

Genome-wide association mapping in a nested population representative of elite breeding in Uruguay

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BACKGROUND

- High malting quality requirements from the industry.
- Strong dependence on modern European germplasm.
- European high quality/yield varieties with limited adaptation in sub-optimal environments.

GOALS

- Identify genetic regions associated with phenology traits in European/Uruguayan crosses.
- Analyze the impact of phenology on agronomic traits.
- Quantify the phenotypic variance explained by individual QTL, and cluster them into hotspot regions.

MATERIALS & METHODS

- We used an elite nested association mapping population representative of local breeding.

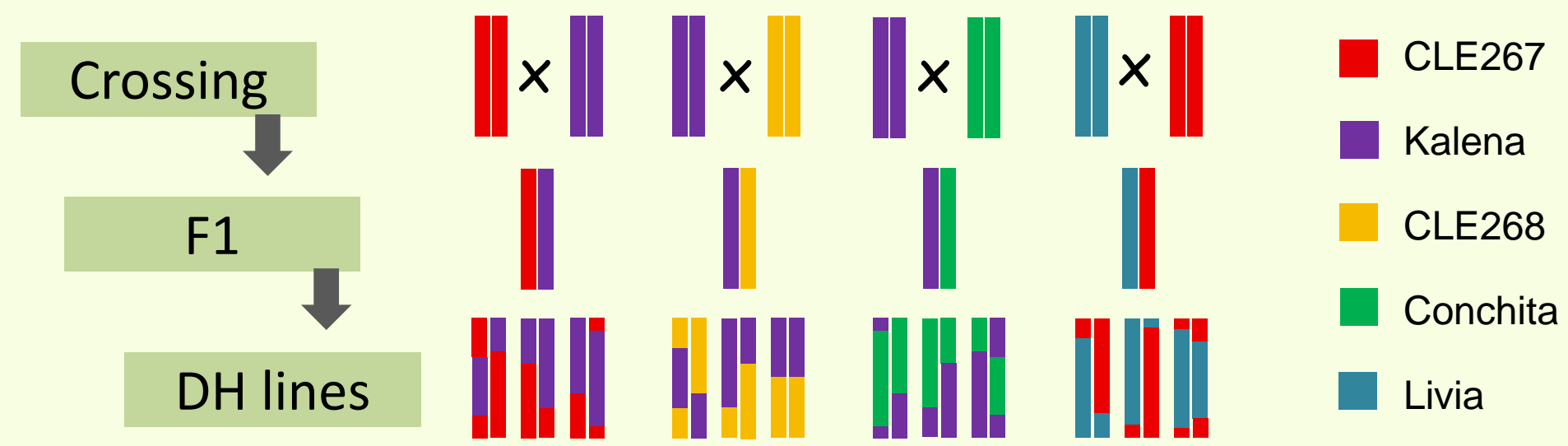


Figure 1. Scheme of NAM population development.

Field trials at four locations during four consecutive seasons (2015-18). Eight agronomic traits were measured: plant height (PH), yield (YLD), plumpness (PML), plump yield (P-YLD), grain weight (TGW), spikes per m² (SM), grains per spike (GS), grains per m² (GN). Additionally, a complete set of phenology related traits was measured (Figure 2), as well as photoperiod response (PPR).

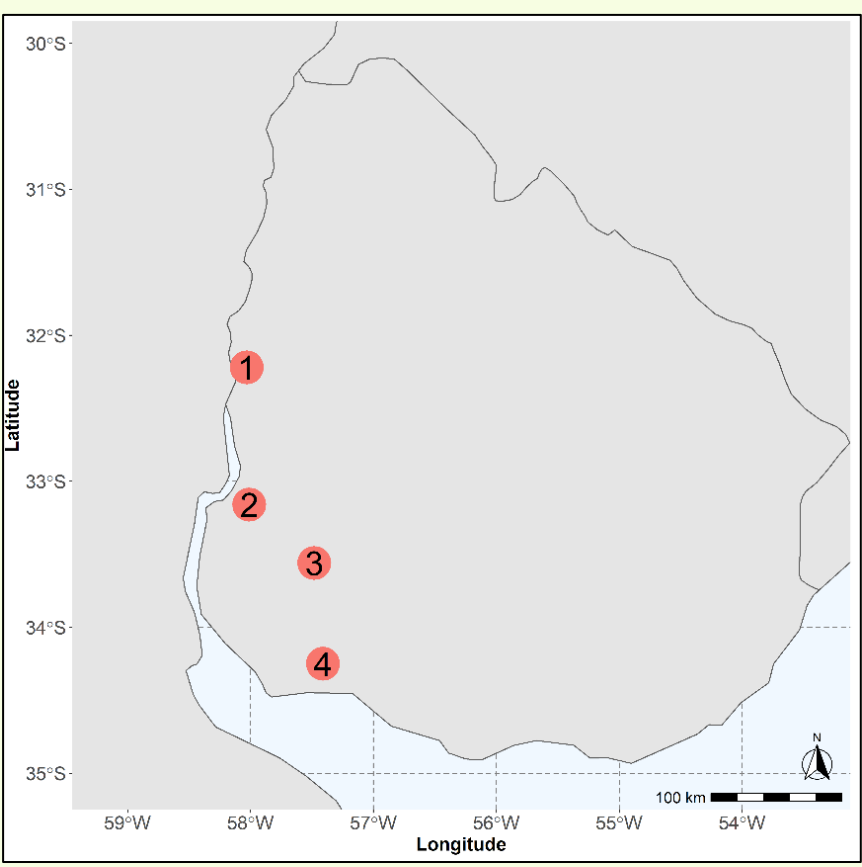


Figure 2. Location of field experiments. 1: Paysandú; 2: Mercedes; 3: Ombúes de Lavalle; 4: Colonia.

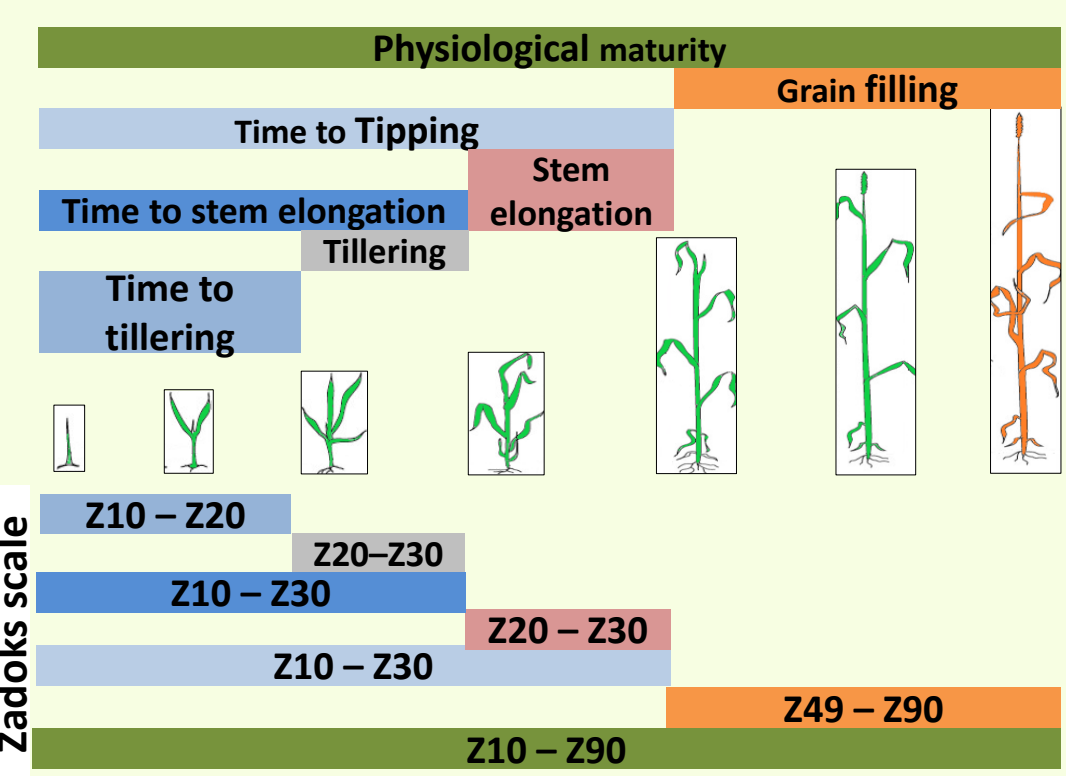


Figure 3. Description of the different phenology phases measured in the field experiments.

- Association studies were performed applying a K+P model using the *rrBLUP* R package (Endelman, 2011). A total of 6340 SNPs from the Illumina 50K iSelect chip (Bayer et al. 2017) were included in the analysis.

- Threshold LOD significance used for marker trait association was 4.
- QTL identification defined on the basis of intercepts of a smoothing spline curve with basal pairwise LD ($r^2 = 0.20$).
- Phenotypic variance explained (PVE) by each QTL was estimated by fitting a multilocus model with all significant markers.



Figure 4. phenotypic difference between genotypes during 2018 at Dr. Mario A. Cassinoni Experimental Station, Paysandú.

RESULTS & DISCUSSION

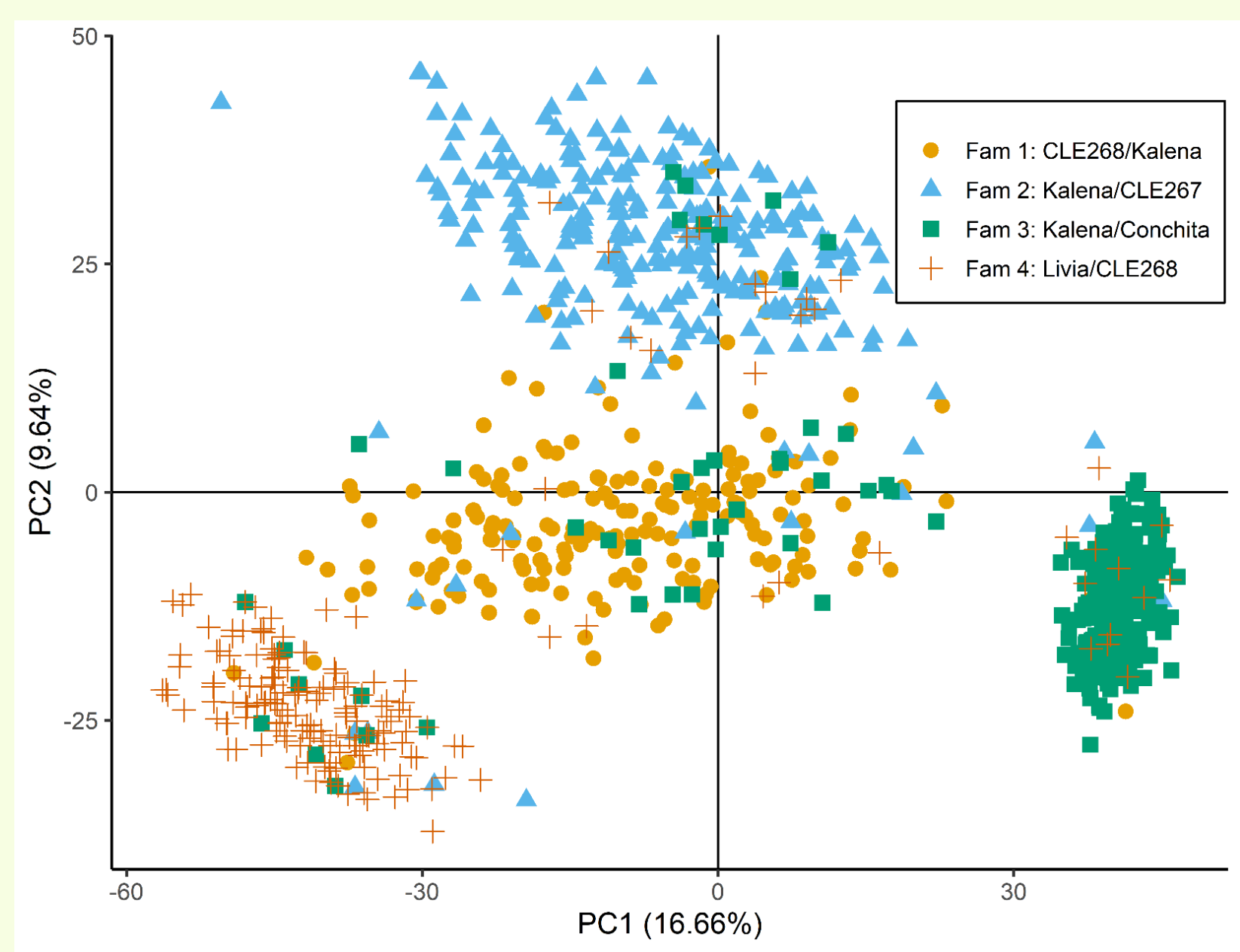


Figure 5. PCA using molecular data.

Table 1. Number of identified QTLs and their phenotypic variance.

Chromosome	QTLs per chromosome	PVE range (%)
1H	12	7.9 – 25.3
2H	19	8.0 – 38.1
3H	11	8.0 – 20.0
4H	-	-
5H	3	6.6 – 8.2
6H	6	3.1 – 10.8
7H	10	7.7 - 17.4

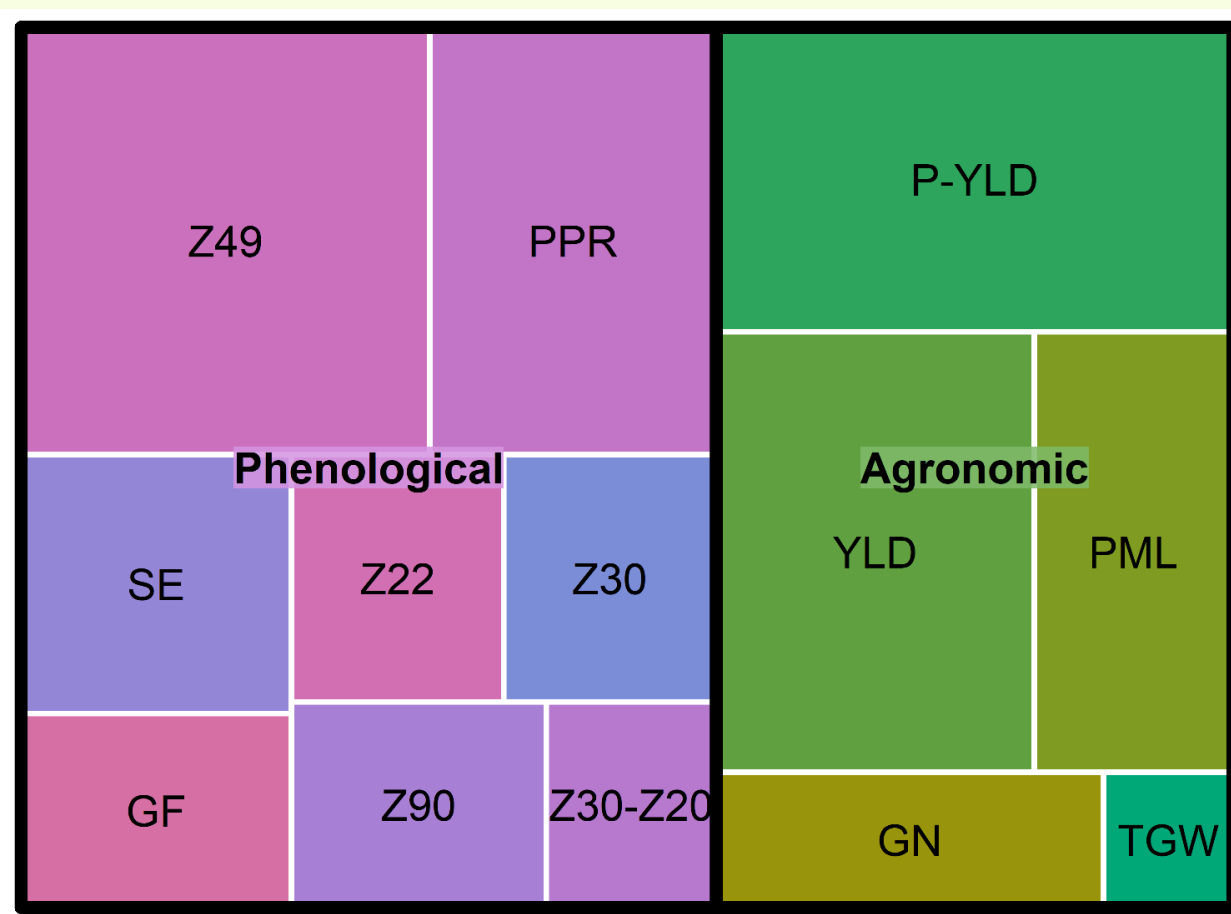


Figure 6. Treemap for phenological and agronomic QTLs.

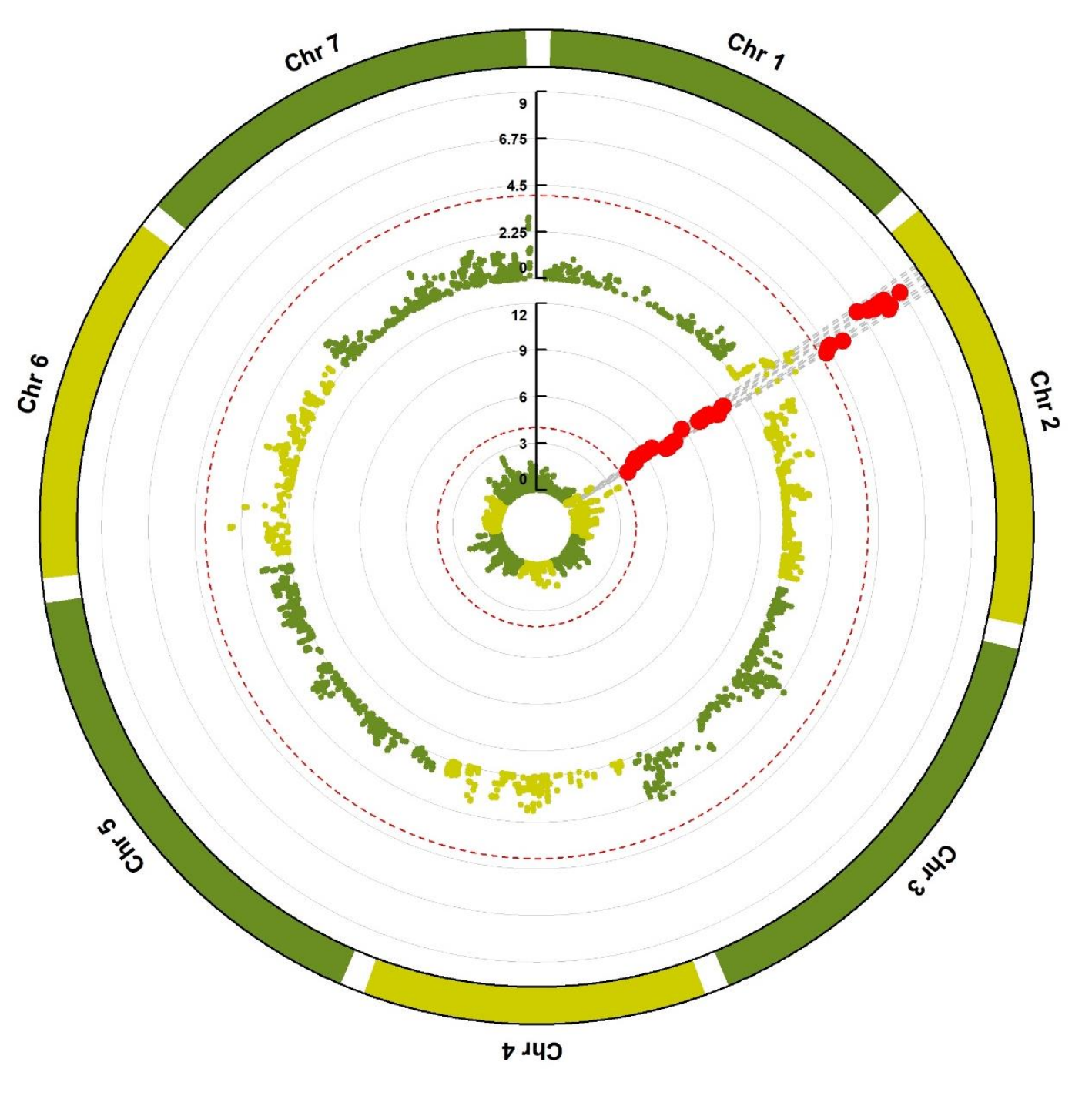


Figure 7. GWAS results for photoperiod response for Z49. Inner circle is 2017. Outer circle is 2018.

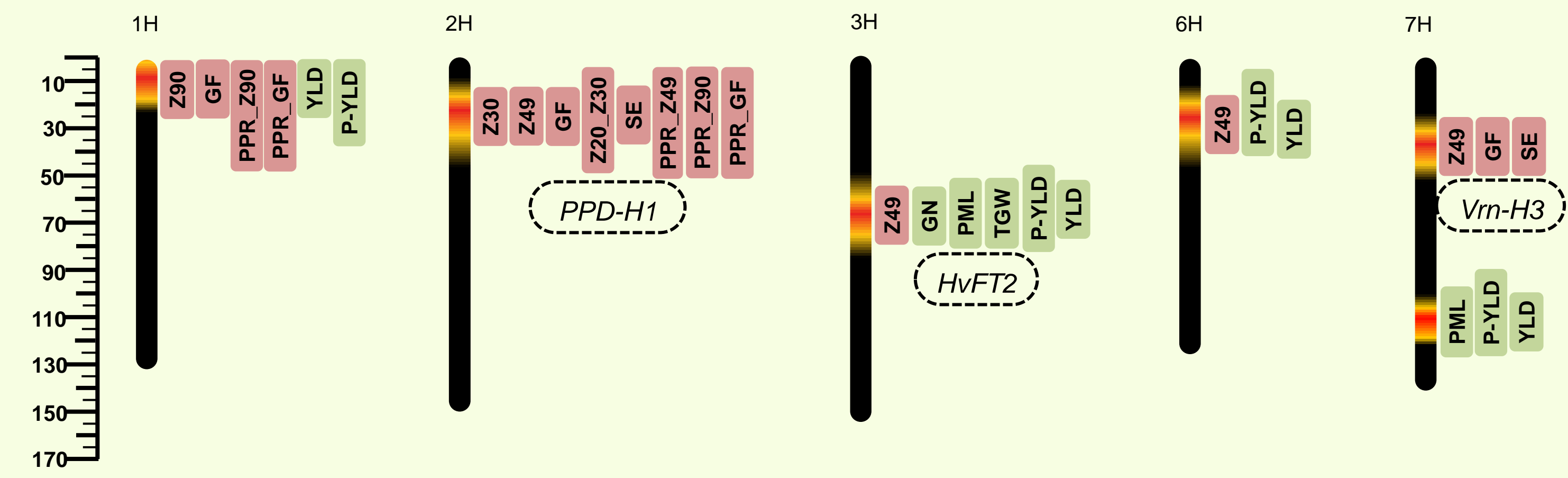


Figure 8. Six identified QTL hotspots and associated traits. Phenological traits colored in purple and agronomic traits in green.

- Hotspots on 1H and 3H associated to yield related traits in normal and late sowing dates.
- Hotspots on 6H and 7H found only in normal sowing dates and associated to yield related traits and phenological phases highly correlated with yield and grain size.
- The hotspot on 2H contribute to better adaptation through photoperiod response.

In our study with elite x elite crosses, locally adapted germplasm can contribute favorable phenology-related alleles under non-optimum environments, without affecting adaptation to high yield conditions