

# Genetic Impacts of the Hull on Barley Grain Quality

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## ABSTRACT

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Barley hull plays an important role in malt and feed quality and processing. In this study we measured the variation in hull content along with other grain quality traits namely, kernel discolouration and degree of pre-harvest sprouting, in a single mapping population. There were significant ( $p < 0.05$ ) genetic as well as environment effects. In addition, heritability was calculated for hull content to be 29% and 47% for two years' data. From the analysis, major QTL markers were identified in controlling the expression of hull content on chromosomes 2 (2H), and 6 (6H) with significant ( $P < 0.05$ ) LOD scores of 5.4 and 3.46 respectively. Minor QTLs were identified on 1 (7H), 4 (4H), 5 (1H) and 7 (5H). The region at marker *Bmac310* on 4(4H) could be associated with dormancy gene SD4. A number of the QTLs also coincided with regions for either kernel discolouration or preharvest sprouting resistance (dormancy). The results indicate that variation exists for hull content, which is influenced by both growing environment as well as genetically, although the genetic variance explained less than half of the total variance. Further, hull content also impacts on other grain quality attributes including dormancy, sprouting resistance and kernel appearance.

**Key words:** Barley, hull, husk, kernel discolouration, pre-harvest sprouting, QTL.

## INTRODUCTION

Barley (*Hordeum vulgare* L.) is one of only four commercial species of grass that retains a hull after harvest. Rice, oats and millet are the other "covered" grains. Thin hulled barley varieties exist but these can suffer from

"skinning" during harvest. Hullless barley varieties are also commercially available. The hull amounts to approximately 13% of grain weight, but can range between 7–25% depending upon type, growing environment and grain size<sup>15</sup>. Variation occurs between row type, with six-row having a larger proportion than two-row barley<sup>15</sup>. Additionally, winter barleys have a higher amount than spring barleys and the hull content increases in regions closer to the equator<sup>15</sup>.

The hull plays an important role before and after harvest. During the later stages of grain ripening, the hull has been considered to have a role in grain dormancy and therefore preharvest sprouting resistance<sup>3</sup>. During harvest, the hull acts to protect the germ during the abrasive threshing process in the harvester<sup>30</sup>. Post harvest, the hull plays a role in processing for the malting, brewing and feed industries. In terms of the malting industry, the hull aids during the malting process by protecting the germ from physical abrasion during handling and preventing the growing acrospire from being damaged during germination and kilning<sup>26</sup>. During brewing, the hull aids during filtration of the brewer's extract from the lautering process. Hullless barley can "gum" up filters, reducing filtration rate and thereby adding to the cost of production and potentially impacting on the quality of beer<sup>10,14</sup>. However, Edney and Langrell<sup>11</sup> recently demonstrated that good quality malt could be produced from hullless barley if the "appropriate malting conditions were used".

The intensive livestock industry also benefits from using a hulled barley grain. The hull aids in holding crushed or pressed grain together. A thinner hull is desirable, as thicker hulls will result in higher levels of deleterious compounds, in particular lignin, which have been shown to have a negative impact on feed performance in ruminants<sup>24</sup>.

Australian barley grain is often required to meet tight quality specifications for malt classification while the feed industry, although less demanding to terms of grain quality, will preferentially purchase grain that is known to be close to malting standards. For both industries, grain appearance and non-sprouted grain is critical. To meet these demands, grain sellers should be able to show that grain is free from fungal contamination. Fungal contamination is usually caused by pre-harvest rain, which could also result in preharvest sprouting. The level of impact of these defects can be influenced by the hull.

Breeding for resistance to kernel discolouration<sup>29</sup> and preharvest sprouting<sup>25</sup> has been possible. Hull content, kernel discolouration and pre-harvest sprouting have been shown to have genetic controls and growing environment

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controls<sup>22,32</sup>. A recent study highlighted the common genetic regions that were associated with either pre-harvest sprouting resistance and/or dormancy<sup>34</sup>. In addition, breeding programs targeting malt quality know that the benefit to be gained with thinner hulled varieties is a higher level of extract<sup>8</sup>. Further, work presented by Somers et al.<sup>33</sup> described the genetic variation associated with hull adherence and peeling resistance. A recent review highlighted the genetic interactions with dormancy, kernel appearance and quality attributes<sup>16</sup>.

At this stage no published work is available detailing either phenotypic or genetic associations for hull thickness and any linkage between kernel discolouration and pre-harvest sprouting. The objectives of this study were to establish phenotypic and genetic variation for hull content and explore any relationship hull content has to kernel discolouration and pre-harvest sprouting.

## MATERIALS AND METHODS

A set of 94 double haploid lines from a mapping population, Patty × Tallon, was assessed for quality traits, with grain samples harvested from field trials grown at a single site, Hermitage Queensland, over two years, 2002 and 2003. The 2002 trial was designed as a single replicate trial of 94 genotypes with interspersed check varieties, in a two-dimensional array of 11 columns by 12 rows. The 2003 trial was designed as a two replicate latinised row-column design of 94 genotypes and interspersed check varieties, in a two-dimensional matrix of 8 columns by 28 rows. Patty (Volla × Athos) was a French malting variety while Tallon (Triumph × Grimmett) was an Australian malting variety.

### Hull

Grain samples for each field plot were taken, split into duplicate samples, and processed in field order in the laboratory, with duplicates immediately following each other. The samples of grain were analysed for hull thickness, by a one fifth scale modification of the European Brewery Convention method 9.1<sup>12</sup>. Ten grams of barley was boiled in a solution of sodium hydroxide and sodium hypochlorite for 80 seconds to remove the hull. The samples were then washed in cold water. The boiled sample was kept at room temperature on blotting paper for 24 h then dried for 3 h at 50°C. The dried samples were then weighed and the difference in weight from initial and final weights was calculated. Duplicates for each sample were averaged for analysis.

### Grain colour

Kernel discolouration was measured using a Minolta Colour meter CR310. A grain sample was taken for each field plot and processed in field order. Samples were placed into a materials granule attachment with a light project tube attached to the meter. The light source was set at D65 which represents a “daylight” light source. The unit was calibrated on a white tile supplied with the instrument. Kernel discolouration was reported as colour components in the CIE (“L”, “a”, “b”) colour space with “L” representing lux or lightness, “a” representing the red to green colour space and “b” representing the blue to

yellow colour space. The scale for these measurements was 0 to 100 for “L” where 0 equals black and 100 equals pure white. Both the “a” and “b” values range in a scale from –60 to +60, where for “a” red equals –60 and green equals +60, while for “b” blue equals –60 and yellow equals +60. The general range of these traits for “L”, “a” and “b” values was generally 55–65, 19–23, 4–6, respectively. The only value usually considered for grain appearance was L with acceptable being ≥ 58.0.

### Pre-harvest sprouting

Preharvest sprouting was measured using the Falling Number method<sup>2</sup>. In this method a sample of grain (approximately 50 g) is ground in a hammer mill through a 0.8 mm sieve. Oven moisture was determined from this sample<sup>10</sup>. This moisture value was then used to weigh, in duplicate, an equivalent amount of flour as described by the method<sup>2</sup>. Weighed samples were mixed with 25 mL of water at room temperature. After the sample and water was mixed, plungers were inserted into the tubes and the tubes were placed in the boiling water bath of the Falling Number instrument. The sample was mixed by the instrument with the plungers moving up and down through the sample, for 55 seconds after an initial five second rest. The plungers were released from the top position and the time for them to reach the base position was recorded in seconds. Results were displayed by the instrument and manually recorded.

### Grain size

Grain size was measured so any variation in hull content could be partitioned and included in the statistical analysis. Field samples were screened through a Sortimat (Germany) for 1 minute. Grain samples were separated into four size fractions, those being <2.2 mm, 2.2–2.5 mm, 2.5–2.8 mm and >2.8 mm. In routine selection for grain size, the screenings (<2.2 mm) and retention (>2.5 mm) and plump grain (>2.8 mm) data were used<sup>16</sup>. In this study, the screenings, plump grain and retention fractions were studied in detail.

### Marker analysis

The molecular map for this population was developed using Amplified Fragment Length Polymorphisms (AFLP) and microsatellite (SSR) markers<sup>6</sup>. Marker identification was carried out using Mapmaker as described in Cakir et al.<sup>6</sup> using the raw phenotypic data. A second marker analysis was conducted using phenotypic data adjusted for field and grain size variance (see below). The adjusted data (best linear unbiased predictors, (BLUPs)) were analysed using a two stage model which includes adjustment for field traits and other traits, such as maturity, proteins or grain size effects, as covariates<sup>9</sup>. In both analyses, a Likelihood of Odds (LOD) score of ≥3.0 was considered significant.

### Statistical analysis

The model for the two years of hull data is a linear mixed model of the form

$$y = X\tau + Z_0u_0 + Z_gu_g + Z_{ge}u_{ge} + Z_1u_1 + b$$

where

$y$  denotes the data vector of hull measurements  
 $\tau$  is the  $p \times 1$  vector of fixed year effects,  
 $u_g$  is the  $m \times 1$  vector of random genotype effects for  $m$  genotypes,  
 $u_{ge}$  is the  $mp \times 1$  vector of random genotype by year effects for  $m$  genotypes and  $p$  years  
 $u_0$  is a vector of additional random effects, e.g. extraneous spatial effects in the field  
 $u_1$  is a vector of field plot effects, and  
 $X, Z_0, Z_g$  and  $Z_1$  are the corresponding design matrices,  
 $e$  is a vector of sample variance for each laboratory run.

The usual assumptions are made for the linear mixed model.

For the traits of grain colour and Falling Number, only single samples were analysed. Error variance from the laboratory was then confounded with field plot variance. In the linear mixed model, the vector of field plot effects,  $u_1$ , is omitted, and the residual vector,  $e$ , is the vector of residual field plot effects.

As data was collected across years, it was of interest to model genetic variance and covariance between years for each trait. A simple model for genotype by year interaction was achieved by the fitting of genotype main effects, and genotype by year interactions, with a separate interaction variance for each year. This model accommodates a separate genetic variance for each year together with a covariance between the two years.

Intertrait correlations were calculated for the 2003 data set, for hull, colour L, colour b and Falling Number. A bivariate model was fitted to pairs of traits in the linear mixed model framework, and contained terms for all effects specified in the previous model.

All models were fitted using Spatial Analysis Mixed Models (SAMM)<sup>5</sup>, a suite of SPlus functions implementing the average information algorithm of Gilmour et al.<sup>20</sup>. In this software, the variance parameters are estimated using the residual maximum likelihood (REML) procedure of Patterson and Thompson<sup>31</sup>. BLUPs were obtained for the random effects and generalised least squares estimates were given for the fixed effects.

## RESULTS

### Hull content

Patty had the thicker hull for both years with the difference being significant ( $p < 0.05$ ) only in 2002. The Patty/Tallon population averaged 12.05% and 12.11% hull content for 2002 and 2003, respectively. The maximum (13.60% and 13.58%) and minimum (10.62% and 11.12%) values for the two years respectively, for the population were outside the values for the parents for both years (Patty 12.94% and 12.30% and Tallon 11.78% and 11.99% for 2002 and 2003 respectively), suggesting transgressive segregation (Fig. 1). The variation between genotypes was significant ( $p < 0.001$ ) within both years, as well as between years. The difference in two years could

be explained partially by the variation in grain size. The 2002 season suffered a severe drought with a high level of screenings (Patty 9.2%, Tallon 9.4%) and low level of retention (Patty 44.2%, Tallon 45.7%). While the 2003 season produced much larger grain size with average screenings of 3.5% and retention of 77.3%. The results for Patty for screenings and retention were 2.3% and 76.3% respectively. While for Tallon, the results were 2.2% and 78.1% respectively for screenings and retention.

The heritability values for the hull content were 29% and 47% for 2002 and 2003 respectively, suggesting a low level genetic variance ( $p < 0.05$ ), especially in 2002. These values were similar to those reported for hull peeling by Aidun et al.<sup>1</sup>, although hull thickness is not the same morphological attribute as hull peeling.

### Discolouration

Kernel discolouration has been measured visually in other studies, which could introduce inconsistent results due to the variability between individual's interpretation of colour. In this study, kernel discolouration was measured only in 2003 when rain occurred pre-harvest. Kernel discolouration was measured objectively using a colour meter. The primary measure was Lux or lightness ("L"). Previously the malting industry has used a standard of greater than 58.0 L as the accepted "L" value. In this trial, Tallon and Patty had "L" values of 57.9 and 58.9 respec-

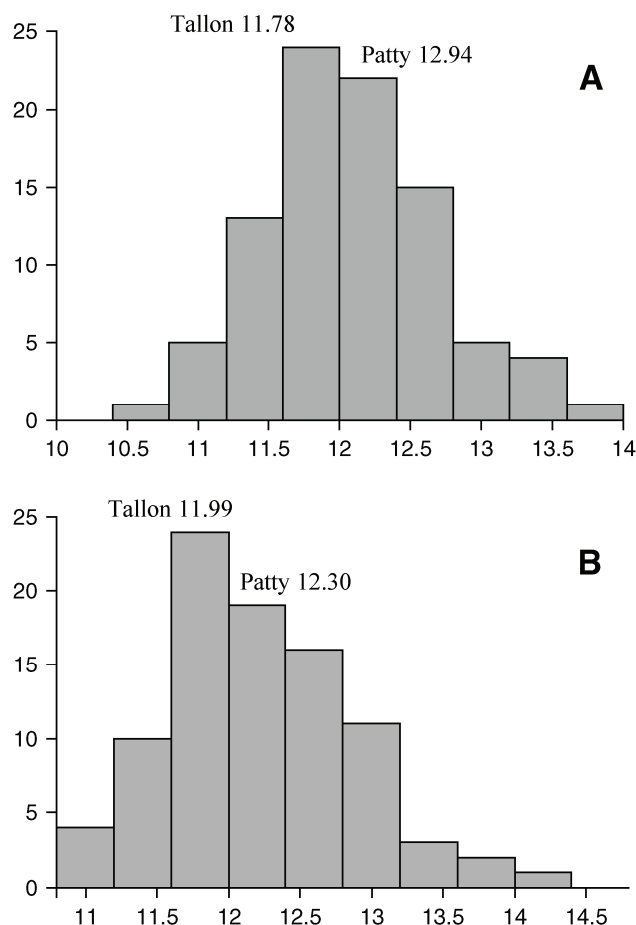


Fig. 1. Patty/Tallon population distribution for hull. (A) 2002 hull (B) 2003 hull.

tively. Results from this population showed an average “L” value of 58.3, with the population range 55.2 to 60.4 “L” indicating that there were lines with grain significantly ( $p < 0.05$ ) darker or lighter in appearance than the parents.

Other values contributing to the overall appearance are the chroma and the hue. The chroma is measured in the red to green colour space and expressed as “a” value. While the hue, measured as the yellow to blue colour space, was expressed as “b” value. The results from the two years data showed Tallon to be significantly ( $p < 0.05$ ) different to Patty for both “a” and “b” values, ie. Tallon was slightly redder (“a”) and more yellow (“b”) in appearance when measured by the colour meter.

Correlation coefficients between hull content and with “L”, “a” and “b” values were 0.123, 0.347 and 0.341, respectively (Table I). There was a low, non-significant ( $p > 0.05$ ) correlation (0.22) between hull and pre-harvest sprouting level. In addition, there was a very low correlation between the colour components and pre-harvest sprouting. Higher levels of correlation were observed between the grain colour components, in particular L and b values (Table II). While there was a low correlation between the colour components for the population used in this study, these values were similar to those reported by Li *et al.*<sup>25</sup>. Li *et al.*<sup>25</sup> presented data on the correlation between the three colour components across a number of populations. The level of hull had a positive correlation with screenings, and a negative relationship with retention in 2002 while the opposite relationship occurred in 2003 (Table II).

### Markers

The results from the marker analysis produced a number of microsatellite markers and AFLP markers closely linked to hull content, kernel discolouration and pre-harvest sprouting. QTLs were identified on five chromosomes, although only three had a LOD score  $> 3.00$ . The phenotyping for the 2002 hull analysis resulted in markers on chromosome 6 (6H) and 7 (5H). For 2003, the marker associations were limited to chromosome 4 (4H).

The hull data was also analysed after being adjusted for grain size effects as described above (see Materials and Methods – Markers). Five QTLs were again identified

for hull content, with the major QTLs identified on 1 (7H), 4 (4H), and 6 (6H). Minor QTLs were located on 2 (2H) and 7 (5H). The LOD scores were again significant ( $p < 0.05$ ) for 1 (7H), 4 (4H), and 6 (6H). The adjusted grain size data failed to identify the QTL on 5 (1H) that was identified in the unadjusted data analysis. In fact, the result of the adjusted hull data analysis (adjusted for grain size) resulted in the marker information being reversed as compared to the first analysis that used unadjusted hull data. In this case, the marker on 4 (4H) was associated with 2003 data while the marker on 6 (6H) was associated with the 2002 phenotypic data. Of the five regions identified for hull content from either analysis, the only region that was common for hull, based on adjusted grain size, was on 1 (7H).

The interval maps highlight the major QTLs on 4 (4H) and 6 (6H) where there were common genetic regions for hull content, and either Falling Number or grain colour components (Fig. 2). For the four markers identified for L, a or b, an association with hull was also present. This would suggest that hull and grain appearance have common chromosomal regions.

## DISCUSSION

The outcomes from this study are the first reported results to indicate genetic and phenotypic relationships between hull content, kernel discolouration and preharvest sprouting. A number of common markers on 5 chromosomes were identified for these attributes.

### Chromosome 1 (7H)

A small region on the long arm of chromosome 1 (7H) around *XP13M55T68* (Tallon allele) was associated with hull thickness (2002 Hermitage) and FN (2003 HRS). This region has also been associated with dormancy derived from a Triumph background<sup>28</sup>. Triumph is a parent of Tallon. Both varieties in this study have been shown to have moderate levels of dormancy<sup>18</sup>.

### Chromosome 2 (2H)

The marker (HVM54) identified on 2 (2H) for hull content was also associated with KD (L). This marker was also identified by Li *et al.*<sup>25</sup>, while Mesfin *et al.*<sup>27</sup> and De la Pena *et al.*<sup>29</sup> associated it with FHB resistance. These results suggest that a decrease in hull thickness could impact on the fungal levels on the seed. A marker for hull thickness on 2H was described previously<sup>8</sup>, however, it was on the short arm of 2H. This marker related to increased hot water extract levels, due to a decrease in hull thickness. A second minor QTL for hull content and hot water extract was also shown around the centromere on 2 (2H)<sup>8</sup>. This region was also identified as being associated with grain colour components, lightness (“L”) and yellow (“b”) using the same population as that in the Collins study. The parent contributing the positive alleles in both studies was Haruna Nijo<sup>25</sup>.

### Chromosome 4 (4H)

The QTL identified on 4 (4H) had associations hull content, Falling Number and grain redness (“a”). Markers on 4 (4H), namely *Ebmac0906* and *Ebmac310* were iden

TABLE I. Genetic correlations.

	Screenings		Plump grain		Retention	
	2002	2003	2002	2003	2002	2003
Correlation with hull	0.65	-0.10	-0.42	-0.13	-0.62	0.048

TABLE II. Correlation coefficients between hull, barley colour components and sprouting.

	Hull	“L”	“a”	“b”	PHS
Hull	—	—	—	—	—
“L”	0.123*	—	—	—	—
“a”	0.347**	0.090	—	—	—
“b”	0.341**	0.200	0.210*	—	—
PHS	0.220*	0.320**	0.019	0.099	—

\* ( $p < 0.05$ )

\*\* ( $p < 0.01$ )



tified for hull thickness (Patty allele) and the red-green colour value ("a"). These have also been identified by Li et al.<sup>25</sup> for blue-yellow in a single population with blue aleurone. Further this region has been associated with KD and FHB resistance in studies from North America. The results for KD colour characteristics reported in this study, as well as the work reported by Li et al.<sup>25</sup> were measured using a colour meter while the work carried out in North America used visual assessment<sup>7,29</sup>. Despite the potential variability between measurements, common markers have been identified. Further mapping of the regions between would help identify the genes involved. In addition, the region around *Ebmac310* has also been associated to hot water extract<sup>4,23</sup> and the seed dormancy (SD4) gene<sup>21</sup>. The hull has an effect on both these traits.

### Chromosome 5 (1H)

The QTL identified on chromosome 5 (1H) was associated with hull content from the 2002 season. There were no linkages to other quality traits reported in this study or from other studies.

### Chromosome 6 (6H)

The 2002 phenotyping for hull content had an association on 6 (6H). This region was also associated with grain colour components, grain lightness ("L") and yellow ("b"). The work reported by Canci et al.<sup>7</sup> showed markers on 6 (6H) for KD also aligned for markers to grain protein concentration.

### Chromosome 7 (5H)

The markers on the short arm of 7 (5H) were associated with hull and "L" value. Markers identified for hull content were *Bmag337*, *P11M48T181* and *P11M49P067*, although the LOD scores were not significant. These markers were associated with the Patty allele. This region has also been identified by Li et al.<sup>25</sup> for lightness and yellow colour. A marker, *PI3M55T212*, associated with KD (lightness only) was located on the distal arm of 7 (5H). This region has been associated with KD colour components ("a" and "b" – Li et al.<sup>25</sup>). This region has also been identified for PHS and dormancy, high extract and high alpha-amylase traits. Li et al.<sup>25</sup> postulated that the same gene, alpha-amylase, may be responsible for a combination of high malt extract, low dormancy and pre-harvest sprouting susceptibility. The dormancy regions on 7 (5H) have also been identified for preharvest sprouting resistance<sup>34</sup> as well as  $\alpha$ -amylase activity. Other regions have also been identified on 7 (5H) for KD<sup>7,29</sup> although these were not common to the regions identified in our study.

The difference between years for hull content and heritability could be explained by the significant variation in grain size. The 2002 season suffered a severe drought with a high level of screenings and a low level of retention. The level of hull had a positive correlation to screenings, with a negative relationship to retention. The reverse relationship occurred for the 2003 set, but the relationships were not as strong. In addition, the chromosomal regions identified for hull content were not the same as those controlling grain size (data not shown). This would

suggest pleiotrophic effects where the hull has a relationship to grain size, but the genetic control is independent of those traits.

The results from this study also indicate that there was genetic control for all the traits measured. The heritability values indicate that breeding varieties with a thinner or thicker hull content would be possible. However, when breeding for resistance to pre-harvest sprouting, generally a thicker hull would be more desirable.

Chromosomal regions with significant LOD scores were identified on chromosomes 4 (4H), 6 (6H) and 7 (5H). All these regions have previously been identified with KD resistance, FHB resistance as well PHS and dormancy.

The results from this study indicate a number of QTLs that contribute to hull content, as well as concomitant attributes, including kernel discolouration and pre-harvest sprouting. Investigation of these QTLs in other populations could provide alternative sources of genetic variation for pre-harvest sprouting tolerance, KD resistance and thin hull. These were limited data sets for all traits, but the results indicate that hull content impacts on grain appearance after pre-harvest rain. In addition, the hull content may also contribute to the level of pre-harvest sprouting resistance. These conclusions were based on the phenotypic relationship between the traits, as well as supporting information associating three molecular regions to hull content, grain appearance and pre-harvest sprouting.

Edney et al.<sup>10</sup> suggested that more research be carried out on kernel discolouration. This work adds to the current knowledge on KD. Future work could expand on this current study with focused phenotyping and fine mapping of the regions identified for KD, hull content and pre-harvest sprouting tolerance.

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#### ERRATUM

A correction was made in this paper on July 18, 2006. The copyright notice on page 101 was incorrect and was replaced with a new statement.