

Japanese Barley Meets Australia: Quality Performance of Malting Barley Grown in Different Countries

K. Ogushi^{1,4}, P. Lim², A. R. Barr³, S. Takahashi¹, T. Asakura¹ and K. Ito¹

ABSTRACT

J. Inst. Brew. 108(3), 303–309, 2002

The aim of this study is to establish whether it is possible to select malting barley showing high quality under Australian conditions on the basis of malting quality data from the crop of the same genotype grown at a breeding station in Japan. Two approaches were taken to analyse the data obtained over several years. The first was a bivariate mixed model used to obtain variety estimates for the various quality traits of interest. The second approach used a univariate mixed model to determine the correlation between the same genotype grown in Australia and Japan, as well as the correlation between the same genotype grown at trial sites within a country. The first analysis found that nitrogen was related to most malting quality traits except for viscosity. The second analysis showed that the performance in Australia and Japan is similar for all malting quality traits. It may therefore be possible to select barley showing high malting quality under Australian conditions on the basis of malting quality data from the Japanese crop of the same genotype.

Key words: Breeding, correlation, malting barley, malting quality, variance.

INTRODUCTION

Since Japan imports more than 90% of the malt used for brewing, the quality of malt and barley produced in the major malt exporting countries is of great interest^{16,27}. For assisting the stable supply of quality malting barley in Australia, the Japanese brewer Sapporo Breweries commenced a collaborative breeding program with Adelaide University in 1993. In this program barley lines with a desirable quality profile were selected and sent to Australia to be selected for agronomic performance¹⁶. The program assumed that barley lines with high malting quality selected in the breeding station in Japan would show a similar quality profile when grown in Australia.

However, barley crops, even of the same genotypes from different areas tend to be variable in malting quality. This is a widely accepted concept for brewers, maltsters and even for breeders²⁵. In addition, the malting quality potential of certain types of barley can be more stable than other varieties and also some quality characters may be more variable than others³¹.

Hot water extract (HWE) is an index of the total extractable material of malt and approximately 90 to 92% of the soluble materials are carbohydrates^{1,6}. The relative level of HWE in one environment is predictive of that in another but such prediction is less reliable than diastatic power³¹. It was observed that HWE varied considerably over sites but compared with a control variety they were constant¹². Similar results were reported by other authors^{9,33}. On the other hand, starch and amylose content were more influenced by environment than genotype⁹.

Diastatic power (DP) is one of the most important quality characters for Japanese brewers when evaluating malting barley. It represents the overall activities of the starch degrading enzymes, such as alpha-amylase, beta-amylase, alpha-glucosidase and limit dextrinase. The major contributing enzyme to DP is beta-amylase, which pre-exists in the endosperm of barley²¹. While it is well established that beta-amylase is highly heritable, the environmental influence of total nitrogen on beta-amylase is also significant²⁵. Sparrow³¹ reported that the relative ranking of DP in one environment was predictive of that in another and that genotype-environment interaction was not present. The same tendency was observed using the Scottish and Spanish crops of two varieties³³. The high DP potential of an Australian variety, Franklin, is more strongly influenced by genotype than environment¹⁹. On the other hand, Petr and co-authors described that DP was mainly influenced by weather, although they did not refer to the varietal effect²⁹. Genotype × environment interaction was not found for DP in one study³¹, while the interaction was detected in alpha-amylase using six varieties in Australia¹⁷.

It is widely accepted that the protein content of barley and malt is mainly influenced by environmental conditions such as weather and soil profiles²⁵. Sparrow³¹ described that barley nitrogen was variable among sites with low heritability, which was supported by the studies^{19,29}. Varietal differences were reported in protein content in another paper, although they were significantly influenced by environment¹⁰. Kolbach index, representing the ratio of soluble nitrogen to total nitrogen of malt, was described to be

¹ Plant Bioengineering Research Laboratories, Sapporo Breweries Ltd., 37-1 Kizaki, Nitta, Gumma 370-0393 Japan

² BiometricSA, Adelaide University, Glen Osmond, South Australia 5064 Australia

³ Department of Plant Science, Adelaide University, Waite Road, Glen Osmond, South Australia 5064 Australia

⁴ Corresponding author. E-mail: kensuke.fukuda@sapporobeer.co.jp

more influenced by environment than by genotype¹⁹. Swanston and co-workers³³ reported that there was a genotype-environment interaction detected for the index.

The endosperm cell walls of barley are comprised of 75% (1-3,1-4)-beta-glucan¹³. Undegraded or partially degraded (1-3,1-4)-beta-glucans in wort may be found in beer and can be precipitated at elevated ethanol concentrations or at low temperatures. Thus they may contribute to haze formation in the final product²². Therefore, wort beta-glucan content is an important quality character for both malt and malting barley. Wort beta-glucan content is mostly related to the following two factors; beta-glucan content in ungerminated barley and beta-glucanase activity of malt. Bourne and Wheeler⁴ found that the ranking order of wort beta-glucan content for different varieties at each site and at each harvest was similar. Total beta-glucan content in barley depended more on genotype than environmental factors³², which was supported by a study using Turkish varieties²⁸, although a significant site effect was found in beta-glucan content by Petr and co-authors²⁹. Beta-glucanase was reported to be influenced more strongly by environmental conditions^{3,32}. Significant genotype × environment interaction was detected for beta-glucanase^{17,33}. However, the relative ranking of beta-glucanase activity among four Australian varieties grown at four different sites was stable¹⁹.

The purpose of this study is to verify whether it is possible to select malting barley showing high quality under Australian conditions on the basis of malting quality data from crops of the same genotype grown at the breeding station in Japan.

MATERIALS AND METHODS

Plant materials

Six different malting barley varieties were included in the analysis: Franklin, Harrington, Haruna Nijo, Lofty Nijo, Schooner and Sloop. These varieties are summarised in Table I.

Field trials

The varieties were grown in Australia and Japan for several years. The field trial of the Japanese crop was carried out in the experimental field of the Plant Bioengineering Research Laboratories (PBRL), Sapporo Breweries Ltd., Kizaki, Nitta, Gumma, Japan. The material was sown in rows of 3.0 m length (1.8 m²) in two replicates, individually harvested and threshed and the replicates of each variety were bulked for micromalting. Trials in Aus-

TABLE I. Names and description of barley varieties included in the analysis.

Variety	Plant type	Country of origin	Pedigree
Franklin	2-row, spring	Australia	Triumph × Shannon
Harrington	2-row, spring	Canada	Klages × F1[F1(Gazelle × Betzes) × Centennial]
Haruna Nijo	2-row, spring	Japan	F1(G65 × K3) × Seijo 15
Lofty Nijo	2-row, spring	Australia	Kita A66-1 × Hokuiku 19
Schooner	2-row, spring	Australia	WI-2128 × WI-2099
Sloop	2-row, spring	Australia	RL-1577/84 × Schooner

tralia were conducted by Adelaide University in the same way as described in a previous report²⁶. The crops from the trial sites (listed in Table II) where samples showed adequate range of grain protein (9.0-12.0%) were used for malting quality analyses. The six varieties did not appear in every field trial in every year, on average there were four varieties in common across all experiments, although some of the sites contained all six varieties. Varieties tested in each field trial are summarised in Table III.

Micromalting and malt analysis

Barley samples for malting quality analysis were shipped to Japan and micromalted in a Phoenix Micromalting Apparatus at PBRL within a few months after harvest. All samples achieved greater than 95% germination at the time of malting according to a 4 mL germination test¹¹. The micromalting program and analysis methods were described in the previous report²⁶. The following quality characters were analysed; hot water extract, diastatic power, total nitrogen, soluble nitrogen, Kolbach index, apparent attenuation limit, Hartong index (VZ45), wort viscosity, friability and wort beta-glucan.

Statistical methods

Due to the small size of the data set (number of varieties and lack of replication at the site level), the use of sophisticated factor analytic models as discussed in Smith³⁰ and by other authors cannot be conducted. This type of analysis would have given a good understanding of the genotype × environment interactions present in this set of experiments and in particular, a good measure of genetic correlations between all sites. There were two approaches taken to analyse the data.

TABLE II. The locations (trial sites) and the year in the data set.

Year	Australia	Japan
1996	Brinkworth, Charlick, Clinton, Sandiland, Weetulta, Yeelana	Nitta
1997	Clinton, Tuckey, Weetulta, Yeelana	Nitta
1998	Borrika, Brinkworth, Bute, Cooke Plains, Keith, Lamerou, Mangalo, Yeelana	
1999	Arthurton, Brentwood, Brinkworth, Cummins, Salter Springs, Wanilla, Weetulta	
2000	Arthurton, Brentwood, Clinton, Yeelana	

TABLE III. Genotypes tested in the field trials in the data set.

Variety	Field trials where the variety appears	
	Year	Trial site
Franklin	Appearing in all the field trials	
Schooner	Appearing in all the field trials	
Sloop	Appearing in all the field trials	
Lofty Nijo	All field trials except for 1996 Charlick and 1997 Yeelana	
Harrington	1996	Brinkworth, Charlick, Clinton, Sandiland, Weetulta, Yeelana
	1997	Clinton, Tuckey, Weetulta, Yeelana
	1998	Yeelana
	2000	Yeelana
Haruna Nijo	1996	Charlick
	1997	Yeelana
	1998	Yeelana
	2000	Yeelana

The first approach was a univariate mixed model which was fitted to obtain variance components, which were then used to estimate genetic correlations. The model that was fitted for the analysis was:

$$Y = c/l * y + g + g:c + g:c:l + g:y + g:c:y + g:c:y:l$$

where g = genotype, c = country, l = location and y = year. These variance components can then be used to estimate the within and between country genetic correlations, using:

$$\rho_{gc} = (\sigma_g^2 + \sigma_{gc}^2) / (\sigma_g^2 + \sigma_{gc}^2 + \sigma_{gcl}^2)$$

$$\rho_c = \sigma_g^2 / (\sigma_g^2 + \sigma_{gc}^2 + \sigma_{gcl}^2)$$

ρ_{gc} is the correlation between the same genotype within the same country, while ρ_c is the correlation between countries. The higher the latter correlation, the more similar are the genotypes in performance across countries.

The second analysis was conducted to determine the varietal performance for each of the traits allowing for genotype \times environment effects. Since there are known relationships between total nitrogen and other quality traits²⁵, a bivariate analysis was carried out, in which total nitrogen and the trait of interest were analysed together. This model allows for variance heterogeneity and correlation of the two traits at the genetic and measurement error levels. A linear mixed model was fitted to the bivariate data. Linear mixed models are of the form:

$$\underline{Y} = X_{\tau} + Z_{\nu} + \underline{e}$$

where Y is the response of interest, X_{τ} are the fixed effects, Z_{ν} are the random effects (e.g. genotype effects) and \underline{e} are the residual phenotypic effects.

From the bivariate analysis, Best Linear Unbiased Predicts (BLUPS) are obtained. All variety BLUPS are adjusted for total nitrogen and the variety BLUPS are averaged over location and year. Variety estimates on the original scale can be obtained to add the variety BLUPS to the overall trait means.

RESULTS AND DISCUSSION

The overall quality data of the six varieties are shown in Table IV as a mean of all the field trials in which a variety was included. The results from the univariate analysis and the BLUPS are summarised in Tables V and VI, respectively. The variance components from the bivariate analysis appear in Table VII.

Hot water extract (HWE)

The bivariate model of total nitrogen (TN) and HWE showed that the genetic correlation between these traits was -0.657 . The correlation at the genotype \times location level was found to be -0.966 . The high correlation implies that TN and HWE were influenced by genotype \times environment interactions. Barley protein content has been considered to be negatively correlated with extract with unknown level of genotype \times environment interaction²⁴.

The present result of genotype \times environment interactions with respect to TN and HWE agrees with the previous studies. It was reported that patterns of relationships between extract and barley protein were different among regions in Europe, where contrasting daylength and temperature regimes were suggested to have strong influences on composition of the barley grain²⁴. Between South Australia and Nitta (Japan), the daylength profile is similar, however, the temperature pattern especially during grain filling is different¹². The interactions observed in the present study might reflect the difference in temperature regime between the two countries.

The genotype \times environment interactions with respect to HWE may be partially explained by Quantitative Trait Loci (QTL) analysis. Barr and co-authors² reported that the HWE QTL on chromosome 1H derived from the Chebec*Harrington mapping population is only expressed in some environments, implying the QTL is subject to interaction effects.

Although significant interactions were detected, the largest variance component was that of genetic variation followed by the unexplained error variance of HWE. The genetic correlation of the same genotype between countries (0.659) was significant but lower than the within country correlation (0.991). The results suggest that the Australian and Japanese crops perform relatively similar for HWE, which supports the results of the previous reports^{9,12,30,32}. Therefore it is possible to select genotypes showing relatively high HWE in Australia on the basis of the data from the same genotypes grown in the breeding station in Japan.

HWE is a complex trait which may be influenced by a number of biochemical factors. Using QTL analysis of DH lines between an Australian variety, Galleon and a Japanese variety, Haruna Nijo, Collins and co-authors⁷ found a QTL region on chromosome 2H associated with both malt extract and husk content. They also reported constant relationships between HWE and malt beta-glucan level⁷ and germination speed⁸. It is reported that barley

TABLE IV. The overall quality profile of the six varieties summarised as a mean of all the field trials in which a variety was included.

Variety	Quality character*									
	TN (%)	HWE (% db)	SN (%)	KI	AAL (%)	DP (WK)	HI	VIS (mPas)	FRI (%)	WBG (mg/L)
Franklin	1.77	80.0	0.609	35.0	83.5	305	32.3	1.55	74.2	167
Harrington	1.67	81.3	0.786	47.7	85.6	305	52.8	1.49	84.6	97
Haruna Nijo	1.85	82.1	0.706	38.7	84.5	266	44.0	1.56	81.9	142
Lofty Nijo	1.74	80.4	0.657	38.2	85.2	276	38.1	1.50	85.0	67
Schooner	1.73	79.5	0.709	41.4	80.2	227	32.8	1.52	83.7	74
Sloop	1.76	79.0	0.721	41.4	82.1	285	33.6	1.48	87.2	49

*TN: total nitrogen in malt, HWE: hot water extract, SN: soluble nitrogen on malt, KI: Kolbach index, AAL: apparent attenuation limit, DP: diastatic power, HI: Hartong index (VZ45), VIS: wort viscosity, FRI: friability, WBG: wort beta-glucan content

varieties with high extract potential tend to have a bigger large starch granule diameter and that the relative ranking of mean large starch granule diameter between varieties was generally the same at the different sites investigated⁹. It may be possible to predict HWE more precisely measuring the grain components described above.

The BLUP estimates for HWE show that Haruna Nijo has the highest HWE (81.6%), followed by Harrington (80.4%) and Lofty Nijo (80.1%) and Sloop is the lowest (78.7%).

TABLE V. The results from the univariate analysis of the data set.

Quality character	Correlation coefficient for the same genotype	
	Within a country	Between countries
Hot water extract (% db)	0.991	0.659
Soluble nitrogen (%)	1.000	0.930
Kolbach index	1.000	0.982
Apparent attenuation limit (%)	0.966	0.893
Diastatic power (WK)	1.000	1.000
Hartong index (VZ45)	0.867	0.820
Viscosity (mPas)	0.901	0.901
Friability (%)	0.861	0.861
Wort beta-glucan (mg/L)	1.000	0.700

All correlations were tested for significance (Ho: rho = 0) and all were found to be highly significant at the 0.05 and 0.01 level. With this set of data, it would be expected to find any correlation greater than 0.13 to be significantly different from zero.

TABLE VI. The variety and variety mean best linear unbiased predicts (BLUPS) for the ten quality characters.

Variety	Quality character*								
	HWE (% db)	SN (%)	KI	AAL (%)	DP (WK)	HI	VIS (mPas)	FRI (%)	WBG (mg/L)
Franklin	79.8	0.595	33.6	83.3	297	30.4	1.55	76.7	156
Harrington	80.4	0.781	45.8	83.9	319	47.4	1.48	79.8	100
Haruna Nijo	81.6	0.680	38.7	83.9	266	37.6	1.54	79.7	125
Lofty Nijo	80.1	0.647	37.6	84.9	271	36.5	1.50	86.5	62
Schooner	79.1	0.700	40.7	79.9	231	31.2	1.52	84.5	70
Sloop	78.7	0.708	41.0	82.0	277	31.7	1.48	88.5	44
Variety mean	79.9	0.685	39.7	83.0	277	35.8	1.51	82.6	93

*See Table IV for the abbreviations.

Table VII. The variance components for the malting quality characters analysed in the present investigation.

Variance component*	Quality character**								
	HWE	SN	KI	AAL	DP	HI	VIS	FRI	WBG
$\sigma_{g:}^2$	1.058	0.004	14.636	3.307	974	42.804	0.906	24.196	1974
$\sigma_{g:c}^2$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
$\sigma_{g:l}^2$	0.016	0.000	0.000	0.155	0.000	6.638	0.000	3.051	0.000
$\sigma_{g:y}^2$	0.000	0.000	0.000	0.297	0.000	1.162	0.000	5.255	363
$\sigma_{g:c:l}^2$	0.000	0.000	0.000	0.000	0.000	0.000	0.099	0.000	0.000
$\sigma_{g:c:v}^2$	0.000	0.000	0.000	0.000	0.000	0.000	0.169	0.000	0.000
σ^2	0.556	0.003	7.384	0.873	1806	4.882	0.000	30.882	2187
$\sigma_{g:l(TN)}^2$	0.002	0.001	0.002	0.002	0.002	0.002	0.000	0.002	0.002
$\sigma_{(TN)}^2$	0.014	0.015	0.014	0.014	0.014	0.001	0.000	0.001	0.001
Correl 1	-0.966	0.000	0.000	-0.236	0.000	0.315	0.000	-0.383	0.000
Correl 2	-0.657	0.514	-0.406	-0.527	0.473	0.043	0.000	-0.602	0.324

* $\sigma_{g:}^2$: genetic variance for the character, $\sigma_{g:c}^2$: genotype × country interaction for the character, $\sigma_{g:l}^2$: genotype × location interaction for the character, $\sigma_{g:y}^2$: genotype × year interaction for the character, $\sigma_{g:c:l}^2$: genotype × country × location interaction for the character, $\sigma_{g:c:y}^2$: genotype × country × year interaction for the character, σ^2 : unexplained error variance for the character, $\sigma_{g:l(TN)}^2$: genotype × location interaction for TN, $\sigma_{(TN)}^2$: unexplained error variance for TN, Correl 1: correlation at genotype × location level for the character, Correl 2: genetic correlation between TN and the character

**See Table IV for the abbreviations.

Soluble nitrogen (SN)

The results of the bivariate analysis (Table VII) showed that there was no genetic correlation at the genotype × location level, however, the overall genetic correlation between SN and TN was 0.514. There were no significant variance components for genotype × location or genotype × year interactions. The results from univariate analysis displayed a correlation of 1.00 for the same genotype within a country, evidenced by the fact that there were neither genotype × location nor genotype × year interactions. However, there was a significant genotype × country interaction, which reduced the correlation of the same genotype between countries to 0.930. These results suggest that it is possible to predict variety performance for SN on the basis of malting quality data from either country. This also suggests that SN is not influenced by genotype × environment effects.

The BLUPS for SN show that Harrington is the highest (0.781%), followed by Sloop (0.708%) then Schooner (0.700%) and Franklin is the lowest (0.595%).

Kolbach index (KI)

The bivariate analysis showed that the genetic correlation between KI and TN was -0.406. The analysis also showed that KI was not influenced by either genotype × location or genotype × year interactions. This is not unexpected due to the fact that $KI = (SN/TN) \times 100^{11}$. As SN

had no genotype \times location interaction and TN had a small component for genotype \times location, it would be expected that KI would not be affected by genotype \times location interactions. The results from the univariate analysis gave a genetic correlation of 1.000 for the same genotype within the same country, which reflected the fact that there was neither significant genotype \times location nor genotype \times year interactions for KI. The correlation between countries was 0.982, which was slightly lower as there was a small variance component for the genotype \times country \times year. These results suggest that it is possible to predict variety performance for KI on the basis of malting quality data from either country.

Although significant genotype \times environment interactions with respect to KI were reported by several authors as cited above^{19,32}, the present investigation did not show such significant interactions. The difference of results may be attributed to the steeping regime applied for the experiments, since the ex-steep moisture level has primary influence on grain modification²⁵. Germination of viable, nondormant barley grain is initiated by the uptake of water¹⁴, and the moisture uptake rate may differ among crops depending on the physical and chemical structure of the grains, for example grain protein content¹. It is preferable to set the ex-steep moisture at the same level for every sample in a batch when comparing the grain modification potential between genotypes.

In the present investigation the ex-steep moisture was set to 43.5%²⁶. The other experiments seemed to apply fixed steeping time to the samples, which might have brought various levels of ex-steep moisture among samples. Therefore, the previous results might be influenced by the grain structure of the samples, which could have been influenced by environmental factors. Such influence might be detected as the interactions in the previous reports.

The varietal performances (rankings) with respect to BLUPS for KI are identical to that of SN, where Harrington is the highest (45.8), followed by Sloop (41.0) then Schooner (40.7) and Franklin is the lowest (33.6).

Apparent attenuation limit (AAL)

The bivariate analysis revealed a genetic correlation between AAL and TN of -0.527 and a genetic correlation at the genotype \times location level of -0.236 . AAL had a significant genotype \times location and genotype \times year interaction. The analysis involving country had significant variance components for genotype \times country, genotype \times country \times location and genotype \times country \times year. This suggest that the performance of a particular genotype is determined by the year of the trial, the location within a country of the trial and also in which country it is grown in. The correlation of a genotype within a country was 0.966, whilst the correlation of the same genotype between countries was 0.893. This is due to the fact that the largest variance component was genetic, the other components make up less than 10% of total variation. The results imply that the varietal ranking with respect to AAL is predictable on the basis of the data from either country, however, the performance of a particular genotype is determined by the year of the trial, the location within a country of the trial and also in which country it is grown in.

AAL has been shown to have relationship with beta-amylase. It was shown that most of the barley varieties were categorised into three types according to the difference of thermostability of their beta-amylase and that the thermostability had a high correlation with apparent attenuation limit²⁰ and that each thermostability type corresponded to a different allele of the beta-amylase structural gene¹⁸. Fukuda and co-workers¹⁵ suggested that selection for apparent attenuation was possible by detecting the beta-amylase thermostability types by using their breeding populations, which is supported by the present results. The stable varietal ranking for apparent attenuation limit in the present study may be attributed to the beta-amylase genotypes of the varieties.

The present investigation showed negative correlation between AAL and TN, implying that the ratio of fermentable extract to total extract seems to decrease as TN increases. KI and FRI also showed the similar tendency, indicating that grain modification has negative correlation with TN. It is probable that malt with lower level of modification tends to give less portion of fermentable sugar giving rise to lower AAL than malt with better modification²⁵. On the other hand, AAL showed a significant association with extract using Alexis barley in South Europe²³. Also, higher TN crops often show lower total starch and lower modification, leading to lower extract²⁵. The negative correlation between AAL and TN observed in the present study might reflect the negative relationship of HWE and grain modification with TN.

The variety estimates for AAL are obtained from the BLUPS, where Lofty Nijo is the highest (84.9%), followed by Harrington (83.9%) and Haruna Nijo (83.9%) and Schooner is the lowest (79.9%).

Diastatic power (DP)

The significant variance components from the bivariate analysis (Table VII) show that DP is not influenced by genotype \times location or genotype \times year interactions. This is due to the fact that the genotype \times country and genotype \times country \times location interactions are not significant. This implies that the performance of a genotype with respect to DP is not influenced by the country of testing. Therefore it is possible to predict variety performance on the basis of malting quality data from either country in terms of DP.

DP represents the overall activities of the starch degrading enzymes, such as alpha-amylase, beta-amylase, alpha-glucosidase and limit dextrinase, where the major contributing enzymes to DP are alpha- and beta-amylase⁵. Significant genotype \times environment interactions were found in alpha-amylase¹⁷, while beta-amylase, which pre-exists in barley endosperm¹⁴, is known to be influenced by nitrogen content of barley grains²⁵, implying significant environment effects on DP. In the present study, the DP values varied between trial sites, while the relative ranking of varieties was stable with respect to DP. The results imply that the activities of the starch degrading enzymes could be influenced by environmental factors, however, the activity per total nitrogen basis might be stable across environments.

The variety estimates for DP are obtained from the BLUPS, where Harrington is the highest (319 WK) fol-

lowed by Franklin (297 WK) and Sloop (277 WK) and Schooner is the lowest (231 WK).

Hartong index (VZ45) (HI)

The bivariate analysis revealed that HI was influenced by genotype \times location and genotype \times year interactions. The correlation between the same genotype in the same country was 0.867. The correlation of the same genotype between countries was 0.820. The genetic variance dominates the variation in HI, with genotype \times county, genotype \times country \times location and genotype \times country \times year only contributing small amounts to the total variation. The results support that it is possible to predict variety performance with respect to HI on the basis of malting quality data from either country.

HI is calculated by expressing the extract yield obtained using the isothermal mashing at 45°C as percentage of the Hot Water Extract¹¹. Higher values are given by better-modified malts, and the value varies with the activities of key heat-labile enzymes in the malt, supposedly proteases and beta-glucanases⁵. This value is influenced by the friability of the malt, the level of pre-formed extract, the variety of barley and the year of its harvest²⁵. HI is an important parameter which predicts the relative extent of endosperm protein degradation. Combined with the results for KI, it is probable that the potential of a genotype with respect to protein degradation may be stable across environments.

The variety estimates for HI are obtained from the BLUPS, where Harrington is the highest (47.4) followed by Haruna Nijo (37.6) and Lofty Nijo (36.6) and Franklin is the lowest (30.4).

Viscosity (VIS)

There were no significant genetic correlations between VIS and TN. The analysis also revealed that VIS had no genotype \times country interaction, although there were significant genotype \times country \times location and genotype \times country \times year interactions. This implies that the performance of varieties with respect to VIS is influenced by year and locations within countries. The genetic correlation between and within countries were expected to be equal, because of the fact that the variance component $\sigma_{g:c}^2$ is zero. The between county correlation was 0.901. The present results suggest that it is possible to predict variety performance with respect to VIS on the basis of malting quality data from either country.

The variety estimates for VIS are obtained from the BLUPS, where Franklin is the highest (1.55 mPas) followed by Haruna Nijo (1.54 mPas), Lofty Nijo (1.52 mPas), Sloop (1.48 mPas) and Harrington (1.48 mPas).

Friability (FRI)

The bivariate analysis showed that FRI was influenced by genotype \times location and genotype \times year interactions. The genetic correlation between FRI and TN was -0.602. The variance components for the genotype \times country interaction was found to be 0.000. However, FRI was influenced by genotype \times country \times location and genotype \times country \times year interactions, suggesting that the perform-

ance of varieties is influenced by both location and year of trials. Having a genotype \times country variance component of 0.000 suggests that the correlation between countries and within a country will be equal. This correlation was found to be 0.861. The present results suggest that it is possible to predict variety performance with respect to FRI on the basis of malting quality data from either country.

The variety estimates for FRI are obtained from the BLUPS, where Sloop is the highest (88.5%) followed by Lofty Nijo (86.5%) and Schooner (84.5%) and Franklin is the lowest (76.7%).

Wort beta-glucan (WBG)

The bivariate analysis showed that WBG was influenced by genotype \times year interactions, although it should be noted that the largest variance component was that of unexplained residual variation. The genetic correlation between genotypes within a country was 1.000. Whereas the genetic correlation between genotypes between countries was 0.700. The present results suggest that it is possible to predict variety performance with respect to VIS, FRI and WBG on the basis of malting quality data from either country.

The variety estimates for WBG are obtained from the BLUPS, where Franklin is the highest (156 mg/L) followed by Haruna Nijo (125 mg/L) and Harrington (100 mg/L) and Sloop is the lowest (44 mg/L).

Viscosity, friability and wort beta-glucan are regarded to be the parameters indicating the modification of barley endosperm cell wall although each parameter represents different physical and biochemical characters of barley. The data implies that the varietal ranking in terms of cell wall modification is stable across environments. The degree of cell wall modification depends on various factors, such as the rate at which moisture distributes through the endosperm, the rate of synthesis of hydrolytic enzymes, the extent of release of these enzymes into the endosperm and structural features of the starchy endosperm¹. The present results suggest that such factors are more strongly regulated by genetic components than environment effects.

However, the genetic correlation with TN is variable among the three parameters. A negative correlation was found for FRI, which represents the physical structure of malt kernel. The parameter gives information on the endosperm cell wall modification at the end of malting. The negative correlation between FRI and TN implies that, in a certain genotype, the cell wall tends to be less modified during malting when TN is at a higher level. It may be explained that barley endosperm structure becomes steeper as TN increases.

On the other hand, the correlation was not significant with respect to VIS and WBG. VIS and WBG are the parameters describing the physical and chemical characteristics of wort, respectively, giving information on the degree of cell wall materials degradation at the end of mashing. The present results suggest that the degradation of cell wall materials after malting and mashing is not significantly influenced by different levels of TN. The variation observed may also be caused by sub-optimal steeping or the changes in moisture during malting, which was not measured in the present investigation.

CONCLUSIONS

Malting quality parameters are not simple genetic characters *per se* but are complex traits which may be influenced by a number of biochemical factors. The present investigation, however, showed that the performance in Australia and Japan is similar for all traits analysed. Because of this it may be possible to select barley variety showing high malting quality under Australian conditions on the basis of malting quality data of the same genotype grown at a Japanese breeding station. It must be noted, however, that the present data set had the only one location from Japan (Nitta). On the other hand, there is good information on the Australian sites. Further analysis including more locations from Japan is underway which should enable a more accurate measurement of genetic correlations between countries.

ACKNOWLEDGEMENTS

The authors would like to thank the members of the SA Barley Improvement Program for the field trials in Australia, the Barley Breeding Group and the Cereal Chemistry Group, PBRL, Sapporo Breweries for their field management in Japan and malting quality analysis. Cordial thanks to Mr. Mont Stuart, Joe White Maltings for critical reading of the manuscript and Dr. Ari Verbyla and Dr. Brian Cullis, NSW Agriculture for the statistical analysis.

REFERENCES

1. Bamforth, C. W. and Barclay, A. H., Malting Technology and the Uses of Malt. In: Barley: Chemistry and Technology, American Association of Cereal Chemists: St. Paul, 1993, 297.
2. Barr, A. R., Jefferies, S. P., Warner, P., Moody, D. B., Chalmers, K. J. and Langridge P., Proceedings of the 8th International Barley Genetics Symposium, Adelaide, 2000, 167.
3. Berbigier, A., Denis, J. B. and Scriban, R., Proceedings of the 4th International Barley Genetics Symposium, Edinburgh, 1981, 204.
4. Bourne, D. T. and Wheeler, R. E., *Journal of the Institute of Brewing*, 1984, **90**, 306.
5. Briggs, D. E., Malts and Malting, Blackie Academic and Professional: London, 1998.
6. Burger, W. C. and LaBerge, D. E., Malting and Brewing Quality. In: Barley, American Society of Agronomy: Madison, 1985, 367.
7. Collins, H. M., Logue, S. J., Jefferies, S. P., Stuart, I. M. and Barr, A. R., Proceedings of the 9th Australian Barley Technical Symposium, Melbourne, 1999, 2.44.1.
8. Collins, H. M., Logue, S. J., Jefferies, S. P. and Barr, A. R., Proceedings of the 8th International Barley Genetics Symposium, Adelaide, 2000, 255.
9. Dunn, C. A., Bonnici, M. J., Logue, S. J., Long, N. R., Allan, G. R. and Stuart, I. M., Proceedings of the Institute of Brewing (Asia Pacific Section) 24th Convention, Singapore, 1996, 120.
10. Dunn, C. A., Long, N. R., Logue, S. J. and Stuart, I. M., Proceedings of the RACI Cereal Chemistry Division, 46th Conference, Sydney, 1996.
11. European Brewery Convention, Analytica 4th Edition, Brauerei und Getraenke Rundschau: Zurich, 1987.
12. Ellis, R. P., Swanston, J. S., Taylor, K. and Bruce, F., *Annals of Applied Biology*, 1989, **114**(2), 349.
13. Fincher, G. B., *Journal of the Institute of Brewing*, 1975, **81**, 116.
14. Fincher, G. B. and Stone, B. A., Physiology And Biochemistry of Germination in Barley. In: Barley: Chemistry and Technology, American Association of Cereal Chemists: St. Paul, 1993, 247.
15. Fukuda, K., Kihara, M., Kaneko, T. and Ito, K., Proceedings of the Institute of Brewing (Asia Pacific Section) 25th Convention, Perth, 1998, 194.
16. Fukuda, K., Takahashi, S. and Aida, Y., Proceedings of the 9th Australian Barley Technical Symposium, Melbourne, 1999, 2.14.1.
17. Henry, R. J. and Johnston, R. P., Barley Genetics VI, Proceedings of the International Symposium, Helsingborg, 1991, 478.
18. Kaneko, T., Kihara, M. and Ito, K., *Plant Breeding*, 2000, **119**(3), 197.
19. Kenn, D. A., Dagg, A. H. S. and Stuart, I. M., *Journal of the American Society of Brewing Chemists*, 1993, **119**, 51.
20. Kihara, M., Kaneko, T., Fukuda, K. and Ito, K., Proceedings of the 8th Australian Barley Technical Symposium, Gold Coast, 1997, 3:5.
21. Kunze, W., Technology – Brewing and Malting, International Edition, VLB: Berlin, 1996, 159.
22. MacGregor, A. W. and Fincher, G. B., Carbohydrates of the Barley Grain. In: Barley: Chemistry and Technology, American Association of Cereal Chemists: St. Paul, 1993, 73.
23. Molina-Cano, J.-L., Polo, J.-L., Sopena, A., Voltas, J., Perez-Vendrell, A.-M. and Romagosa, I., *Journal of the Institute of Brewing*, 2000, **106**, 117.
24. Molina-Cano, J.-L., Rubio, A., Igartua, E., Gracia, P. and Montoya, J.-L., *Journal of the Institute of Brewing*, 2000, **106**, 111.
25. Narziss, L., *Technologie der Malzbereitung*, 6. Auflage: Ferdinand Enke Verlag: Stuttgart, 1976.
26. Ogushi, K., Barr, A. R., Takahashi, S., Asakura, T. and Ito, K., *Journal of the Institute of Brewing*, 2002, **108**, 13.
27. Ogushi, K., Takahashi, S. and Ito, K., Proceedings of the 8th International Barley Genetics Symposium, Adelaide, 2000, 94.
28. Ozkara, R., *Journal of the Institute of Brewing*, 1998, **104**, 217.
29. Petr, J., Skerik, J., Psota, V. and Langer, I., *Monatsschrift für Brauwissenschaft*, 2000, **52**(5/6), 90.
30. Smith, A. B., Multiplicative mixed models for the analysis of multi-environment trials data, Ph.D. Thesis, Adelaide University, 1999.
31. Sparrow, D. H. B., Barley Genetics II, Proceedings of the Second International Barley Genetics Symposium, 1970, 559.
32. Stuart, I. M., Loi, L. and Fincher, G. B., *Journal of Cereal Science*, 1988, **7**, 61.
33. Swanston, J. S., Ellis, R. P., Rubio, A., Perez-Vendrell, A. and Molina-Cano, J.-L., *Journal of the Institute of Brewing*, 1995, **101**, 261.

(Manuscript accepted for publication July 2002)