

# Proteomics of Wheat Bran

(*Triticum aestivum* var. Babbler)

A thesis submitted in fulfilment of the requirements  
for the Honours Degree of Master of Science

By

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October 2006

## **Declaration**

The work presented in this thesis was carried out between March 2005 and October 2006 on a full-time basis. This work represents original research which has not been submitted for any other degree. All work was carried out by the author unless otherwise acknowledged.

Candidates Signature

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## **Acknowledgements**

I would like to thank Associate Professor Robert Willows for his guidance, help and support during the past few years. Thank you for this great opportunity and also the weekly squash games.

Thank you to Dr Ron Bradner, Dr Alison Kriegel and Artur Sawiki with whom I share the office, for the fun and help, and for having to listen to my procrastinating (I will eventually do all those things). A special thank you to Ron for your wealth of suggestions and for being so helpful in keeping me organised and on track (“Thanks Ron!”).

I would like to thank my parents for supporting me at home over the years during my career change and my sister and brother for their support also. Big thanks to all my friends for their encouragement and understanding.

I would also like to thank the following people who have helped me during this project: Debra Birch and Nicole Vella from microscopy, for their help and suggestions in getting wonderful pictures of bran tissue for my thesis. Matt Laver, Julie Soon, Thiri Winn, Narelle Jay, Alamgir Khan, Brett Cooke, Nasreen Yaghoutyfam, Rebecca Touma, Lewis Adler and Xiaomin Song from APAF who have been so friendly and helpful in every step of proteomic analysis. My co-supervisor Associate Professor Brian Atwell for his guidance and suggestions throughout this project. Tom Roberts for his editorial advice/proof reading at the last minute. Finally, I also acknowledge the contribution made by Robert Willows for constructing the wheat EST database.

Last but not least, I would like to thank the Grain Foods CRC for the financial support in offering me the scholarship to do this project. Also, I have thoroughly enjoyed the experience working as part of the Grain Foods CRC as it was challenging in that the project was commercially focused and I was able to present my work at annual research meetings.

## **Abstract**

Wheat is a major crop in Australia with around 25 million tonnes of grain harvested in an average year. Improved wheat grain cultivars and wheat grain milling can result in higher biological yields and flour quality. The introduction covers the general aspects of the wheat grain from bran development and structure through to milling and the importance of flour quality in flour-based products. It also highlights the problem with bran contamination in flour during milling and other factors that may have an effect on flour quality. Proteomics was used to identify proteins in three separate bran tissue fractions: the inner fraction (aleurone), intermediate fraction (nucellar tissue, testa, tube cells and cross cells) and the outer fraction (hypodermis and epidermis). The aim of the project was to identify proteins in bran tissue fractions which may potentially be useful in improvements in wheat quality for farmers and consumers and flour yield for millers. The results show that more than 80% of the identified proteins in the outer and intermediate tissue fractions are defence-and stress-related proteins (chitinase, xylanase, thaumatin-like protein, wheatwin 1, lipid-transfer protein, oxalatae oxidase (OXO), polyphenol oxidase (PPO), peroxidase (POX). Almost 60% of the proteins identified in the inner tissue fraction are 7S Globulin storage proteins and around 15% are protein synthesis-and energy-related. Water-soluble proteins were also identified and it was found that endochitinase, OXO, PPO and POX all leach out from the grain during imbibition. This study has added to the knowledge of bran tissue-specific proteins and has broad implications for improving crop yield and flour quality.

## Abbreviations

<b>1-DE</b>	One-dimensional gel electrophoresis
<b>2-DE</b>	Two-dimensional gel electrophoresis
<b>ABA</b>	Absciscic acid
<b>ABI</b>	Applied Biosystems International
<b>ACTH</b>	Adrenocorticotrophic hormone
<b>APS</b>	Ammonium persulphate
<b>AR</b>	Acquired resistance
<b>ATP</b>	Adenosine triphosphate
<b>AX</b>	Arabinoxylan
<b>BSA</b>	Bovine serum albumin
<b>BLAST</b>	Basic Local Alignment Tool (from NCBI)
<b>BTH</b>	Benzothiadiazole
<b>CHAPS</b>	3-[-1-propanesulfonate
<b>DPA</b>	Days post anthesis
<b>DTT</b>	1,4-Dithio-DL-threitol
<b>ESI</b>	Electrospray ionization
<b>EST</b>	Expressed sequence tag
<b>GA</b>	Gibberellic acid
<b>IAA</b>	Indole-3-acetic acid
<b>IDA</b>	Information dependent acquisition
<b>IEF</b>	Iso-electric focussing
<b>IPG</b>	Immobilised pH gradient
<b>kDa</b>	kilo Da
<b>LC</b>	Liquid chromatography
<b>LOX</b>	Lipoxygenase
<b>LTP</b>	Lipid transfer protein
<b>MALDI-TOF MS</b>	Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry
<b>MS</b>	Mass spectrometry
<b>MS/MS</b>	Tandem mass spectrometry

<b>MudPIT</b>	Multi dimensional protein identification technology
<b>NCBI</b>	National Center for Biotechnology Information
<b>OXO</b>	Oxalate oxidase
<b>PAGE</b>	Polyacrylamide gel electrophoresis
<b>PCD</b>	Programmed cell death
<b>PCT</b>	Patent Cooperation Treaty
<b>PDI</b>	Protein disulfide isomerase
<b>PHYLIP</b>	Phylogeny Inference Package
<b>PMF</b>	Peptide mass fingerprinting
<b>POX</b>	Peroxidase
<b>PPO</b>	Polyphenol oxidase
<b>PR</b>	Pathogenesis related
<b>SDS</b>	Sodium dodecyl sulfate
<b>TBP</b>	Tributyl phosphine
<b>TCA</b>	Trichloroacetic acid
<b>TEMED</b>	N,N,N',N'-Tetramethylethylenediamine
<b>TFA</b>	Trifluoroacetic acid
<b>TL</b>	Thaumatococcus
<b>TOF</b>	Time of flight
<b>VDAC</b>	Voltage dependant anion channel
<i>A. fatua</i>	<i>Avena fatua</i>
<i>A. oryzae</i>	<i>Aspergillus oryzae</i>
<i>H. vulgare</i>	<i>Hordeum vulgare</i>
<i>M. viride</i>	<i>Mesostigma viride</i>
<i>O. sativa</i>	<i>Oryza sativa</i>
<i>P. glaucum</i>	<i>Pennisetum glaucum</i>
<i>P. miliaceum</i>	<i>Panicum miliaceum</i>
<i>S. cereale</i>	<i>Secale cereale</i>
<i>T. aestivum</i>	<i>Triticum aestivum</i>
<i>X. oryzae</i>	<i>Xanthomonas oryzae</i>
<i>Z. mays</i>	<i>Zea mays</i>

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- Protein ID Tables (Excel format) with links to mass spectra
- Mass spectra link file