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## Location of a gene regulating cold-induced carbohydrate production on chromosome 5A of wheat

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**Abstract** Major changes in osmotic potential during cold acclimation are due to changes in sugar concentration, and there is a good correlation between sugar content and frost tolerance. The objective of the present study was to localize a gene(s) responsible for carbohydrate accumulation during cold acclimation on chromosome 5A of wheat using recombinant lines developed from the cross between the substitution lines Chinese Spring (Cheyenne 5A) and CS (*Triticum spelta* 5A). Previously, major genes influencing frost resistance (*Fr1*) and vernalization requirement (*Vrn1*) had been localized on the long arm of that chromosome. The *T. spelta* 5A chromosome carrying the *Fr1* (frost-sensitive) allele for frost tolerance and the *Vrn1* (spring-habit) allele for vernalization requirement did not have a major effect on the sucrose and fructan contents in the Chinese Spring background. On the other hand, the presence of Cheyenne alleles for vernalization requirement, *vrn1*, and frost tolerance, *fr1*, significantly increased sugar concentrations. A recombinant line thought to exhibit recombination between the *Vrn1* and *Fr1* loci suggested that the gene regulating sucrose accumulation was closely associated with, or else represented a pleiotropic effect of, *Vrn1*, but was separable from the *Fr1* locus.

**Key words** Carbohydrate · Frost resistance · Fructan · RFLP mapping · Sucrose · Wheat

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### Introduction

Winter exposes young wheat seedlings to many stresses including a direct effect of frost, ice-encasement, flooding, heaving, desiccation and various diseases usually known as snow moulds. However, tolerance to low freezing temperatures has been considered as the primary limiting factor for survival in most regions (McKersie and Leshem 1994). To achieve the full genetic potential of frost tolerance the plant must be hardened. Under natural conditions the cold hardening (acclimatization) takes place in autumn when the temperature gradually decreases to 0°C over several weeks. Temperatures of 2–5°C and photoperiods of about 12 h are considered to be optimal for cold hardening under controlled environmental conditions, although sublethal freezing temperatures may induce a second phase in the hardening process leading to the maximal expression of freezing tolerance (Fowler et al. 1983; Kacperska 1993).

Numerous reports have shown that the accumulation of various osmotically active solutes, such as sucrose, fructan, quaternary ammonium compounds and proline, takes place during hardening (Thomashow 1990; Galiba 1994; McKersie and Leshem 1994). These may function as cryoprotectants, helping to avoid cellular dehydration during extracellular ice formation, and many of these compounds may also stabilize membranes. Carbohydrate changes during hardening are of particular importance because of their direct relationship with such physiological processes as photosynthesis, translocation and respiration. Among the soluble carbohydrates, sucrose and fructans have some potential role in adaptation to cold stress (Housley and Pollock 1993; McKersie and Leshem 1994). Sucrose can act in water replacement to maintain membrane phospholipids in the liquid-crystalline phase and to prevent structural changes in soluble proteins.

In addition to acting as plant carbohydrate reserves, fructants may have other functions, including involvement in drought and frost tolerance in many grasses, e.g. wheat and barley. The accumulation of fructans is induced by unfavourable conditions, such as cold or drought, that reduce plant growth. Under these conditions, photosynthesis is less inhibited than growth, sucrose concentrations will increase (as a substrate for fructan synthesis), which may further enhance fructan biosynthesis (Housley and Pollock 1993). Recent studies of overwintering cereals have shown that freezing tolerance is strongly correlated with the capacity to increase photosynthesis and with the capacity to increase soluble carbohydrate pools during cold hardening (Tognetti et al. 1990; Öquist et al. 1993). Furthermore, field studies have shown that plants become vulnerable to freezing when the fructan pool becomes depleted and simple sugars can no longer be released into the cytosol and intracellular liquid (Olien and Clark 1993). Hurry et al. (1995) compared the carbon metabolism in spring and winter cultivars of wheat and oil-seed rape during long-term exposure to low temperature. They found increased enzyme activity (fructose-1,6-bisphosphatase and sucrose-phosphate synthase) only in the winter cultivars. This was associated with increased soluble/insoluble carbohydrate ratios in winter cultivars while spring wheats showed a relative decrease in soluble carbohydrates. Roberts (1993) studied the effect of continuous sucrose feeding on the cold hardiness of 'Kharkov 22 MC' wheat plants. His data suggested that increases in sugar content increase hardiness.

Certain chromosomes are known to carry genes that play an important role in the development of frost tolerance. For instance, if the 5A chromosome of the frost-sensitive genotype Chinese Spring (CS) is replaced by the corresponding chromosome from the winter variety Cheyenne (Ch), which possesses excellent frost tolerance, the frost tolerance of CS is greatly increased (Sutka 1981; Veisz and Sutka 1989). Major genes influencing frost tolerance (*Fr1*) and vernalization requirement (*Vrn1*) were mapped on the long arm of chromosome 5A (Roberts 1989; Sutka and Snape 1989; Galiba et al. 1995) using recombinant lines developed from the cross between the substitution lines CS(Ch 5A) and CS (*Triticum spelta* 5A) (Galiba et al. 1995). The data showed that although a close genetic linkage exists between the loci *Fr1* and *Vrn1*, they appeared to be separable. The location of *Vrn1* suggests that it is homoeologous to other vernalization genes in related species, particularly to the *Sh2* locus on chromosome 7(5H) of barley (Laurie et al. 1995) and to the *Sp1* locus on chromosome 5R of rye (Plaschke et al. 1993). An association between frost tolerance and fructan content was reported by Hayes et al. (1993) in barley, and QTLs controlling traits associated with winter hardiness (field survival, LT50, vernalization

response and fructan content) have also been mapped to chromosome 7(5H).

In a preliminary experiment the elevated carbohydrate levels during cold stress of the CS(Ch) chromosome-substitution lines were studied. This showed that the Ch 5A chromosome raised total sugar, fructan and invertase activity as well frost tolerance in the CS background (Housley et al. 1993). These results prompted us to investigate in greater detail the sugar concentrations of CS, Ch and the 5A recombinant-substitution lines, and the results of these analyses are reported here.

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## Materials and methods

### Genetic stocks

The eight recombinant lines studied here were developed from the cross between the substitution lines, CS (*T. spelta* 5A) and CS (Ch 5A), described above (Galiba et al. 1995).

### Plant growth and cold treatment

Cold hardening was carried out using the method developed at Martonvasar (Sutka 1981). Briefly, the seedlings were grown in wooden boxes, and subjected to gradually decreasing temperature and illumination in a Conviron growth chamber for 5 weeks as follows: day and night temperatures, respectively, of 15°C and 10°C in the 1st week, 10°C and 5°C in the 2nd and 3rd weeks, 5°C and 0°C in the 4th and 5th weeks. The duration of the illumination was 12 h for 3 weeks, after which it was shortened to 8 h for the last 2 weeks. The photosynthetic photon flux during the growth of the plants was 260  $\mu\text{mol m}^{-2} \text{s}^{-1}$ .

### Chemical analysis

Water-soluble carbohydrate content was determined on fresh plant material (shoot bases including crown and leaf sheaths). Samples of 2 g fresh weight were extracted twice under reflux using 40 ml of boiling water for 15 min, and twice using 40 ml of 80% boiling ethanol for 15 min (Kerepesi et al. 1996). Fractions were collected and cleared by filtering through Whatman No. 42 papers. Filtrates were dried under reduced pressure at 40°C (vacuum evaporator Buchy model ASB, Sweden) and dissolved in distilled water. Oligosaccharides were hydrolysed by boiling in 0.5% HCl for 30 min. Amounts of free (analysed before hydrolysis) and bound (analysed after hydrolysis) glucose (Glu), fructose (Fru) and sucrose (Suc) were measured using Boehringer Mannheim GmbH Glu/Fru/Suc, No. 716 260 Kits (Wagner et al. 1983). Total amounts of water-soluble carbohydrates were determined using the phenol-sulphuric-acid method (Dubois et al. 1956).

### Statistical analysis

Four replicate samples of each plant material were taken from each genotype. The data were analysed by the STATGRAPHICS statistical package, using the *t*-test and ANOVA functions, to assess significant differences between genotype and treatment means.

## Results

### Carbohydrate content in the stems of CS and Cheyenne

#### Control plants

Total water-soluble carbohydrate (WSC) contents were significantly lower ( $P > 0.05$ ) in the non-hardened (NH) control plants of CS than in Ch (Table 1), which would be expected from their frost tolerance levels. The mono- and di-saccharide contents were similar, although the values were higher in Ch. The Fru concentration was approximately 2.5-times higher in the Ch shoots, whilst the glucan contents were similar.

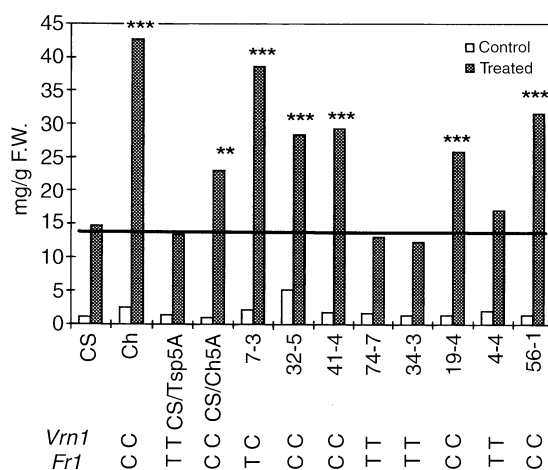
#### Cold-hardened plants

Cold treatment increased the carbohydrate concentration considerably in both cultivars. The cold-hardened (CH) shoots of both parents showed approximately a 10-fold increase in WSC. Concentrations of all of the main sugar components (Glu, Fru and Suc) increased in both genotypes in the same manner, where Suc increased approximately 15-fold, while Glu and Fru concentrations increased approximately 4-fold and 5-fold (Table 1). The sugar contents in the NH winter wheat plants were higher than in the spring line, and this difference was reflected in CH plants where the Suc contents in Ch and CS were 43 and 15 mg/g F.Wt., respectively. Of the polysaccharides, the Fru contents of Ch and CS increased approximately 18- and 22-fold, respectively. Glu content increased 10-fold in Ch and 7-fold in CS following CH. Examination of the proportions of different sugar components of WSC suggests that CH increased the percentage of Suc and Fru and decreased the proportions of monosaccharides and Glu in both varieties. The proportion of Suc increased slightly from 6% to 8% in CS while Glu and the Fru decreased considerably from 40% to 19% and 17% to 12%, respectively, but still remained higher than the Suc level. The percentage of Fru increased from 19% to 46%. In Ch the incremental change of Suc from 8% to 13% during CH was greater than that of each mono-

saccharide. The Glu and Fru percentages decreased from 31% to 11% and 14% to 9%, respectively. The contribution of Fru to WSC increased from 29% to 50%. These changes show that the large CH-induced Fru and Suc accumulation is an adaptive response to cold. Moreover the concentrations of these sugars in Ch were considerably higher than in CS, independent of the growing conditions. These genetic differences between CS and Ch prompted the investigation of the Suc and Fru contents of the 5A recombinant-substitution lines.

#### Distribution of sugars in the recombinant lines

The presence of the *T. spelta* *Fr1* (frost-sensitive) allele and the *Vrn1* (spring-habit) allele for vernalization requirement (symbolised in Fig. 1 as "T") did not change



**Fig. 1** Effect of cold hardening on sucrose concentration in stems of spring wheat 'Chinese Spring' (CS), winter wheat 'Cheyenne' (Ch), CS (*T. spelta* 5A) and CS (Ch 5A) substitution lines and eight of the single-chromosome recombinant lines developed from these 5A substitutions. The frost-tolerance (*Fr1*) and vernalization-requirement (*Vrn1*) genes representing *T. spelta* and Ch alleles are symbolised by T and C, respectively. Each column represents the mean of four stems. The differences from the mean of CS (*T. spelta* 5A), marked with a horizontal line, were calculated among the cold-hardened samples only. Significant differences were calculated at the  $P < 0.05$  (\*),  $P < 0.01$  (\*\*) and  $P < 0.001$  (\*\*\*) levels

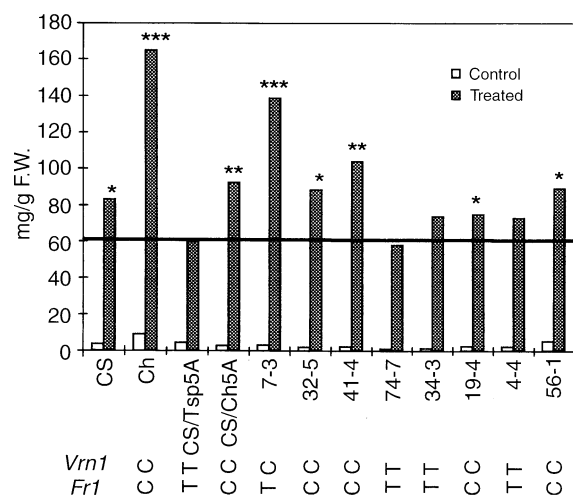
**Table 1** Carbohydrate content of non-hardened (NH) and cold-hardened (CH) stems of spring wheat Chinese Spring and winter wheat Cheyenne. Each value represents the mean  $\pm$  SD of four stems

Carbohydrates	Carbohydrate content (mg/g fresh wt)			
	Chinese Spring		Cheyenne	
	NH	CH	NH	CH
Glucose	7.9 $\pm$ 0.6	33.4 $\pm$ 1.8	10.1 $\pm$ 1.0	36.3 $\pm$ 0.8
Fructose	3.3 $\pm$ 0.4	20.8 $\pm$ 1.3	4.6 $\pm$ 0.3	29.4 $\pm$ 0.7
Sucrose	1.1 $\pm$ 0.6	14.7 $\pm$ 2.0	2.5 $\pm$ 1.0	42.5 $\pm$ 3.0
Glucan	3.8 $\pm$ 2.0	27.3 $\pm$ 2.5	5.3 $\pm$ 2.9	51.7 $\pm$ 4.5
Fructan	3.7 $\pm$ 0.5	83.1 $\pm$ 10.7	9.3 $\pm$ 1.9	165.0 $\pm$ 7.8
Total WSC <sup>a</sup>	19.8 $\pm$ 4.3	179.3 $\pm$ 18.6	31.8 $\pm$ 6.9	324.9 $\pm$ 27.3

<sup>a</sup> WSC = water-soluble carbohydrate

the Suc content in the 'Chinese Spring' background (Fig. 1). On the other hand, the presence of the 'Cheyenne' allele (symbolised as "C") for vernalization requirement, *vrn1*, significantly increased the sucrose concentration. From the genotype of the recombinant between these loci, 7-3, the gene regulating sucrose accumulation seems to be closely associated with the *Vrn1* locus but separable from the *Fr1* locus. This was also the case with a gene affecting ABA accumulation (Quarrie et al. 1994 a).

The presence of the complete *T. spelta* 5A chromosome in the 'Chinese Spring' background decreased the



**Fig. 2** Effect of cold hardening on fructan concentration in stems of spring wheat 'Chinese Spring' (CS), winter wheat 'Cheyenne' (Ch), CS (*T. spelta* 5A) and CS (Ch 5A) substitution lines and eight of the single-chromosome recombinant lines developed from these 5A substitution. Otherwise, as in Fig. 1

rate of Fru accumulation during cold treatment (Fig. 2) whilst the 'Cheyenne' 5A increased the Fru content. From the genotype of the recombinant line, 7-3, the *Vrn1* locus again appears linked to the gene(s) controlling stress-induced fructan accumulation. However, the effect is less pronounced and variation between the lines may indicate that another gene(s) on 5A may be segregating for Fru accumulation independent of *Vrn1*.

## Discussion

Measurements of sugar concentrations on the 5A recombinant-substitution lines (Table 2, Figs. 1 and 2) clearly shows that there is close genetic linkage between the genes responsible for cold-induced sugar accumulation and the *Fr1* and *Vrn1* loci. Although several papers have indicated a positive correlation between sugar accumulation and frost tolerance, this is the first report which represents data on the close genetic linkage between the major genes influencing winter hardiness and the genes that regulate cold-induced sugar production. Based on this result the monitoring of Suc or Fru contents in breeding programs could be used as a selection criterion to achieve better winter hardiness.

The presence of three known RFLP loci in this region of chromosome 5A (Galiba et al. 1995) may make this region amenable for gene isolation and cloning, following the recent mapping results of Gill et al. (1996). For chromosome 5A they found that more than 60% of the markers (marker distribution may represent the distribution of genes) were present in three major clusters that physically encompassed less than 18% of the long arm of chromosome 5A. According to their map, the *Fr1* and *Vrn1* genes are flanked by two probes

**Table 2** The genomic composition of the single-chromosome recombinant lines developed from the intercross of CS (*T. spelta* 5A) and CS (Ch 5A) substitution lines. The RFLP probes representing *T. spelta* and Ch alleles are symbolised by T and C, respectively

Distance (cM)	Marker	T.sp5A 55-6	Ch 5A 67-3	Single-chromosome recombinants						
				7-3	32-5	41-4	74-7 34-3	19-4	4-4	56-1
0	<i>psrB85</i>	T	C	T	T	C	T	C	C	C
	<i>psrB85</i>	T	C	T	T	C	T	C	C	C
6.4	<i>psr911</i>	T	C	T	T	C	T	C	C	C
15	<i>psr637</i>	T	C	T	T	C	T	C	C	C
56.7	<i>Xpsr2021</i> ( <i>dhn2</i> )	T	C	C	T	C	T	C	T	C
65.4	<b><i>Vrn1</i></b>	T	C	C	C	C	T	C	T	C
	<i>Xcdo504</i>	T	C	C	C	C	T	C	T	C
	<i>Xwg644</i>	T	C	C	C	C	T	C	T	C
	<i>Xpsr426</i>	T	C	C	C	C	T	C	T	C
67.5	<b><i>Fr1</i></b>	T	C	T	C	C	T	C	T	C
113.1	<i>Xpsr805</i> ( <i>Embp</i> )	T	C	T	T	T	C	T	C	T
117.7	<i>Q</i>	T	C	T	T	T	C	T	C	T
122	<i>Xpsr370</i>	T	C	T	T	T	C	T	C	T
	5A/4A break point									
128.4	<i>Xpsr164</i>	T	C	T	T	T	C	T	C	T
178.9	<i>B-amy-A1</i>	T	C	T	T	C	T	C	C	T

mapped in the gene cluster at FL 0.75. In this particular submicroscopic region ten other probes were mapped. The bp/cM estimates for this region may be anywhere from 40 to 120 kb/cM, which is similar to other crop plants possessing smaller genomes like tomato (Ganal et al. 1989; Zhang et al. 1994) or rice (Umehara et al. 1995).

It is not clear how carbohydrate biosynthesis is regulated during cold hardening and what is the role of the genes on chromosome 5A. Housley and Pollock (1993) pointed out that there are at least six possible sites for the regulation of carbohydrate metabolism in leaf cells of temperate grasses. In winter rye, in parallel with the increase in photosynthetic capacity following cold hardening, there is an increase in ribulose-1,5-bisphosphate carboxylase/oxygenase and sucrose-phosphate synthase activity and 3- to 4-fold increases in the pools of associated metabolites (Hurry et al. 1994). The regulation of fructan metabolism is based on its possible function, namely the control of sucrose content within the vacuole (Housley and Pollock 1993). Understanding the control of sucrose content is important because of its major role in higher-plant carbohydrate partitioning. It is also believed to be responsible for changes in gene expression including the induction of fructan metabolic enzymes (Housley and Pollock 1985, 1993; Olien and Clark 1993). These findings support the proposal of Guy et al. (1992) that the increase in the activity and amount of enzymes of the photosynthetic carbon reduction cycle and of those responsible for Suc synthesis is not simply an adjustment for overcoming the slower enzyme kinetics at low temperature.

A polygenic regulation pattern might be required for the control of these rather complicated processes. The region around the *Vrn1* and *Fr1* genes may therefore contain a complex of regulatory genes. Dubcovsky et al. (1995) investigated the linkage relationships among genes responding to water-deficit, salt stress and heat shock in diploid wheat (*Triticum monococcum* L.). They mapped a relatively high number of genes (two dehydrin and four early salt-induced (*Esi*) genes and a duplicate heat-shock locus *Xttu1934(Hsp16.9b)*, which co-segregated with the *Xwg644* RFLP locus, in a 54.6-cM region on the telomeric end of chromosome 5A<sup>m</sup>L. Moreover a QTL for drought-induced ABA accumulation was also found in this region (Galiba et al. 1994; Quarrie et al. 1994a, b). Clearly much more detailed genetic information is required by further fine mapping of this region.

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