

Copyright is owned by the Author of the thesis. Permission is given for a copy to be downloaded by an individual for the purpose of research and private study only. The thesis may not be reproduced elsewhere without the permission of the Author.

**Fructan biosynthesis**  
**in *Lolium perenne***

**Tissue, cultivar and temperature effects  
on gene expression and protein accumulation profiles**

A thesis presented in  
partial fulfilment of the requirements  
for the degree of  
Master of Science in Plant Biology  
at  
Massey University  
Palmerston North  
New Zealand

**Hong Xue**

**2008**

## ACKNOWLEDGEMENTS

I wish to express my gratitude to my supervisors Dr. Susanne Rasmussen (Grasslands, AgResearch Ltd., New Zealand) and Professor Michael McManus (Institute of Molecular BioSciences, Massey University), for their excellent supervision, constant encouragement, moral support, and critical discussion throughout all stages of my study. Without their persistent support, it would have been impossible for me to complete this work.

Throughout this study, I have received lots of help and kindness from many other people. I would like to express my special thanks to: Professor Jonathan A. Newman (University of Guelph, Canada) for his help with the statistical analysis; to Dr Anthony J. Parsons (Grasslands, AgResearch Ltd., New Zealand) for his consistent encouragement and advice; to Chunhong Chen (Grasslands, AgResearch Ltd., New Zealand) for his technical advice.

I would also like to thank all the staff of the Forage Biotechnology Section, Grasslands, AgResearch Ltd., New Zealand and the academic and administrative staff of the Institute of Molecular BioSciences, Massey University, who have helped me on various occasions.

Finally, my immense gratitude to my family members, most importantly to my parents, husband (Qianhe Liu) and son (Lisheng Liu) for their love and excellent support throughout.

## ABSTRACT

Cultivars of *Lolium perenne* with high concentrations of water soluble carbohydrates (WSCs) offer opportunities to mitigate greenhouse gas emissions (nitrous oxides) from grazed pastures and improve meat and milk production in livestock. Our previous studies demonstrated that fructan accumulation in the blades of high WSC grasses involves a strong gene x environment interaction. To identify the temperature effects on the expression of high sugar trait in the high sugar cultivars, we conducted a pot trial in climate chambers with temperature regimes set at 10/10, 20/10 and 20/20°C (day/night), respectively. Water soluble carbohydrate concentrations, the expression of the key genes and proteins: 1-SST (sucrose: sucrose 1-fructosyltransferase), 1-FFT (fructan: fructan 1-fructosyltransferase), 6G-FFT (fructan: fructan 6G-fructosyltransferase) and 1-FEH (1-fructan exohydrolases) involved in the fructan biosynthetic pathway of *L. perenne* were compared in blades and sheaths of three selected high sugar cultivars (P, A and H) and a common cultivar (F) grown under the three temperature regimes. We found that amongst the selected 3 high sugar cultivars, high molecular weight (HMW) WSC content was significantly higher in P and A cultivars, regardless of the temperature regimes. As expected, sheaths contained significantly higher concentrations of HMW WSCs (fructans) compared to leaf blades. The highest WSC contents in both leaf and sheath tissues accumulated at 10/10°C while the lowest accumulated at 20/20°C. Gene expression profiles demonstrated that all four genes studied were more significantly expressed in sheaths compared to blades, and the expression levels were highly correlated with fructan accumulation in this tissue. Low temperature resulted in significant up-regulation of 1-SST in sheaths, but not in blades. 1-FFT was highly expressed in blades of A and P cultivars. Unexpectedly, 6G-FFT was expressed more significantly in the control F cultivar, but not in the high sugar cultivar P. Protein expression profiles showed that 1-SST protein accumulated to high levels in sheaths, whereas protein levels of 1-FFT and 1-FEH were higher in blades. 1-SST protein levels in both blades and sheaths generally increased in plants grown at low temperatures, whereas 1-FFT protein was not affected by low temperatures in blades and sheaths, furthermore, in both tissues there was no consistent effect observed between the different cultivars and temperature regimes on 1-FEH protein levels.

## ABBREVIATIONS

<b>1-FEH:</b>	1-fructan exohydrolases
<b>1-FFT:</b>	Fructan: fructan 1-fructosyltransferase
<b>1-SST:</b>	Sucrose: sucrose 1-fructosyltransferase
<b>6G-FFT:</b>	Fructan: fructan 6G-fructosyltransferase
<b>6-SFT:</b>	Sucrose: fructan 6-fructosyltransferase
<b>AP:</b>	Ammonium persulfate
<b>bp:</b>	Base pair
<b>cDNA:</b>	Complementary deoxyribonucleic acid
<b>C<sub>T</sub>:</b>	Threshold cycle
<b>C-terminus:</b>	Carboxyl-terminus
<b>DEPC:</b>	Diethylpyrocarbonate
<b>DM:</b>	Dry mass
<b>DNA:</b>	Deoxyribonucleic acid
<b>DNase:</b>	Deoxyribonuclease
<b>dNTPs:</b>	Dinucleotide triphosphates
<b>DP:</b>	Degree of polymerisation
<b>EDTA:</b>	Ethylenediaminetetraacetic acid
<b>FEHs:</b>	Fructan exohydrolases
<b>g:</b>	Relative centrifuge force
<b>h:</b>	Hour(s)
<b>His:</b>	Histidine
<b>HMW:</b>	High molecular weight fructans
<b>HSD:</b>	Honestly Significant Different test
<b>HSG:</b>	High sugar grass
<b>IPTG:</b>	Isopropyl- $\beta$ -D-thiogalactopyranoside
<b>kDa:</b>	Kilodaltons
<b>LB:</b>	Luria-Bertani
<b>LMW:</b>	Low molecular weight
<b>mA:</b>	Milli ampere
<b>min:</b>	Minute(s)
<b>NCBI:</b>	National Center for Biotechnology Information

<b>Ni-NTA:</b>	Nickel-nitrilotriacetic acid
<b>PBS:</b>	NaH <sub>2</sub> PO <sub>4</sub> - NaCl buffer
<b>PCR:</b>	Polymerase chain reaction
<b>PMSF:</b>	Phenyl methyl sulfonyl fluoride
<b>PVDF:</b>	Polyvinylidene difluoride
<b>qPCR:</b>	Quantitative polymerase chain reaction
<b>RNA:</b>	Ribonucleic acid
<b>RNase:</b>	Ribonuclease
<b>rpm:</b>	Revolutions per minute
<b>rRNA:</b>	Ribosomal RNA
<b>RT-PCR:</b>	Reverse transcription polymerase chain reaction
<b>Rubisco:</b>	Ribulose 1,5-bisphosphate carboxylase
<b>SDS:</b>	Sodium dodecyl sulfate
<b>SDS- PAGE:</b>	Sodium Dodecyl Sulfate-Polyacrylamide Gel Electrophoresis
<b>sec:</b>	Second(s)
<b>TAE:</b>	Tris-acetate-EDTA buffer
<b>Taq:</b>	<i>Thermus aquaticus</i>
<b>TBST:</b>	Tris-HCl-NaCl-Tween 20 buffer
<b>TEMED:</b>	N,N,N',N'-tetramethylethylenediamine
<b>Tris:</b>	Trishydroxymethylaminomethane
<b>UV:</b>	Ultraviolet light
<b>V:</b>	Voltage
<b>WSCs:</b>	Water soluble carbohydrates
<b>X-gal:</b>	5-bromo-4-chloro-3-indolyl- $\beta$ -D-galactopyranoside

# TABLE OF CONTENTS

ACKNOWLEDGEMENTS.....	i
ABSTRACT .....	ii
ABBREVIATIONS.....	iii
TABLE OF CONTENTS.....	v
LIST OF FIGURES.....	viii
LIST OF TABLES.....	x

## CHAPTER ONE: Fructan biosynthesis in *Lolium perenne*

### - A Literature Review

1.1. Practical importance of high sugar grass cultivars in agriculture.....	2
1.2. Physiology of fructan biosynthesis in plants.....	3
1.3. Biosynthetic pathway of fructans in plants.....	5
1.4. Fructan metabolism in <i>Lolium perenne</i> .....	11
1.4.1. Fructan accumulation in <i>Lolium spp</i> .....	11
1.4.2. Fructan distribution in <i>L. perenne</i> .....	12
1.4.3. Fructan metabolism-related genes and enzymes in <i>L. perenne</i> .....	14
1.5. Summary and research objectives.....	19

## CHAPTER TWO: Materials and Methods

2.1. Plant materials.....	21
2.2. Analysis of water soluble carbohydrates (WSC).....	22
2.3. General DNA, RNA and protein methods.....	23
2.3.1. Polymerase Chain Reaction (PCR).....	23
2.3.2. TA cloning.....	23
2.3.3. Plasmid DNA isolation.....	24
2.3.4. Restriction Enzyme Digestion.....	25
2.3.5. Agarose gel electrophoresis.....	25
2.3.6. Purification of DNA fragments from agarose gels.....	25

2.3.7. <i>Ligation of DNA fragments</i> .....	26
2.3.8. <i>Plasmid DNA isolation using the Qiagen Miniprep Kit</i> .....	26
2.3.9. <i>DNA Sequencing</i> .....	26
2.3.10. <i>Sodium Dodecyl Sulfate Polyacrylamide Gel Electrophoresis</i> <i>(SDS- PAGE)</i> .....	27
2.3.11. <i>Coomassie Blue staining</i> .....	28
2.3.12. <i>Western blotting</i> .....	28
<b>2.4. Gene expression profiling</b> .....	29
2.4.1. <i>cDNA synthesis</i> .....	29
2.4.1.1. Isolation of total RNA with TRIzol Reagent.....	29
2.4.1.2. Removal of genomic DNA from total RNA.....	30
2.4.1.3. Quantification of RNA.....	30
2.4.1.4. Reverse transcription of RNA into cDNA.....	31
2.4.2. <i>Primers designed for RT qPCR</i> .....	31
2.4.3. <i>Plasmid DNA standards for qPCR</i> .....	33
2.4.4. <i>qPCR analysis</i> .....	33
2.4.5. <i>Analysis of results</i> .....	34
<b>2.5. Antibody generation</b> .....	34
2.5.1. <i>Expression of recombinant proteins in a bacterial expression system</i> .....	34
2.5.1.1. Cloning <i>Lp1-SST</i> , <i>Lp1-FFT</i> and <i>Lp1-FEH</i> into pET 22b(+) (Novagen) vector.....	34
2.5.1.2. Induction of pET 22b(+) vector.....	36
2.5.1.3. Cell disruption and extraction of inclusion bodies.....	36
2.5.2. <i>Purification of recombinant proteins</i> .....	37
2.5.2.1. Purification of recombinant proteins using Ni-NTA affinity column.....	37
2.5.2.2. SDS-PAGE whole gel elution of Ni-NTA affinity column purified proteins.....	37
2.5.3. <i>Production of polyclonal anti-Lp1-SST, -Lp1-FFT and -Lp1-FEH antisera in rabbits</i> .....	38
2.5.4. <i>Determination of antibody quality</i> .....	38
<b>2.6. Plant protein expression profiling</b> .....	39
2.6.1. <i>Protein extraction</i> .....	39
2.6.2. <i>Protein separation and Western blotting</i> .....	39



2.7. Statistical analysis.....	40
--------------------------------	----

## **CHAPTER THREE: Experimental Results**

<b>3.1. Water soluble carbohydrate (WSC) concentrations.....</b>	<b>41</b>
3.1.1. <i>Cultivar effects</i> .....	41
3.1.2. <i>Tissue effects</i> .....	41
3.1.3. <i>Tissue by temperature interactions</i> .....	44
<b>3.2. Gene expression profiling .....</b>	<b>44</b>
3.2.1. <i>Methodological tests for RT- qPCR quantification</i> .....	44
3.2.1.1. RNA quality.....	44
3.2.1.2. Primer design and primer specificity.....	45
3.2.1.3. qPCR amplification efficiencies and linearity.....	48
3.2.2. <i>Gene expression profiling</i> .....	48
3.2.2.1. Tissue effects.....	48
3.2.2.2. Cultivar by tissue interactions.....	52
3.2.2.3. Tissue by temperature interactions.....	52
<b>3.3. Protein expression profiling.....</b>	<b>52</b>
3.3.1. <i>Antibody generation</i> .....	52
3.3.1.1. Expression of recombinant proteins.....	52
3.3.1.2. Purification of the recombinant proteins.....	54
3.3.2. <i>Determination of antibody quality</i> .....	58
3.3.3. <i>Analysis of 1-SST, 1-FFT and 1-FEH protein levels</i> .....	59

## **Chapter FOUR: Discussion and Conclusions**

<b>4.1. Tissue effects.....</b>	<b>64</b>
<b>4.2. Cultivar by tissue interactions.....</b>	<b>66</b>
<b>4.3. Temperature by tissue interactions.....</b>	<b>68</b>
<b>4.4. Conclusions.....</b>	<b>70</b>
<b>REFERENCE LIST.....</b>	<b>71</b>

## LIST OF FIGURES

<b>Figure 1.1</b> Molecular structures of the three trisaccharide precursors of plant fructans.....	6
<b>Figure 1.2</b> Model of the enzymology of fructan biosynthesis and breakdown in plants.....	7
<b>Figure 1.3</b> Hypothetical pathway of fructan synthesis in <i>L. perenne</i> and proposed activities of the enzymes implicated.....	16
<b>Figure 3.1</b> Main effect of cultivar on the concentration of (A) – HMW WSCs and (B) – LMW WSC.....	42
<b>Figure 3.2</b> Main effect of tissue on the concentration of (A) – HMW WSCs and (B) – LMW WSC.....	42
<b>Figure 3.3</b> Tissue by temperature interactions on the concentration of (A) – HMW WSCs and (B) – LMW WSC.....	43
<b>Figure 3.4</b> Agarose gel electrophoresis analysis of RNA integrity after DNase treatment and purification.....	45
<b>Figure 3.5</b> (a) Representative melting curve analysis of the qPCR amplicons generated from cDNA of blades and sheaths. (b) The amplicons were separated by electrophoresis on a 2.5% (w/v) agarose gel and visualized with ethidium bromide staining. (c) Amplification profile of the selected primers.....	47
<b>Figure 3.6</b> Main tissue effects on the expression of <i>Lp 1-SST</i> (A), <i>Lp1-FFT</i> (B), <i>Lp 6G-FFT</i> (C) and <i>Lp1-FEH</i> (D) gene expressions.....	49
<b>Figure 3.7</b> Interactions of cultivar and tissue on the expression of <i>Lp 1-SST</i> (A), <i>Lp1-FFT</i> (B), <i>Lp 6G-FFT</i> (C) and <i>Lp1-FEH</i> (D).....	50

<b>Figure 3.8</b> Temperature by tissue interactions on the expression of <i>Lp 1-SST</i> (A), <i>Lp1-FFT</i> (B), <i>Lp 6G-FFT</i> (C), and <i>Lp1-FEH</i> (D).....	51
<b>Figure 3.9</b> SDS–PAGE analysis of recombinant proteins of <i>L. perenne</i> 1-SST, 1-FFT, and 1-FEH proteins in <i>E. coli</i> .....	55
<b>Figure 3.10</b> SDS–PAGE analysis of purified recombinant proteins from <i>E.coli</i> .....	56
<b>Figure 3.11</b> Mass spectrometry analysis of recombinant 1-SST, 1-FFT and FEH proteins. Probability based Mowse score and the peptides detected by the peptide fragment mass fingerprint.....	57
<b>Figure 3.12</b> Determination titres of the three antibodies by detecting 100 ng antigen with different concentrations of antisera.....	58
<b>Figure 3.13</b> Sensitivity determination of the three antibodies with 1:10,00 diluted antisera to different amounts of antigens.....	59
<b>Figure 3.14</b> Western blot analysis of <i>Lp1-SST</i> , 1-FFT and 1-FEH using polyclonal antibodies.....	60
<b>Figure 3.15</b> WSC levels, gene transcript levels (qRT-PCR), and Western blot analysis of <i>Lp1-SST</i> , 1-FFT and 1-FEH proteins in blades.....	62
<b>Figure 3.16</b> WSC levels, gene transcript levels (qRT-PCR), and Western blot analysis of <i>Lp1-SST</i> , 1-FFT and 1-FEH proteins in sheaths.....	63

## LIST OF TABLES

<b>Table 2.1</b> Primer sequences used in this study.....	32
<b>Table 3.1</b> qPCR amplification efficiencies and linearity.....	48