Genomic Responses to Artificial Selection in Maize

Han Zhao\(^1\), Martha Schneerman\(^1\), Elizabeth Wragge\(^1\), Ayna Salas\(^1\), George Singletary\(^2\), Steve Morse\(^1\)

\(^1\) Department of Crop Sciences, University of Illinois at Urbana-Champaign
\(^2\) 2 Pioneer Hi-Bred, Int'l., Johnston, Iowa.

Abstract

Prior studies have detected evidence for selection among maize genes associated with domestication and crop improvement (1,2). However, it is more difficult to demonstrate selection upon individual genes or alleles associated with quantitative traits in recent breeding populations. The Illinois Protein Strains represent four related populations (Illinois High Protein, Illinois Low Protein, Illinois Reverse High Protein, Illinois Reverse Low Protein) that have been subjected to 105 cycles of artificial divergent recurrent selection for grain protein concentration. The application of functional genomics approaches to the unique genetic resource of the Illinois Protein Strains promises to reveal mechanistic insights into the responses of the complex maize genome to artificial selection. Our results to date have identified a number of genes whose RNA expression appears to be responsive to selection for grain protein concentration, including the zein seed storage protein genes and a number of genes predicted to function in pathways associated with nitrogen accumulation in developing maize seeds.

Experimental Methods

- Developing seeds of self-pollinated field-grown plants of inbred lines derived from the Illinois Protein Strains were sampled at 16 days after pollination. Five ears were sampled from each inbred.
- mRNA was extracted from whole seeds of these ears, reverse-transcribed to cDNA, and hybridized to long-array chips produced by the Maize Olignucleotide Array Project. Hybridized cDNAs were post-labeled using the Genisphere amplification system and then scanned using an Axon GenePix scanner. Dye swaps were conducted in the 5 replicate labelings.
- After spot finding, raw data was normalized using programs within Biocomductor, then imported into GeneSpring v. 7.2 for further analysis.

Table 1. Microarray results.

<table>
<thead>
<tr>
<th>Comparison</th>
<th># Significant Features*</th>
<th># Differentially Expressed Features*</th>
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</thead>
<tbody>
<tr>
<td>IHP vs. ILP</td>
<td>42,896 (76%)</td>
<td>530 (2.2%)</td>
</tr>
<tr>
<td>IHP vs. IRHP</td>
<td>40,595 (72%)</td>
<td>661 (1.6%)</td>
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<tr>
<td>IHP vs. ILP &amp; IRHP</td>
<td>30,993 (7%)</td>
<td>97 (0.3%)</td>
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*Features that showed significance difference by t-test, p < 0.05, following Bonferroni correction for multiple tests.

Table 2. Microarray results for zeins and zein regulators.

The relative expression of microarray features specific to zein family classes or subclasses, the OZ and PFB transcription factors, and the BPI ER protein chaperone are shown. The number of features present on the array for each gene class is indicated below each gene name in parentheses. *not significantly different expression level: by t-test at p<0.05

The coordinated directional changes in different a-zein gene subfamilies indicate that a-zein responses to selection in IHP and ILP are mediated by a post-transcriptional mechanism.

Table 3. Additional non-zein candidate genes whose expression changes greater than 5-fold between IHP and ILP.

References


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