Experimental evolution in barley – 2 decades of natural adaptation to farming systems

Sustainable food production for a growing world population will pose a central challenge in the coming decades. Organic farming is among the most feasible approaches to achieving this goal if the yield gap to conventional farming can be decreased. However, uncertainties exist whether organic and conventional agro-ecosystems require different breeding strategies.

A heterogeneous spring barley population was established between a wild barley and an elite cultivar to examine this question. The population was divided into organic and conventional agro-ecosystem, without any artificial selection for two decades. The parents and five generations from both environments up to the 23rd generation were whole-genome pool-sequenced to identify adaptation patterns towards ecosystem and climate conditions in the allele frequency shifts. Additionally, based on previously published QTLs in barley, a meta-data analysis was conducted to link genomic regions’ increased fitness to agronomically related traits.

Methods:

A Cultivar

<table>
<thead>
<tr>
<th>Wild form (ISR 42-8)</th>
<th>Conventional</th>
<th>Organic</th>
</tr>
</thead>
<tbody>
<tr>
<td>BC2F2</td>
<td>BC2F1</td>
<td>BC2F3</td>
</tr>
<tr>
<td>F1</td>
<td>X</td>
<td>Golf</td>
</tr>
</tbody>
</table>

B Population construction

- Selecting population samples (generations) to genotype

C Genotyping

- BC2F16
- BC2F22
- BC2F23
- BC2F24
- BC2F3
- BC2F4
- BC2Fn
- BC2F23 allele frequency patterns changes compared to original F3

Results: BC2F23 allele frequency patterns changes compared to original F3

A Evolution

- 0.6
- 0.4
- 0.2
- 0.0

System

- Conventional
- Organic

Trait associated with genomic region

- Biotic resistance
- Drought tolerance
- Nutrients

B Loci clustered by trait category – across generations

For each:

- 2 samples
- 300 genotypes pooled to one sample
- DNA extraction from pooled sample
- WGS 10x sequencing

Details about the frequency estimate methodology using pool seq

Validation exp.

Observation:

- The genomic data indicates more wild type like roots in the organic environment

Hypothesis:

- Organic populations tend to produce longer roots to access nutrients in deep soil layers

Methods:

1. Measure 100 BC2F24 genotypes from both farming systems
   1. in hydroponics (seedling)
   2. in field (flowering time)
2. Harvesting roots, washing and using WinRHIZO for assessment

Results:

1. Mean root length is higher in the organically adapted population
2. The diversity in the organic was higher than in the conventional population after 21 generations of adaptation to a specific farming practice

Find out more about this validation study

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