 Increased copy number at the \textit{HvFT1} locus is associated with accelerated flowering time in barley

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Abstract  A precise regulation of flowering time is critical for plant reproductive success, and therefore, a better understanding of the natural variation in genes regulating the initiation of the reproductive phase is required to develop well-adapted varieties. In both monocot and dicot species, the \textit{FLOWERING LOCUS T (FT)} is a central integrator of seasonal signals perceived by the leaves. The encoded mobile protein (florigen) is transmitted to the apical meristem where it induces flowering. The \textit{FT} homolog in barley (\textit{Hordeum vulgare} L.), designated \textit{HvFT1}, was shown to correspond to the vernalization locus \textit{VRN-H3}, and natural alleles for spring and winter growth habit were identified. In this study, we demonstrate that the \textit{HvFT1} allele present in the barley genetic stock (BGS213) associated with a dominant spring growth habit carries at least four identical copies of \textit{HvFT1}, whereas most barley varieties have a single copy. Increased copy number is associated with earlier transcriptional up-regulation of \textit{HvFT1} and a spring growth habit. This allele is epistatic to winter alleles for \textit{VRN-H1} and \textit{VRN-H2}. Among accessions with one \textit{HvFT1} copy, haplotype differences in the \textit{HvFT1} promoter and first intron are also associated with differences in flowering time, which are modulated by genetic background. These different \textit{HvFT1} alleles can be used to develop barley varieties adapted to different or changing environments. Our results, together with studies of other wheat and barley flowering genes, show that copy number variation plays an important role in the regulation of developmental processes in the temperate cereals.

Keywords  Vernalization · Barley · \textit{Hordeum vulgare} · Flowering · FT

Introduction

Plant reproductive success is highly dependent on a precise targeting of flowering time to a narrow seasonal window that maximizes resources for the developing seeds. In cereal crops, the correct targeting of this optimal reproductive period is translated into increased grain yields. A clear understanding of the natural variation in the genes that regulate flowering time is important to develop varieties adapted to different or changing environments.

In the temperate cereals, which include barley (\textit{Hordeum vulgare} L.) and wheat (\textit{Triticum aestivum} L.), the initiation of the reproductive phase is regulated by the integration of two main seasonal signals: photoperiod (day-length) and vernalization (extended exposures to low temperatures). Based on the response to photoperiod, barley varieties are divided into photoperiod sensitive (accelerated flowering under long days) and insensitive (limited response of flowering time to long days) classes. Based on the response to vernalization, barley varieties are
divided into winter (vernalization accelerates flowering) and spring (early flowering irrespective of vernalization) classes.

Most of barley’s natural variation in photoperiod response is associated with allelic differences in the photoperiod genes PPD-H1 and PPD-H2. PPD-H1 encodes a pseudo-response regulator (PRR) protein that is part of the circadian clock (Turner et al. 2005) and promotes flowering under long days. Recessive mutations in the PPD-H1 gene reduce expression of HvFT1 and result in delayed flowering under long days (Hemming et al. 2008; Turner et al. 2005). The PPD-H1 gene acts in conjunction with CO-H1 (Campoli et al. 2012), which is one of the barley homologs of the Arabidopsis photoperiod gene CONSTANS (CO). In Arabidopsis, long days result in the stabilization of CO proteins, which up-regulate FT resulting in the acceleration of flowering (Corbesier and Coupland 2005). This function seems to be conserved in barley since overexpression of CO-H1 results in the up-regulation of HvFT1 and the acceleration of flowering (Campoli et al. 2012). The second photoperiod gene, PPD-H2 (HvFT3) is a paralog of HvFT1, but its effect on flowering is not as strong as HvFT1 (Kikuchi et al. 2009). The induction of flowering by PPD-H2 seems to be restricted to winter genotypes under non-inductive conditions (short days or long days without vernalization, Casao et al. 2011).

Natural variation in barley vernalization requirement is predominantly found in the vernalization loci VRN-H1, VRN-H2, and VRN-H3 (Dubcovsky et al. 2005; Fu et al. 2005; Takahashi and Yasuda 1971; Yan et al. 2005, 2006). The VRN-H1 gene is closely related to the Arabidopsis gene APETALA1, which encodes a MADS-box protein responsible for the transition of the shoot apical meristem (SAM) from the vegetative to the reproductive stage (Danyluk et al. 2003; Trevaskis et al. 2003; Yan et al. 2003). Deletions of regulatory regions in the VRN-H1 first intron result in a dominant spring growth habit (Fu et al. 2005; Hemming et al. 2009; von Zitzewitz et al. 2005). The second vernalization locus, VRN-H2, includes three closely related genes characterized by a putative zinc finger and a CCT-domain, designated as ZCCT genes (Yan et al. 2004). These genes function as flowering repressors and deletions of all three copies result in spring growth habit independently of the VRN-H1 alleles (Dubcovsky et al. 2005; Yan et al. 2004). Finally, VRN-H3 is a functional homolog of Arabidopsis flowering promoting gene FLOWERING LOCUS T (FT) (Yan et al. 2006) and will be referred hereafter as FT1 (HvFT1 in barley and TaFT1 in wheat).

In both monocot and dicot species, the signals from the vernalization and photoperiod pathways converge at the regulation of FT1, which is considered to be a central flowering integrator (Turck et al. 2008). When temperate cereals germinate during the fall, FT1 is repressed by VRN2, which competes with the photoperiod protein CO for the regulation of FT1 (Hemming et al. 2008; Trevaskis et al. 2007; Yan et al. 2006, Li et al. 2011). During the winter, vernalization up-regulates VRN1 (Oliver et al. 2009), which results in the repression of VRN2 in the leaves and the release of FT1 transcription in the spring (Loukoianov et al. 2005; Trevaskis et al. 2006; Hemming et al. 2008; Sasani et al. 2009; Chen and Dubcovsky 2012).

In Arabidopsis and rice, it has been demonstrated that FT encodes a mobile protein (florigen) that travels through the phloem and transmits signals perceived in the leaves to the SAM (Corbesier et al. 2007; Tamaki et al. 2007; Turck et al. 2008). Once FT arrives to the SAM it forms a complex with the bZIP transcription factor FD that physically interacts with the promotors of the meristem identity genes AP1 (Arabidopsis; Wigge et al. 2005), VRN1 (rice; Li and Dubcovsky 2008) or FUL2 (rice; Tsuji et al. 2011), and up-regulates transcription to levels that induce the transition of the SAM to the reproductive stage. In rice, it has been shown that the FT-FD complex also includes 14-3-3 proteins (Taoka et al. 2011).

In barley and wheat, there are other FT-like genes (Faure et al. 2007; Kikuchi et al. 2009). However, FT1 shows the most robust induction of flowering when transformed into rice and wheat (Kikuchi et al. 2009; Yan et al. 2006) and is highly expressed under long days, which indicates that it is likely the key gene in the induction of flowering under long days.

In Arabidopsis, the FT promoter and first intron have been shown to contain cis-regulatory sites that are important for the transcriptional regulation of this gene (Adrian et al. 2010; Helliwell et al. 2006; Schwartz et al. 2009; Tiwari et al. 2010). However, the FT1 regulatory regions of barley and wheat are not as well characterized. Based on the few sequences available at the time of the cloning of HvFT1, Yan et al. (2006) found an association between growth habit and intron haplotypes. However, the sequencing of HvFT1 alleles from populations previously used to map QTL for flowering time, such as Dicktoo x Morex (Pan et al. 1994) and Sloop x Halcyon (Read et al. 2003; Hemming et al. 2008) failed to reveal any significant association between the intron one haplotypes and flowering time. Inconsistent results were also observed in recent surveys of HvFT1 allelic variation (Cuesta-Marcos et al. 2010; Casas et al. 2011). In this study, we demonstrate that these inconsistencies were generated by previously unknown copy number variation at the HvFT1 locus. We found that high HvFT1 copy number is associated with early flowering, and is epistatic to the vrn-H1 and Vrn-H2 alleles for winter growth habit (independently of PPD-H1). Finally, once we separated the effects of copy number variation, we were able to better characterize the effect of haplotype variation in HvFT1 regulatory regions on barley flowering time.
Materials and methods

Plant materials

Parental lines used in the different crosses were selected based on their HvFT1 alleles, including different combinations of promoter and first intron haplotypes. Their growth habits, vernalization and photoperiod alleles, and HvFT1 haplotypes are indicated in Table 1. All accessions except H. vulgare ssp. spontaneum Koch (OSU6, PBI004-7-0-015) belong to the sub-species H. vulgare ssp. vulgare. Hayakiso 2 and Iwate Mensury C (IMC) are commercial barley varieties from Japan and Igri is a variety from Germany, whereas E878 (Ethiopia) and U672 (Russia) are accessions received from the Okayama University barley collection (http://www.shigen.nig.ac.jp/barley/).

BGS213 is the designated genetic stock for the barley VRN-H3 (=Sgh3) allele associated with a dominant spring growth habit (Franckowiak and Konishi 1997). BGS213 is a line derived from the cross Tammi × Hayakiso 2 (GSHO 764) which has been selected for the dominant Vrn-H3 allele from Tammi (early flowering variety from Finland) and for recessive vrn-H1 and dominant Vrn-H2 alleles for winter growth habit (Takahashi and Yasuda 1971). Two additional sets of spring VRN-H3 isogenic lines were developed by backcrossing the Vrn-H3 allele from Tammi into the winter varieties Hayakiso 2 and Dairokkaku 1 for eleven generations (Takahashi 1983), designated hereafter as Hayakiso 2-Tammi and Dairokkaku 1-Tammi.

Haplotypes

Based on a limited number of barley lines, it was initially hypothesized that haplotype variation in HvFT1 was associated to differences in flowering time (Yan et al. 2006). To facilitate the description of the different haplotypes used in this study, we assigned names to each of the haplotype found in the promoter and intron one regions. The promoter haplotype present in E878, U672, BGS213, Hayakiso 2, and IMC is referred hereafter to as PE (promoter-early) whereas the promoter haplotype in Igri and H. vulgare ssp. spontaneum is referred to as PL (promoter-late). These two promoter haplotypes differ in nine linked SNPs and indels (Table 1). The two linked SNPs in the first intron are used to name the intron haplotypes as either ITC or IAG. Copy number variation is indicated separately in Table 1.

Segregating populations and growing conditions

A summary of the crosses and segregating populations included in this study is available in Table 2. The two crosses between BGS213 and winter lines H. vulgare ssp. spontaneum and Igri were published before (Yan et al. 2006) but are re-analyzed here in the light of the new copy number variation in HvFT1 presented in this study. Two additional crosses include the varieties Morex (Morex × H. vulgare ssp. spontaneum) and IMC (IMC × Hayakiso 2), which have identical HvFT1 haplotypes as BGS213 but different copy number. A third cross was

Table 1 Parental lines used in the different segregating populations

| Line     | Growth habit | PPD-H1 | VRN-H1 | VRN-H2 | HvFT1 hapl. copy number | HvFT1 haplo. abbr. | Promoter | Intron 1 |
|----------|--------------|--------|--------|--------|-------------------------|-------------------|----------|---------|
|          |              |        |        |        |                         |                   |          |         |
| BGS213   | S pdl        | vnI    | Vn2    | 4      | PE IAG                  | 4GC G A C T i T C C A G |
| IMC      | S Pd1        | vn1    | Vn2    | 1      | PE IAG                  | 4GC G A C T i T C C A G |
| Morex    | S pdl        | Vnl    | Vn2    | 1      | PE IAG                  | 4GC G A C T i T C C A G |
| E878     | S pdl        | Vnl    | Vn2    | 1      | PE ITC                  | 4GC G A C T i T C C T C |
| U672     | S pdl        | Vnl    | Vn2    | 1      | PE ITC                  | 4GC G A C T i T C C T C |
| Hayakiso2| W Pd1        | vn1    | Vn2    | 1      | PE ITC                  | 4GC G A C T i T C C T C |
| Igri     | W Pd1        | vn1    | Vn2    | 1      | Pt ITC                  | 8GC A G G C d C G T T C T C |
| H. v. spont. | W Pd1     | vn1    | Vn2    | 1      | Pt ITC                  | 8GC A G G C d C G T T C T C |

Growth habit, alleles at different vernalization genes, and HvFT1 copy number and haplotypes at the promoter (PE and PL) and intron one regions (IAG and ITC) are described for each line. Positions of the polymorphisms are reported as bp upstream of the start codon (promoter) or downstream of the start of intron one (intron) in Igri (i = insertion, d = deletion)

a PPD-H1: the recessive pdl allele is associated with photoperiod insensitivity and the dominant Ppd1 allele with photoperiod sensitivity

b VRN-H1: the recessive vn1 allele is associated with vernalization requirement (winter growth habit) and the dominant Vrn1 allele is associated with the lack of vernalization requirement (spring growth habit)

c VRN-H2: the dominant Vrn2 allele is associated to vernalization requirement (winter growth habit) and the recessive vrn2 allele is associated with the lack of vernalization requirement (spring growth habit)
made between BGS213 and IMC to test the effect of HvFT1 copy number variation on flowering time in lines with identical promoter and intron one haplotypes.

Finally, the effect of the different HvFT1 promoter haplotypes in varieties with identical HvFT1 copy number was tested in two F2 segregating spring x winter populations from crosses E878 × H. vulgare ssp. spontaneum and U672 × H. vulgare ssp. spontaneum and in one winter x winter population from the cross Hayakiso 2 × H. vulgare ssp. spontaneum. The effect of the different intron one haplotypes was only explored in the IMC × Hayakiso 2 segregating population.

All populations were produced and grown in greenhouse under long day (LD) photoperiod (15–16 h day length) generated by extending natural light conditions with supplementary lights as needed. Temperatures were held at non-vernalizing conditions (21–25 °C during the day and 12–18 °C during the night).

Markers

The Vrn-H1 and vrn-H1 alleles were identified using the UCW133 marker (Table 3), which detects a small indel near the end of the first intron that is linked to the larger functional deletion in the same intron. The two recessive vrn-H1 alleles in the Hayakiso 2 × H. vulgare ssp. spontaneum population were characterized using HvV1PromF2 and HvV1PromR2 primers that detect a promoter indel (Table 3). PPD-H1 alleles were identified using a Cleaved Amplified Polymorphic Sequence (CAPS) marker digested with restriction enzyme BstUI (Table 3; Turner et al. 2005). VRN-H2 was genotyped using primers VRN-H2aF and VRN-H2aR (Table 3), or when a codominant marker was necessary, with a marker for the tightly linked SNF2 gene (Table 3). The HvFT1 marker based on a 4-bp indel in the promoter was used for genotyping the populations segregating for the HvFT1 promoter haplotypes (Table 3; Yan et al. 2006), whereas the UCW133 marker was used to differentiate the intron haplotypes (Table 3).

Determination of copy number variation (CNV) by quantitative PCR

Genomic DNA was extracted using the CTAB (cetyltrimethylammonium bromide) extraction method (Murray and Thompson 1980). Samples were treated with RNase A, and a phenol:chloroform:isoamyl alcohol purification step was used to remove possible RNA contamination, which might interfere with normalization. DNA concentration was normalized using a Nanodrop instrument (Thermo Fisher Scientific, Waltham, MA) to a concentration of 20 ng/μl, and 1 μl was used for each 20 μl Fast Sybr® Green reaction. These reactions were performed on an AB7500 Fast Real-Time PCR System (Applied Biosystems by Life Technologies, Grand Island, New York), using identical programs for all primer pairs ((95 °C 20 s) × one cycle, (95 °C 3 s, 60 °C 30 s) × 40 cycles). The parental lines were tested with various pairs of primers in the HvFT1 region (Table 3), and a pair of primers in the SNF2 control gene, which has been shown before to have a single copy in the barley genome (Yan et al. 2002). The \( 2^{-\Delta\Delta Ct} \) method was used to estimate copy number (Weaver et al. 2010), with Morex as a calibrator and C T = threshold cycle. We first calculated \( \Delta Ct = Ct - C T \) and then calculated the difference between the two as \( -\Delta Ct = \Delta Ct - \Delta Target \). Previous sequencing of Bacterial Artificial Chromosomes (BACs) containing HvFT1 has shown that only one copy of this gene is present in Morex, making it a good calibrator variety (Yan et al. 2006). Table 3 describes the primers used for quantitative PCR and their efficiency.

Table 2 Segregating populations

| Parental lines | CNV | HvFT1 alleles | Number of plants tested (selected alleles) |
|----------------|-----|---------------|------------------------------------------|
| BGS213 × H. vulgare ssp. spontaneum | 4 × 1 | \( P_b I_{AG} \times P_l I_{TC} \) | 72 (F2) |
| BGS213 × Igri \(^{a}\) | 4 × 1 | \( P_b I_{AG} \times P_l I_{TC} \) | 96 (F2) |
| BGS213 × IMC | 4 × 1 | \( P_b I_{AG} \times P_e I_{AG} \) | 164 (F2, Vrn-H2/-, Ppd-H1/-) |
| Morex × H. vulgare ssp. spontaneum | 1 × 1 | \( P_b I_{AG} \times P_l I_{TC} \) | 81 (F2) |
| IMC × Hayakiso 2 | 1 × 1 | \( P_l I_{TC} \times P_l I_{TC} \) | 70 (F2, Vrn-H2/-) |
| E878 × H. vulgare ssp. spontaneum | 1 × 1 | \( P_b I_{TC} \times P_l I_{TC} \) | 47 (F3, Ppd-H1) |
| U672 × H. vulgare ssp. spontaneum | 1 × 1 | \( P_b I_{TC} \times P_l I_{TC} \) | 89 (F3, Ppd-H1) |
| Hayakiso 2 × H. vulgare ssp. spontaneum | 1 × 1 | \( P_b I_{TC} \times P_l I_{TC} \) | 125 (F3) + 134 (F2) |

\(^{a}\) Yan et al. 2006
The first HvFT1 primer pair (CNV_FT1_F2 and CNV_FT1_R2) was designed on the border between the first exon and the first intron. This region was selected because it includes several SNPs that differentiate HvFT1 from other members of the FT family. Copy number in the recombinant BGS213 lines was determined using these primers.

To determine the borders of the duplication in the BGS213 lines, additional primers were designed inside and flanking the HvFT1 gene. In the HvFT1 promoter region, a set of primers was designed 656–727 bp upstream of the start codon (CNV_FT1p_F2 and CNV_FT1p_R2). Another set of primers amplified a region from a 22-bp upstream to 97-bp downstream of the start codon (CNV_FT1p_F5 and CNV_FT1p_R4). Within the gene, an additional set of primers was designed at exon three to determine if the complete gene was duplicated (CNV_FT1_F4 and CNV_FT1_R3, 778–902 bp downstream from the start codon). Markers were also designed outside the HvFT1 gene. One pair of primers was designed for gene UCW123, located 6.6 kb downstream from HvFT1 on Morex BAC clone 440G4 (GenBank DQ900686, CNV_UCW123_F1 and CNV_UCW123_R1). The nearest known genes on flanking BACs 455J22 (GenBank DQ900687) and 761F04 (GenBank DQ900685, Yan et al. 2006) were also tested, including UCW120 (CNV_UCW120_F1 and CNV_UCW120_R1) and UCW118 (CNV_UCW118_F1 and CNV_UCW118_R1).

### Results

**Variation in flowering time among lines with identical HvFT1 haplotypes**

The HvFT1 sequences from Morex, IMC, and BGS213 are identical (Table 1). However, segregating populations including the first two varieties (Morex × H. vulgare ssp. spontaneum and IMC × Hayakiso 2) showed that plants...

### Table 3  Primer names, sequence, amplification temperatures, and amplification efficiencies

| Genotype | Primer name | Forward primer | Reverse primer | A.T. | Enzyme |
|----------|-------------|----------------|----------------|------|--------|
| Vrn-H1   | UCW132_F/R  | TGGTTGCAAACTATTTGACCAG | TAGGCCATCATACGTTCAAG | 59°  | –      |
| vrn-H1   | HvV1PromF/R2 | ACTTCACCACCAACACCTGAC | CTGCGGGTGATCTCTGTTCT | 55°  | –      |
| Vrn-H2   | VRN-H2a_F/R | CATGAAACACGCACCTCCAGA | TTGGGCTCTCTTCCTGTCAAG | 59°  | –      |
| SNF2     | SNF_F/R     | TTGGTACCTGAATGCCGTTGAAA | ATGGCACAATTTGAGATATGGA | 60°  | –      |
| Ppd-H1   | PPD/H1_F/R  | CTGAGCCTGAAGAGGTCGAG | GTGGCGGGGATCTATCTCTCT | 57°  | BsaI   |
| HvFT1 Prom. | HvFT1F/R1 | AGTGGACATGGAAACCTGCACT | TGGTGTAGTGATGTTGGGCC | 55°  | –      |
| HvFT1 Intron | UCW133_F/R | TGGCGACCATGGCAGTGA | GCAGACGGGAGAACGACTAA | 55°  | Real   |
| EBmac603 | EBmac603F/R | ACCGGAACAACTAAATGACTACTGC | TGGCAACTGTGCTAATTAGG | 56°  | –      |
| Bmac914  | Bmac914F/R  | GGGCAATTATACAGTTCAACTC | ATGAACTGGGAGGGAGAAA | 57°  | –      |

### qRT-PCR

| Gene | Primer name | Forward primer | Reverse primer | Efficiency % |
|------|-------------|----------------|----------------|--------------|
| UCW118 | CNV_UCW118_F1/R1 | CAGTAAAGCCGGAACCATGTCATC | TGGCACAACACAGGACAGC | 99.9 |
| FT1 Prom. | CNV_FT1p_F2/R2 | CGGCCGACTCGACTGCTGTATCT | GCCATAATCCGCCCTTCTT | 99.9 |
| FT1 ATG | CNV_FT1p_F5/R4 | TGGTCCTAAGAGGAGGGAGGAGAG | GAAGTGCAATGGCCTGTTG | 99.8 |
| FT1 Ex1 | CNV_FT1_F2/R2 | CGTGACGTACCAATACCACTACATCTCAATG | GAGAGCGGACCTGCTGCAAT | 99.8 |
| FT1 Ex3 | CNV_FT1_F4/R3 | GCAGGTTGGTGACGATATCCC | GGAAGAGCAGGACAGGAA | 89.3 |
| UCW123 | CNV_UCW123_F1/R1 | ACTGCAAGAGGCTAGGCTAGTCCA | GTACCGGCGCAGACGATCTAG | 99.9 |
| UCW120 | CNV_UCW120_F1/R1 | GCGGACGACGAAATGACG | CGGGTCGCGGATCAGGAA | 99.9 |
| SNF2  | CNV_SNF2_F1/R1 | ATTAGCCCTGCTGCTGCGGATTA | AAATGAGGCTGCTGAAGGTGT | 93.4 |

* PCR program:(95° 20 s) × one cycle, (95° 3 s, 60° 30 s) × 40 cycles
with winter alleles for the VRN-H1 and VRN-H2 genes flowered very late independently of HvFT1. This observation was inconsistent with the results from Yan et al. (2006), which have previously shown that the HvFT1 allele from BGS213 was sufficient to confer a spring growth habit when introgressed into winter barley varieties. To test if additional polymorphism were present among these three HvFT1 alleles, we sequenced a 9,250-bp region starting 1,499-bp upstream of the start codon and ending 6,690-bp downstream of the stop codon. No polymorphisms were detected in the HvFT1 coding and flanking sequences of Morex, IMC, and BGS213. The segregating populations including these varieties are described in detail below.

Morex (P_E I_AG) × H. vulgare ssp. spontaneum (P_L I_TC)

This population of 81 F2 plants segregated for the VRN-H1, VRN-H2, and HvFT1 loci. To study the effect of the HvFT1 alleles in a winter background, we first selected plants homozygous for vrn-H1 and homozygous or heterozygous for the Vrn-H2 alleles for winter growth habit. The 11 selected plants carrying these alleles flowered relatively late (91–106 days after sowing) and showed no significant differences between the different HvFT1 alleles (P = 0.32), even when the 11 plants were divided in photoperiod sensitive and photoperiod insensitive groups.

IMC (P_E I_AG) × Hayakiso 2 (P_E I_TC)

A similar result was observed in a population of 92 F2 lines from the cross between the photoperiod sensitive varieties IMC and Hayakiso 2. IMC is a spring barley variety that carries an HvFT1 allele with identical sequence to the BGS213 allele and a vrn-H2 allele for spring growth habit, whereas Hayakiso 2 is a winter variety (Table 1). In the F2 segregating population, 22 plants homozygous for the IMC vrn2 allele were identified using the tightly linked SNF2 molecular marker and were discarded. The remaining 70 plants, carrying vrn-H1 and Vrn-H2 alleles for winter growth habit, flowered relatively late (100–250 days, average 167 days) and showed no significant differences between the different HvFT1 alleles (P > 0.05). Plants homozygous for the functional Vrn-H2 allele flowered 29 days later than the plants carrying the heterozygous allele (P = 0.02) suggesting some dosage effect of VRN-H2. No significant interaction was detected between HvFT1 and VRN-H2 (P = 0.74).

The results from the IMC × Hayakiso 2 and Morex × H. vulgare ssp. spontaneum populations suggest that, in spite of their identical sequence, the HvFT1 alleles present in Morex and IMC have a smaller effect on inducing flowering than the HvFT1 allele present in BGS213. To test this hypothesis, we developed a third population segregating for the HvFT1 alleles of BGS213 and IMC, which have identical sequence and contrasting phenotypes.

BGS213 (P_E I_AG) × IMC (P_E I_AG)

Since no polymorphisms were found between the two parental lines in HvFT1 or in the genes tightly linked to HvFT1 (Yan et al. 2006), we screened linked SSR markers and found Bmag914 and EBmac0603 (GrainGenes database, http://wheat.pw.usda.gov/) to be polymorphic between BGS213 and IMC. These two markers flanking the HvFT1 locus were located approximately 14 cM apart in this mapping population.

The complete segregating population was genotyped with the HvFT1 flanking SSR markers and with markers for VRN-H2 and PPD-H1 genes. To focus on the effect of HvFT1, plants homozygous for the vrn-H2 allele for spring growth habit or for the photoperiod insensitive allele (ppd-H1) were eliminated. The remaining 167 F2 lines showed a highly significant (P < 0.0001) effect on flowering associated with the SSR markers flanking the HvFT1 locus. The HvFT1 locus alone explained 96 % of the variation in flowering time among the selected 167 plants, indicating that no other major flowering gene was segregating in this selected sub-population.

Plants heterozygous or homozygous for the BGS213 HvFT1 allele showed a spring growth habit (33 days to 76 days from sowing to heading time) whereas plants homozygous for the IMC SSR markers flanking the HvFT1 locus showed no signs of flowering 125 days after planting, when the experiment was terminated. This population showed a clear 3:1 ratio between spring and winter plants (122 spring/45 winter, χ² P = 0.56). In summary, these results confirmed that the largest differences in flowering time in this segregating population were linked to the HvFT1 region in spite of the identical HvFT1 sequences between BGS213 and IMC.

Variation in HvFT1 copy number

Possible explanations for the previously described differences in flowering time include an unknown gene tightly linked to HvFT1, a regulatory sequence beyond the HvFT1 sequenced region or copy number variation (CNV) in HvFT1. To test the last hypothesis, we determined the number of HvFT1 copies in BGS213, IMC, Morex, and other accessions used as parental lines in different segregating populations.

DNAs were extracted from approximately 10 plants from each variety, and HvFT1 copy number was determined by quantitative PCR for the exon one region (Table 3) using the single copy gene SNF2 as an internal
The results indicated that BGS213 has four to five copies of HvFT1 whereas IMC has a single copy (Fig. 1). The increase of HvFT1 copy number found in the BGS213 allele was confirmed in the two backcross substitution lines of the Tammi HvFT1 allele into the winter varieties Hayakiso 2 and Dairokkaku 1, which also showed four to five copies of HvFT1 each. All other varieties tested in this experiment (E878, H. vulgare ssp. spontaneum, Hayakiso 2, Golden Promise, Igri, U672 and Morex) showed only one copy of HvFT1.

To test if the multiple HvFT1 copies were linked, we estimated HvFT1 copy number with the same exon one primers in 45 BGS213 x IMC F2 lines selected for recombination between the HvFT1 flanking markers Bmag914 and EBmac0603. The lines that flowered earlier (30–39 days) showed the highest average copy number (∼5 copies), whereas the lines that flowered later (>110 days) showed an average of one HvFT1 copy. Plants with intermediate flowering times are likely heterozygous since they showed an intermediate copy number (∼3 copies). These results confirmed that HvFT1 copy number co-segregates with flowering time (Fig. 2), and that the different HvFT1 copies are linked.

We performed an additional experiment to determine the extension of the duplicated region. Primer pairs within loci UCW118 and UCW120 located in Morex’s HvFT1 flanking BACs 455J22 and 761F04 (Yan et al. 2006), showed no evidence of duplication in BGS213 (Fig. 3). These results indicated that the duplication of the HvFT1 region did not include the adjacent BACs. Therefore, we designed additional primers within the Morex BAC 440G04, which includes the HvFT1 gene. The primer set for the HvFT1 promoter region located 655–700 bp upstream of the ATG start site showed no increase in copy number (Fig. 3). Since the start codon region shows four to five copies, the duplicated region must start within the 600-bp region of the HvFT1 promoter upstream of the start codon. The primers for the third exon of HvFT1 and for the UCW123 marker located 6.6-kb downstream from HvFT1 showed that the duplicated region extended beyond the coding region of HvFT1 and into this marker (Fig. 3).

Differences in HvFT1 expression in alleles with different copy number

To study the relationship between HvFT1 copy number variation and expression, we crossed Hayakiso 2 with its near isogenic line containing the Tammi allele (Hayakiso 2-Tammi), selected eight plants homozygous for each of the parental alleles and eight heterozygous plants from the segregating F2 population, and characterized HvFT1 expression profiles in the leaves by qRT-PCR.

Hayakiso 2-Tammi lines showed earlier expression of HvFT1, with significantly higher transcript levels of HvFT1 expression than the two other genotypes just 2 weeks after planting (three leaf stage; Fig. 4, P = 0.002). Plants homozygous for the Tammi HvFT1 allele flowered around seven to 8 weeks, after which HvFT1 transcripts fell back to lower levels. The heterozygous plants showed an increase of HvFT1 transcript levels at the last time point of the experiment (11 weeks), when approximately one-third of the plants had already headed. At this same time point,
Plants homozygous for the HvFT1 alleles from Hayakiso 2 showed no detectable levels of HvFT1 and no signs of flowering induction (Fig. 4). These results show that the transcript levels of HvFT1 are affected by copy number, with larger copy number resulting in earlier HvFT1 expression and early flowering.

**Association between differences in HvFT1 haplotypes and heading time**

Since HvFT1 copy number differences have such a large effect on flowering time, the effect of the different HvFT1 haplotypes needs to be tested using varieties with the same copy number.

Only one population was available to study the effect of the HvFT1 first intron haplotypes in lines with a single HvFT1 copy and identical HvFT1 promoter haplotypes (Table 1).

**IMC (P_E I_AG) × Hayakiso 2 (P_E I_TC)**

Both IMC and Hayakiso 2 are photoperiod sensitive, and carry a single copy of HvFT1 with the same promoter haplotype, but they differ in their first intron haplotypes (Table 1). Plants homozygous for the I_AG allele flowered on average 10 and 13 days later than the plants heterozygous and homozygous for the I_TC allele, respectively. However, these differences were not significant ($P = 0.19$ within the VRN2 heterozygous class) likely due to the large variability of late flowering plants (100–250 days) that resulted in a reduced statistical power. The late flowering observed in all plants indicates that none of the HvFT1 alleles segregating in this population was epistatic to the VRN-H1 and VRN-H2 alleles for winter growth habit.

Three additional populations were used to study the effect of the HvFT1 promoter haplotypes in lines with a single HvFT1 copy (Fig. 3) and identical HvFT1 intron one haplotypes (Table 1).

**E878 (P_E I_TC) × H. vulgare ssp. spontaneum (P_L I_TC)**

This F2 population segregated for HvFT1, VRN-H1 and PPD-H1. To simplify the analysis, two separate F3 segregating populations were derived in which the photoperiod sensitive (Ppd-H1) and photoperiod insensitive (ppd-H1) alleles were fixed. The ANOVA models including the VRN1 and HvFT1 loci, and their interactions explained 92 and 94 % of the variation in heading time in the photoperiod sensitive and insensitive subpopulations, respectively, which indicates that these two genes account for most of the variation in heading time in these two subpopulations. Both sub-populations showed highly significant interactions between the VRN-H1 and HvFT1 loci ($P < 0.0001$) and therefore, the effects of the HvFT1 alleles on heading time are described separately for the recessive and dominant (homozygous plus heterozygous) VRN-H1 classes.

The statistical analysis of the photoperiod sensitive F3 family (47 plants, Fig. 5a) showed significant effects of the HvFT1 alleles within both the dominant Vrn-H1 class
The difference, interaction in E878 (PE ITC) alleles show significant minus one standard error of the Vrn HvFT1 of the vrn and HvFT1 homozygous for the HvFT1 HvFT1 the Photoperiod sensitive F3 a Photoperiod sensitive F3 family, the lack of parallelism between lines reflects the significant interaction between VRN-H1 and HvFT1 alleles (larger effect of the HvFT1 alleles within the vrn-H1 class than within the Vrn-H1 class). Bars are plus-minus one standard error of the means.

In both E878 and U672 populations, the HvFT1 P_E ITC haplotype was associated with early flowering and was epistatic to the winter VRN-H1 and VRN-H2 alleles. However, the same P_E ITC haplotype is also present in the variety Hayakiso 2 (Table 1), which has a winter growth habit. To test if this effect was caused by unlinked epistatic genes in Hayakiso 2 or by a specific characteristic of the HvFT1 region in Hayakiso 2, we crossed this variety with H. vulgare ssp. spontaneum to generate a third population segregating for the HvFT1 promoter haplotype. These two varieties are photoperiod sensitive and have a winter growth habit.

Hayakiso 2 (P_E ITC) × H. vulgare ssp. spontaneum (P_L ITC)

This population was characterized in two separate experiments performed in California (125 F2) and Oklahoma (134 F2). The effect of the HvFT1 alleles was consistent across experiments (no significant experiment × HvFT1 interaction), so the results from the two experiments were analyzed in a single factorial ANOVA including experiment, VRN-H1 and HvFT1 as factors. This analysis showed significant differences in heading time between the two recessive vrn-H1 alleles (P < 0.0001) and also between the HvFT1 P_E and P_L alleles (P < 0.0001), but no significant interaction between the two loci (P = 0.36). On average, F2 plants carrying the vrn-H1 allele from H. vulgare ssp. spontaneum (average 106 days after sowing) flowered 31 days earlier than those carrying the corresponding allele from Hayakiso 2 (135 days after sowing, Table 4). These results indicated that even though both varieties have recessive vrn-H1 alleles for winter growth habit, the vrn-H1 region from Hayakiso 2 is associated with a stronger vernalization requirement than the one from H. vulgare ssp. spontaneum. The earlier vrn-H1 allele was dominant, since the difference in heading time between plants...
heterozygous and homozygous for the *H. vulgare* ssp. *spontaneum* VRN1 allele was less than 1 day (Table 4). Surprisingly, plants carrying the *HvFT1* allele from Hayakiso 2 (P_E promoter) were on average 10 days later than the heterozygous plants and 14 days later than the plants homozygous for the *HvFT1* allele from *H. vulgare* ssp. *spontaneum* (P_L promoter), and the differences were highly significant (*P* < 0.0001, Table 4).

### Discussion

*HvFT1* increases in copy number are associated with a spring growth habit

Previous studies demonstrated that the BGS213 *HvFT1* allele is sufficient to confer spring growth habit and therefore that it is epistatic to the VRN-H1 and VRN-H2 alleles for winter growth habit (Takahashi and Yasuda 1971; Yan et al. 2006). In the two F2 populations reported by Yan et al. (2006) (BGS213 × *H. vulgare* ssp. *spontaneum* and BGS213 × Igri), plants heterozygous or homozygous for the BGS213 *HvFT1* allele had a spring growth habit (average heading time 40 and 59 days, respectively) and the plants homozygous for the *H. vulgare* ssp. *spontaneum* or Igri alleles showed very late flowering or failed to flower (average heading time 106 and >130 days, respectively; Yan et al. 2006). In addition, the introgression of the *HvFT1* early flowering allele from Tammi into the winter-photoperiod sensitive varieties Hayakiso 2 and Dairokkaku 1 also resulted in spring growth habit (Yan et al. 2006). Results from the BGS213 × IMC population in this study confirmed the previous results. Taken together, these experiments indicated that the epistatic effect of the BGS213 *HvFT1* allele on the VRN-H1 and VRN-H2 alleles for winter growth habit is effective across multiple genotypes.

Although the sequences of the coding and flanking regions of the *HvFT1* alleles from barley varieties Morex, IMC, and BGS213 were identical, only the BGS213 allele was sufficient to induce early flowering in the presence of vrn-H1 and Vrn-H2 alleles for winter growth habit. These differences motivated the study of *HvFT1* copy number in these varieties and led to the discovery of the increased *HvFT1* copy number in BGS213. Surprisingly, the BGS213 allele included 4–5 copies of *HvFT1*, which was confirmed in the two backcross introgression lines Hayakiso 2-Tammi and Dairokkaku 1-Tammi (Fig. 1). No *HvFT1* duplications were observed among the other eight varieties characterized for *HvFT1* copy number in this study. This observation, together with the lack of sequence differences among the 4–5 *HvFT1* copies present in the BGS213 allele, suggest that this duplication is of recent origin.

The *HvFT1* allele for spring growth habit found in BGS213 comes from the spring variety Tammi (Olli/Asplund, both spring), which was released in Finland prior to 1950 (received by the National Small Grain Collection in 1949 as PI 175505). This variety can be found in the pedigrees of barley varieties from Finland, Sweden, Canada, and Alaska, where the short growing seasons require varieties with very early flowering and short life cycles.

Additional *HvFT1* alleles dominant for spring growth habit have been reported in barley accessions from North Pakistan, North India, Tibet, and Ethiopia in the germplasm collection at Okayama University (Takahashi 1983). Here, we confirmed the presence of dominant spring *HvFT1* alleles in one accession from Ethiopia (E878) and another one from Russia (U672), and showed that these two alleles were not associated with differences in *HvFT1* copy number (both alleles showed the P_E ITC haplotype combination).

With the identification in this study of CNV at the *HvFT1* locus, all four major flowering genes in the *Triticaceae* have been reported to have some level of CNV. Two

| VRN-H1 allele | *HvFT1* allele | Heading time (days) | ±SEM | Tukey |
|---------------|----------------|---------------------|------|------|
| *H. v. spontaneum* | *H. v. spontaneum* | 97.9 | 4.1 | a |
| *H. v. spontaneum* | Heterozygous | 103.5 | 3.7 | ab |
| *H. v. spontaneum* | Hayakiso 2 | 115.3 | 4.3 | b |
| Avg. *H. v. spontaneum* vrn-H1 | Heterozygous | 98.1 | 3.1 | a |
| Heterozygous | Heterozygous | 106.9 | 2.5 | ab |
| Heterozygous | Hayakiso 2 | 109.5 | 3.1 | b |
| Avg. heterozygous vrn-H1 | 104.8 | 3.1 | a |
| Hayakiso 2 | *H. v. spontaneum* | 124.7 | 3.7 | a |
| Hayakiso 2 | Heterozygous | 140.9 | 3.8 | b |
| Hayakiso 2 | Hayakiso 2 | 137.9 | 3.4 | b |
| Avg. Hayakiso 2 vrn-H1 | 134.5 | 3.1 | b |

Different letters in the last column indicate significant differences between the mean values using the Tukey test (*P* < 0.05)

* Both VRN-H1 alleles in this population are recessive vrn-H1

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Table 4 Hayakiso 2 (P_E ITC) × *H. vulgare* ssp. *spontaneum* (P_L ITC): average heading time plus-minus standard error of the means
to four copies of the *Photoperiod-B1* gene were identified on wheat chromosome 2B and two to three copies of the vernalization gene *VRN-A1* were detected recently on wheat chromosome 5A (Díaz et al. 2012). We reported before the presence of CNV of the ZCCT genes in both wheat and barley (Dubcovsky et al. 2005; Distelfeld et al. 2009). Other important agronomic genes in the *Triticaceae* also show CNV, including a tandem segmental duplication of the wheat dwarfing gene *Rht-D1* (Li et al. 2012), and duplications of the frost tolerance *CBF* transcription factors in barley and wheat (Knox et al. 2010). The rapid increase in CNV examples reported in barley and wheat genes likely reflects the relatively high frequency of gene copy number differences in these species. It has been proposed that the abundance of repetitive elements in the large genomes of the *Triticaceae* species might be associated with the faster rates of duplications and deletions observed in these species (Dubcovsky and Dvorak 2007; Saintenac et al. 2011; Wicker et al. 2011).

**Effect of increased copy number on gene expression and phenotype**

In *Arabidopsis*, which has a small genome and limited numbers of repetitive sequences, copy number variation affects approximately 9% of the genes (Gan et al. 2011). Many of these CNV are likely pseudogenes since only a small proportion is expressed. Among the 388 expressed genes with CNV, only 54 showed differences in expression that were attributed to CNV, which suggested that CNV has a modest effect on differences in gene expression in *Arabidopsis*. However, several examples of differential expression of genes associated with CNV and phenotypic changes have started to emerge in barley and wheat, suggesting that the faster rates of duplications (Dubcovsky and Dvorak 2007), together with the strong selection pressures imposed by agriculture may contribute to a larger role of CNV on expression and phenotypic differences in these species than in *Arabidopsis*.

In wheat, the increased copy number observed in the *Ppd-B1* locus was associated with significantly higher transcript levels particularly at dawn when expression in the wild type was very low (Díaz et al. 2012). In contrast, the increased copy number of recessive *vrn-A1* alleles was associated with slower induction of expression, which is consistent with the increased vernalization requirement and the delayed flowering time observed in the varieties with higher *vrn-A1* copy number (Díaz et al. 2012). Large dosage effects of the *VRN-H2* locus were observed here in the IMC x Hayakiso 2 segregating population, suggesting that the natural variation in *VRN-H2* copy number should also have an effect on flowering time. Natural variation in *VRN2* copy number has been previously described in wheat (Distelfeld et al. 2009). Additional CNV affecting gene expression and phenotype have been reported in genes affecting other important agronomic traits in barley and wheat (Li et al. 2012; Knox et al. 2010; Stockinger et al. 2007; Ragupathy et al. 2008). These examples show that CNV can contribute to important adaptive variation in the *Triticaceae* species through changes in the patterns of gene expression.

Using the Hayakiso 2 × Hayakiso 2-Tammi population, we showed that CNV can influence the timing of expression. Plants homozygous for the Tammi *HvFT1* allele (4–5 *HvFT1* copies) had earlier *HvFT1* expression during development than the near isogenic lines with a single *HvFT1* gene. Heterozygous plants (average ~ 3 copies per genome) showed an intermediate initiation time of *HvFT1* expression levels (Fig. 4) providing additional evidence of the association between *HvFT1* copy number, expression levels and flowering time.

A correlation between earlier increases in *HvFT1* transcript levels and earlier heading time was also observed in wheat. Recombinant substitution lines carrying the *TaFT-B1* allele from the variety Hope, which has a retrotransposon insertion in the promoter showed higher *FT1* transcript levels and earlier flowering time than the isogenic lines carrying the wild type *TaFT-B1* allele (Yan et al. 2006). Similarly, a winter wheat line transformed with the *TaFT-B1* Hope allele showed early flowering even in the absence of vernalization (Yan et al. 2006). To test if the early flowering was associated with CNV we estimated *TaFT-B1* copy number in the transgenic lines relative to the non-transgenic Hope allele. Analysis of genomic DNAs from multiple plants from two independent transgenic events (Yan et al. 2006) showed that these transgenic lines have approximately four (3.7 ± 0.27, 8 plants) and five (4.70 ± 0.14, 12 plants) *TaFT-B1* copies. Although these differences in copy number may explain the earlier induction of *TaFT-B1* in the transgenic wheat plants, we cannot rule out alternative explanations. Since these transgenic events were produced by bombardment, some of the inserted copies may not be functional. Altered transcript levels can be also generated by the truncation of critical regulatory regions in the construct and/or rearrangements during the transformation.

**Haplotype differences in *HvFT1* promoter and first intron**

Based on the early flowering associated with the Tammi and BGS213 *HvFT1* alleles, Yan et al. (2006) hypothesized that the I*AC* intron one haplotype present in these varieties might be associated with their early flowering time, but cautioned that the number of varieties analyzed was insufficient to make valid conclusions. The results from the
Marcos et al. (2010) also reported the presence of the IAG flowering than the ITC haplotype and showed a high correlation with latitude (Adrian et al. 2010; Helliwell et al. 2006; Schwartz FT intron 1 polymorphisms on flowering reported in other species (Ponce-Molina et al. 2012). In our E878 (PE ITC) × H. vulgare ssp. spontaneum (PE ITC) segregating population, the effects of HvFT1 on heading time was significant both in photoperiod sensitive and insensitive backgrounds.

Epistatic interactions between VRN-H1 and HvFT1 alleles

The heterogeneity of the effects of the promoter haplotypes on heading time was also evident in their epistatic effects. In the E878 × H. vulgare ssp. spontaneum and U672 × H. vulgare ssp. spontaneum populations, the plants carrying the HvFT1 PE ITC haplotype showed a spring growth habit irrespectively of the VRN-H1 allele. This result indicates that this HvFT1 allele is epistatic to the VRN-H1 and VRN-H2 alleles for winter growth habit present in these populations (Fig. 5). In spite of having an identical HvFT1 haplotype (PE ITC), the Hayakiso 2 allele was not able to overcome the vernalization requirement in the Hayakiso 2 × H. vulgare ssp. spontaneum population (Table 4).

Based on this result, we conclude that the currently known differences in the sequences of the HvFT1 promoter haplotypes are not sufficient to explain the different epistatic interactions involving this locus.

The increased HvFT1 copy number found in the BGS213 and Tammi alleles was associated with stronger and more consistent epistatic interactions than the haplotype differences among single copy alleles described above. In the BGS213 × H. vulgare ssp. spontaneum and BGS213 × Igri populations, the early flowering HvFT1 allele from BGS213 was epistatic to the alleles for winter growth habit (Yan et al. 2006). Similar epistatic interactions and early flowering were observed when the HvFT1 allele with increased copy number was introgressed into the varieties Hayakiso 2 and Dairokkaku 1, which have a
strong vernalization requirement (Yan et al. 2006), and in the early experiments using the barley variety Tammi (Takahashi and Yasuda 1971). These results indicate that epistatic effects of the $HvFT1$ allele from BGS213/Tammi are consistent across different genotypes.

Conclusions and practical applications

From a practical point of view, our results have clarified the effects of $HvFT1$ natural variation on barley flowering time. We demonstrated that the BGS213 genetic stock used to define the dominant $Vrn-H3$ spring allele includes multiple copies of $HvFT1$ that result in earlier expression and earlier flowering time. The large effect of this allele on flowering time may restrict its use to areas or cropping systems that require short growing cycles. In contrast, the allelic differences in $HvFT1$ first intron are associated with smaller effects on flowering time that can be used to fine tune flowering time of barley varieties to different or changing environments. The presence of multiple $HvFT1$ alleles with diverse effects on flowering time suggests that natural variation at this locus may have contributed to the wide adaptation of barley to different environments.

From a more basic point of view, our results add to a rapidly growing literature on CNV in the Triticeae species. CNV has been found for most of the flowering genes studied so far in the temperate grasses, suggesting that this mechanism plays an important role in the generation of novel diversity. This is not surprising given the dynamic nature of the large genomes of the Triticeae species that exhibit rates of duplications and deletions several orders of magnitude faster than the rates of nucleotide substitution (Dubcovsky and Dvorak 2007; Saintenac et al. 2011; Wicker et al. 2011). In the long term, gene duplications play an important evolutionary role, as they provide opportunities for diversification and sub-functionalization that can increase adaptative plasticity.

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