Genetic Dissection of Quantitative Disease Resistance in Maize

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The Maize Diversity Project \textsuperscript{1,2,4,5,6,7,8}, Rebecca J. Nelson\textsuperscript{1}

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Resistant, Susceptible, and shades of gray...

Phenotype

R

Gene-for-gene

S

Specific

General

Interaction

Non-host

Multiple Disease Resistance

Quantitative Resistance
Research Approach: Genetic Platforms

- Selection Mapping
- Nested Association Mapping
- Maize Diversity Panel
- Near-Isogenic Lines

Phenotype

Interaction

R

S

Specific

General

Gene

Quantitative Resistance

Multiple Disease Resistance
Utility of Genetic Platforms

- Selection Mapping
- Nested Association Mapping
- Maize Diversity Panel
- Near-Isogenic Lines

Phenotyping Power

Allelic Diversity

Interaction

Quantitative Resistance

Phenotypic Power

Maize Diversity Panel

Multiple Disease Resistance

R

S

Gene
Utility of Genetic Platforms

- Nested Association Mapping
  - enrichment for resistance alleles
  - breeding material
- Maize Diversity Panel
  - diversity
  - high resolution
- Near-Isogenic Lines
  - uniform background
  - detailed phenotyping

- Selection Mapping
  - power!
  - resolution

Allelic Diversity

Phenotyping Power
Evidence for Multiple Disease Resistance in the Maize Diversity Panel

Phenotypic Evaluations
- SLB: 4 environments
- NLB: 3 environments
- GLS: 3 environments

Analysis:
- Linear Mixed Model
- Covariates:
  - Population Structure (K)
  - Relatedness (Q)
  - Relative maturity (days to anthesis)

<table>
<thead>
<tr>
<th>disease</th>
<th>GLS</th>
<th>NLB</th>
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<tbody>
<tr>
<td>SLB</td>
<td>***0.61</td>
<td>***0.62</td>
</tr>
<tr>
<td>GLS</td>
<td>-</td>
<td>***0.45</td>
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</table>

Genetic component of multiple disease resistance

Phenotypic Evaluation: P.Balint-Kurti, J.Kolkman, R.Wisser
Genotyping: The Maize Diversity Project, E.Bucker et al.
Analysis: R.Wisser
Candidate genes for quantitative disease resistance

Genotypes:
~850 genome-wide SNPs

Analysis:
Linear Mixed Model
Covariates: Population Structure (K), Relatedness (Q), and relative maturity (days to anthesis)

Sequence candidate gene from diversity panel (includes 26 NAM parents) and test for association

Analysis: R. Wisser
NESTED ASSOCIATION MAPPING (NAM)

NAM is a QTL mapping strategy that simultaneously exploits the advantages of \textit{linkage analysis} and \textit{association mapping} for high resolution genome scans.

Use sequence information from parents for association analysis

✓ Parental sequence imputed to RILs
## Multiple disease resistance in NAM

### Diversity Panel

<table>
<thead>
<tr>
<th></th>
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<th>GLS</th>
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<tr>
<td>SLB</td>
<td>0.62</td>
<td>0.61</td>
</tr>
<tr>
<td>NLB</td>
<td>0.45</td>
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*mixed model correction for population structure, flowering time*

### NAM

#### COVARIATES

<table>
<thead>
<tr>
<th></th>
<th>NLB</th>
<th>GLS</th>
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<tr>
<td>NONE</td>
<td>SLB</td>
<td>0.5</td>
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<tr>
<td></td>
<td>NLB</td>
<td>0.44</td>
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#### w/Population

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<thead>
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<tr>
<td>NLB</td>
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#### w/ flowering time

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<td>0.28</td>
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<tr>
<td>NLB</td>
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<td>0.24</td>
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#### w/ Population & flowering time

<table>
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<th>NLB</th>
<th>GLS</th>
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<tbody>
<tr>
<td>SLB</td>
<td>0.18</td>
<td>0.17</td>
</tr>
<tr>
<td>NLB</td>
<td>0.11</td>
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Position and relative effect of QRL identified in NAM

- B97
- CML103
- CML228
- CML247
- CML277
- CML322
- CML333
- CML52
- CML69
- Hp301
- Il14H
- Ki11
- Ki3
- Ky21
- M162W
- M37W
- Mo17
- Mo18W
- MS71
- NC350
- NC358
- Oh43
- Oh7B
- P39
- Tx303
- Tzi8

Legend:
- Red: SLB
- Blue: NLB
- Green: GLS

Inset graph:
- SLB
- NLB

Numbers 1 to 10 represent different categories or conditions.
Characterizing and Fine-mapping a Quantitative Resistance Loci on Chr. 8

Near Isogenic Lines: DK888/S11 F₇ lines from HIF (heterozygous inbred family)

Further detailed phenotyping possible in NILs (race-testing)

NIL development, evaluation, fine-mapping – C.Chung; NAM evaluation - J.Poland;
Characterizing Resistance Effect in Near Isogenic Lines

Near Isogenic Lines from Tx303 in B73 background

- Conidium
- Appressorium
- Initial infection
- Successful infection
- Infection hyphae

**Infection efficiency of* E. turcicum* (Northern Leaf Blight)**

- - QTL
- + QTL @ 1.02
- + QTL @ 1.06

**Number of hyphae growing into the xylem* (E. turcicum)**

- - QTL @ 1.02
- + QTL @ 1.02

+ QTL @ 1.06
Reduce infection efficiency

+ QTL @ 1.02
Reduce fungal growth in xylem
(no effect on infection)

NIL development, evaluation – C. Chung
Moving forward

- Selection Mapping
- Maize Diversity Panel
- Nested Association Mapping
- Near-Isogenic Lines

- ✓ Evaluation of selected alleles in RIL population
  ✓ Follow-up in BC lines

- ✓ Cross validate associations

- ✓ Test Candidate Genes
- ✓ Race-testing
- ✓ Microscopic phenotypes
- ✓ Fine mapping
- ✓ Map based cloning

- ✓ QTL characterization / confirmation
- ✓ 3rd season for NLB
- ✓ 2nd & 3rd seasons for GLS
- ✓ Test SNP associations

- ✓ Sequencing candidate genes
- ✓ Test for association
Thank you

Rebecca Nelson Lab
The Generation Challenge Program
The McKnight Foundation
Cornell University

Peter Balint-Kurti Lab
The Generation Challenge Program
USDA-ARS
North Carolina Corn Growers

Erik L. Stromberg Lab

The Maize Diversity Project
NSF (DBI-0321467: Molecular and Functional Diversity in the Maize Genome)
USDA-ARS
Dissection of a QRL for multiple diseases

Allele effects for QRL in bin 6.05: A region conferring resistance to multiple pathogens

Northern Leaf Blight

Common Rust

Anthracnose Stalk Rot

No effect on SLB severity

RILs: CML52/B73 Population (S5 inbred lines)

NILs: CML52/B73 S6 lines derived from HIF (heterozygous inbred family)

NIL development, evaluation – C.Chung; RIL evaluation - J.Poland;
Trypan blue staining

- Targeted stages: penetration, initial intracellular hyphal growth
- Microscopic parameter: infection efficiency

Successful infection
Infection efficiency of *E. turcicum*

Maize genotype

![Bar graph showing infection efficiency of *E. turcicum* across different maize genotypes and time points (2 dpi, 4 dpi, 7 dpi).]
**Recurrent Selection and Selection Mapping**

**Recurrent Selection:** Improving the mean performance of a population through iterative cycles of selection by

1) Identifying the superior individuals/families
2) Intercrossing superior individuals to form the next generation
Recurrent Selection Population:

Significant improvement for NLB resistance

mean AUDPC decreased by an average of 17% cycle\(^{-1}\)

CIMMYT; Ceballos et al., 1991 Crop Sci 31: 964-971
MDR in recurrent selection population

- Significant improvement for unselected diseases (SLB and GLS)

- Correlated response = genetic correlation = MDR

*evaluated at NCSU 2007*
Northern Leaf Blight

Disease Severity

P < 0.0001***

RILs  
NILs

B73  
CML52

qEt6.05_{B73}  
qEt6.05_{CML52}
Anthracnose Stalk Rot

ASR

- B73
- CML52

P = 0.0001***

RILs  NILs

Stalk Rot Severity

$qE6.05_{B73}$  $qE6.05_{CML52}$
Stewart’s wilt

Resistance to Stewart's wilt in CML52 NILs differing for bin 6.05

Allele(s) at bin 6.05

P < 0.0001***
Common Rust

Rust

$qET6.05$ – Multiple disease resistance effect

- NLB
- ASR
- Stewart’s wilt
- Common rust (?)
Nelson Lab Activities

- Test effect of selection on candidate genes
- Nested Association Mapping
- Selection Mapping
- Maize Diversity Panel
- Survey allele series
- Fine-mapping QTL
- Near-Isogenic Lines
- Near-Isogenic Lines

Phenotyping Power
sqrtAUDPC
sqrtAUDPC