

# YIELD EFFECTS OF FLOWERING TIME GENES IN MEDITERRANEAN CONDITIONS

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## INTRODUCTION.

A majority of Spanish landraces are intermediate types, with a vernalization requirement, but of lower duration than that of typical winter varieties. They also present an active *PpdH2* allele, contrary to most winter cultivars. Why were these haplotypes empirically selected in these landraces? Do they provide any agronomic advantage? This study uses several biparental crosses of cultivars with landraces to explore this hypothesis.

The experiment was run in field trials comparing bulks of lines selected with markers for specific allelic combinations. Three populations were used, segregating for 2 or 3 genes. Segregation of

other genes potentially affecting grain yield and earliness was partially controlled (not shown).

Sets of lines of **three biparental populations** were **bulked** together, 4-8 bulks per population. The lines were selected according to their haplotypes at target genes, different at each population. The genes targeted, involved in the vernalization and photoperiod pathways, are indicated in the figure below. It was assumed that segregation of genes in the rest of the genome occurred at random, and that any significant difference observed in the bulks would likely be caused by the fixed target genes.

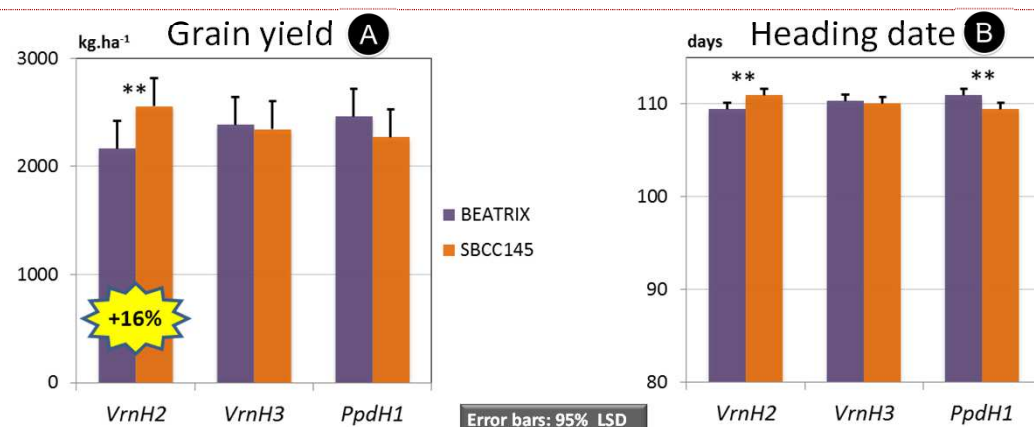
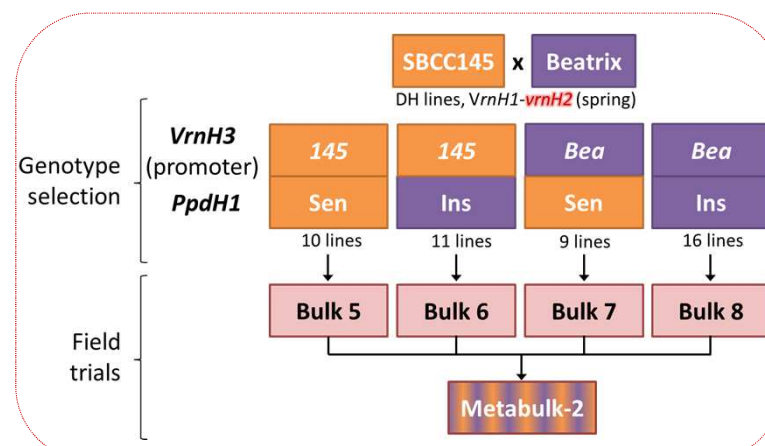
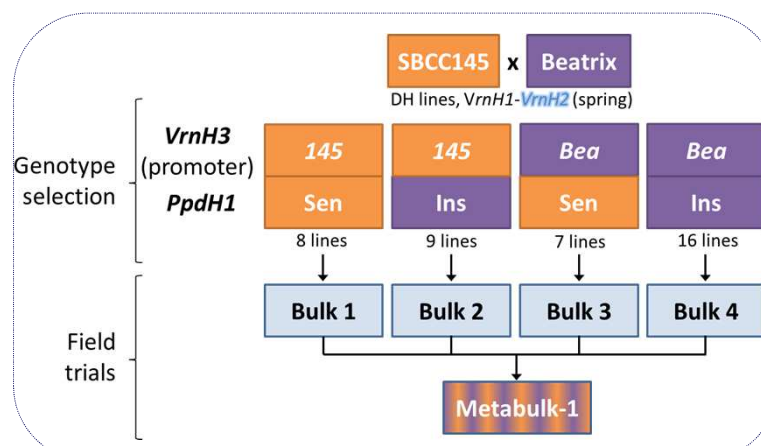
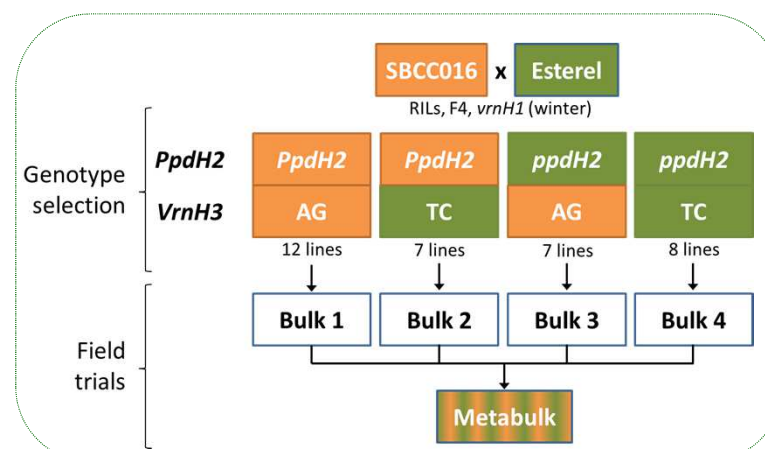
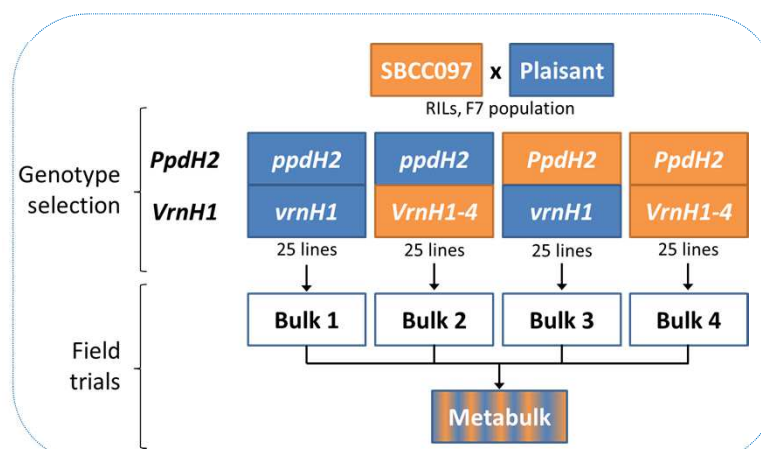
## PLANT MATERIAL

A total of 16 bulks of lines (and 4 metabulks, see below) were sown in Spanish locations. Seed for field trials was prepared at once, before the start of the experiment, by bulking equal amounts of seed per line, to a total of 2500 seeds per field plot. The trials followed a RCBD with 3 replicates, with individual plot size of 1.2 x 6 m.

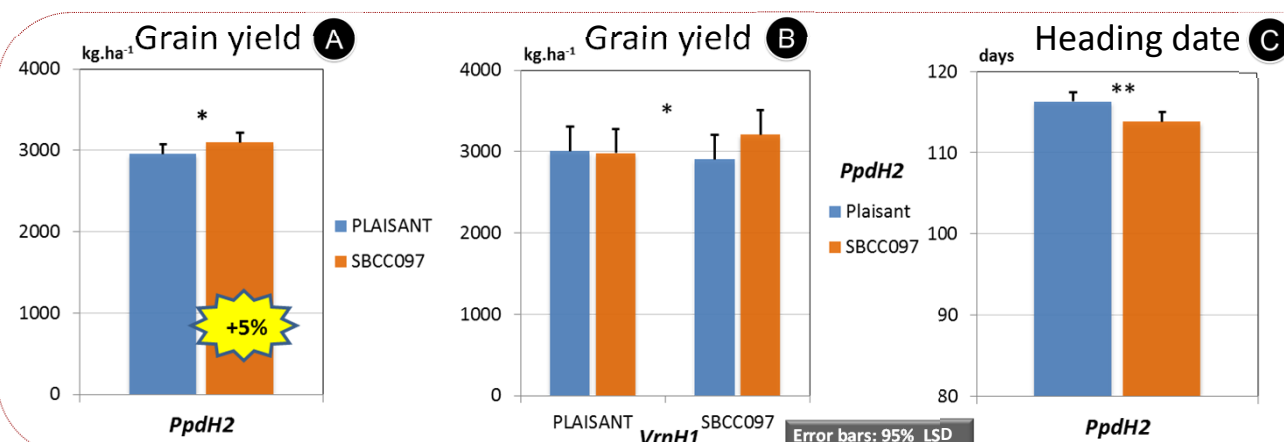
## FIELD TRIALS

Yield trials were carried out for the **bulks** of lines for up to 2-3 years per population, and two sowing dates per year, November (standard) and February (late), 3 reps, 7.2 m<sup>2</sup> plots, in up to two locations.

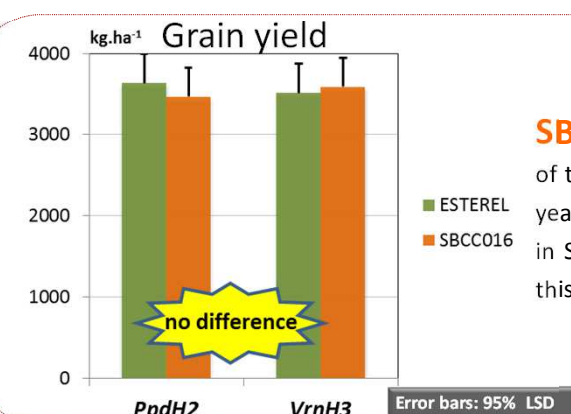
The **metabulks** were hand-harvested each time. Seed was kept and used for next season's sowing. After at least 3 seasons (for each sowing date), marker frequencies will be compared between the original lines and the final populations, to look for selection bias.



**SBCC145 x Beatrix** Yield advantage of bulks with the dominant (presence) allele of *VrnH2*, contributed by landrace SBCC145 (A), across 5 field trials (3 years, 2 sowing dates). Probably not related to earliness (B). No yield difference for *VrnH3* and *PpdH1* (A).



**SBCC097 x Plaisant** Yield advantage of bulks with the dominant (presence) allele of *PpdH2* contributed by landrace SBCC097 (A), measured across 7 field trials (3 years, 2 sowing dates, 2 locations). Could be related to earliness (C). No difference in grain yield for *VrnH1*, except in interaction with *PpdH2* (B).



**SBCC016 x Esterel** No yield difference of bulks with any of the *VrnH3/PpdH2* haplotypes, recorded across 6 field trials (2 years, 2 locations, 2 sowings). This result contrasts with the result in SBCC097 x Plaisant. The fact that *VrnH1* is not segregating in this population could have an influence.

## COMMENTS, FURTHER WORK

Metabulks will be analyzed using genome markers covering the whole genome, to look for selection biases in allele frequencies. A QTL study with population SBCC145 x Beatrix will be attempted in the future, including work on yield components.