of leaves below the ear
- Flowering time
 - Days to anthesis
 - Days to silking
 - Anthesis-silking interval

Correlation of SAM Architecture with Other Morphological Traits



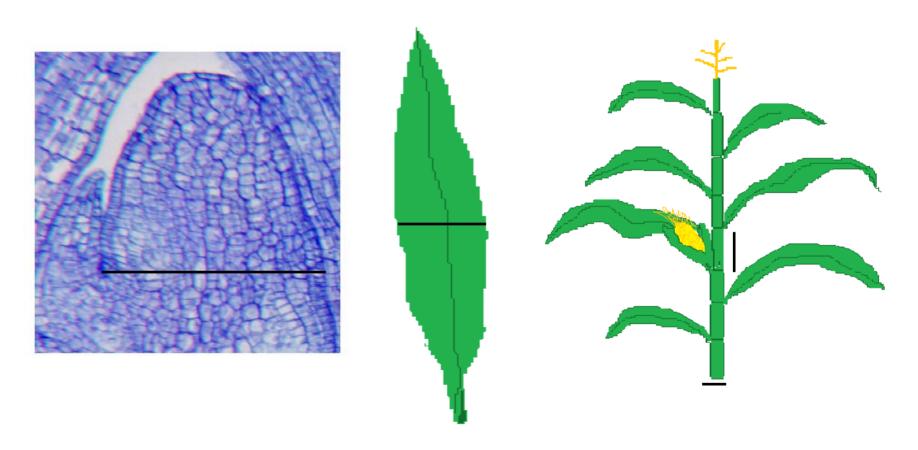
Tall, large volume

Meristem

Longer leaves

Lower ear height on plant

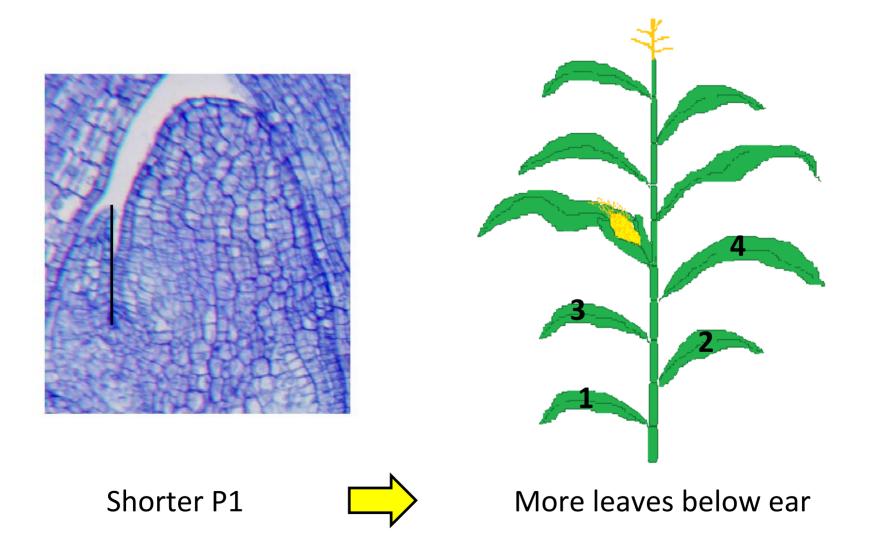
Correlation of SAM Architecture with Other Morphological Traits



Wide Meristem Wider leaves

Wider stem diameter Shorter internode length

Correlation of SAM Architecture with Other Morphological Traits



QTL Mapping of SAM Architecture

- SNP map
 - Developed from RNA-seq of IBMRILs
 - Over 7800 high-quality SNPs

Many small-effect SAM QTL

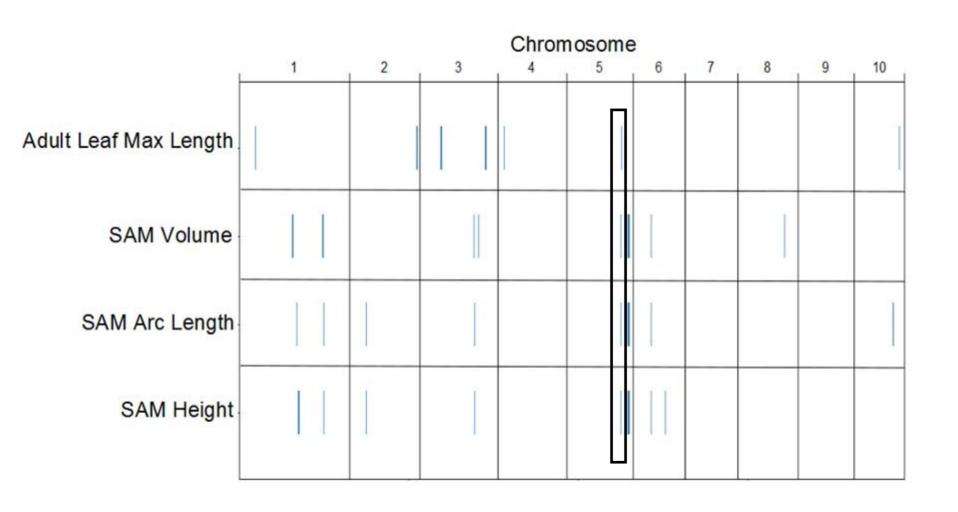
All SAM QTL

Chromosome

ı	1	2	3	4	5	6	7	8	9	10
SAM Cell Size	1									
SAM Height/Width						1				
SAM Volume					П					
SAM Cell count						П				
SAM P1 Length										
SAM Midpoint Width										
SAM Width					- 1					
SAM Arc Length										
SAM Height										

SAM Trait	Number of QTL	Total R2	Total Effect (um)	Effect Range (um)
Height	8	0.632	18.73	-4.57 to 6.1
Width	8	0.885	3.36	-3.58 to 4.87

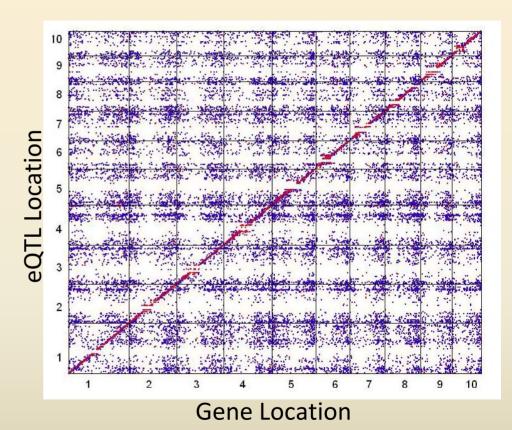
Coincident QTL



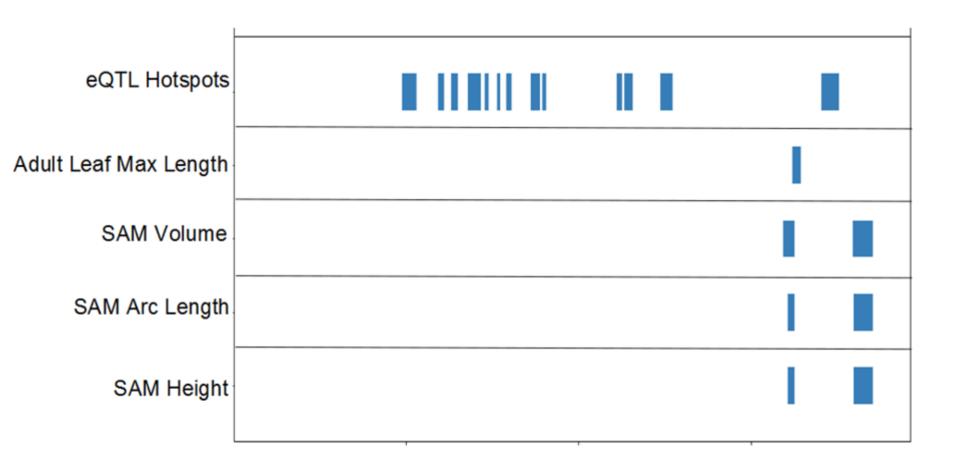
eQTL Mapping



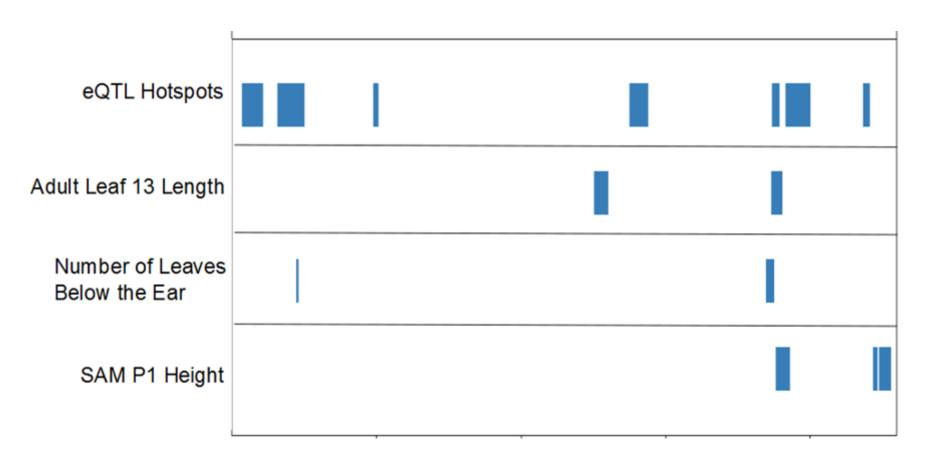
- RNA-seq of SAMenriched tissue from 120 IBMRIL
- Identified cis, trans, hotspots
 - Chi-sq p<0.05
- Identify regions that may contain master regulators via coincidence of pQTL and eQTL



Chromosome 5



Chromosome 3



Summary

- SAM height and volume are correlated with leaf length and ear height
- SAM width is correlated with leaf width, stem diameter, internode length
- P1 length is correlated with leaf number
- SAM architecture is controlled by many small effect QTL, one-third of which co-localize with other phenotypic QTL
- Half of co-localized physical QTL coincide with trans eQTL hotspots

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Maize Trait Datasets

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SNP map

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