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# Is Malting Barley Better Feed for Cattle than Feed Barley?

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## ABSTRACT

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Barley grain from a combined intermediate and advanced barley breeding trial was assessed for grain, feed and malt quality from two sites over two consecutive years, with the objective to ascertain relationships between these traits. Results indicated there were genetic effects for both malt (hot water extract and friability) and “feed” traits (as measured by hardness, acid detergent fibre, starch and *in-sacco* dry matter digestibility). The feed trait values were generally independent of the malt trait values. However, there were positive relationships between friability, hardness and protein, as well as a negative relationship between extract and husk. Extract also had a positive relationship with test weight but appeared to be independent from the feed traits. Test weight also showed little relationship to the feed traits. Heritability values ranged from low to high for almost all traits. This study details where both malt and cattle feed parameters have been compared and the results indicated that while malt and feed traits do not correlate directly, malt cultivars can exhibit excellent feed characteristics, equal to or better than feed cultivars. This data highlights the benefit of selecting for malt quality even if a breeding program would be interested at targeting specific feed quality.

**Key words:** extract, feed quality, friability, malt quality.

## INTRODUCTION

The use of barley grain is primarily for feeding animals but the value-added market is for malt and beer production and as such the malting and brewing industry has set the quality specifications for barley grain being delivered

after harvest. While the grain traits of retention, weight and protein level dictate the barley grain suitable for malt production, the key malt trait for selection within a breeding program or for brewers purchasing malt is hot water extract (HWE). High levels of HWE are desirable as it provides an indication of malt quality as well as potential brewhouse performance<sup>24</sup>. Studies have shown the expression of this trait was controlled by genotype and environment<sup>4,23,49,53,68,70,79</sup> and processing<sup>12,47,67,69</sup>.

A number of grain characteristics also contributed to variation in HWE including:

- protein content and composition<sup>40,52,54,56,82</sup>,
- starch content<sup>11,13,46</sup>,
- $\beta$ -glucan content<sup>37,55,86</sup>,
- husk content<sup>1,18,33,48</sup>,
- grain hardness<sup>2,27,28,38,63,66,78</sup> and
- cell wall, protein and starch degrading enzyme levels in both resting grain and synthesised during malting<sup>4,12–14,43,44,50,64,80,81,83</sup>.

A second important trait that provides an early indication of malt potential is friability, although this is a relatively new method compared to the HWE method. Friability is a measure of the breakdown of endosperm cell wall components and protein matrix. Measuring the friability of commercial malt has increasingly been used as an indicator of malting and brewing quality as well as trouble shooting samples of poor malt quality. The relationship between other malt quality parameters and friability has been well documented. Biochemical measures of endosperm modification include malt and wort  $\beta$ -glucan, Kolbach Index and wort viscosity. All of these parameters have been correlated with friability<sup>20,28,77,84</sup>. Most of these studies reported the strong negative relationship between friability and wort viscosity.

In regards to feed quality, very little feed grade barley attracts a premium. However, the feed industry understands that barley provides energy as well as fibre. One relatively new trait has been emerging as a sound indicator of feed quality. Measurement of *in-sacco* dry matter disappearance (*ISDMD*) uses a methodology where grain is placed into an animals' stomach and the amount of disappearance measured. A recent review highlights the important aspects of *in vivo* studies<sup>44</sup>. This process has been shown to provide data on performance of different grain species, and differences between cultivars<sup>6,7,10,34,60,61</sup>. In addition, the *in-sacco* method has been shown to provide more discrimination between or within species than an *in-vitro* assay. *ISDMD* has been shown to provide reliable

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feeding performance results on a range of grains, including barley. Previous reports have shown the positive relationship between this assay and estimated feed performance<sup>8,10</sup>. A review by O'Brien<sup>58</sup> suggested that there is a lack of studies with sufficient experimental design to provide data on genotype and environment effects for *in vivo* assays. Subsequent studies have investigated the *in-sacco* assay using barley grown in trials from multiple locations and years, with differences between genotypes and environments reported<sup>134,35</sup>.

Barley processed for feedlots is generally steam flaked or rolled. The hardness of the grain impacts on the pressing and processing efficiency and, hence, the accessibility of the endosperm material. While hardness is not routinely measured when evaluating barley grain quality, recent studies have demonstrated the relationship between barley hardness (milling energy) and grain and malt quality parameters<sup>2,28,38,77,78</sup>. In addition, the effect of growing environment impacts on grain components such as  $\beta$ -glucan as well as protein content and protein composition, where high  $\beta$ -glucan and / or protein levels related to harder grain<sup>29,63,77,78</sup>. Other methods using milling and particle size separation have demonstrated genetic and environment effects<sup>29,59</sup>. Barley hardness, as measured by the Single Kernel Characterization System, has been shown to impact on malt quality<sup>41,59</sup>, shochu quality (a Japanese distilled spirit)<sup>42,72</sup> and feed quality<sup>5</sup>.

Processing of barley grain for brewing, i.e. the malting process, has a direct impact on malt and beer quality. The most obvious effects occur through manipulating the level of endosperm modification during malting and mashing, as well as controlling the particle size of the milled malt going into the mash. Similarly, processing of grain in the feed industry would appear to impact on feed performance. Bowman et al.<sup>9,10</sup> have reported a negative correlation between particle size (hardness), acid detergent fibre (ADF) and dry matter disappearance (DMD), but a positive correlation with daily live weight gain. Particle size has been shown to have a direct impact on animal performance.

Limited data has been published on the relationship between feed and malt quality. The review by O'Brien<sup>58</sup> detailed previous studies where research was conducted using malting and feed (non-malting) cultivars, although none of these studies actually included any malting analysis. However, a number of those studies reviewed detailed comparisons of cultivars, with malting cultivars showing to be equal or better than the feed varieties for animal performance measured through *in-vivo* assays.

An early study reported on the relationship between a decoction style malt extract method with barley fibre components (acid detergent fibre (ADF) and neutral detergent fibre (NDF))<sup>15</sup>, while two studies in 1984<sup>39,74</sup> also showed correlations between ruminant feed quality and malt quality attributes. Recently, it has been proposed to use the European Brewing Convention (EBC) extract as an indicator of feed quality. This would also be useful in a combined feed/malt quality testing program within a barley breeding program.

The objective of this study was to compare the performance of malting and feed cultivars grown over multiple locations and years. The level of heritability was

quantified for these feed and malt traits, and phenotypic relationships between these traits were explored.

## MATERIAL AND METHODS

### Barley samples

The data set was comprised of barley cultivars, including commercial cultivars and breeding lines, selected from a combined intermediate and advanced breeding trial series. There were eleven Australian commercial malt and feed cultivars as well as two international cultivars. The breeding lines represented a diverse range of genetic backgrounds. This trial series was grown in a replicated trial at two sites (Kaimkillenbun and Breeza) over two years (2002 and 2003).

A number of measurements were carried out on the grain samples obtained from these trials and the methodology for measuring each trait is described below. In terms of statistical design, differing levels of duplication and randomisation were employed for the grain, feed and malt measurements. Grain and feed trait measurements were all obtained from replicated plots from the field and processed in field order. There was no extra duplication of samples made of the grain and feed traits. However, a two stage experiment was undertaken for the malt traits. Grain from field plots was split into duplicate samples for the micromalting process, and an incomplete block design was used to allocate individual samples to the malt runs and position within the micromalter. The designs contained only partial duplication of the field plots and laboratory samples as described previously<sup>17</sup>.

### Grain quality

**Grain size.** Grain size was measured following the procedure outlined previously<sup>25</sup> where approximately 120 g was screened in a Sortimat for 1 min. The percentage of the grain size distribution was calculated based on the weight of four fractions, namely <2.2 mm (screenings (Scr)), 2.2–2.5 mm, 2.5–2.8 mm and >2.8 mm (>2.8 mm). Retention (Ret) was the combination of >2.5 and >2.8 fractions. Plump grain (PG) is the fraction above 2.8 mm. For micromalting, grain above 2.2 mm was retained.

**Grain protein.** Whole grain barley samples were scanned as whole grain through a NIRSystems 6500 near infrared spectrophotometer. Spectra were recorded between 1100 nm to 2500 nm. In-house calibrations, built using a broad range of commercial cultivars and breeding lines, were used to predict grain moisture and protein (as is) values. The moisture value was used to correct protein to a dry basis.

**Husk.** Husk content was measured as described previously<sup>26</sup> where 10 g of grain was boiled for 2 min in a solution of sodium hypochlorite and hydrogen peroxide. Grain was weighed before and after boiling to determine the percentage of husk.

**Hardness.** For Particle Size Index (PSI) analysis, 50 g of barley was pearled for ten sec in a barley pearler (Strong-Scott). The recovered grains were then milled using a Falling Number 1600 disc mill with a sieve size of 1.0 mm<sup>29</sup>. Ten grams of the milled sample was then sieved in a Fritch Sieve Shaker for 10 min. The weight of the

material that passed through the sieve was weighed. This value was multiplied by 10 and recorded as PSI. The results are reported as arbitrary units with values 10–15 being hard and 18–30 being soft.

**Feed analysis.** All feed analysis was carried out at Montana State University, as described by Bowman et al.<sup>10</sup> Grain samples from each line were individually ground to pass through 0.5 mm screen using a Udy-Cyclone Mill (Ft. Collins). Characterisation of chemical composition was calculated on a dry basis. Dry matter (DM) content was determined following the Association of Official Analytical Chemists (AOAC) method (AOAC 934.01)<sup>3</sup>. ADF content was determined using an ANKOM 200 Fiber Analyzer (ANKOM Technology Crop, Fairport, NY)<sup>75</sup>. Starch content was determined by the amyloglucosidase/ $\alpha$ -amylase method (Megazyme, Sydney, Australia).

**Particle size.** Grain samples were cracked using a Buhler mill (Buhler-Miag, Braunschweig, Germany) to simulate dry rolling. Particle size was determined on the cracked samples by dry sieving with two replicates per sample<sup>22</sup>. Ground matter retained on 3350  $\mu\text{m}$ , 2360  $\mu\text{m}$ , 1700  $\mu\text{m}$ , 850  $\mu\text{m}$  and 425  $\mu\text{m}$  sieves, along with material retained in the bottom collection pan, was used to estimate particle size.

**Dry matter digestibility.** ISDMD estimation was carried out according to the procedure of Vanzant et al.<sup>76</sup>, using two ruminally cannulated beef cows that consumed low quality grass hay *ad libitum* and 3.6 kg day<sup>-1</sup> of barley. Four 5 g samples of each entry were placed in 10 × 20-cm, 50- $\mu\text{m}$  pore size polyester bags (Ankom Technology, Fairport, NY). Twenty-eight polyester bags containing experimental samples, one blank bag and one bag containing Harrington as a check cultivar, were placed in the rumen at the same time and incubated for 3 h. After removal from the rumen, the bags were manually rinsed under cold water until the wash water ran clear. The bags were dried at 60°C for 48 h and then weighed. Dry-matter content of the cracked barley samples was estimated by measuring the DM content and calculating the mean value. Ruminal DMD was calculated according to the following equation: *in sacco* DMD% = 100 – (((dry sample and bag wt. out – bag weight) – (blank bag wt. in – blank bag wt. out))/(sample wt. in × DM)) × 100. These average values were then used in regression equations to derive estimations of Net Energy (NE), Average Daily Gain (ADG) and Efficiency (Eff). The development of these equations has been described previously<sup>10</sup>.

### Malt quality

**Micromalting.** Barley samples were screened over a 2.2 mm sieve prior to malting. The malt process was as follows Steep 8:10:6 (17°C), germination 96 h at 17°C, kilning 6 h ramp to 65°C, 5 h ramp to 75°C, 6 h ramp to 85°C hold for 4 h at 85°C. The kiln was then cooled and held at 50°C until malt was removed. Rootlets were removed using an in-house built machine where the sample is placed into a drum (20 cm diameter × 15 cm long) where paddles thresh the malt for 5 min. Rootlets fall through a perforated wall. The finished malt is then removed and stored in plastic airtight jars until analysis. All sites were malted as separate batches. As there was a difference in

protein between the Breeza and Kaimkillenbun sites (9.0% and 12.0% respectively), from 2002 the first air-rest in the steep was reduced by 1 h for the Breeza samples to obtain similar modification levels for each site.

**Malt evaluation.** Friability and malt extract were analysed as per EBC methods 4.2 and 4.5 respectively<sup>21</sup>.

**Statistical analysis.** The model for analysing the combined grain data across the multiple environments is a linear mixed model. In this mixed model formulation, within-trial variation is modelled simultaneously with effects for genotype<sup>31</sup>. A factor analytic (FA) form<sup>65</sup> is fitted to the variance of the interaction effects between cultivar and environment (G×E) and allows for heterogeneous genetic variances between sites, and different covariances between each pair of sites; two assumptions deemed necessary to appropriately model the genetic variance across environments for these measurements. Based on this FA form for the genetic variance matrix, genetic correlations between environments are calculated to indicate the closeness in genotype ranking for each pair of environments.

This FA model has been shown to perform well for these types of MET data<sup>25–29</sup>. This same statistical model was adopted for the feed grain traits. Feed grain samples were processed in field order with no blocking or randomisation of duplicates. Error variance was then a pooled estimate for the field trial and feed trial stages of testing. The model for the malt analysis includes an additional strata due to the two-stage process<sup>16</sup>, including a term for residual variance due to field plots, and a term for residual variance from the micromalting samples.

Heritability ( $h^2$ ) for individual environments was estimated directly from the average pairwise prediction error variances (apev)<sup>16</sup>, as  $h^2 = 1 - \text{apev}/(2 \sigma_g^2)$ , where  $\sigma_g^2$  is the genetic variance for each environment.

Each model was fitted using *samm*, a suite of Splun functions implementing the average information algorithm<sup>31</sup>. In this software, the variance parameters were estimated using the residual maximum likelihood (REML) procedure<sup>62</sup>, best linear unbiased predictors (BLUPs) were obtained for the random effects and generalised least square estimates were given for the fixed effects.

Genotype predictions from the analysed data for all malt and feed traits were subjected to principal component analysis to explore the inter-trait relationships. Biplots were used to display the relationships between these traits, and similarities between the genotypes

## RESULTS AND DISCUSSION

This study used a range of breeding lines, commercial malting and non-malting (feed) varieties. Summaries of the grain, feed and malt quality for the genotypes evaluated and four sites tested are shown in Tables I and II respectively. Table I details the individual genotype performance, and Table II summaries the analysis across environments through site means, genetic correlations and heritability of each trait.

### Grain quality

Recent studies have highlighted the benefits of using liner mixed models over traditional analysis of variance to

**Table I.** Summary of grain, malt and feed quality for 40 cultivars grown in four environments<sup>a</sup>.

Cultivar	Scr	PG	Ret	GP	HLW	PSI	PS	Husk	ADF	St	ISDMD	NE	ADG	Fri	HWE
Feed cultivars															
Binalong	7.6	10.5	55.9	12.1	71.5	22.2	1250	10.7	4.3	57.6	33.7	2.51	1.64	68.7	76.7
Grout	7.2	24.8	72.2	11.5	69.9	22.7	1247	11.9	4.4	58.0	34.3	2.50	1.62	60.6	78.9
Kaputar	4.1	31.0	73.4	12.0	68.2	29.8	1290	11.2	4.6	55.9	38.2	2.44	1.57	76.6	77.4
Mackay	5.9	19.3	65.0	10.9	72.0	19.4	1228	10.6	4.1	59.1	35.9	2.49	1.61	76.0	79.0
Tantangara	6.4	10.9	49.8	11.8	70.7	27.4	1211	10.5	4.8	56.2	35.6	2.48	1.60	74.5	77.5
	6.2	19.3	61.2	11.7	70.5	24.3	1245	11.0	4.4	57.3	35.4	2.48	1.61	71.3	77.9
Malt cultivars															
Fitzroy	4.2	22.8	73.7	11.3	68.4	25.5	1235	11.3	4.3	58.8	30.3	2.55	1.67	77.5	78.8
Gairdner	5.5	13.1	64.7	12.6	70.6	24.2	1318	10.7	4.1	56.9	35.4	2.48	1.62	77.1	78.6
Grimmett	5.1	21.6	68.0	11.8	72.2	21.0	1210	10.7	3.9	57.1	36.7	2.47	1.61	76.6	77.6
Lindwall	8.9	10.9	51.5	12.0	71.8	18.9	1205	10.4	4.0	57.2	30.4	2.54	1.69	85.6	78.7
Schooner	2.7	32.2	77.7	12.3	72.2	24.7	1167	11.1	4.6	58.0	37.8	2.46	1.58	76.3	78.4
Tallon	7.0	12.6	57.6	11.4	70.5	22.6	1219	10.9	4.1	57.2	35.4	2.48	1.62	80.3	78.5
	5.6	18.9	73.7	11.9	71.0	22.8	1226	10.9	4.2	57.5	34.3	2.50	1.63	78.9	78.4
Scarlett	2.9	28.4	80.1	11.2	71.6	21.8	1222	10.2	3.90	57.0	36.7	2.47	1.61	82.5	79.3
Valier	5.1	28.3	73.3	11.4	72.3	21.8	1196	11.1	4.08	58.6	37.7	2.46	1.59	72.7	80.4
NRB01002	6.3	34.0	68.9	11.4	68.2	25.6	1222	10.9	5.01	55.3	31.8	2.52	1.65	78.8	77.8
NRB01004	4.5	20.3	72.7	11.7	71.6	20.2	1205	10.6	3.91	58.3	33.9	2.51	1.64	71.6	78.3
NRB01020	4.8	32.1	71.1	11.5	68.5	24.8	1247	14.0	4.39	58.0	34.3	2.51	1.62	61.0	76.4
NRB01077	2.2	33.2	82.2	11.6	70.3	24.1	1293	11.0	4.27	56.7	37.3	2.46	1.59	72.3	77.6
NRB01126	12.6	22.9	53.2	11.2	68.5	27.2	1312	12.0	4.31	58.2	35.3	2.49	1.61	72.5	78.2
NRB01133	6.3	22.4	63.5	11.4	70.4	26.2	1275	11.0	3.92	57.4	35.7	2.48	1.62	70.3	78.3
NRB01134	5.9	25.5	58.2	10.9	69.6	26.3	1290	11.8	4.16	55.8	33.7	2.50	1.64	82.7	78.3
NRB01139	5.8	40.8	71.7	11.3	67.5	26.3	1275	11.7	4.82	57.4	35.1	2.49	1.60	82.3	77.7
NRB01145	4.4	43.0	78.3	10.8	68.5	24.0	1252	11.3	4.62	57.8	35.9	2.48	1.60	82.3	78.2
NRB01173	3.9	33.1	72.5	11.0	67.1	26.3	1267	11.8	4.38	57.0	37.4	2.46	1.59	82.8	77.5
NRB01179	8.0	17.6	56.2	12.0	70.2	22.5	1217	10.3	3.95	58.3	37.1	2.47	1.60	74.8	78.4
NRB01181	4.6	18.7	57.8	11.4			1265	11.2	4.04	61.5	43.3	2.42	1.50	79.0	78.0
NRB01183	7.5	17.9	52.7	11.1		21.8	1288	11.1	4.01	60.1	37.9	2.47	1.57	85.9	78.4
NRB01186	5.2	17.6	66.5	11.3	70.5	22.1	1245	10.7	4.42	57.0	34.8	2.49	1.62	74.8	78.2
NRB01210	5.1	21.5	69.4	11.1	72.5	20.1	1221	11.0	3.81	57.3	38.4	2.45	1.59	71.7	78.7
NRB01230	4.7	27.9	71.6	12.0	70.7	23.0	1258	11.1	3.79	59.2	37.3	2.47	1.59	80.7	78.1
NRB01231	3.7	33.2	76.5	11.7	70.8	23.2	1252	11.0	4.17	57.6	37.4	2.46	1.59	77.4	78.6
NRB01240	4.2	21.6	71.6	11.9	71.1	21.3	1220	10.9	4.03	57.7	41.8	2.41	1.54	80.6	78.8
NRB01244	2.1	49.7	87.2	12.4	71.1	24.1	1191	10.6	3.67	58.1	46.1	2.36	1.49	77.3	79.5
NRB01251	3.8	24.2	74.5	11.4	72.7	21.5	1277	10.1	4.09	59.5	36.0	2.49	1.60	63.1	78.0
NRB01298	4.1	26.8	72.1	11.2	72.3	20.8	1218	10.9	4.31	56.8	33.6	2.50	1.64	77.2	78.2
NRB01333	2.8	39.9	82.1	11.2	72.6	19.1	1225	11.1	3.94	57.5	37.1	2.46	1.60	75.0	77.9
NRB01345	5.4	17.2	62.6	11.2	72.2	18.4	1211	11.3	4.67	56.4	34.0	2.50	1.63	70.1	76.9
NRB01346	4.5	24.3	69.6	11.0	70.2	20.9	1301	11.5	4.61	57.3	35.7	2.48	1.60	70.0	77.8
	5.0	27.8	69.9	11.4	70.5	22.9	1247	11.2	4.2	57.8	36.7	2.47	1.6	75.7	78.2

<sup>a</sup> Scr – Screenings (% <2.2mm); PG – Plump Grain (% >2.8mm); Ret – Retention (% >2.5mm); GP – % Grain protein (dry basis); HLW – Hectolitre weight (kg/100 litres); PSI – Particle Size Index (arbitrary units); Husk – Husk Content (%); ADF – Acid Detergent Fibre (%); ST – Starch (% dry basis); ISDMD – *In-Sacco* Dry Matter Digestibility (%); PS – Particle size (µm); NE – Net Energy (MJ/kg); ADG – Average Daily Gain (kg/day); Fri – Friability (%); HWE – Hot Water Extract (% dry basis)

calculate genetic and environmental effects for barley breeding data<sup>25–29</sup>. Using this mixed model analysis, we identified differences in genotypic responses across environments for the grain, malt and feed quality attributes measured in this study.

Genetic variation in grain quality was observed in the commercial varieties as well as within the breeding lines. Only two of the commercial malting varieties met the Australian Malt 1 standard for retention (min 70%) when the results for the four sites used in this study were averaged. However, the international varieties, Scarlet and Valier, met this standard. A number of breeding lines were also above the retention standard but most averaged well below the standard (Table I).

Four of the six Australian commercial malt varieties, as did Scarlet, met the industry specifications for averaged protein content (max 12.0% db). However, while there are no feed industry specifications for protein content, four of the five Australian feed varieties and Valier were less than

or equal to 12.0% db. Most of the breeding lines averaged protein data fell within the protein specifications although there were marked differences between genotypes for protein content (Table I). These differences demonstrated selecting for low protein barley was achievable as a breeding target when breeding for malting varieties that could be grown in a broad range of environments. The moderate to high level of genetic selection suggests this trait could be selected for across a number of environments (Table II). This also supports previous studies identifying low protein progeny in breeding populations<sup>20,32,57</sup>.

Another industry specification used for both malt and feed classification is Hectolitre Litre Weight (HLW). Only the samples from 2003 were tested for HLW. All the malt and feed cultivars averaged >65 kg/hectolitre which is the industry standard. There was a broad range amongst the breeding lines for HLW and the range in genetic correlations suggests the trait could be selected for across environments (Table II).

**Table II.** Summary of grain, malt and feed quality, heritability and genetic correlation between sites<sup>a</sup>.

Site	Year	Ret	GP	HLW <sup>b</sup>	PSI	Husk	ADF	ST <sup>b</sup>	ISDMD <sup>b</sup>	PS <sup>b</sup>	NE	ADG	Fri	HWE
Breeza	2002	91.5	9.8		22.9	10.2	4.1	59.2	41.5	1259	2.42	1.53	87.3	79.8
Breeza	2003	74.8	10.3	71.0	24.5	10.5	5.0	57.2	34.4	1204	2.45	1.61	85.2	78.7
Kaimkillenbun	2002	59.5	12.4		20.1	11.4	3.9	57.9	38.5	1275	2.50	1.58	82.4	77.7
Kaimkillenbun	2003	61.4	13.5	70.1	22.4	11.5	3.6	56.6	33.7	1239	2.50	1.66	55.6	77.5
Genetic Correlation (range)		0.42–0.70	0.20–0.75	0.58	0.51–0.99	0.57–0.79	0.76–0.95	–0.60–0.90	0.13–0.98	0.47–0.99	0.08–0.99	0.11–0.99	0.57–0.85	0.39–0.92
Heritability (range)		0.89–0.99	0.60–0.80	0.74	0.37–0.94	0.66–0.90	0.56–0.71	0.30–0.90	0.55–0.63	0.47–0.73	0.31–0.48	0.44–0.51	0.05–0.45	0.86–0.92

<sup>a</sup> Ret - % > 2.5mm; GP - % Grain protein (dry basis); HLW - Hectolitre weight (kg/100 litres); PSI - Particle Size Index (arbitrary units); Husk - Husk content (%); ADF - Acid Detergent Fibre (%); ST - Starch (% dry basis); ISDMD - *In-Sacco* Dry Matter Digestibility (%); PS - Particle size (µm); NE - Net Energy (MJ/kg); ADG - Average Daily Gain (kg/day); Fri - Friability (%); HWE - Hot Water Extract (% dry basis)

<sup>b</sup> Only measured in 2003.

In this study, two hardness methods were used, both based on a milling and sieving process, with the difference being the PSI method used a single sieve with the amount of ground barley passing through the sieve used to calculate hardness. The PS method used six sieves to calculate an average particle size. Both methods have previously been shown to distinguish between cultivars<sup>10,29</sup>. The feed varieties averaged slightly harder grain by the PSI method and slightly larger particle size (Table I). There was a range of hardness within the malting and feed varieties. Lindwall, an outclassed malting variety, had the hardest grain *albeit* it was still within the soft region as defined for wheat<sup>71</sup>. Schooner, a malting variety released over 25 years ago, had the softest grain by the PS method. The breeding lines all fell between the malting and feed ranges for hardness regardless of method. Barley is generally a soft grain compared to other cereals such as bread wheat or durum wheat.

The results for husk content showed a broad range between cultivars. There was also a difference between the averaged data between sites. A number of breeding lines had values lower than most of the current malting cultivars which is desirable as lower husk content is required for increased extract potential<sup>1,19</sup>. As this breeding program has had malting quality as one of its breeding targets for over thirty years, then it would be reasonable to expect reduced husk content on some cultivars which have some, but not all, desirable malt quality traits.

For acid detergent fibre, there was both genetic and environmental variation. ADF is a component within the total fibre fraction and used as a feed quality characteristic, with lower levels of ADF being linked to improved feed performance. The range of ADF was within the range reported in other studies<sup>9,10,36,46</sup>.

### Malt and feed quality

There were marked differences in genetic variance between environments for both malt and feed quality. As malt quality has been the breeding target for over thirty years in our program, most of the lines that progressed to the intermediate and advanced breeding stages, have malt potential which was determined primarily by the HWE values. This can be seen by all breeding lines having hot water extract values equal to or greater than the value for Grimmett, the oldest commercial malting cultivar (released in 1982). The most recently released malting variety, Fitzroy, had one of the highest HWE values. There were a number of breeding lines that had averaged HWE

values similar to Fitzroy. Of interest was the performance both the international varieties, Scarlet and Valier as these had HWE values greater than Fitzroy. Valier, a feed cultivar released by Montana State University, averaged the highest HWE value of all the commercial varieties tested.

Friability is an important malt trait that can provide an indication of malt modification. The results from our study show the commercial malt varieties had much higher friability values than the feed varieties, which would be expected. Scarlett also had a high friability while Valier had a friability similar to the Australian feed varieties. A number of breeding lines had friability levels similar to the malting varieties.

There were differences between all genotypes for the feed traits ISDMD, Average Daily Gain (ADG) and Net Energy (NE). The malt varieties averaged the lowest ISDMD (lower values indicate slow disappearance which is more desirable) than the feed varieties. In addition, Fitzroy and Lindwall (malting varieties) had the lowest averaged ISDMD for any genotype. Of interest, all of the commercial malt varieties, and a number of feed varieties and breeding lines had better ISDMD than Valier.

The malt varieties also had slightly higher ADG and NE values suggesting cattle fed on the samples from these malt varieties could achieve a target weight or be heavier within a defined time period than animals fed on the feed varieties. The range observed for all of these traits falls within previously published ranges<sup>8,10</sup>.

### Site effects

The trial was grown at two sites in each of two consecutive years. Genotype responses at the two sites, Breeza and Kaimkillenbun, were considerably different for grain, feed and malt qualities (Table II). Breeza gave protein values within the industry standard (<12.0% db) for both years. In addition, both years met the specification (70% >2.5 mm) although screenings from the 2003 season were just above the industry standard (5% <2.2 mm). Conversely, Kaimkillenbun failed to meet any industry specification for grain quality in either year. However, while this data was averaged from forty replicated genotypes, there were individual samples that met the industry specifications for protein, grain size or both parameters.

Grain samples from all sites were tested for feed and malt quality, and results were used to explore the relationship between malt and feed quality traits. Breeza produced grain of excellent quality in both years, while

Kaimkillenbun generally produced grain outside malting industry specifications. This is shown in the overall malt quality of the samples with high levels of HWE and friability. In addition, Breeza samples had a lower husk content and a softer grain texture (higher PSI) for both years, which would also have had a positive effect on malt performance. Grain from Kaimkillenbun produced much lower malt quality over the two years. The malt performance matched the grain quality results with the highest HWE and friability levels being obtained from the sites with the lower protein content (or larger grain size), while the poor malting performance was associated with high protein (and smaller grain size) sites. In addition, samples from the 2002 season averaged slightly higher HWE and friability than those from the 2003 season. This data is consistent with previous reports on site and season effects on malt quality<sup>70,73</sup>.

There were site effects on both NE and ADG. However, the NE and ADG values for the sites tested did not follow the same pattern as for malt quality. While the lowest protein site (Breeza 2002) produced the lowest NE and ADG values, the highest NE value (2.61) was produced at 2003 Breeza and 2003 Kaimkillenbun. The highest ADG site was 2003 Kaimkillenbun, but the ranking of genotypes for ADG did not match the rankings for protein. There were also seasonal effects on feed quality, with the 2003 season averaging slightly better feed quality than 2002.

Genetic correlations are an important parameter describing the nature of the genotype by environment interaction for each trait. The genetic correlations quantify the degree of rank change in genotype performance across environments, and range in value from +1 to -1, with a high positive value indicating nearly complete agreement in ranking of genotype performance across these environments. The results from this study show that for most traits there were strong positive genetic correlations between environments (Table II), with starch being the only trait that showed any negative correlation. For a number of traits the correlation between environments was high to very high, suggesting ranked genotype performance was consistent across environments.

### Heritability

Heritability was calculated for all measured quality traits, and quantifies the proportion of variation in a trait that can be attributed to the genotype. It provides a numerical value to define the level of genetic and environment effects on expression of a trait. High heritability values indicate a relatively high level of genetic variance when compared to total variance. The grain traits (grain size, protein and test weight), were highly heritable with values ranging from 89–99%, 60–80% and 74–94% respectively (Table II). For the hardness (PSI) and husk thickness, heritability was moderate to high with 37–90% and 66–71% respectively (Table II). The heritability values for protein (60–80%) were similar to the ranges reported in some previous studies but considerable higher than data reported by Brennan et al.<sup>11</sup> The heritability values for HLW from the 2003 sites were 74 and 94%.

The heritability values for the feed traits were low to moderate (Table II). For ADF the range was moderate at

values 56 to 68%. The starch heritability values were low at 30 to 39%. Particle size had moderate heritability values range from 47 to 73%. The *ISDMD* heritability was also moderate in range from 55 to 63%. For NE and ADG, the values were 31 to 48% and 44 to 51% respectively. The results from this study show similar results from previous reports of barley feed quality. Bowman et al.<sup>9</sup> reported heritability of 58% for starch, 90% for crude protein and 50% for *ISDMD* from the Steptoe × Morex population. Hussein<sup>41</sup> reported in more detail heritability values of 61.8% to 92.5% for *ISDMD* and 48% to 63% for PS in a Valier × PT370970 mapping population, grown at dry and irrigated sites. For *ISDMD*, individual heritability values of 61.8% to 92.5% were reported for dry, irrigated and combined sites, while for the population  $h^2$  values of 76.1% to 92.5% were reported. Molina-Cano et al.<sup>51</sup> reported a broadsense heritability of 55% for apparent metabolisable energy.

There was a range for the malt quality traits from low to high heritability values. Husk content can be considered as a malt trait as thinner husk can result in higher extract, and hence could be a malting barley breeding objective. The range of heritability reported here was moderate to high (Table II). These results agree with one previous report<sup>84</sup>. The range in heritability for HWE was very low to high (39–92%) while for friability the range was 5–85%. The HWE results were similar to previously reported data<sup>48</sup>. The heritability values for friability were slightly lower than those reported previously<sup>30</sup>.

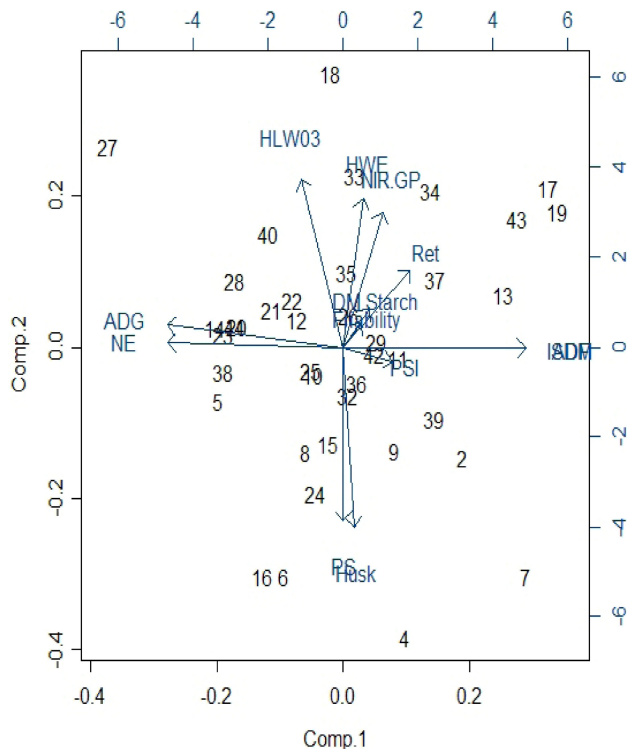
The irrigated sites produced the higher heritability values which suggested that better growing conditions resulted in high genetic variance and low environmental variance. The comparison of “hard” and “soft” sites thus provides greater understanding of the genetic and environmental effects on specific quality traits. If heritability was high under both hard and soft conditions, it would suggest that the trait was more easily improved through breeding.

### Relationship between malt and feed quality

Malt and feed data were subjected to principal component analysis (PCA) so as to examine the trait relationships based on the overall genotypic predictions from across sites analysis. Biplots were used to summarise the relationships between traits (Figs. 1 and 2). The first three axes of the PCA explained 31, 22 and 12% of the variation, respectively. Figure 1a plots PC one against PC two, accounting for 53% of the variation in the multi-trait data. The main contrast in component one was between NE and ADG against *ISDMD* and ADF, with most of the other traits appearing to be independent of those four. Conversely, *ISDMD* was negatively correlated with ADG but independent to HWE, protein and grain size.

Figure 1b plots PC two and three against each other. HWE showed a negative correlation with hardness, fibre, particle size and husk. The secondary malting trait of friability had a strong positive relationship with PSI (for this trait a high value means softer grain), and negative correlations with starch and retention. Friability was somewhat independent of husk, particle size, extract and test weight. Component three made little differentiation between the feed traits, as the greatest variation between these had already been explained by component one.





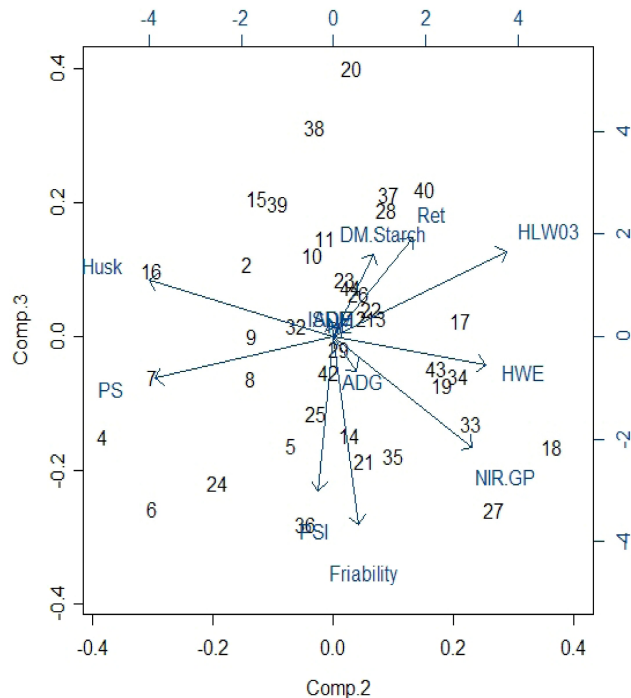
**Fig. 1.** Biplot for principal component 1 (31%) and 2 (22%) for all traits.

## CONCLUSIONS

This study reports on a large number of cultivars tested for a comparison between malt and ruminant feed quality. The sample set used was a combined intermediate and advanced breeding trial with a number of commercial malting and feed cultivars, together with two international cultivars used as breeding parents. The results from this study show a generally positive relationship of the key malt trait (hot water extract), and feed traits, such as *ISDMD* and *ADG*. The positive relationship between some feed and malt quality characteristics agrees with previous studies that highlighted how some malt cultivars performed equal to or better than feed varieties.

There were genetic effects for all traits, with some variation in each trait attributable to environment, and to genotype by environment interaction. These results agreed with limited data available in assessing genetic and environmental effects on feed quality and also agreed with the numerous reports on the genetic and environmental impacts on malt quality.

The variation evident within the cultivar set and the environments facilitated an important breeding trait to be calculated, namely heritability. The results showed most traits with a moderate to high level of heritability, suggesting it would be possible to set breeding targets. In particular, the *ISDMD* trait was highly heritable. The *ISDMD* method for substrate degradation is similar to the *HWE* procedure where the barley components are attacked by enzymes to produce products which are more easily consumed. However, the enzymes in cattle must work slowly on the cell walls and protein, then act quickly on the starch when it reaches the small intestine. Conversely, in



**Fig. 2.** Biplot for principal component 2 (22%) and 3 (12%) for all traits.

the malting process and the trait of *HWE*, the grain enzymes must degrade the cell walls and protein quickly to allow the starch to be attacked.

The use of *ISDMD* or *HWE* as the key end-use quality trait would allow breeders and chemists to make appropriate decisions on the material to be advanced for the specific end-use markets, but the cost of undertaking each of these analyses would impact on the quality evaluation program. While malting and malt evaluation are relatively inexpensive, the cost of maintaining fistulated cattle over a number of years is considerable. Hence the use of *HWE* delivered results that would suit either end-use.

The data reported here adds to the growing body of evidence of the similar performance in feed nutritional value of varieties accredited as malting against those cultivars that are classified as feed (non-malting quality). Selecting for malting quality cultivars could easily satisfy quality requirements for feed cattle.

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