Engineering light response pathways in crop plants for improved performance under high planting density

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How do crop plants perceive and respond to their light environment?

Can we manipulate light response pathways to improve crop yields?
Canopy Shade is Enriched in Far-Red Light
Canopy Shade is Enriched in Far-Red Light

A - Open  B - 1 Maize leaf  C - Under Maize Canopy

Photon Flux (μmol m⁻² sec⁻¹ nm⁻¹) vs Wavelength (nm)
Shade Avoidance Responses (SAR) in maize

Alterations of Growth Patterns and Resource Partitioning
  Increased plant height
  Reduced vegetative branching (tillering)
  Elongated Internodes (increased lodging)
  Acceleration of flowering
Holophytochromes

Pr → Pfr

Red

Far-Red

Phytochromes

Nucleus

Responses

Phytochromobilin

Plastid

Heme

Biliverdin

Phytochromobilin

Apophytochromes

Holophytochromes
Response mode (trait)

Arabidopsis thaliana

Oryza sativa (rice)
Sorghum bicolor
Maize phytochrome gene family
Maize phytochrome gene family

Maize phytochrome genes map to homeologous regions of the genome
Phytochrome gene family

Eudicot

- PhyA
  - PhyC
  - PhyE
  - PhyD
  - PhyB

Arabidopsis thaliana

Monocot

- PhyA
  - PhyC
  - PhyB

Oryza sativa (rice)
Sorghum bicolor (sorghum)

Zea mays (corn)

Allotetraploid event

Adapted from Mathews and Sharrock, 1997 *Plant Cell & Environment* **20**:666-671.
Identification of *phy* mutants

**PHYB1**

- phyB1-567
- phyB1-563

**PHYB2**

- phyB2-CSHL

**phyB1-563** homozygotes have a unique phenotype in the F2 inbred

- *phyB1-563* was introgressed into four genetic backgrounds:
  
  a) B73 (BC3)
  b) Mo17 (BC4)
  c) W22 (BC5)
  d) F2 (BC4)

- Plants were grown under greenhouse conditions
*phyB2-F2 lacks canonical ATG*
phyB1 phyB2 double mutants

PhyB1  phyB1 phyB2
PHYB1 and PHYB2 act redundantly in the control of several adult traits

- Examined phy control of ear node height, plant height, stem diameter and leaf sheath-internode difference

- Means groups are shown in lower case letters.
Control of flowering time in response to photoperiod is mediated predominately by PHYB2
## Summary of morphological measurements

<table>
<thead>
<tr>
<th>Effect</th>
<th>Trait</th>
<th>ANOVA</th>
</tr>
</thead>
<tbody>
<tr>
<td>PhyB1 only</td>
<td>Mesocotyl length</td>
<td>***</td>
</tr>
<tr>
<td>PhyB1 &gt; PhyB2</td>
<td>Plant height</td>
<td>**</td>
</tr>
<tr>
<td>PhyB1 &lt; PhyB2</td>
<td>Male flowering time (DAS)</td>
<td>***</td>
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<tr>
<td>PhyB1 = PhyB2</td>
<td>Ear height</td>
<td>***</td>
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<tr>
<td></td>
<td>Full height</td>
<td>***</td>
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<tr>
<td></td>
<td>Leaf sheath minus internode length</td>
<td>***</td>
</tr>
<tr>
<td></td>
<td>Stalk diameter</td>
<td>***</td>
</tr>
<tr>
<td>No PhyB effect</td>
<td>Internode length</td>
<td>NS</td>
</tr>
<tr>
<td></td>
<td>Tassel stem length</td>
<td>NS</td>
</tr>
</tbody>
</table>

P value: *** < .0001, ** < .0002, NS=Not Significant
Light control of axillary branch development
PhyB control of axillary branch development
PhyB regulation of axillary shoot development
FR light regulates *Tb1* expression in sorghum

PHYB1 regulates \textit{Tb1} expression

High R:FR \rightarrow \text{PhyB} \rightarrow \text{TB1} \rightarrow \text{Tiller bud outgrowth}

Low R:FR
QTL Analysis of SAR
Mimicking Canopy Shade: end-of-day-FR
Identification of Highly Responsive Traits

IBM#118, Day 6

EOD-FR

Control

IBM#118, Day 6

1st Leaf Sheath

Mesocotyl
PhyB1 predominates in control of seedling SAR.
1st Leaf Sheath Length in IBM

Transgressive Segregation: EOD-FR and Control
QTL Analysis of SAR

α = 0.01, 0.05, and 0.10
Maize Genome Sequencing

http://maizesequence.org
**Ds insertional Mutagenesis**

Goal: Generate a sequenced indexed collection of 10,000 Ds insertion lines

Update
- approx. 8,000 Ds elements have been distributed throughout genome (F1 seed)
- approx. 1800 F2 families have been generated
- approx. 600 fDs sequences amplified from F2 families
- amplifying at rate of 200/300 fDs/month

http://www.plantgdb.org/prj/AcDsTagging/
**GSS Contig**

Learn more about PlantGDB GSS assembly

**Sequence ID:** ZmGSSuc11-12-04.8509.1  
**Title:** Maize GSS contig assembled from B73 GSS  
**Type:** GSS Contig  
**Length:** 4187 bp  
**Organism:** Zea mays

**Search MaizeGDB for ZmGSSuc11-12-04.8509.1**  
**Search ZmGDB for ZmGSSuc11-12-04.8509.1**

Putative homologous gene products:  
PGL1: [Arabidopsis thaliana] At3g15510.1 - 68416.m00966 no apical meristem (NAM) family protein (NAC2) identical to ANAC2 [Arabidopsis thaliana] GI:12060426; contains Pfam PF02366: No apical meristem (NAM) domain; similar to jasmonic acid 2 GB_AAF04915 from [Lycopersicon]

**Diagram of ZmGSSuc11-12-04.8509.1 GSS contig assembly**

- **GSS contig:** repeat Mask:  
- **exon:** intron:

**PGL.60S (Predicted Gene Location/Alternative Gene Structure):**

- 3' UTR: 4055 - 4077
- 5' UTR: 4007 - 4055
- PGL.60S:
  - Exon: 1234
  - Intron: 1234
  - PGL.60S:
  - Exon: 1234
  - Intron: 1234

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The Shade of Things to Come
Light signaling in maize

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