High-Resolution Study of Wheat Transcriptomes in Response to Drought and Salinity & Ontologies

Pankaj Jaiswal
jaiswalp@oregonstate.edu
IWGSC Standards and Protocols Workshop
XXV PAG 2017, San Diego, California
January 17, 2017

Wheat lines being analyzed for their transcriptome sequencing, performance and genetic variation

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Specific De-novo Transcript Assemblies</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control</td>
<td></td>
</tr>
<tr>
<td>Drought</td>
<td></td>
</tr>
<tr>
<td>Salt</td>
<td></td>
</tr>
</tbody>
</table>

An Example of Differentially Spliced Transcript Isoforms Under Different Treatments

About wheat genomes

Number of Homeologous Genes Expressed Under Salt and Drought Conditions

Chinese Spring | Drought | Salt |
----------------|---------|------|
181             | 94      | 56   |
Kukri          | 1726    | 360  |
Ladd           | 3407    | 60   |
Kaseberg       | 1971    | 12   |
Bobtail        | 1410    | 2270 |

For samples from 89 samples (colored cells) there is a high degree of expression. Wheat plants were grown in the OSU greenhouses under normal 12h light/12h dark photoperiod cycle at 28°C temperature. When the plants reached the booting stage, the treatments were given and only the topmost leaf was harvested for isolating the mRNA. The plants continued to complete their lifecycle under normal conditions after the treatment and were observed for yield traits like average grain number and weight, after undergoing stress shock during their reproductive phase. Ideally stress during reproductive phase would negatively impact the yield.
Common & Treatment-Specific Homeologues in Hexaploid Accessions

SNP Identification and Their Consequences

Planteome: Reference Ontologies for Plants

Planteome Ontologies Maintained on the GitHub
Integration of Species-Specific Terms (e.g. Wheat Growth Stages)

Mapping of Species-specific Traits to Reference Trait Ontology

Acknowledgments

Planteome

Planteome Partners

User and resource databases who have adopted the Planteome Ontologies and contributed data:

Wheat Transcriptome Work

Matthew Geniza

Terry Nipp

John Talbott

Chris Daly