Low temperature tolerance (LTT) - an important component of winter hardness in barley.

Three major QTLs identified for LTT - mechanisms not fully understood.

Reported QTLs - FR-H1 and FR-H2 - 30 cM apart on chromosome 5H and FR-H3 on the short arm of chromosome 1H.

FR-H1 cosegregates with VRN-H1.

FR-H2 locus consists of two physically linked clusters of C-repeat binding factor (CBF) genes.

FR-H1, FR-H2, and FR-H3 characterized in bi-parental mapping populations.

Vernalization (VRN) - a low temperature response trigger for vegetative-to-reproductive transition.

Three major QTLs identified for VRN - controlling growth habits (spring, facultative, & winter).

Reported QTLs – VRN-H1 on chromosome 5H, VRN-H2 on chromosome 4H, and VRN-H3 on chromosome 7H.

Facultative growth habit defined as spring allele at VRN-H2 & winter alleles at LTT-related loci & FPD-H2.

Objectives

1) Identify novel LTT & VRN QTLs(s).

2) Identify novel alleles at known LTT & VRN QTL(s).

3) Estimate effects and interactions in a large and diverse panel of germplasm.

Material & Methods

The LTT panel - 941 accessions with low temperature tolerance selected by 21 barley breeders around the world.

The panel includes 300 lines from the TCAP Winter-Facultative 6 row set, and winter lines from the AGOUEB and ExBarDiv Projects.

The panel genotyped with the Illumina iSelect 9k chip.

LTT - Planted 2013/14 (14 locations) & 2014/15 (12 locations): Alberta (Canada), Oregon, Idaho, Nebraska, Ohio, Minnesota (USA), France (2 locations), Germany (2 locations), Spain, Hungary, Scotland (UK), Japan.

VRN – Planted in greenhouse under non-vernalized conditions to measure max days-to-flowering.

The experimental design - Type II Modified Augmented Design with 5 replicated checks: Alba (winter), Maja (facultative), Full Pint (spring), winter wheat, and a local cold tolerant check.

Future

Further characterization of best accessions - phenotypically and genotypically.

Identify candidate genes at novel LTT QTLs.

LTT and VRN allele introgression into adapted germplasm.

Results

Differential survival data obtained from 2014 & 2015 Idaho, Minnesota, Ohio (USA), Alberta (Canada), and 2015 Germany (BLL), Hungary, & Nebraska. Otherwise complete survival or minimal differential survival, except Nebraska 2014, where there was 0 survival.

41/941 potential facultative accessions based on 2014 greenhouse days-to-flowering (46-96 DTF) and LTT (>75%) (Figures 1, 2, 3 & 4).

Normal distribution of winter survival (%) across 2014 & 2015 differential environments (Figure 2) with 114/941 accessions with >75% survival.

No correlation between spike type (2-row vs. 6-row) and LTT (Figure 5).

FR-H1 & FR-H2 are the largest effect and consistent LTT QTLs (Figure 6).

VRN-1 & VRN-2 are the largest effect and consistent VRN QTLs (Figure 6 & 7).

Potentially novel QTLs to explore and characterize.

Discussion

The panel contains non-VRN germplasm with excellent LTT, useful starting points for breeding.

Encouraging prospects for maintaining, improving LTT.

Introduction

Figure 1. Frequency distribution of 2015 greenhouse days-to-flowering/vernalization sensitivity data of the LTT GWAS panel.

Figure 2. Frequency distribution of 2015 and 2015 winter survival (%) of the LTT GWAS Panel in differential environments.

Figures 3-5. Principle component analysis of (3) 2015 greenhouse days-to-flowering/growth habit data (Facultative: DTF= 46-96 days & LTT>75%) (4) combined 2014 and 2015 environments with differential low temperature tolerance data (1= 0-25%; 2= 26-50%; 3= 51-75%; 4= 76-100%), and (5) Spike type (2-row & 6-row).

Figure 6. Manhattan plot of marker: trait associations from genome-wide association of 2015 greenhouse days-to-flowering/vernalization data of the LTT GWAS panel.

Figure 7. Manhattan plot of marker: trait associations from genome-wide mapping of combined 2014 and 2015 environments winter survival (%) of the LTT GWAS panel.

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