A high density GBS map of bread wheat and its application for genetic improvement of the crop

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OUTLINE

- Over-view: SeeD-Wheat
- High density GBS map
- GWAS: examples
- Conclusion

The Scope of SeeD

Strategic focus on “characterization for use in breeding” and pre-breeding (priority traits = breeding targets)

Anchoring GBS tags on chromosomes

<table>
<thead>
<tr>
<th>Population</th>
<th>Number of markers</th>
<th>Number of individuals</th>
</tr>
</thead>
<tbody>
<tr>
<td>PBW343 x Kingbird</td>
<td>13123</td>
<td>198</td>
</tr>
<tr>
<td>PBW343 x MUU</td>
<td>6936</td>
<td>148</td>
</tr>
<tr>
<td>PBW343 x K.Swara</td>
<td>18612</td>
<td>109</td>
</tr>
</tbody>
</table>

Genetic linkage mapping to construct a consensus map containing 28644 GBS markers.
Consensus map – 3757 unique positions
Total length of the map – 3302.5 cM
Proportion of common GBS markers across three populations

Validation of GBS map & Genetic dissection of complex traits in wheat

Distribution of segregation distortion loci across three RIL mapping populations

Identified chromosomal regions (QTLs) harboring APR to wheat rusts

Identified chromosomal regions (QTLs) harboring TS resistance-PBW343/Kingbird population

<table>
<thead>
<tr>
<th>Trait</th>
<th>Chro</th>
<th>Position</th>
<th>Left-Marker</th>
<th>Right-Marker</th>
<th>LOD</th>
<th>PVE(%)</th>
<th>Add</th>
</tr>
</thead>
<tbody>
<tr>
<td>TS</td>
<td>5B</td>
<td>263</td>
<td>1100641[F][0]</td>
<td>1069940[F][0]</td>
<td>21.6214</td>
<td>50.6367</td>
<td>-0.3248</td>
</tr>
<tr>
<td>TS</td>
<td>5A</td>
<td>124</td>
<td>2328786[F][0]</td>
<td>18641811[F][0]</td>
<td>4.4252</td>
<td>7.537</td>
<td>0.1238</td>
</tr>
<tr>
<td>TS</td>
<td>1B</td>
<td>93</td>
<td>3029257[F][0]</td>
<td>1130776[F][0]</td>
<td>4.1395</td>
<td>7.0445</td>
<td>-0.1201</td>
</tr>
<tr>
<td>TS</td>
<td>3A</td>
<td>56</td>
<td>1100113[F][0]</td>
<td>3029754[F][0]</td>
<td>4.6102</td>
<td>7.9568</td>
<td>-0.1275</td>
</tr>
<tr>
<td>TS</td>
<td>7A</td>
<td>165</td>
<td>1226998[F][0]</td>
<td>1128339[F][0]</td>
<td>13.0078</td>
<td>25.6901</td>
<td>0.2291</td>
</tr>
</tbody>
</table>

Genomic associations - Yield in PBW343 derived populations
Blast the GBS markers against the genome sequence of Chinese Spring

- BLASTN 2.2.26
- E-value < 1e-4

Averaged hits to the Chinese Spring genome, and rye genome on across chromosome 1B within sliding window with 30 markers in length and 15 markers overlapped between neighboring windows.

Clear enrichment for rye hits indicating known IB/IR translocation

Frequency of the sequences of GBS markers in the Chinese Spring genome.

Mexican landrace: GWAS for Zn

Iranian landrace: GWAS for Zn

Iranian landrace: GWAS for Tan spot

Frequency (%)
A. Hit to the Chinese Spring genome with correct chromosome
B. Hit to the Chinese Spring genome with wrong chromosome
C. No hit to the Chinese Spring genome
Iranian landrace: GWAS for SBN

GBS query sequences blasted in IWGSC and filtered using best score criterion for each sequence

BLAST Results

Sequences with highest Blast score and with 100% identity were downloaded for each sequence and blasted in NCBI

BLAST Results

Region containing GBS query sequence

Gene structure of Acc-2

The gene Acc-2 has 29 exons and 28 introns. Acc-2 is associated with grain yield, grain harvest index and panicle yield under irrigated and drought stress conditions in pearl millet (Sehgal et al. 2015 - PLOS One)

BAC clone containing putative gene(s) identified; putative acetyl-CoA carboxylase (Acc-2) and amino acid permeases (AAP)

Triticum aestivum clone BAC: 1825717D cytotoxic acetyl-CoA carboxylase (Acc-2) and putative amino acid permease genes, complete cds

28 | 6A | 28

Exons

Introns

Acetyl-CoA carboxylase (Acc-2) Amino acid permease (AAP)
The AAP genes have 5 or 6 exons and 4 or 5 introns. AAPs are the integral membrane proteins which mediate the transport of amino acids across cellular membranes in higher plants, and play an indispensable role in various processes of plant growth and development, including long distance amino acid transport, response to pathogen and abiotic stresses (Zhao et al. 2012 PLOS One).

**Gene structure of AAPs**

**Conclusion**

- High-density genome profiles, generated using the GBS platform, have the potential to stimulate genetic improvement of wheat
- Validated known genes controlling disease resistance; and detected new genetic regions for resistance.
- Facilitate genetic dissection of complex trait in wheat and genomics-assisted breeding.