

# **Genetic mapping of noodle quality characters and rust resistance in hexaploid wheat**

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**Plant Breeding Institute, Cobbitty  
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## **Declaration**

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The text of this thesis contains no materials which has been accepted for the award of any other degree or diploma in any University and to the best of my knowledge, is original and contains no material previously published or written by another person, except where due reference is made.

**ABDUS SADEQUE**

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## **ABSTRACT**

Polyphenol oxidase (PPO) catalyses undesirable darkening in wheat products such as Asian noodles. Genetic variation for PPO activity is characterized in bread wheat. Australian wheat breeding programmes recognize that reduced PPO activity is an important quality target. Despite this interest from breeders, no varieties possessing extremely low and null PPO activity exist. The development of null PPO wheat varieties is dependant on an understanding of the genetic control of the null phenotype. Knowledge of these factors will accelerate efforts to develop them.

The inheritance of PPO activity was investigated in two populations that were derived from hybrids between a null PPO genotype and Australian wheat varieties Lang and QALBis. Observed genetic ratios were consistent with two and three gene control, respectively in these populations.

QTL mapping was performed in the QALBis x VAW08-A17 population. The Diversity Array Technology (DArT) approach was employed to genotype the QALBis x VAW08-A17 population. Three highly significant QTLs that control PPO activity were identified on chromosomes 2AL, 2BS and 2DL. Close associations between PPO activity and DArT marker loci wPt-7024, wPt-0094 and wPt-2544 were observed, respectively. Collectively, these loci explained 74% of the observed variation in PPO activity across seasons. Significant QTLs on chromosomes 1B and 3B were also identified that together explained an additional 17% of variation in PPO activity.

The relationship between PPO activity and yellow alkaline noodles (YAN) colour stability parameters was investigated in a DM5637\*B8 x H45 doubled

haploid population. PPO activity and changes in YAN brightness ( $\Delta L^*$  0-24h) and yellowness ( $\Delta b^*$  0-24h) in both seasons were analysed.

Quantitative trait analyses of PPO activity, flour yellowness ( $b^*$ ) and YAN colour stability was also conducted in this population. QTL mapping of variation in PPO activity in the DM5637\*B8 x H45 DH population identified a highly significant QTL on chromosome 2AL, which explained 52% of the observed variation across seasons. Regression analysis identified that wPt-7024 was highly significantly associated with PPO activity in this population. A highly significant association between this marker and PPO was also identified in the QALBis x VAW08-A17 population. Collectively, the three identified QTLs (on chromosomes 2AL, 7A and 7B) explained 71% of variation in PPO activity across seasons.

A highly significant ( $P < 0.001$ ) QTL on chromosome 2B along with significant ( $P < 0.01$ ) QTLs on the chromosomes 1A, 3B, 4B and 5B were found to control flour yellowness. The QTLs on 2B, 4B and 5B were detected in both seasons analysed and accounted for 90% of variation in flour  $b^*$  across seasons.

The study on YAN colour stability located two highly significant ( $P < 0.001$ ) QTLs and two significant ( $P < 0.01$ ) QTLs that controlled the change in brightness of yellow alkaline noodle. The 2A QTL accounted for 64% of observed variation across seasons. It was in the same location as the PPO QTL and shared a common closest marker wPt-7024. Only one significant QTL for YAN  $\Delta a^*$  (0-24h) was identified. It accounted for 12% of variation across seasons and was only detected in one season. One highly significant ( $P < 0.001$ ) QTL and two significant ( $P < 0.01$ ) QTLs were identified that controlled the change in yellowness of yellow alkaline noodle. The 2A QTL accounted for 68% of observed variation across seasons. The location of this QTL corresponded with that of 2A QTLs for PPO activity and  $\Delta L^*$  of YAN in this

study. Furthermore, wPt-7024 was also identified as the marker with the most significant association with  $\Delta L^*$ . The identification of a correlation between the characters and a common location of a highly significant QTL for each of these characters indicates that it is likely that PPO activity is directly responsible for a large proportion of the changes in brightness and yellowness of YAN.

QTLs for  $\Delta L^*$  and  $\Delta b^*$  of YAN were detected in a common location on chromosome 1A. However, no corresponding QTL was identified that controls PPO activity, highlighting the complexity of the relationship between these traits.

Resistance to three rust pathogens (*Puccinia graminis*, *Puccinia striiformis*, and *Puccinia triticina*) was also investigated in the DM5637\*B8 x H45 DH population because they are major yield limiting diseases in wheat. Disease response data at the seedling stage were converted to genotypic scores for rust genes *Sr24/Lr24*, *Sr36*, *Lr13* and *Yr7* to construct a genetic linkage map. No recombination was observed between rust resistance genes *Sr36*, *Lr13* and *Yr7* in this DH population. Therefore, these genes mapped in the same position on chromosome 2B. The *Lr24/Sr24* locus was incorporated into the chromosome 3D map. Interval mapping analysis identified QTLs on chromosomes 2B, 3B, 4B and 5B that control adult plant resistance (APR) to stripe rust. Two QTLs on chromosomes 2B and 3D were identified that controlled APR to leaf rust in this DH population.

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# ACRONYMS AND SYMBOLS

A	Absorbance in nm (nona metre)
a*	Lightness which is red-green scales
AACC	American association of cereal chemistry
AFLP	Amplified fragment length polymorphism
APR	Adult plant resistance
b*	Lightness which is yellow-blue scales
bp	Base pair
CIE	International Commission on Illumination
cm	Centimeter
cM	Centimorgan
CS	Chinese spring
CTAB	Cetyltrimethylammonium bromide
CV	Coefficient of variation
cv.	Cultivar
d f	Degrees of freedom
DArT	Diversity Array Technology
DH	Doubled Haploid
DMAB	3-dimethylamino benzoic acid
<i>dmh45</i>	DM5637*B8 x H45 (used for QTL nomenclature)
DNA	Deoxy ribonucleic acid
dNTPs	Dinucleotide triphosphates
EC	Enzyme Commission
EDTA	Ethylene diamine tetraacetic acid
EST	Expressed sequence tags
h	Hour(s)
Hb	Hemoglobin
IM	Interval mapping
IT	Infection type
L*	Lightness which is white-black scales

L-DOPA	L-Dihydroxyphenylalanine
LOD	Log 10 of the odds ratio
LOX	Lipoxygenase
Lr	Leaf rust
LRS	Likelihood static ratio
LSD <sub>0.05</sub>	Least significant difference at 5% level
M	Meter
M	Molar
MAS	Marker Assisted Selection
MBTH	3-methyl-2-benzothiazolinone
MgCl <sub>2</sub>	Magnesium chloride
min	Minute(s)
mM	Millimolar
NaAc	Sodium Acetate
nm	nona meter
NSW	New South Wales
P	Probability
PAGE	Polyacrylamide gel electrophoresis
PBIC	Plant Breeding Institute Cobbitty
PBIN	Plant Breeding Institute Narrabri
PCR	Polymerase chain reaction
pers. comm.	Personal communication
PIC	Polymorphic information content
POD	Peroxidase
Pgt	<i>Puccinia graminis</i> f.sp. <i>tritici</i>
Pmol	Picomolar
PPO	Polyphenol oxydase activity
<i>Pst</i>	<i>Puccinia striiformis</i> f.sp. <i>tritici</i>
<i>Pt</i>	<i>Puccinia triticina</i>
PVE	Phenotypic variation explained
<i>Q</i>	Quantitative trait loci (used for QTL nomenclature)
QLD	Queensland
<i>qp</i>	QALBis x VAW08-A17 (null PPO line) (used for QTL nomenclature)

QTL	Quantitative trait locus/loci
RAPD	Random Amplified Polymorphic DNA
RFLP	Restriction Fragment Length Polymorphism
SNP	Single nucleotide polymorphisms
SE	Standard Error
STDEV	Standard Deviation
spp.	Sub species
SSR	Simple sequence repeats
Sr	Stem rust
STMP	Sequence-tagged microsatellite profiling
STS	Sequence-tagged sites
TBE	Tris/ Borate/ EDTA
TE	Tris-EDTA
U	Unit
UV	Ultra Violet
VAWCRC	Value Added Wheat Co-operative Research Centre
YAN	Yellow alkaline noodles
Yr	Stripe rust
wPt	Wheat:Pst 1/Taq 1
WSN	White salted noodles
WSU	Washington State University
WWQL	Western Wheat Quality Laboratory
μl	Microlitre
$\chi^2$	Chi-squared
Δ	Delta