

# NATURAL VARIATION IN FLOWERING LOCUS T, HvFT1

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## INTRODUCTION

The barley ortholog of *FLOWERING LOCUS T*, *HvFT1*, also called *VrnH3*, is the main integrator of the photoperiod and vernalization signals leading to the transition from the vegetative to the reproductive stage. Results gathered by several groups over the last years have repeatedly identified QTL for flowering time at the region of this locus. This communication updates and summarizes on the richness of polymorphisms found at this gene, and their associated phenotypic effects.

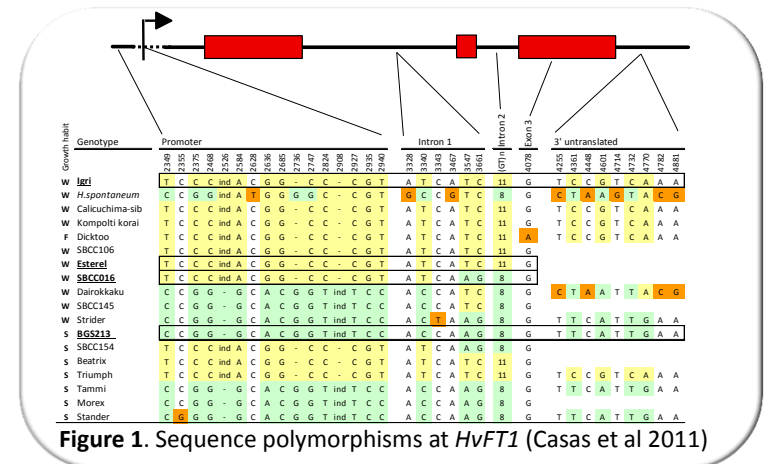


Figure 1. Sequence polymorphisms at *HvFT1* (Casas et al 2011)

## RESULTS

***HvFT1* polymorphisms and effects.** These have been found first at the first intron (Yan et al. 2006), at the promoter (Casas et al. 2011, Figure 1) and also as gene copy number variation (Nitcher et al. 2013). QTL in the *HvFT1* region in biparental crosses with all these types of polymorphisms have been reported (Table 1), reflecting ample phenotypic variation available for plant breeders to choose from.

In some crosses, the QTL at the *HvFT1* region has shown significant interaction with other flowering time QTL (some representing major genes). Therefore, management of *HvFT1* alleles in breeding programs must take into account the possibility of interactions.

Population	Field trials	1st intron	Promoter	CNV	Effect (early parent)	Interactions	Ref.
Beka x Logan	7, fall and spring sowings	–	Late vs Early	2 vs 1 copies	2.8 days (Logan)	QTL in HvCEN, HvELF3 regions	unpublished
Beka x Mogador	6, fall and winter sowings	–	–	2 vs 1 copies	2.2 days (Beka)	No	Cuesta-Marcos et al. 2008
Henni x Meltan	4, fall sowings	–	Late vs Early	–	1.5 days (Meltan)	Not tested	Borraàs-Gelonch et al. 2010
SBCC154 x Beatrix	1, fall sowing	AG vs TC	–	4 vs 1 copies	2.5 days (Beatrix)	No	Loscos et al. 2014
SBCC145 x Beatrix	2, fall and winter sowings	–	Early vs late	–	4.7 days (SBCC145)	QTL at PpdH1 region	Ponce-Molina et al. 2012
SBCC016 x Esterel	2, fall and winter sowings	AG vs TC	–	–	7.4 days (SBCC016)	Not tested	Casas et al. 2011

Table 1. Summary of polymorphisms and effects found in biparental populations

***HvFT1* copy number variation.** There is variation in the number of copies of the *HvFT1* gene, apparently related to growth habit. A large set of winter genotypes, with a functional *VrnH2* allele, has one copy of *VrnH3*, whereas variable number (1-5), was found in also a large set of spring or facultative barleys (without *VrnH2*), as shown in Figure 2.

The dominant *VrnH3* allele, which overrides the vernalization requirement of winter *VrnH1* and *VrnH2* alleles, reported by Nitcher et al. (2013) is found only in Nordic barleys and carries a particular structure of the gene, with one promoter and variable number of transcribed regions.

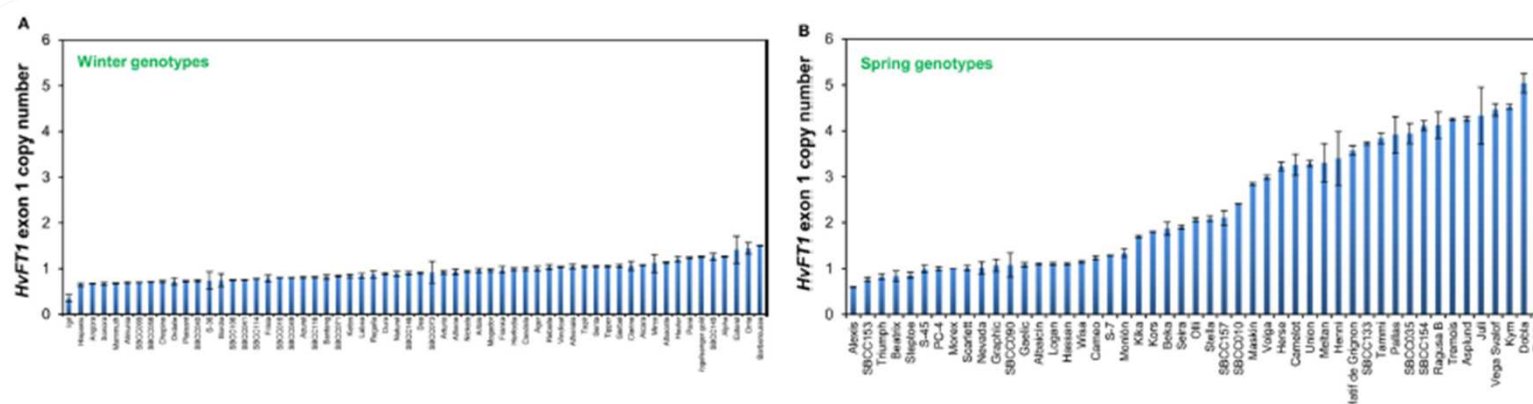


Figure 2. There is copy number variation in *HvFT1*: winter genotypes have one copy whereas spring barleys have a variable number of copies (1-5)

Association studies with geo-referenced barley landraces from Spain revealed:

- Clear association of 1st intron polymorphism with flowering time (Figure 3), and
- Latitudinal variation for the 1st intron polymorphism (Figures 4, 5), with high geographical autocorrelation, at the extreme of the distribution of 7447 markers

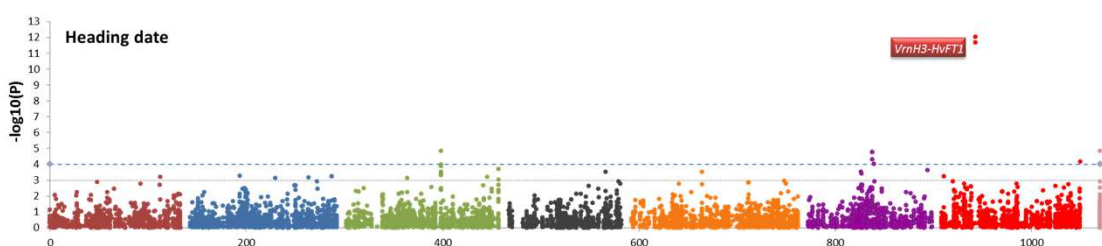


Figure 3. GWAS, K model, for flowering time in the Spanish barley core collection, evaluated at a series of field trials, for over 8000 SNPs.

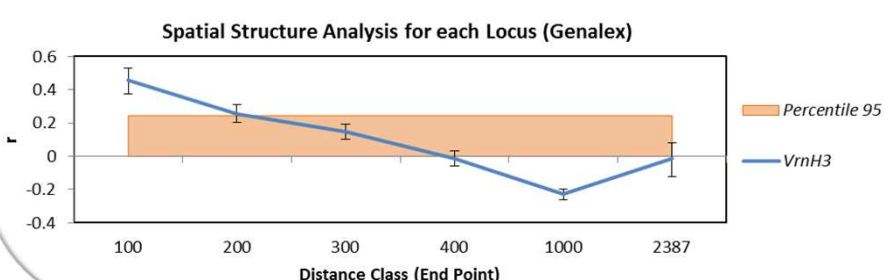


Figure 4. Spatial autocorrelation for *HvFT1*, compared to autocorrelation of 7447 markers distributed over the whole genome.

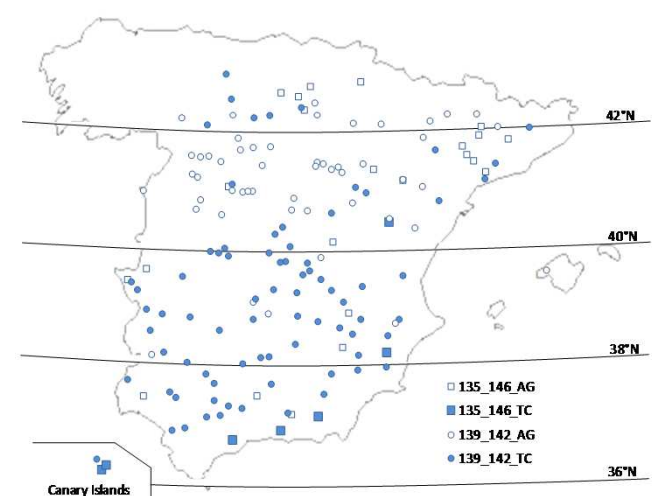


Figure 5. Latitudinal variation for *HvFT1* polymorphism, 1<sup>st</sup> intron, found in the Spanish barley core collection (Casas et al. 2011)

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