Opportunities to Improve an Elite Barley Cultivar Using Spanish Landraces

Arantxa Monteagudo, Ana M. Casas, Carlos P. Cantalapiedra, Bruno Contreras-Moreira, M. Pilar Gracia, Ernesto Igartua

6th March 2019, Córdoba
80’s → Lack of adaptation of the European commercial varieties to semiarid dry lands of the Mediterranean area.

“The Spanish Barley Core Collection (SBCC) is representative of ancient barley genotypes grown in Spain.

Some of the SBCC lines have shown good performance in low productivity sites and, thus, they could be good candidates to introgress drought adaptation to commercial cultivars.

(Yahiaoui et al. 2014)
Would these well-adapted materials report benefit in other backgrounds?
Materials and Methods

SBCC
- donor parent, with good yield performance under drought conditions

Cierzo
- elite barley cultivar in Mediterranean conditions

BC$_2$F$_5$
- 264 lines
Materials and Methods

Two years field evaluation (2014-2015; 2015-2016)
Validation (2017-2018)

Autumn sowings
Augmented design

Moving grid spatial correction
Results

Grain yield, plant height, flowering date and other agronomic and drought-related traits were evaluated.

2015 → 3 t ha\(^{-1}\)
2016 → 5-6 t ha\(^{-1}\)

Differences in PH, TKW and HW

87.5% genome contributed by Cierzo.
Cierzo contributed with shorter plants and similar flowering time
Results

Cierzo contributed with higher HW and lower TKW.
Early vigor (February)
Results

SBCC042 x Cierzo

12893 SNPs
1080.5 cM

SBCC073 x Cierzo

12026 SNPs
1115.8 cM

Genotyping of 264 lines using the Barley Illumina iSelect 50k SNPchip

Mascher et al. (2017) Nature 544, 427-433

Genetic maps
Colour denotes association with higher phenotypic value for:

- Cierzo allele
- Landrace allele
Results

Grain yield were contributed by the elite parent, whereas plant height and TKW were contributed by the landrace allele.

Ground cover QTLs were detected only in SBCC042xCierzo, with trait-increasing alleles contributed by the landrace.

Validation showed that Cierzo contributed to grain yield with more grains per spike.

Colour denotes association with higher phenotypic value for:

- Cierzo allele
- Landrace allele

<table>
<thead>
<tr>
<th>Trait</th>
<th>Cierzo allele</th>
<th>SBCC073 allele</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grain yield (kg/ha⁻¹)</td>
<td>2918</td>
<td>2619**</td>
</tr>
<tr>
<td>Thousand kernel weight (g)</td>
<td>29.4</td>
<td>32.1**</td>
</tr>
<tr>
<td>Harvest index</td>
<td>52.4</td>
<td>49.2**</td>
</tr>
<tr>
<td>Grains per spike</td>
<td>29.5</td>
<td>25.5**</td>
</tr>
</tbody>
</table>

Results of the validation trial for the marker at the peak of GY in 6H, in the 2017-18 season.
Results

Genomic regions surrounding the QTL, and their physical positions.

Not candidates: huge density of markers, size and type of populations were limitants.

QTL flanking markes from the literature were cross-referenced \(\Rightarrow\) Information with biological meaning.
Results

Hassan et al. 2017
Arabinoxylan content

Pauli et al. 2014
Grain Plumpness

Houston et al. 2014
β-glucan content
Conclusions

1. The **Barley Illumina iSelect 50k SNPchip** was very useful to determine consistencies and unconsistencies with positions in the barley genome, and also crossing the information with that of other authors.

2. We did not detect direct grain yield QTLs with the superior allele coming from the landraces, even in the lower-yielding year. There were QTLs for TKW, HW and FD with trait-increasing alleles from both sides of each cross, indicating that breeding is possible in either direction of these crosses for each of these traits.

3. In 6H, QTL hotspot in both populations, for GY and PH, carry also negative effects on TKW.

4. Another option: Improve landrace lines or at least, use as parent in plant breeding.
Future Perspectives

There were 16 and 14 lines in each population with yield values above the elite parent’s values in each year. These lines will be further tested in field trials, and some may become candidate cultivars.
THANK YOU FOR YOUR TIME