



Title	Comparative study of transgenic <i>Brachypodium distachyon</i> expressing sucrose:fructan 6-fructosyltransferases from wheat and timothy grass with different enzymatic properties
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3 **Title:** Comparative study of transgenic *Brachypodium distachyon* expressing

4 sucrose:fructan 6-fructosyltransferases from wheat and timothy grass with different

5 enzymatic properties.

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16

1 **Abstract**

2 Fructans can act as cryoprotectants and contribute to freezing tolerance in plant species,
3 such as in members of the grass subfamily Pooideae that includes Triticeae species and
4 forage grasses. To elucidate the relationship of freezing tolerance, carbohydrate
5 composition and degree of polymerization (DP) of fructans, we generated transgenic
6 plants in the model grass species *Brachypodium distachyon* that expressed cDNAs for
7 sucrose:fructan 6-fructosyltransferases (6-SFTs) with different enzymatic properties;
8 one cDNA encoded PpFT1 from timothy grass (*Phleum pratense*), an enzyme that
9 produces high DP levans, a second cDNA encoded wft1 from wheat (*Triticum*
10 *aestivum*), an enzyme that produces low DP levans. Transgenic lines expressing *PpFT1*
11 and *wft1* showed retarded growth; this effect was particularly notable in the *PpFT1*
12 transgenic lines. When grown at 22°C, both types of transgenic line showed little or no
13 accumulation of fructans. However, after a cold treatment, *wft1* transgenic plants
14 accumulated fructans with DP = 3 – 40, whereas *PpFT1* transgenic plants accumulated
15 fructans with higher DPs (20 to the separation limit). The different compositions of the

1 accumulated fructans in the two types of transgenic line were correlated with the
2 differences in the enzymatic properties of the overexpressed 6-SFTs. Transgenic lines
3 expressing *PpFTI* accumulated greater amounts of mono- and disaccharides than wild
4 type and *wft1* expressing lines. Examination of leaf blades showed that after cold
5 acclimation *PpFTI* overexpression increased tolerance to freezing; by contrast, the
6 freezing tolerance of the *wft1* expressing lines was the same as that of wild type plants.
7 These results provide new insights into the relationship of the composition of
8 water-soluble carbohydrates and the DP of fructans to freezing tolerance in plants.
9

1 **Key words:** *Brachypodium*, Degree of polymerization, Freezing tolerance, Fructan, Fructosyltransferase,
2 Timothy, Wheat.

3 **Abbreviations:**

4 ***DP***
5 Degree of polymerization

6 ***DTT***
7 Dithiothreitol

8 ***FEH***
9 Fructan exohydrolase

10 ***1-FFT***
11 Fructan:fructan 1-fructosyltransferase

12 ***HPAEC-PAD***
13 High-performance anion exchange chromatography with pulsed amperometric detection

14 ***HPLC***
15 High-performance liquid chromatography

16 ***LE***
17 Ligand exchange

18 ***RI***
19 Refractive index

20 ***SE***
21 Size exclusion

22 ***1-SST***
23 Sucrose:sucrose 1-fructosyltransferase

24 ***6-SFT***
25 Sucrose:fructan 6-fructosyltransferase

26 ***PFT***
27 Transgenic line expressing *PpFTI*

28 ***WFT***
29 Transgenic line expressing *wft1*

30 ***WT***
31 Wild type

1 **Introduction**

2 Fructans are soluble fructose polymers derived from sucrose that are synthesized and
3 assimilated as storage carbohydrates during photosynthesis in many plant species. The
4 structures of fructans vary widely among plant species (Vijn and Smeekens 1999) and
5 this variation is exemplified in plants belonging to the tribes Poeae and Triticeae
6 (family Poaceae, subfamily Pooideae). In the Poeae, timothy grass (*Phleum pratense*),
7 orchard grass (*Dactylis glomerata*), and big blue grass (*Poa secunda*) accumulate a
8 simple levan comprised of linear $\beta(2,6)$ -linked fructose units with a terminal glucose
9 (Chatterton et al. 1993; Bonnett et al. 1997; Chatterton and Harrison 1997; Cairns et al.
10 1999). However, Triticeae species, such as wheat (*Triticum aestivum*) and barley
11 (*Hordeum vulgare*), produce mixed levans, called graminans, composed of
12 branched-type fructans containing $\beta(2,6)$ - and $\beta(2,1)$ -linked fructose residues (Carpita
13 et al. 1989; Bonnett et al. 1997). The degree of polymerization (DP) of fructans also
14 differs among plant species (Vijn and Smeekens 1999). The DPs of the major
15 components of wheat fructan range from 3 to 20, while some varieties accumulate
16 fructans with a higher DP during the winter (Yoshida and Tamura 2010). By

1 comparison, the DP of the fructans found in timothy grass may be 90 in leaf tissue
2 (Cairns et al. 1999) and as high as 260 in the stem base (Grotelueschen and Smith
3 1968). The variation in structure and DP of fructans arises from differences in the
4 substrate specificities and the combined actions of different fructosyltransferases. In
5 timothy grass, levans with high DPs are thought to be produced by sucrose:fructan
6 6-fructosyltransferase (6-SFT) which transfers fructosyl units from sucrose to a target
7 sucrose or fructan molecule with a $\beta(2,6)$ -linkage (Cairns et al. 1999; Tamura et al.
8 2009). In wheat, graminans are produced by the combined activities of 6-SFT,
9 sucrose:sucrose 1-fructosyltransferase (1-SST) and fructan:fructan
10 1-fructosyltransferase (1-FFT) (Kawakami and Yoshida et al. 2002, 2005). A cDNA for
11 a protein with 6-SFT activity has been identified in timothy grass as *PpFT1* (Tamura et
12 al. 2009) and in wheat as *wft1* (Kawakami and Yoshida 2002). Comparison of the
13 activities of recombinant PpFT1 and Wft1 enzymes identified quite different
14 enzymatic properties as follows: (i) When sucrose is an only substrate, PpFT1 mainly
15 synthesizes a $\beta(2,6)$ -linked, linear fructan series, whereas Wft1 preferentially uses

1 1-kestose ($\beta(2,1)$ -linked fructan with DP = 3 produced by sub-activity of Wft1) as an
2 acceptor and generates branched fructans ($\beta(2,1)$ - and $\beta(2,6)$ -linked) in addition to a
3 $\beta(2,6)$ -linked, linear fructan series. (ii) PpFT1 has a higher affinity for high DP
4 fructans as acceptors than Wft1; thus, PpFT1 produces longer fructans than Wft1. (iii)
5 PpFT1 has a lower substrate affinity for sucrose than Wft1 (Kawakami and Yoshida
6 2002; Tamura et al. 2009).

7 During cold acclimation before winter, fructans are accumulated in Triticeae
8 and forage grass species. Later they may be used as an energy source under snow
9 during winter. In addition to their role as carbohydrate storage molecules, fructans
10 have been suggested to have a role as a cryoprotectant and to directly or indirectly
11 contribute to freezing tolerance at the cellular level (Valluru and Van den Ende 2008;
12 Livingston et al. 2009). Currently, several possible mechanisms for fructan activity
13 against freezing damage have been proposed: membrane protection, reduction in water
14 potential, freezing point depression, and scavenging of reactive oxygen species (ROS)
15 (Gaudet et al. 1999; Valluru and Van den Ende 2008; Livingston et al. 2009; Van den

1 Ende and Valluru 2009; Keunen et al. 2013). Recently, it is hypothesized that small
2 fructans act as phloem-mobile signaling compounds under stress (Van den Ende 2013).
3 Cryoprotectant activity is thought to differ among fructans with different structures and
4 different DPs. For example, Cacela and Hinch a (2006) found increased protection of
5 dry model membranes with an increase in the DP of inulin (a $\beta(2,1)$ -linked, linear
6 fructan) from 2 to 5. However, fructans with DPs between 7 and 17 from oat and rye
7 do not provide cryoprotection of liposomes, whereas smaller fructans do have a
8 protective activity (Hinch a et al. 2007). Vereyken et al. (2003) reported that a bacterial
9 levan with a DP of approximately 125 has a protective activity in liposomes during
10 air-drying. Dionne et al. (2009) reported that freezing tolerance in bluegrass ecotypes
11 was correlated with the amount of higher DP fructans rather than with lower DP
12 fructans. Moreover, simple sugars such as glucose and sucrose, which are accumulated
13 before winter and are the products of hydrolysis of fructans, are also reported to be
14 involved in freezing tolerance and play crucial roles in ROS homeostasis (Valluru and
15 Van den Ende 2008; Livingston et al. 2009; Bolouri-Moghaddam et al. 2010).

1 The *in vivo* physiological roles of fructan can be investigated using
2 transgenic plants. Thus, transgenic tobacco plants overexpressing Bp6-SFT from
3 *Bromus pictus* and 1-SST from *Lactuca sativa* accumulate fructans and show increased
4 freezing tolerance compared to wild type plants that do not accumulate fructans (Li et
5 al. 2007; del Viso et al. 2011). Hisano et al. (2004) generated transgenic *Lolium*
6 *perenne*, a species that normally accumulates fructans, that overexpressed *wft1* (6-SFT
7 cDNA) and *wft2* (1-SST cDNA) from wheat; they found an increase in fructan
8 accumulation and freezing tolerance at the cellular level.

9 In this study, we sought to examine the relationship of freezing tolerance,
10 carbohydrate composition and the DP of fructans. We generated two different types of
11 transgenic line of the model species *Brachypodium distachyon* by inserting the 6-SFT
12 cDNA *PpFT1* from timothy grass or *wft1* from wheat. *B. distachyon* is closely related
13 to timothy grass and wheat but does not have fructosyltransferases (Li et al. 2012). The
14 inserted gene was expressed and the freezing tolerance of the two transgenic types was
15 compared with regard to their accumulation of fructans with different structures and

1 DPs, and to the levels of water-soluble carbohydrates.

2

3 **Materials and methods**

4 Plant materials

5 A *PpFTI* cDNA (AB436697, Tamura et al. 2009) or a *wft1* cDNA (AB029887,
6 Kawakami and Yoshida 2002) coding an enzyme that works as sucrose:fructan
7 6-fructosyltransferase (6-SFT) in plant cells with different properties described in the
8 introduction was inserted into the Ti-based vector pMLH7133 (Mitsuhara et al. 1996),
9 downstream of the maize ubiquitin promoter (Christensen and Quail 1996) that was
10 substituted for the CaMV 35S promoter to ensure a high level of expression of the gene
11 in grass. The resulting plasmids were used for transformation of the *Brachypodium*
12 *distachyon* diploid inbred line ‘Bd21-3’ by the *Agrobacterium*-mediated method using
13 a previously reported protocol (Vogel and Hill 2008) except that *Agrobacterium* strain
14 EHA101 was used. Regenerated T₀ plants with hygromycin resistance were screened
15 for the presence and expression of the transgene. T₁ generation lines were screened by

1 an analysis to detect fructans. For the *wft1* expressing lines, homozygous T₃ lines were
2 used for subsequent analyses. For the *PpFT1* expressing lines, homozygous plants
3 could not be generated; therefore, only transgenic plants from T₃ heterozygous lines
4 were used after PCR confirmation of the genotype. Plants were grown in cell pots (3.5
5 × 3.5 cm) under normal temperature conditions of 10 hours light, 100 μmol m⁻² s⁻¹
6 PFD, and 22°C for 7 weeks or under cold acclimation conditions of 8 hours light, 75
7 μmol m⁻² s⁻¹ PFD, 22°C for 8 weeks and 4°C for 5 weeks. Plant height and fresh
8 weight were measured after growth under normal temperature conditions.

9

10 Carbohydrate extraction and analysis

11 Total water-soluble carbohydrates were extracted from 20-50 mg of fully expanded
12 leaves by boiling for 1 hour in 500 μl - 1 ml deionized water. After filtration, the
13 qualitative analysis of carbohydrate profiles in tissues were analyzed by
14 high-performance anion exchange chromatography and pulsed amperometric detection
15 (HPAEC-PAD) (DX-500, Dionex) with a Carbo Pac PA-1 anion-exchange column

1 (Dionex) as described by Tamura et al. (2009). Glucose, fructose, sucrose,
2 1-kestotriose (Wako Chem.) and 6-kestotriose (Iizuka et al. 1993) were used for known
3 standards to identify peaks. Products of the Wft1 and PpFT1 recombinant enzyme
4 generated by *Pichia pastoris* with sucrose (Tamura et al. 2009) were used as standards
5 for polymerized fructans. Extracted sugar solutions were treated with mild acid or
6 fructan exohydrolase (FEH) to degrade fructans. Mild acid treatment was performed
7 using 0.06 N HCl at 70°C for 1 hour. Recombinant enzyme solution of Pp6-FEH1
8 produced by *P. pastoris* prepared as in Tamura et al. 2011 (0.1 mg/ml) was incubated
9 with the extracted sugar solution at 30°C for 13 hours in 20 mM citrate-phosphate
10 buffer (pH 5.2). The quantitative measurements of carbohydrate contents were
11 performed according to the method as described by Yoshida et al. (1998). The filtrated
12 carbohydrate solution was measured by high-performance liquid chromatography
13 (HPLC) using Shodex KS-802 and KS-803 columns with the size exclusion (SE) and
14 ligand exchange (LE) separation mode (Showa Denko), and an L-2490 refractive index
15 (RI) detector (Hitachi). Propylene glycol (1 mg ml⁻¹) was used as the internal standard

1 to control the extraction efficiency.

2

3 Assay of fructosyltransferase activities in crude enzymatic extracts

4 Crude enzymatic extracts were prepared using 20 mM citrate-phosphate buffer (pH

5 5.2) containing 1 mM dithiothreitol (DTT) and 0.2 to 1.0 g of shoots from plants

6 grown under normal temperature conditions. Following centrifugation at 8000 g for 15

7 min, proteins in the resulting supernatants were concentrated by precipitation with 70%

8 ammonium sulfate. The pellets were dissolved in 0.1 to 0.5 ml of 20 mM

9 citrate-phosphate buffer (pH 5.2) with 1 mM DTT and desalted using a Biospin-30

10 column (Bio-Rad). Twenty μl of enzymatic solution including ca $0.7 \mu\text{g} \mu\text{l}^{-1}$ of protein

11 were incubated with 20 μl of a solution containing 2 M sucrose, 0.2% bovine serum

12 albumin, 20 mM citrate-phosphate buffer, and 1 mM DTT at 37°C for 4 hours. The

13 reaction was terminated at 95°C for 3 min. The enzymatic products were analyzed by

14 HPAEC-PAD as described above.

15

1 Freezing tolerance assay

2 Fully expanded leaf blades from each plant were used to test freezing tolerance. Two or
3 three leaf blade segments of approximately 2 cm were placed on ice produced by
4 freezing 100 µl deionized water in a 1.5 ml tube. The temperature was held at -2.5°C
5 for 16 hours and then decreased by 1°C per hour to a minimum temperature of -12°C
6 using a programmed freezer (MPF-1000, Eyela, Tokyo, Japan). As the temperature
7 decreased, samples were taken at each temperature. Deionized water (1.2 ml) was
8 added to each tube, and the samples were incubated with shaking at room temperature
9 for 4 hour. Electrical conductivities of the resulting solutions were measured using a
10 conductance meter (Twin Cond B-173, Horiba, Kyoto, Japan). Electro leakage was
11 estimated as the ratio of electro conductivity at each freezing temperature to that at
12 -80°C.

13

14 **Results**

15 Two lines of *B. distachyon* overexpressing *PpFTI* and three lines overexpressing *wft1*

1 were analyzed in this study. Under normal conditions (22°C), the growth rate of all five
2 transgenic lines was slower than that of the wild type (WT) plants as evidenced by
3 reductions in plant height and in fresh weight (Fig. 1). The *PpFTI* expressing lines
4 were smaller than *wftI* expressing lines (Fig. 1).

5 The components of the water-soluble carbohydrates that accumulated in the
6 leaf blades of transgenic and non-transgenic lines were qualitatively and quantitatively
7 analyzed. Under normal temperature conditions, the qualitative analysis by
8 HPAEC-PAD detected 6-kestotriose ($\beta(2,6)$ -linked fructan with DP = 3) only in *wftI*
9 transgenic plants, whereas fructans with DP > 4 could not be unambiguously identified
10 in any transgenic plant or in the WT (Fig. 2). The quantitative HPLC analysis revealed
11 significantly higher oligosaccharide amounts in *wftI* plants as compared to WT and
12 *PpFTI*. However, these levels were low compared to those of glucose, fructose and
13 sucrose (Table 1). Polysaccharides corresponding to polymerized fructans were not
14 detected also in this quantitative analysis. The average amount of sucrose in transgenic
15 lines expressing *PpFTI* was slightly lower than in WT and *wftI* transgenic lines (Table

1 1). To investigate the carbohydrates in the cold acclimated plants, leaves of plants
2 treated at 4°C for 5 weeks after grown at room temperature for 8 weeks were analyzed.
3 In the qualitative HPAEC-PAD analyses, WT had sequential small peaks around the
4 region corresponding to fructans with DP > 5; however, the retention times of these
5 peaks did not coincide with those of $\beta(2,6)$ -linked fructans in the products of the
6 PpFT1 recombinant enzyme with sucrose or $\beta(2,1)$ -branched $\beta(2,6)$ -linked fructans in
7 the products of the Wft1 recombinant enzyme (Fig. 3). These retention times also did
8 not accord with those of $\beta(2,1)$ -linked or linear fructans (inulins) (data not shown).
9 Furthermore, mild acid treatment (data not shown) or incubation with a recombinant
10 Pp6-FEH1 that preferentially hydrolyze $\beta(2,6)$ -linked fructans but also could hydrolyze
11 $\beta(2,1)$ -linked fructans (Tamura et al. 2011, Fig S1), did not alter the pattern of these
12 unidentified peaks. In transgenic plants expressing *wft1*, peaks corresponding to linear
13 $\beta(2,6)$ -linked fructans with DP = 3 – ca. 40 were detected. By comparison, the *PpFTI*
14 transgenic plants had similar peaks to those in WT and also sequential peaks at
15 retention times corresponding to those of fructans with DP > 20 to the separation limit

1 (Fig. 3). These peaks were not observed in extracts of WT leaves and they were
2 selectively removed by a treatment with Pp6-FEH1 (Fig. S1). There was no clear peak
3 corresponding to 1-kestotriose in both WT and transgenic lines (Fig. S2). In the
4 quantitative HPLC analysis, broad peaks corresponding to polysaccharide were
5 detected in cold-treated *wft1* and *PpFTI* transgenic plants, and they were at negligible
6 level in extracts of WT (Fig. S3). The polysaccharide peak in the *PpFTI* transgenic
7 plant positioned at higher molecular weight than that in the *wft1* transgenic plant (Fig.
8 S3). These broad peaks were drastically decreased by the recombinant Pp6-FEH1
9 treatment (data not shown). The mean amounts of oligo- and polysaccharides in the
10 transgenic lines were similar and were significantly higher than in WT (Table 2). In
11 *PpFTI* transgenic lines, the amounts of fructose, glucose and sucrose were
12 significantly higher than those in extracts of WT and *wft1* overexpression plants,
13 resulting in a higher total water-soluble carbohydrate content in *PpFTI* transgenic lines
14 (Table 2). In particular, the glucose content of transgenic lines expressing *PpFTI* was
15 more than 10 times greater than in WT and in those expressing *wft1* (Table 2).

1 To confirm that the transgenic plants had fructosyltransferase activity, crude
2 enzyme extracts from shoots grown under normal temperature conditions and their
3 enzymatic products with sucrose (a substrate of fructosyltransferase) were analyzed by
4 HPAEC-PAD. Significant 6-SF(S)T and 1-SST activities were confirmed by the
5 generation of fructans with DP = 3, namely, 6-kestotriose and 1-kestotriose, in *PpFTI*
6 and *wft1* transgenic lines (Fig. 4). In the reaction mixture of the crude enzyme extract
7 from the *PpFTI* transgenic line, production of 6,6-kestotetraose (DP = 4) and
8 6,6,6-kestopentaose (DP = 5) by 6-SFT activity was also observed under this reaction
9 condition (Fig. 4). In the reaction solution from WT plants, signals corresponding to
10 1-kestotriose and 6-kestotriose were detected at a very low level that was much weaker
11 than in the reaction products of the enzyme extracts from the fructosyltransferase
12 expressing lines.

13 To compare the freezing tolerance of the transgenic and WT plants, the
14 degree of electrolyte leakage after freezing (termed the index of freezing tolerance) at
15 the cellular level was measured. In leaf blades from plants grown under normal

1 temperature conditions, the degree of electrolyte leakage after freezing at -5°C did not
2 differ significantly among transgenic plants expressing *wft1* or *PpFTI* and the WT
3 plants (58.9, 59.7 and 54.2%, respectively). After cold acclimation, electrolyte leakage
4 in two transgenic lines expressing *PpFTI* was significantly lower than in WT and in
5 those expressing *wft1* at -8°C and -10°C of freezing temperatures, whereas difference
6 of freezing tolerance was not clearly confirmed in WT and the *wft1* overexpressing
7 lines (Fig. 5).

8

9 **Discussion**

10 *B. distachyon* was the first Pooideae species to have its genome fully sequenced (Vogel
11 et al. 2010). It has proved a valuable model plant species for cereals, temperate grasses
12 and dedicated biofuel crops, due to its short lifespan, small genome size, and ease of
13 transformation (Opanowicz et al. 2008). Li et al. (2012) confirmed that cold responsive
14 genes, such as those for ice recrystallization inhibition proteins and C-repeat binding
15 factor genes, were conserved among *B. distachyon* and core Pooideae species. They

1 proposed the use of *B. distachyon* as a model for the specific molecular mechanisms
2 involved in low temperature responses in Pooideae species. The fact that the
3 semi-lethal temperature decreases in *B. distachyon* following a low temperature
4 conditioning treatment (ca -5°C to -10°C), indicates that this species can respond to
5 cold and increase its freezing tolerance. In the present study, we confirmed that only
6 weak fructosyltransferase activity was present in crude enzyme extracts of WT plants;
7 however, in the extracted water-soluble carbohydrate solution, our HPAEC-PAD
8 analysis did not confirm the presence of $\beta(2,6)$ and $\beta(2,1)$ -linked fructans even after
9 cold acclimation. Mild acid and FEH treatments revealed that the unidentified peaks
10 that appeared after cold acclimation did not correspond to fructans, since fructans
11 should have been hydrolyzed by these treatments. It can be concluded that *B.*
12 *distachyon* does not accumulate fructans. Small fructosyltransferase activity in *B.*
13 *distachyon* can be regarded as a side activity of invertases because synthesis of the
14 DP3 fructans at high sucrose is a general property of invertases (De Coninck et al.
15 2005; Ritsema et al. 2006). These suggest that the metabolism of water-soluble

1 carbohydrates, especially for storage, shows evolutionary diversity between *B.*
2 *distachyon* and core Pooideae species such as wheat and timothy grass.

3 The significant increase in fructosyltransferase activity and the elevation of
4 oligo- and polysaccharide contents following overexpression of the
5 fructosyltransferase cDNAs, *PpFT1* and *wft1*, indicated the initiation of a heterologous
6 novel fructan synthetic pathway in *B. distachyon*. When testing a crude extract of
7 *PpFT1* transgenic plants with sucrose as the only substrate, higher amounts of
8 1-kestotriose were generated as compared to 6-kestotriose and more polymerized
9 $\beta(2,6)$ -linked fructans. This is in accordance with the fact the 6-SST activity of
10 recombinant PpFT1 was lower compared to its 1-SST activity (Tamura et al. 2009).
11 Under cold acclimation conditions, affecting growth more than photosynthesis,
12 increasing sucrose supplies sustain fructan synthesis in PpFT1 transgenic plants. This
13 indicates that PpFT1 acts as a 6-SFT *in planta*, and that endogenous invertases are not
14 able to prevent the accumulation of the synthesized levan-type fructans. Generally,
15 plant fructosyltransferases show low affinity for sucrose as a substrate (high apparent

1 Km; > 280 mM); therefore, sucrose availability is a limiting factor in fructan
2 production (Cairns 2003). Under cold acclimation conditions, a significantly higher
3 rate of accumulation of fructans was observed in transgenic plants expressing
4 fructosyltransferases compared to under normal temperature conditions; this may
5 reflect higher substrate availability in source leaves, due to the altered source/sink
6 balance under cold. The increase in fructan content in transgenic lines expressing *wft1*,
7 but not in those expressing *PpFT1*, under normal temperature conditions might be due
8 to the higher affinity of Wft1 for sucrose compared to PpFT1 (Tamura et al. 2009). The
9 difference in the DPs of the accumulated fructans, i.e., short fructans (DP = 3 - 40) in
10 *wft1* transgenic plants and long fructans (DP > 20) in *PpFT1* plants, is consistent with
11 the different affinity of the two fructosyltransferases for fructans of different DPs as
12 acceptors; this difference in affinity was first identified by analysis of yeast
13 recombinant enzymes (Tamura et al. 2009). Little accumulation of low-DP fructans in
14 the *PpFT1* transgenic plants seemed to be caused by the higher 6-SFT activity of
15 PpFT1 to high-DP fructans than to low DP ones as acceptors, which was previously

1 revealed in the recombinant enzyme analysis (Tamura et al. 2009). As a result,
2 generated low-DP fructans seemed to be gradually converted to high DP fructans,
3 resulting in the little accumulation of low-DP fructans. In transgenic plants expressing
4 *PpFTI*, the linkage forms of the accumulated fructans could not be determined as the
5 DPs were too high to be separated in this HPAEC-PAD analysis. However, with
6 respect to the known enzymatic properties of PpFT1, it is likely that they had linear
7 $\beta(2,6)$ linkages similar to those fructans that accumulated in *wft1* expressing plants;
8 further analysis is needed to confirm this supposition. In addition to fructan
9 accumulation, higher levels of hexose and sucrose per unit fresh weight were present in
10 transgenic lines expressing *PpFTI* compared to WT and *wft1* expressing lines. In
11 plants grown under more intense light conditions, a higher accumulation of glucose
12 was also observed in *wft1* expressing lines (data not shown). A significant increase in
13 glucose and/or fructose concentration has been reported in several studies on
14 plant-derived 6-SFT expressing lines (Hisano et al. 2004; Kawakami et al. 2008).
15 Accumulation of these hexoses might result from the release of glucose from sucrose

1 by a fructosyltransferase reaction, hydrolysis of fructans by native invertases, and /or
2 hydrolysis of sucrose by invertase activity of introduced fructosyltransferases.
3 However, it is possible that the reduced growth phenotypes of the transgenic lines,
4 particularly those expressing *PpFTI*, might also affect carbohydrate metabolism, and
5 cause a relatively low consumption of sugars.

6 The freezing tolerance at the cellular level in leaf blades of *wft1* lines did not
7 differ from that of WT plants despite the former having approximately six times higher
8 accumulation of oligo- and polysaccharides. This suggests that accumulation of
9 fructans might not lead directly to an increase in freezing tolerance. The *PpFTI*
10 expressing lines showed accumulation of oligo- and polysaccharides at a similar level
11 to *wft1* lines and also showed a significant increase in freezing tolerance. The major
12 differences in water-soluble carbohydrate compositions between *wft1* and *PpFTI*
13 plants were (i) the structure of the fructans, especially their DP, and (ii) the amount of
14 mono- and disaccharides, i.e. higher accumulation in *PpFTI* expressing lines and
15 similar levels in WT and *wft1* lines under cold acclimation conditions. Several studies

1 have reported that mono- and disaccharides are involved in freezing tolerance in plant
2 cells (reviewed by Valluru and van den Ende 2008; Livingston et al. 2009). Soluble
3 sugars are also believed to play crucial roles in overall cellular ROS homeostasis
4 (Couée et al. 2006; Keunen et al. 2013; Van den Ende 2013 and references therein).
5 Therefore, the accumulation of high levels of mono- and disaccharides might be
6 involved in the enhanced freezing tolerance of the leaf blades of *PpFT1* expressing
7 plants. Hisano et al. (2004) reported that in perennial ryegrass the overexpression of
8 *wft1* improves freezing tolerance, which was not seen in the *B. distachyon*
9 overexpressing lines in this study. Different response to freezing in the *wft1*
10 overexpressing lines of perennial ryegrass and *B. distachyon* compared to WT might be
11 due to the difference of mono- and disaccharide content; mono- and disaccharide
12 content increased in perennial ryegrass (Hisano et al. 2004) but not in *B. distachyon*.
13 The evidence described above suggests that the enhancement of freezing tolerance
14 caused by 6-SFT overexpression might be related to the increased accumulation of
15 mono- and di-saccharides in addition to fructans. It has also been reported that tobacco

1 plants with heterologous expression of 6-SFT show accumulation of fructans and
2 enhancement of freezing tolerance (del Viso et al. 2011; Bie et al. 2012); however,
3 determination of mono- and disaccharide contents were not performed in these studies.
4 Yoshida et al. (1998) reported that highly freezing-tolerant winter wheat varieties
5 grown under autumn field conditions accumulate high amounts of simple sugars
6 (mono- and disaccharides) and fructans, whereas other varieties (snow mold-resistant
7 cultivars) with higher amounts of fructans and lower amounts of mono-and
8 disaccharides do not have high freezing tolerance compared to varieties with high
9 freezing tolerance. This also suggests the higher contribution of simple sugars than
10 fructans for freezing tolerance.

11 The effect of the DP of the accumulated fructans on freezing tolerance was
12 more difficult to ascertain in this study because the contents of other forms of
13 carbohydrate (especially mono- and disaccharides) were very different between *wft1*
14 and *PpFTI* expressing plants. In a study of liposome membrane stability, it was found
15 that a combination of the high glass transition (T_g) effect of hydroxyethyl starch and

1 the depression of gel phase transition temperature (T_m) by glucose could preserve dry
2 liposomes (Crowe et al. 1997). Hinch et al. (2007) also reported “synergistic effects”
3 of low and high molecular weight carbohydrates on membrane stability. Thus, the
4 enhanced freezing tolerance of *PpFTI* expressing lines might be a synergistic effect of
5 simple sugars and high DP fructans.

6 Transgenic plants expressing fructosyltransferases, particularly those
7 expressing *PpFTI*, showed reduced growth phenotypes. Aberrant phenotypes have
8 been reported for transgenic plants with bacterial levansucrase genes (Cairns et al.
9 2003). Overexpression of *wft1* in perennial ryegrass and rice did not cause aberrant
10 phenotypes (Hisano et al. 2004; Kawakami et al. 2008) as observed in *B. distachyon*
11 (this manuscript) and *Paspalum notatum* (dwarf phenotype, Muguerza et al. 2013),
12 suggesting that growth aberrations are species-specific. As growth retardation occurred
13 here under normal temperature conditions in which there is little, if any, accumulation
14 of fructans, then the accumulation of fructans is not likely to be a major cause of the
15 phenotypic effect. Further studies will be required to clarify the reason of growth

1 aberrations by the overexpression of plant fructosyltransferases.

2 In this study, relationship between the structures of fructans and freezing
3 tolerance could not be clarified. However, our analyses here indicate that the increased
4 freezing tolerance after overexpression of 6-SFT genes is caused by the increase of
5 mono- and disaccharides and of fructans with high DPs. Findings obtained in a
6 monocot grass model species *B. distachyon* in this study would contribute to the
7 improvement of the freezing tolerance of plants, especially the most economically
8 important Poaceae family including cereals, temperate forage grasses and dedicated
9 biofuel crops.

10

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1 6-kestotriose, respectively. We thank Ms. Yukari Ikenobe and Satomi Shimada for their

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3

4

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1 **Figure legends**

2

3 **Fig. 1 a** Phenotypes of transgenic *B. distachyon* expressing *wft1* and *PpFT1* driven by
4 the maize ubiquitin gene promoter. Plants were grown at 22°C, under 10 hours light for
5 7 weeks. WT, wild type; WFT, *wft1* expressing transgenic plant; PFT, *PpFT1*
6 expressing transgenic plant. **b** The height and fresh weight of each transgenic line and
7 WT are given as means \pm SD ($n = 5$ plants for each line). The means of each line with
8 the same small letter do not differ at $p < 0.05$ by Tukey's HSD test

9

10 **Fig. 2** Anion exchange HPLC (HPAEC-PAD) analysis of water-soluble carbohydrates
11 from the leaf blades of transgenic and wild type *B. distachyon* grown under normal
12 temperature conditions. Extracted solutions from fully expanded leaves of wild type
13 **(b)**, plants of a transgenic line expressing *wft1*, WFT1-20 **(c)** and plants of a transgenic
14 line expressing *PpFT1*, PFT1-31 **(d)** were analyzed with a standard **(a)**. Abbreviations
15 for each sugar peak are: G, glucose; F, fructose; S, sucrose; 1K, 1-kestotriose; 6K,
16 6-kestotriose; The *numbers* indicate the putative DPs of $\beta(2,6)$ -linked and linear

1 fructan oligomers

2

3 **Fig. 3** Anion exchange HPLC (HPAEC-PAD) analysis of water-soluble carbohydrates

4 from the leaf blades of cold acclimated transgenic and wild type *B. distachyon*.

5 Extracted solutions from fully expanded leaves of cold acclimated wild type plants (**d**),

6 plants from a transgenic line expressing *wft1*, WFT1-20 (**e**) and plants from a

7 transgenic line expressing *PpFT1*, PFT1-31 (**f**) were analyzed. Standard (**a**), products

8 of the *wft1* and *PpFT1* recombinant enzyme solution with sucrose (**b** and **c**) were also

9 analyzed. Chromatograms at the latter retention time are redrawn using an extended y

10 axis scale (**d**, **e** and **f**). Abbreviations for each sugar peak are: G, glucose; F, fructose; S,

11 sucrose; 1K, 1-kestotriose; 6K, 6-kestotriose; The *numbers* indicate the putative DPs of

12 β (2,6)-linked and linear fructan oligomers and the *numbers with asterisks* indicate the

13 putative DPs of β (2,6)-linked branched fructan oligomers produced by polymerization

14 of fructose units linked to 1-kestotriose

15

1 **Fig. 4** Anion exchange HPLC analysis (HPAEC-PAD) of the enzymatic products of
2 crude enzyme extracts with sucrose. Crude enzymatic extracts from wild type plants
3 **(d)**, a transgenic line expressing *wft1*, WFT1-20 **(e)** and a transgenic line expressing
4 *PpFTI*, PFT1-31 **(f)** grown under normal temperature conditions were incubated with
5 1 M sucrose. Standard **(a)**, products of the PpFT1 recombinant enzyme solution with
6 sucrose **(b)** and sucrose incubated with buffer not including enzyme extracts **(c)** were
7 also analyzed. Abbreviations for each sugar peak are: G, glucose; F, fructose; S,
8 sucrose; 1K, 1-kestotriose; 6K, 6-kestotriose; The *numbers* indicate the putative DPs of
9 β (2,6)-linked and linear fructan oligomers

10

11 **Fig. 5** Freezing tolerance of leaf blades of transgenic *B. distachyon* expressing *wft1* or
12 *PpFTI*. The leaf blades of cold acclimated plants were used for the freezing test.
13 Electrolyte leakage was calculated from the value of electrical conductivity after
14 freezing ($n = 5$). The *asterisks* indicate significant differences compared to wild type
15 by Dunnett's test (*, $P < 0.05$; **, $P < 0.01$)

16

1 **Supplemental material**

2 **Figure S1** Anion exchange HPLC (HPAEC-PAD) analysis of water-soluble
3 carbohydrates from the leaf blades of cold acclimated plants, treated with the
4 recombinant Pp6-FEH1 enzyme. **a** Authentic standards; **b** and **c** untreated and treated
5 extracted solutions from fully expanded leaves of cold acclimated wild type plants; **d**
6 and **e**, untreated and treated extracted solutions from a transgenic line expressing *wft1*,
7 WFT1-20; **f** and **g**, untreated and treated extracted solutions from a transgenic line
8 expressing *PpFT1*, PFT1-31. Chromatograms at the latter retention time are redrawn
9 using an extended y axis scale (**f** and **g**). Abbreviations for each sugar peak are: G,
10 glucose; F, fructose; S, sucrose; 1K, 1-kestotriose; N, nystose

11

12 **Figure S2** Low molecular parts of the anion exchange HPLC (HPAEC-PAD) analysis
13 of water-soluble carbohydrates from the leaf blades of cold acclimated plants. **a**
14 Authentic standards; **b** wild type; **c** a transgenic line expressing *wft1*, WFT1-20; **d** a
15 transgenic line expressing *PpFT1*, PFT1-31. Abbreviations for each sugar peak are: G,

1 glucose; F, fructose; S, sucrose; 1K, 1-kestotriose

2

3 **Figure S3** HPLC chromatograms of water-soluble carbohydrates from the leaf blades

4 of cold acclimated transgenic and wild type *B. distachyon* analyzed by the SE and LE

5 separation mode with the RI detection. Extracted solutions from fully expanded leaves

6 of cold acclimated wild type plants (a), plants from a transgenic line expressing *wft1*,

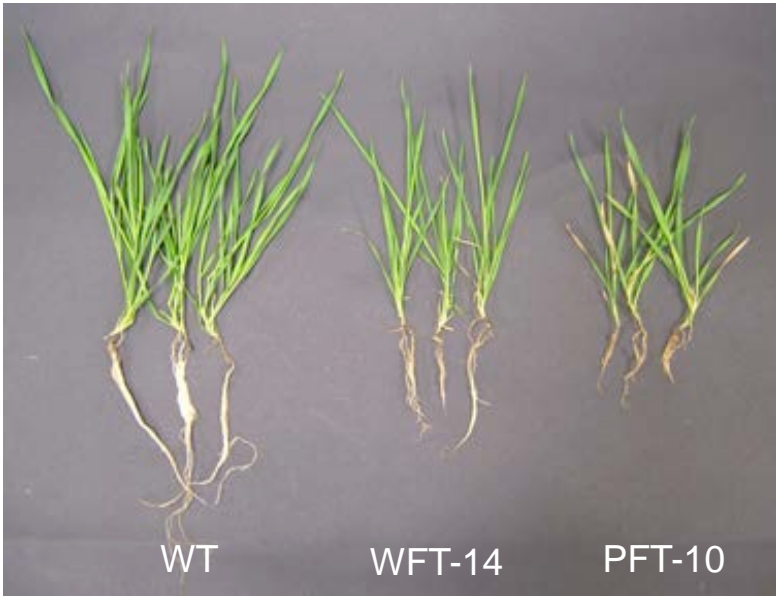
7 WFT1-20 (b) and plants from a transgenic line expressing *PpFTI*, PFT1-31 (c) were

8 analyzed. Abbreviations for each sugar peak are: G, glucose; F, fructose; S, sucrose; O,

9 oligosaccharide; P, polysaccharide. The leftmost peak in each chromatogram does not

10 show any sugars

a



b

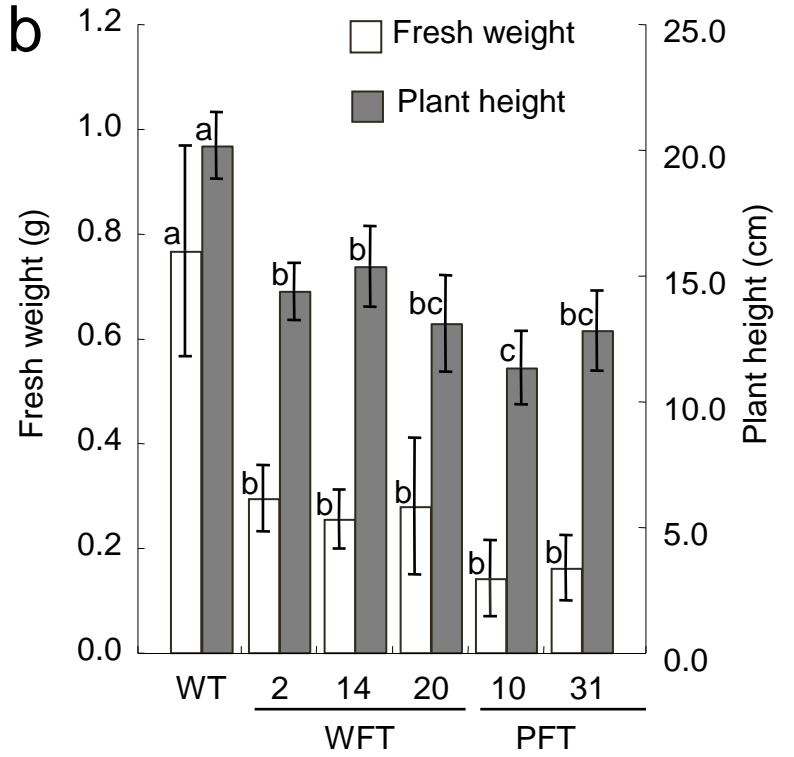


Fig.1

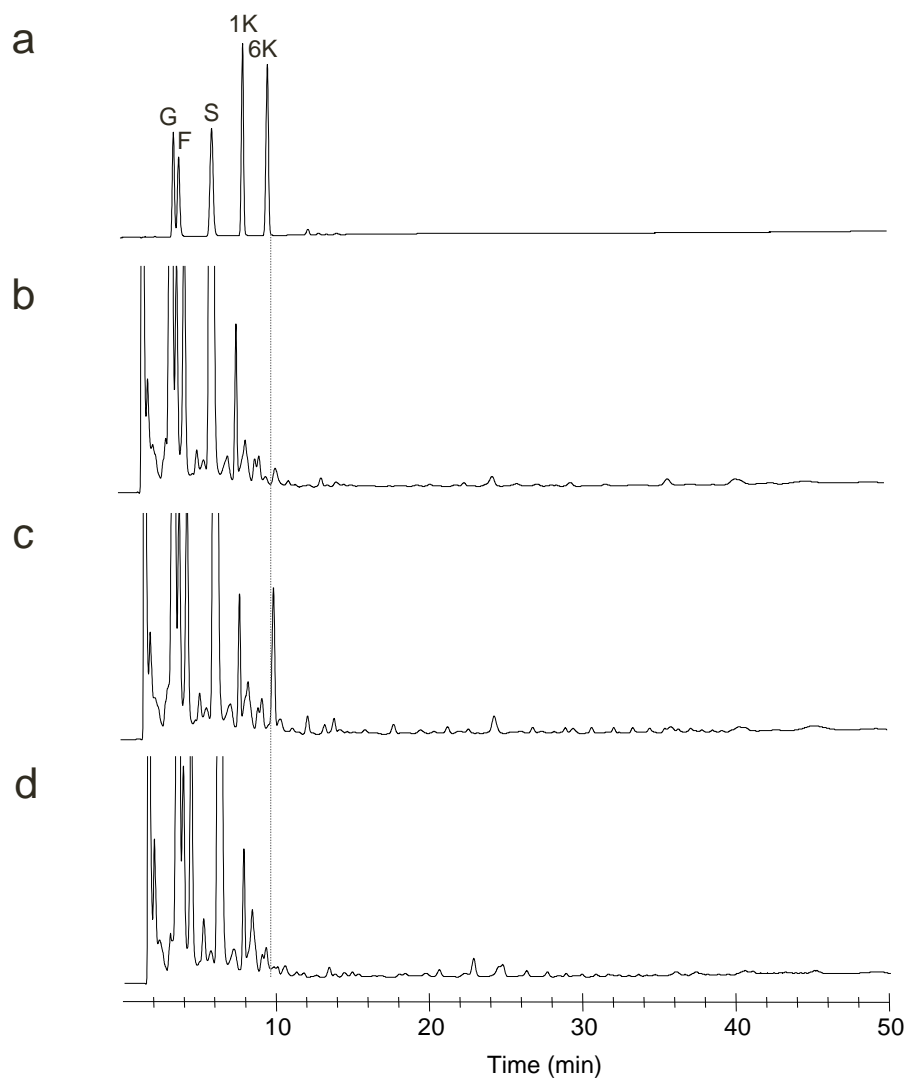


Fig. 2

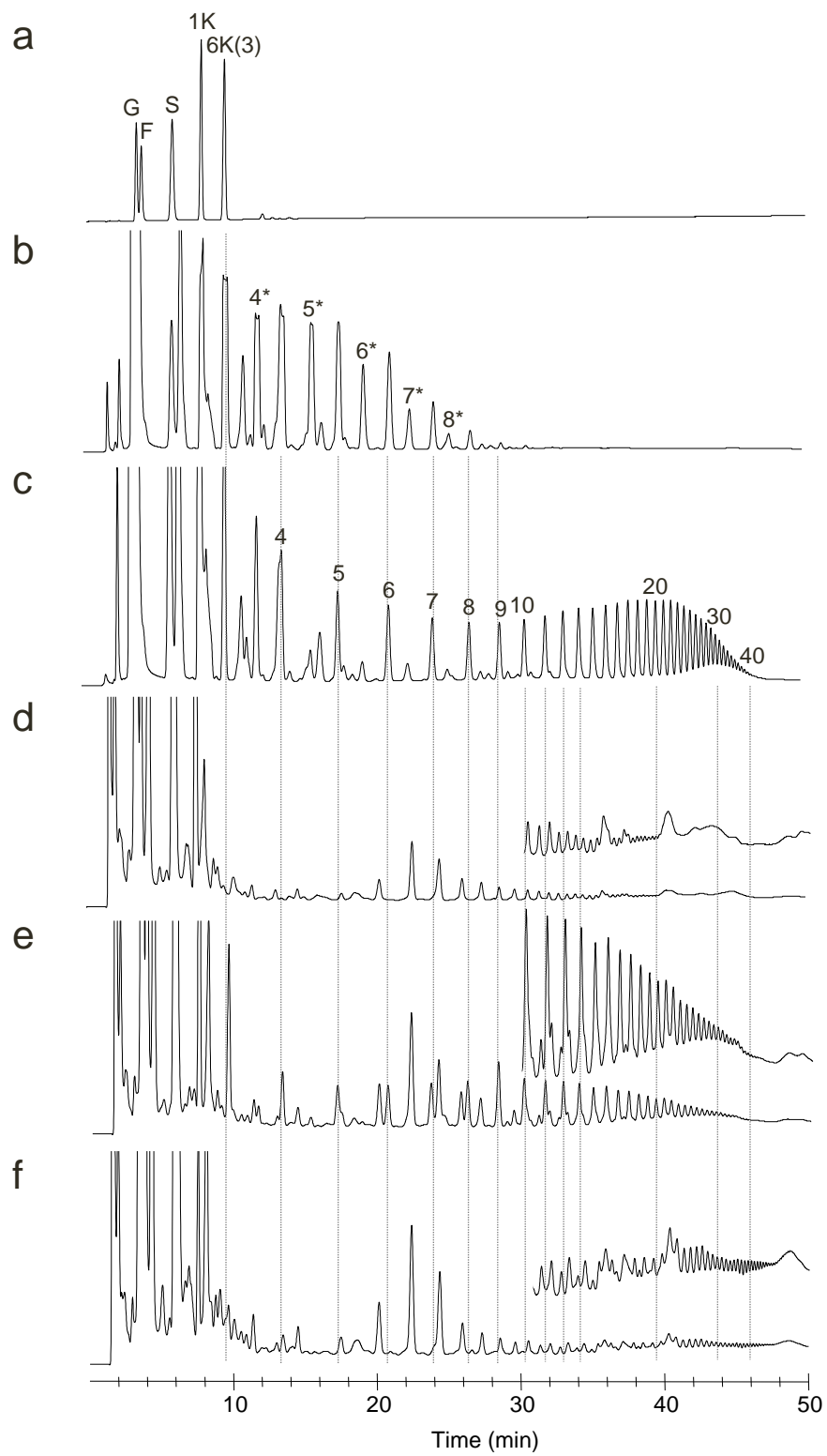


Fig. 3

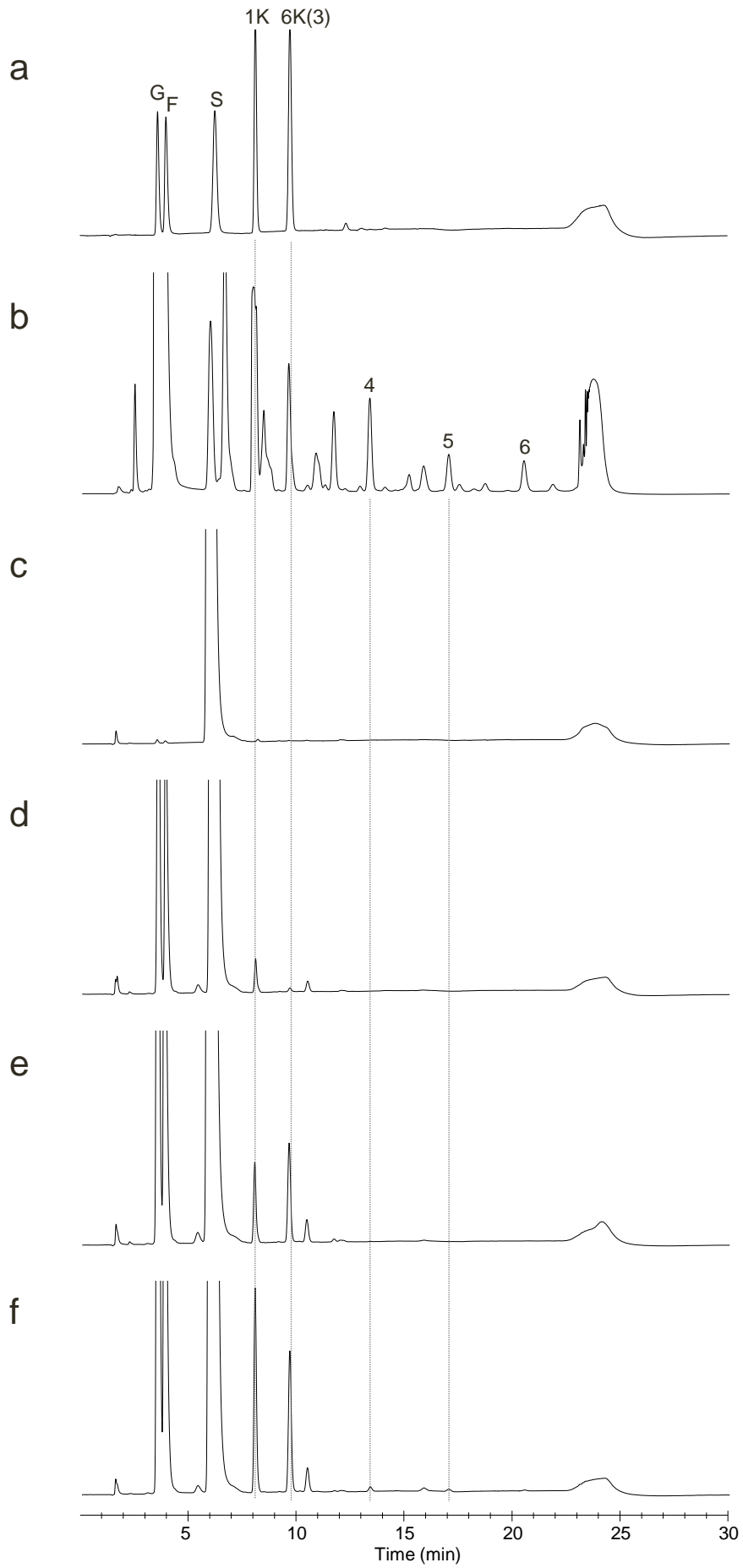


Fig. 4

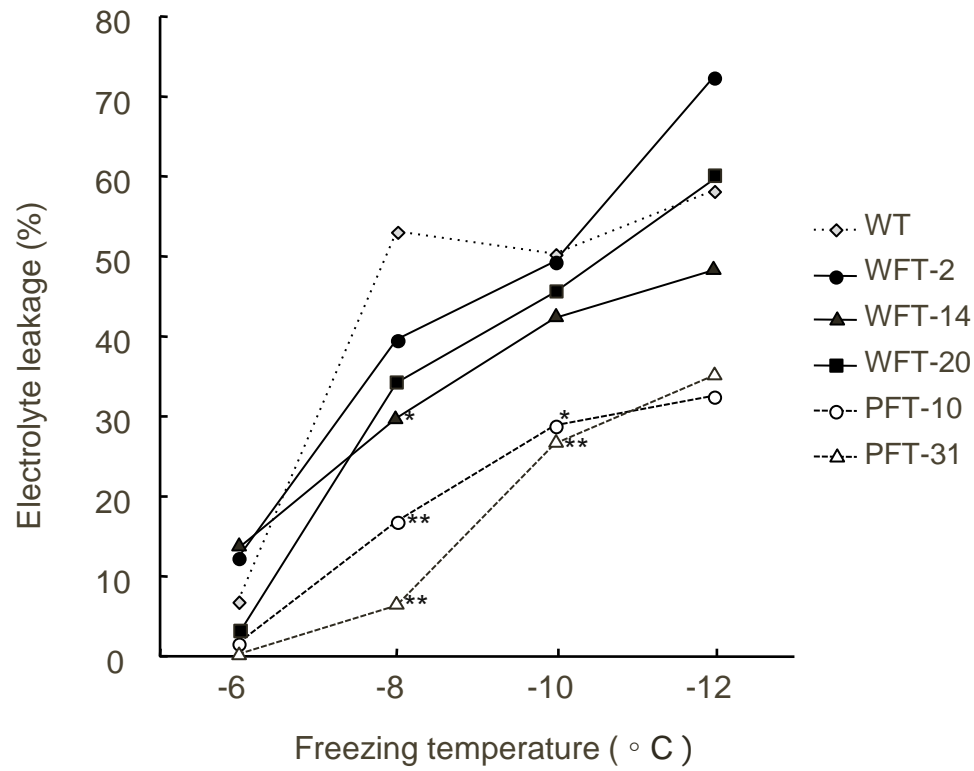


Fig. 5

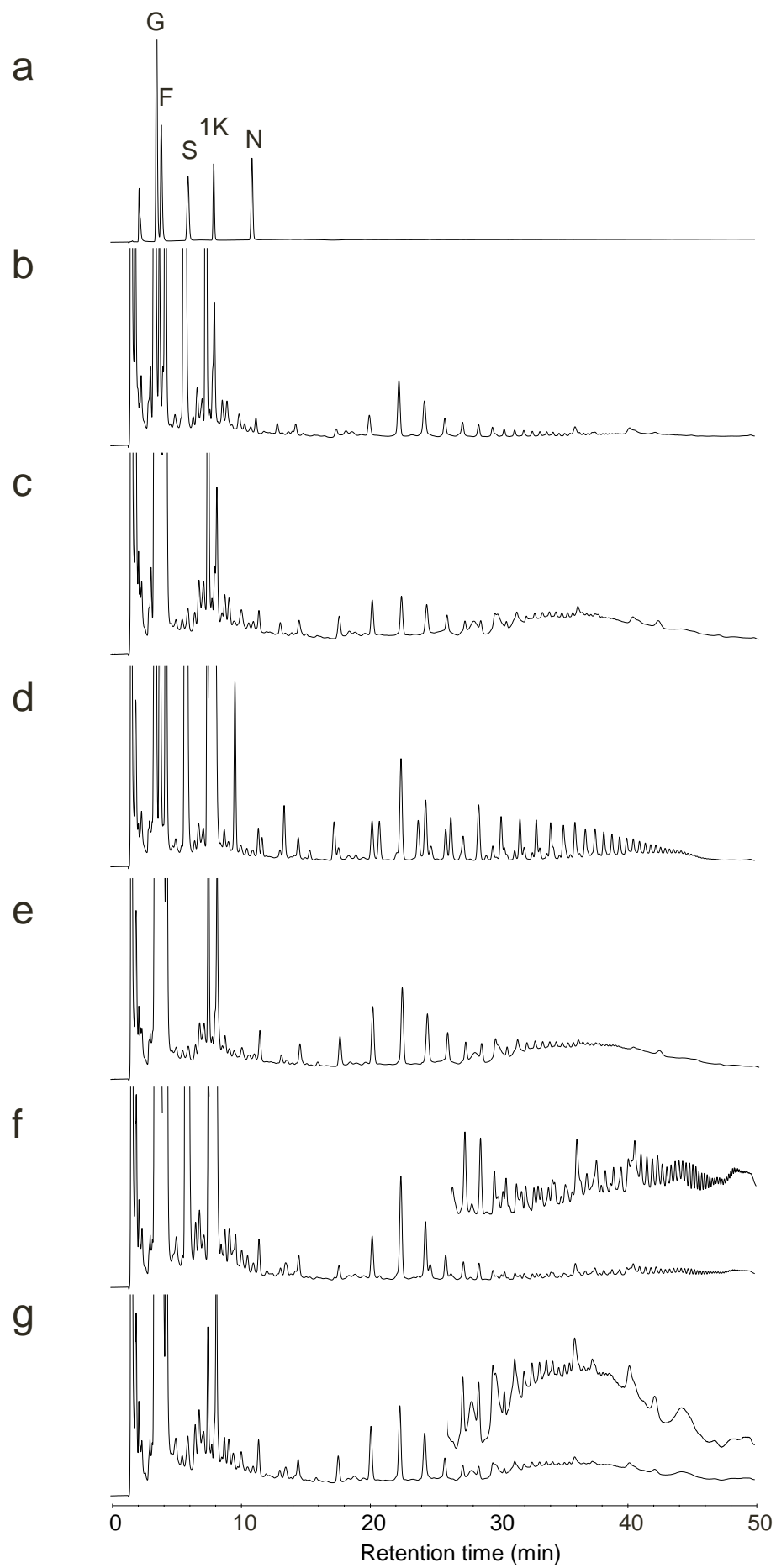


Fig. S1

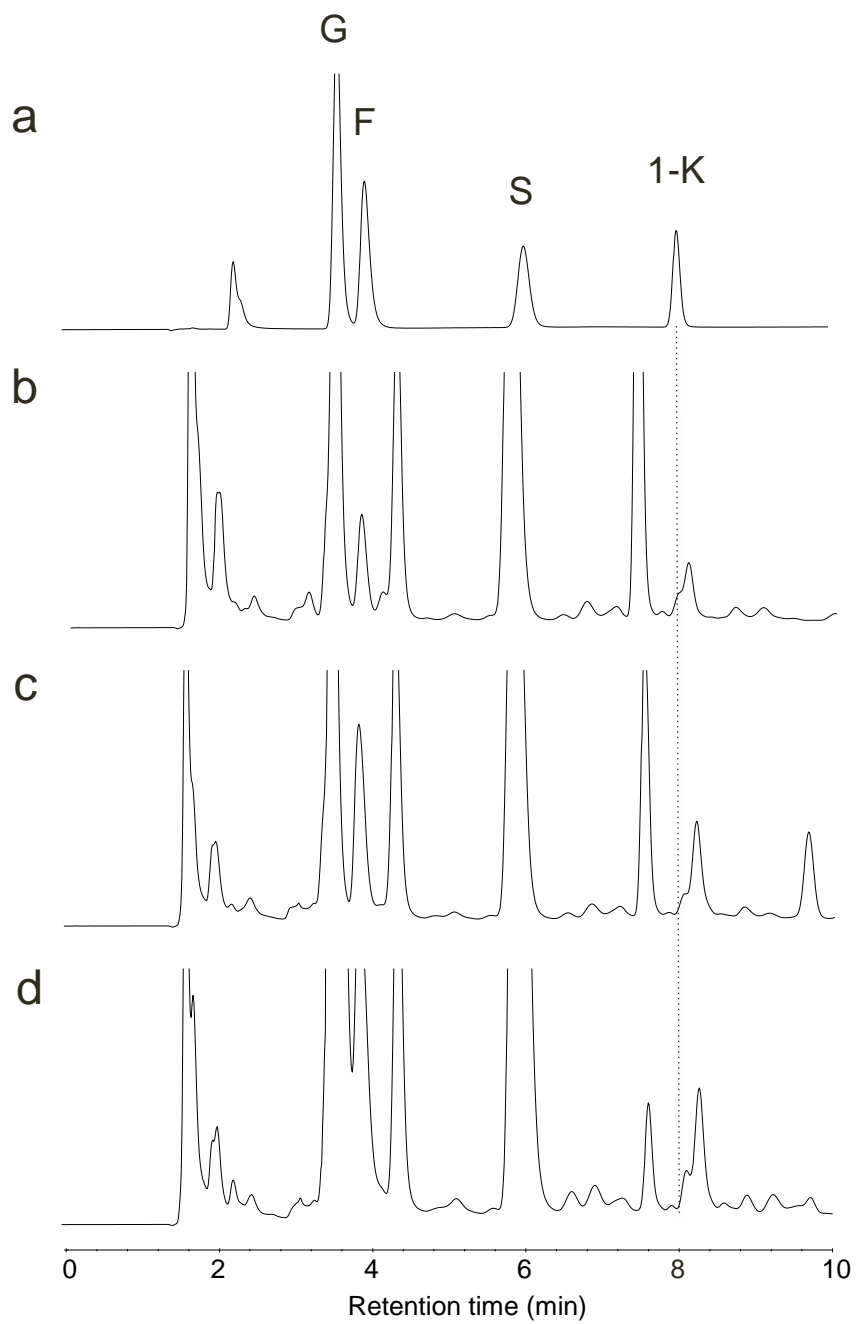


Fig. S2

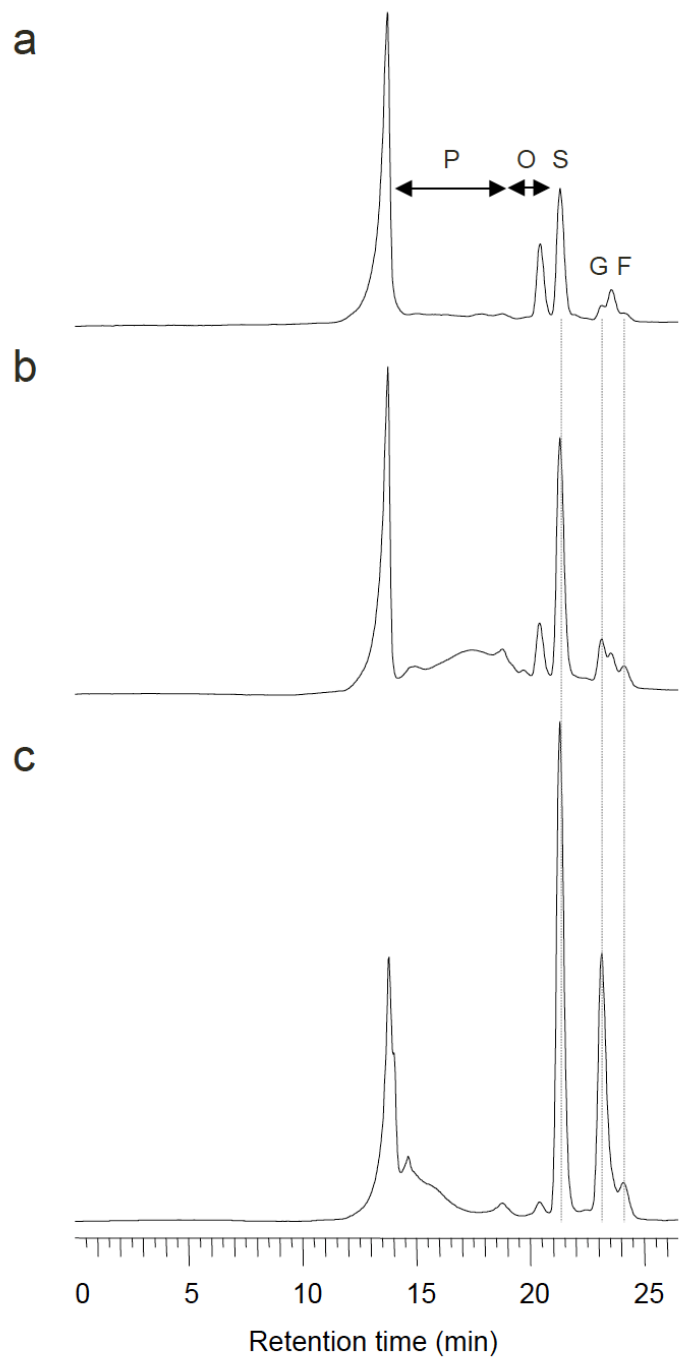


Fig. S3

1 **Table 1** Sugar contents (mg g⁻¹ fresh weight) of transgenic and wild type plants under
 2 normal temperature conditions

Line	Fructose	Glucose	Sucrose	Oligosaccharide	Total water-soluble carbohydrate
PFT-10	0.7 (±0.3) a	1.2 (±0.5) a	8.5 (±1.7) a	0.4 (±0.1) a	13.5 (±4.5) a
PFT-31	0.7 (±0.2) a	1.2 (±0.3) a	8.7 (±1.1) ab	0.4 (±0.1) ab	14.5 (±2.2) a
WFT-2	0.8 (±0.1) a	1.3 (±0.1) a	10.0 (±1.1) ab	0.8 (±0.1) c	14.9 (±1.7) a
WFT-14	0.8 (±0.1) a	1.3 (±0.1) a	11.0 (±1.0) b	0.8 (±0.1) c	14.8 (±1.5) a
WFT-20	0.7 (±0.1) a	1.0 (±0.2) a	10.4 (±1.5) ab	0.6 (±0.1) b	14.1 (±1.7) a
WT	0.9 (±0.1) a	1.2 (±0.1) a	10.2 (±0.9) ab	0.5 (±0.1) ab	13.5 (±2.6) a
PFT average	0.7 (±0.2) a	1.2 (±0.4) a	8.6 (±1.4) a	0.4 (±0.1) a	14.0 (±3.4) a
WFT average	0.8 (±0.1) a	1.2 (±0.2) a	10.5 (±1.2) b	0.7 (±0.1) b	14.6 (±1.6) a
WT	0.9 (±0.1) a	1.2 (±0.1) a	10.2 (±0.9) ab	0.5 (±0.1) a	13.5 (±2.6) a

3 Fructans were included in the oligosaccharide category. WT, wild type; WFT,
 4 transgenic lines expressing *wft1*; PFT, transgenic lines expressing *PpFT1*. The results
 5 for each line ($n = 5$ plants) and for the combined data of each transgenic type (WFT, n
 6 = 15; PFT, $n = 10$) are given as means ± SD. Means with the same *small letter* do not
 7 differ at $P < 0.05$ by Tukey's HSD test

1 **Table 2** Sugar contents (mg g⁻¹ fresh weight) of transgenic and wild type plants under
 2 cold acclimation conditions

Line	Fructose	Glucose	Sucrose	Oligo- and polysaccharide	Total water-soluble carbohydrate
PFT-10	3.2 (±1.3) ab	28.5 (±16.8) a	28.2 (±6.5) a	28.8 (±12.4) a	88.8 (±26.4) a
PFT-31	4.5 (±2.1) a	18.1 (±3.0) a	35.2 (±5.4) a	34.8 (±13.8) a	92.6 (±19.7) a
WFT-2	0.5 (±0.4) c	1.4 (±0.4) b	11.1 (±3.6) b	19.0 (±10.1) ab	32.1 (±13.6) b
WFT-14	2.2 (±1.5) abc	2.6 (±1.8) b	16.6 (±4.6) b	23.1 (±12.7) a	50.0 (±22.9) b
WFT-20	1.8 (±0.5) bc	2.7 (±1.4) b	14.8 (±4.0) b	30.6 (±7.4) a	49.8 (±12.7) b
WT	1.2 (±0.8) bc	2.0 (±0.6) b	10.1 (±0.8) b	4.3 (±0.5) b	17.5 (±1.4) b
PFT average	3.9 (±1.8) a	23.3 (±12.6) a	31.7 (±6.7) a	31.8 (±12.8) a	90.7 (±22.1) a
WFT average	1.6 (±1.1) b	2.3 (±1.4) b	14.4 (±4.4) b	26.6 (±12.4) a	44.8 (±18.0) b
WT	1.2 (±0.8) b	2.0 (±0.6) b	10.1 (±0.8) b	4.3 (±0.5) b	17.5 (±1.4) c

3 Fructans were included in the oligo- and polysaccharide category. WT, wild type; WFT,
 4 transgenic lines expressing *wft1*; PFT, transgenic lines expressing *PpFT1*. The results
 5 for each transgenic line (n = 5 plants) and for the combined data of each transgenic
 6 type (WFT, n = 15; PFT, n = 10) are given as means ± SD. Means with the same *small*
 7 *letter* do not differ at $P < 0.05$ by Tukey's HSD test