PROJECT REPORT No. 324

CHARACTERISING WHEAT FLOUR PROTEIN QUALITY FROM REOMIXER TRACES

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CHARACTERISING WHEAT FLOUR PROTEIN QUALITY FROM REOMIXER TRACES

by

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CONTENTS **Page No.**

Erratum

The set-up file for the Reomixer used at CCFRA in this study had settings such that 1.0 second as recorded is 1.063 seconds (S.I. unit). All times reported for this instrument are based on this recorded unit. The report is internally consistent and the conclusions drawn are not affected. If time values are required in S.I. units, then the reported value must be multiplied by 1.063. The Reomixer used for the breeders' assessments was not affected.

It is recommended that future purchasers of a Reomixer confirm the time base with the supplier.

1. ABSTRACT

The project aim was to evaluate the ability of the Reomixer (a planetary pin mixer with computer interface designed to be similar to a Mixograph) to provide useful protein quality information, particularly for varietal testing in Recommended List (RL) and National List (NL) trials. The white flours from the 2001 and 2002 harvests were studied on the Reomixer. Other analytical data on the flours were also available.

The instrument provides practical, rapid small-scale wheat protein quality measurements derived from dough mixing characteristics. It was used with two recipes. These were 1) flour-SDS solution dough (SDS-dough) where SDS is sodium dodecyl sulphate, a detergent, and 2) flour-salt-water dough (standard-dough). The time to reach the peak of the mixing curve is taken from SDS-dough. The mixing curve data from standard-dough is reduced by calculation to two co-ordinates that are plotted on a quality map that discriminates between varying dough development, peak time, peak height and differing breakdown. Comparisons of the plotted positions of test samples are made with reference quality areas derived separately from established varieties or from a quality score (e.g. for breadmaking).

The peak time of the mixing curve from SDS-dough provided a dough strength measure that has the potential to replace the current strength measurement with the use of equipment of reduced capital cost. For breadmaking varieties, it enables assessment for weak and very strong gluten (less likely to be suitable for high energy dough mixing) and strong gluten (less likely to be suitable low energy dough mixing). For biscuit making varieties, it enables screening for relatively stronger dough (more likely to be acceptable).

For quality maps, the characteristic regions for the established varieties were determined. The relationship of position on the quality map with other individual flour quality parameters (e.g. loaf volume) showed trends in direction diagonally across the map. A quality area, plotting outside of which was definitely negative for overall bread score, was identified. Although plotting inside this area is not necessarily positive, virtually all the averaged values for the established RL varieties plotted in this area. A biscuit flour score region giving a very high likelihood of the required Extensograph resistance and extensibility was also found.

As an example, using varieties on the first year of National List testing, the Reomixer data was shown to have potential in providing relevant quality information from both recipes. The dough strengths of potential biscuit making varieties varied, with several below an indicated target for acceptance to the RL of 60 s: they also plotted outside the biscuit flour score region. Varied positions on the quality map were also observed for breadmaking varieties where they did not all correspond with the areas of the established varieties: some also plotted outside the bread quality region. This demonstrates that breeders could use the technique to better target varieties for National List testing. Use on National List varieties would provide additional information for decisions regarding selection for the Recommended List trials, thus ensuring use of HGCA funds for testing more appropriate varieties. Use across the varietal assessment chain (from breeders to millers) would allow direct comparison of values with improved understanding of quality requirements.

2. SUMMARY

INTRODUCTION

The project aim was to evaluate the ability of the Reomixer (a planetary pin mixer with computer interface designed to be similar to a Mixograph) to provide useful protein quality information, particularly for varietal testing in Recommended List (RL) and National List (NL) trials.

Currently in the RL and NL trials, direct assessment of gluten quality is limited for breadmaking varieties (apart from baking bread) to measurement of gel protein weight and elastic modulus (G´) and for biscuit making varieties to Extensograph resistance and extensibility measurements. Gel protein measurement is only carried out in a few cereal research laboratories because of equipment expense. Extensograph measurement requires a large sample (at least 300 g) and the equipment is also costly. Protein quality measurement using lower-cost accessible equipment and less material would enable plant breeders and end-users to perform the same tests, allowing direct comparison of protein quality measurements with improved understanding of quality requirements.

The Reomixer produces torque-time traces while mixing dough. It is used with two recipes: 1) flour-salt-water dough (standard-dough) and 2) flour-SDS solution dough (SDS-dough) where SDS is sodium dodecyl sulphate. Using equations determined at CCFRA, the smoothed standard-dough traces are converted into two numbers (principal component scores) that are used to plot the position on a quality map, which summarises the trace characteristics of varying dough development, peak time, peak height and differing breakdown. Points from the same variety generally plot in a characteristically positioned group on the map. A boundary around an area for a reference variety defines the region on the map where the plotted position of a test sample would denote a torque-time profile that matches that variety: quality is defined in terms of mixing characteristics. SDS-dough data provide complementary information on dough strength.

This work additionally explored the relationships between other analytical data (e.g. loaf volume, Extensograph resistance and extensibility) and both the SDS-dough data and the quality maps to determine whether supplementary quality information was obtainable.

MATERIALS AND METHODS

The Bühler-milled flours from the 2001 and 2002 harvests from the RL and NL wheat varieties that were also assessed at CCFRA for breadmaking and biscuit making quality were analysed on the Reomixer by mixing both SDS-dough and standard-dough (except for two breadmaking varieties in the NL1 2002 trial). For SDS-dough, 10.0 g flour and 10.0 g 5% SDS solution were mixed for 4 minutes at 30 °C. For standard-dough, 10.0 g flour, 4.2 g 5% salt solution (equivalent to 2% salt on the flour) and total water to the Farinograph water absorption level were mixed for 10 minutes at 30 °C. Torque was recorded in volts (V) where 1V equals 220 g cm. Additional flour analytical data (Farinograph water absorption, NIR protein, gel protein elastic modulus, CBP loaf volume and texture (high energy mixing) and Spiral loaf volume (low energy mixing)) were provided from the trials results: they were obtained using the Recommended List trials protocol. Measured values for a variety were either used as individual sample results or as a varietal average for each harvest year.

The peak time was extracted from the smoothed SDS-dough trace. For breadmaking varieties, comparison was made with the current measure of protein strength, gel protein elastic modulus (G´), and with baking results. For biscuit making varieties, it was compared with Extensograph resistance and extensibility.

The principal component scores (PC1 and PC2) were calculated from the standard-dough torque-time traces. Values corrected for protein content were also calculated: this enables comparisons to be made at constant protein values. Reference areas on the quality map were constructed for the established RL varieties (note that for the 2002 harvest, there was a change in the RL testing procedure such that for the established varieties only the controls were tested for flour quality). The consequence is that there are limited data for establishing varietal reference areas for this harvest year. The plotted positions of test varieties (e.g. NL flours) were compared with these reference areas.

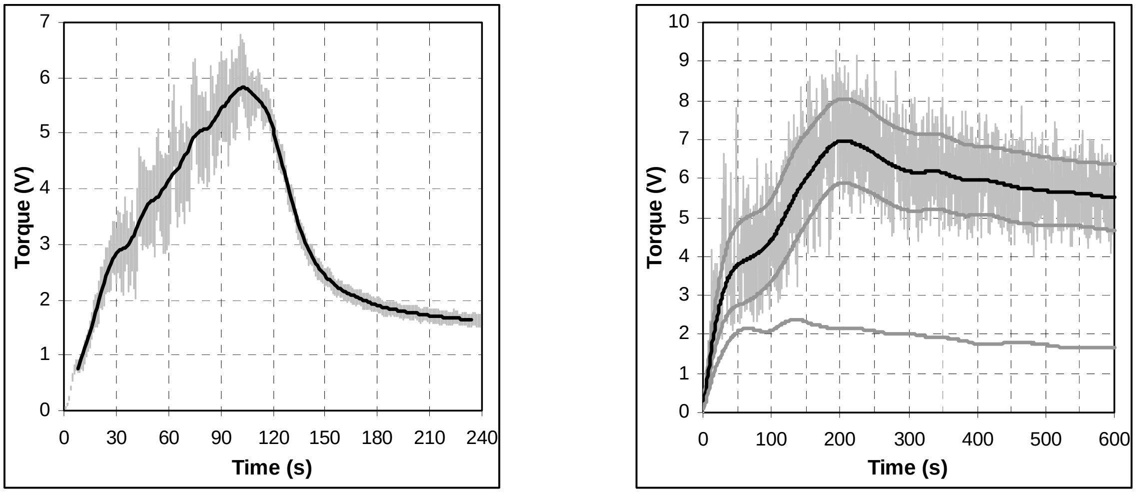
Relationships between plotted positions and other individual quality measures were investigated. Two composite quality measures were also calculated and assessed. They were 1) a bread score, calculated for each breadmaking variety for each year from the averaged values for CBP loaf volume and texture and Spiral loaf volume and 2) a biscuit making flour quality score calculated for each biscuit making variety for each year from the averaged values for Extensograph resistance and extensibility and SDS-dough peak time.

RESULTS AND DISCUSSION

Torque-time traces

Example torque-time traces are given in Figure Aa for SDS-dough and Figure Ab for standard-dough. Smoothed centre lines are shown in black and envelope lines are in grey (upper, lower and difference).

Figure A. Example torque-time traces



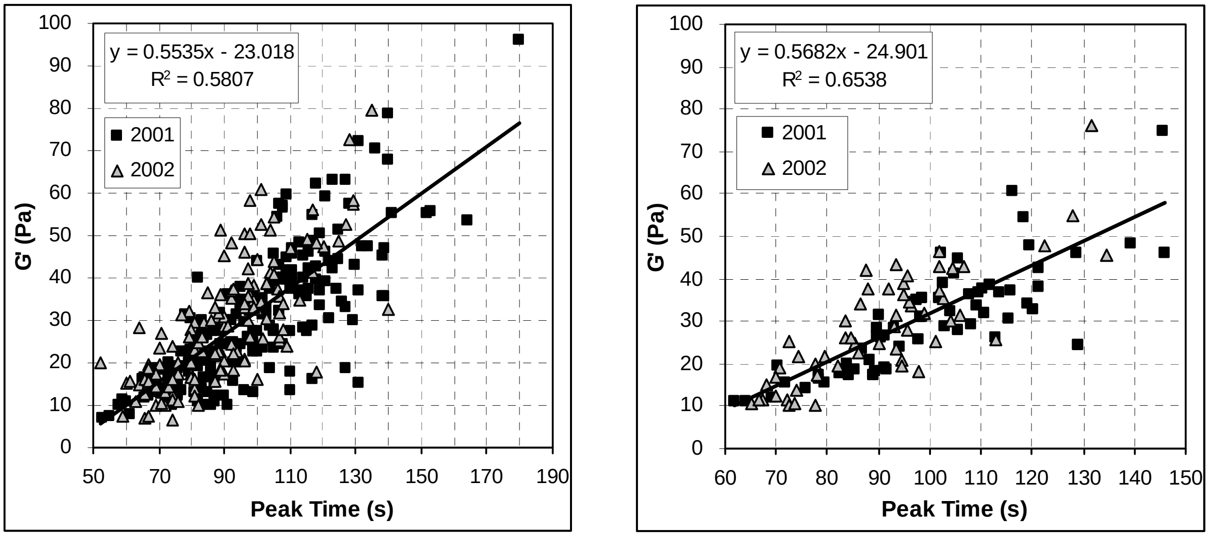
a) SDS-dough

b) Standard-dough (note the scale differences)

SDS-dough – breadmaking varieties

The relationship between gel protein elastic modulus (G´) and SDS-dough peak time is shown in Figure Ba for individual results and in Figure Bb for averaged data. The values for each harvest year are separately identified and an overall regression line has been drawn.

Figure B. Relationships between G' and SDS-dough peak time


a) Individual data

b) Average data

G´ is used as a measure of protein strength. The fact that there is a very significant relationship between peak time and G´ shows that it also is providing a strength measurement. G´ is measured on an extract from flour and is a direct measure of the high molecular weight glutenins. SDS-dough peak time is measured on whole dough. There will therefore be additional flour components affecting the latter result; hence the lack of high correlation is not unexpected. The residual errors (variation unexplained by the relationship) are too large for precise estimation of G´: the relationship could be used to estimate whether the G´ value is likely to be high or low. However, the value should be viewed as a strength measurement in its own right.

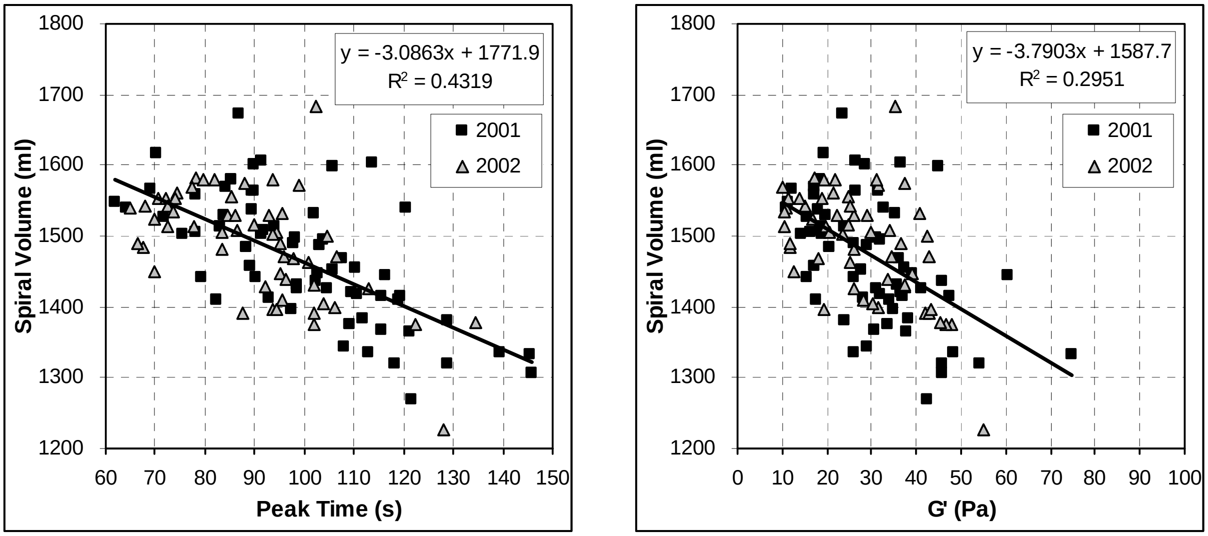
For averaged data, the relationship between Spiral loaf volume and peak time is shown in Figure Ca and that between Spiral loaf volume and G´ is shown in Figure Cb. The values for each harvest year are separately identified and an overall regression line has been drawn.

The trend is for Spiral loaf volume to decrease with increasing peak time and G´. The correlation is higher for SDS-dough peak time and therefore it is a better measure of dough strength in this context. This reinforces its use in its own right.

No useful specific relationships between CBP loaf volume and either SDS-dough peak time or G´ were found. However, they are useful in screening for weak and very strong gluten, both of which are likely to be unsuitable for the CBP process.

Figure C. Relationship between Spiral loaf volume and a) SDS-dough peak time and b) G'

a) SDS-dough peak time b) G´



SDS-dough – biscuit making varieties

Gel protein elastic modulus is not measurable in biscuit making varieties, as the quantity of gel protein obtained is too low. The SDS-dough peak time variety averages were ordered by harvest year and value to examine whether useful information was being provided. Averaged values ranged from 50 – 80 s in 2001 and from 33 – 72 s in 2002: the average values for Claire were 71 s in 2001 and 65 s in 2002. In 2001, the four varieties promoted to RL for 2002 had mean peak times of at least 69 s. The 3 varieties promoted to RL for 2003 had peak time values of at least 61 s in 2002 (they also had values of at least 60 s in 2001). This indicates that selection for the RL is favouring the stronger varieties and that a consistent average value of at least 60 s is required. In 2002, five of the seven varieties in NL1 had mean values of 53 s or less with the lowest mean being 33 s. This suggests a low probability of acceptance. Such data, if obtained when a breeder is considering varieties for trial testing, might be viewed as discouraging.

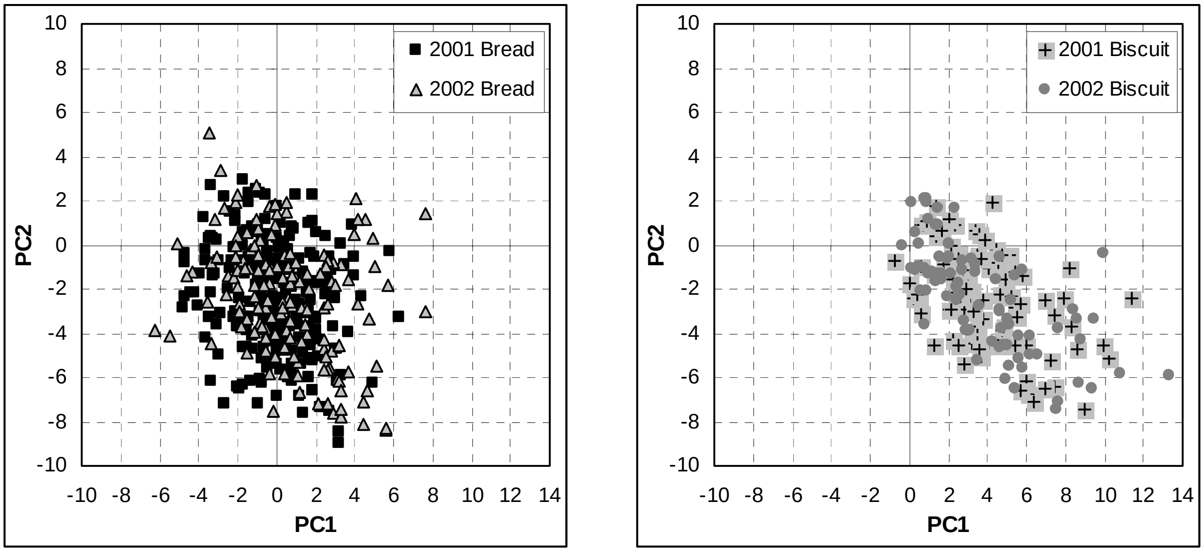
The relationship with resistance and extensibility was not of practical value.

Standard-dough – quality maps and dough mixing quality comparisons

Figure D shows quality maps with all the points for the traces from this work (excluding anomalies) identified by year. Although excessive for any more than general interpretation, they illustrate the potential advantage of condensing the data. With values held in a spreadsheet database, filtering can be used to rapidly obtain plots from more meaningful sub-sets. The general spread of points is similar for the two years.

The map surface covers the complete range of trace shapes expected as summarised in Table A, and is therefore universally applicable. In the top-left, the trace rises rapidly to a high peak and remains relatively high (trace characteristics are high – high). In the bottom-left the trace starts low with a delayed rise to a high

Figure D. Quality maps showing all samples tested


a) Breadmaking

b) Biscuit making

second half (the trace is low – high). In the bottom-right the trace is low throughout (low – low). Towards the top-right there is rapid rise and more breakdown (high – low). In the centre, both the initial and final trace heights are in middle positions (middle – middle).

Table A. Trace characteristics at various map positions
(given as the relative height of the trace in the first half followed by that in the second half)

Map Position	Left	Right
Top	High - High	High - Low
Bottom	Low - High	Low - Low

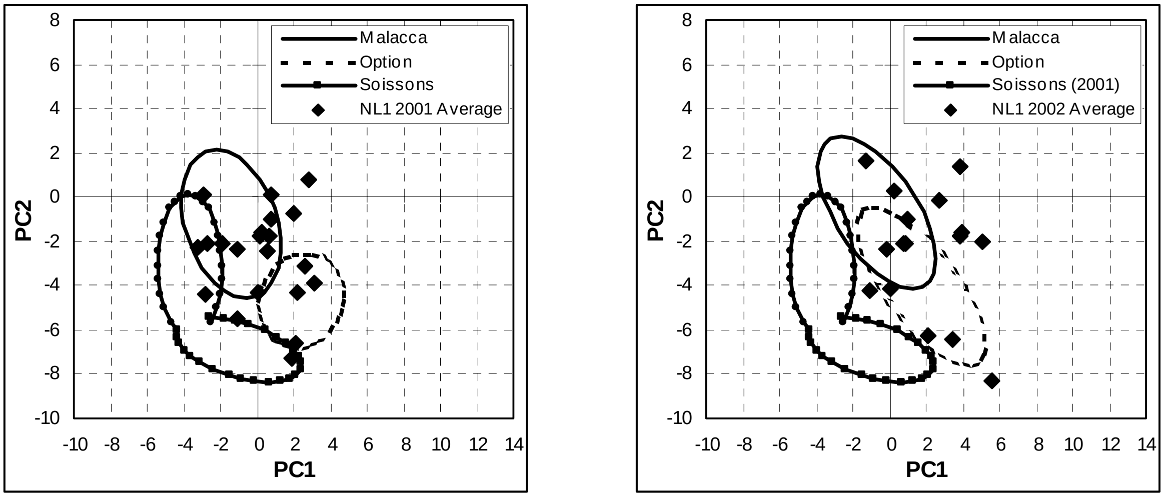
Reference areas for established values were constructed. The established **nabim** group 1 varieties (Malacca, Hereward and Shamrock) had PC1 values that were mainly less than zero and therefore tended to plot to the left of the y-axis. The newer group 1 variety Xi19, with a tendency to lower protein content, plotted mainly to the right of the y-axis. The **nabim** group 2 varieties (Option, Rialto and Charger) had PC1 values that were mainly greater than zero and therefore tended to plot to the right of the y-axis. Soissons (**nabim** group 2) plotted to the left of the y-axis but is in a region of the map (towards the bottom left) showing strong gluten characteristics. Examples of the Malacca, Option and Soissons areas are given in Figure E.

Claire (**nabim** group 3) plots around the diagonal downward to the right from the origin. The ‘as-is’ areas were very similar for the two harvest years. The protein corrected area for 2002 was smaller than in 2001 but the latter completely overlaps the area for 2002. The area for Consort (2001 only) is very similar to that for Claire, but does not extend quite so far towards the bottom left. This indicates that some samples of Claire are stronger than any of Consort. This is consistent with their relative SDS-dough peak time values.

The bulk of the Paragon samples plotted just inside the top-left quadrant (similar to Hereward). However, in 2002 there were two samples (of lower protein content) that plotted diagonally downwards to the right, producing a larger area than for 2001. After protein correction, all samples plotted in a relatively small region. Chablis plotted mainly below Paragon and slightly more to the left with some overlap. Like Paragon there were two lower protein samples in 2002.

The use of the quality maps for assessing varieties in relation to reference varieties is illustrated in Figure E. The reference areas are constructed from individual values whereas the plotted positions are from averaged values. Therefore, where the average value plots within the boundary but near the edge it is likely that some individual samples of that variety plotted outside the boundary.

Figure E. Quality maps with positions of NL1 winter varieties



a) 2001 harvest

b) 2002 harvest

In 2001, there were several varieties with average PC1 values less than zero (more likely to be **nabim** group 1, although only one is near the top left quadrant). There are two varieties low down to the right with positive PC1 in an area of poor loaf volume and with trace characteristics of later peak development and with lower peak height (possibly stronger gluten). There are two varieties outside to the right of the Malacca area, which is characteristic of satisfactory Spiral loaf volume but unsatisfactory CBP loaf volume. One variety plotted near the junction of the two Soissons ellipses showing stronger gluten characteristics.

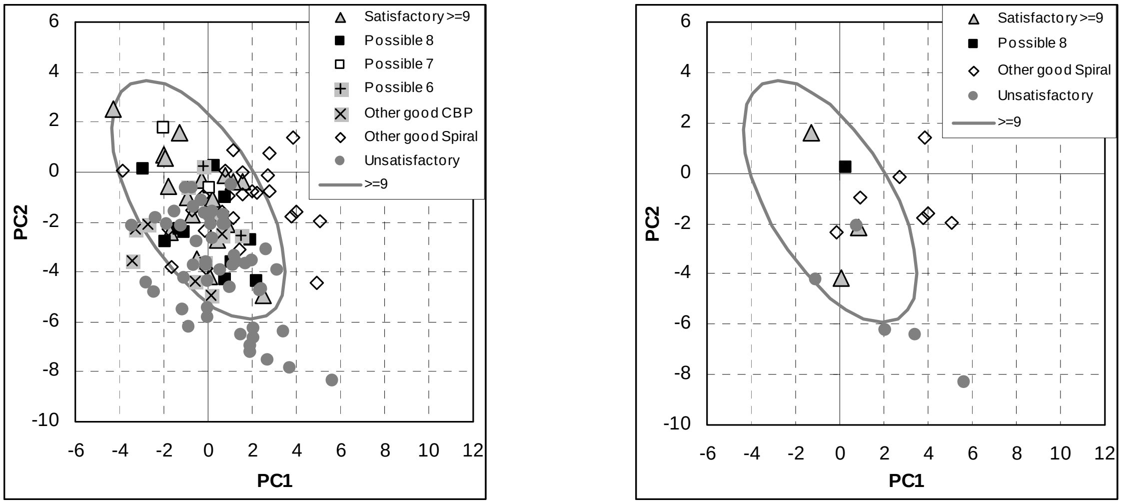
In 2002, the varietal averages had predominantly positive PC1 values. Of the varieties with a negative PC1 value (more likely to be **nabim** group 1), only one plotted in the top left quadrant. There are three varieties low down to the right with positive PC1 in an area of poor loaf volume and with trace characteristics of later peak development and with lower peak height (possibly stronger gluten). There are five varieties outside to the right of the Malacca area which is characteristic of good Spiral loaf volume but poor CBP loaf volume.

Relationships between PC plots (quality maps) and other quality measures – breadmaking varieties

Diagonal relationships from bottom left towards the top right with G´ (decrease with slope = 0.7), SDS-dough peak time (decrease with slope = 1.0) and Spiral loaf volume (increase with slope = 2.9) were found. These relationships are not sufficiently good for prediction purposes but indicate that protein strength is high towards the bottom left (e.g. Soissons) and decreases moving upwards diagonally to the right. As Spiral loaf volume increases with decreasing strength, the trend of increase in volume in this upward direction is consistent with this. For CBP loaf volume and texture, the relationships were not of much value. There was a tendency for higher values moving from right to left (in a slight diagonal upward direction for loaf volume). This is consistent with established **nabim** group 1 varieties generally plotting at PC1 values less than zero and with Hereward plotting mainly just inside the top left quadrant.

Plots for the averages for breadmaking varieties identified by overall bread score are shown in Figure Fa for all varieties and in Figure Fb for 2002 harvest NL1 winter varieties.

Figure F. Breadmaking quality score plots



a) All varieties

b) NL1 Winter, 2002 harvest

A score of 9 or above is satisfactory overall. A ‘possible’ category (scores of 8, 7 or 6) denotes just below satisfactory for 1, 2 or 3 characteristics of CBP loaf volume and texture and Spiral loaf volume. The ‘other good CBP’ category is satisfactory for CBP loaves but is unsatisfactory for Spiral loaves, and *vice-versa* for ‘other good Spiral’. The remainder are unsatisfactory. The boundary surrounding the points of score of 9 or above was calculated statistically and is also drawn on the map. All the ‘possible’ points also plot within this area. However, examples of the other categories do also. Plotting within the area is a requirement for a potentially satisfactory performance but it is not a guarantee (note that there are no unsatisfactory points in the top left quadrant). Conversely, plotting outside the area is neither satisfactory nor ‘possible’.

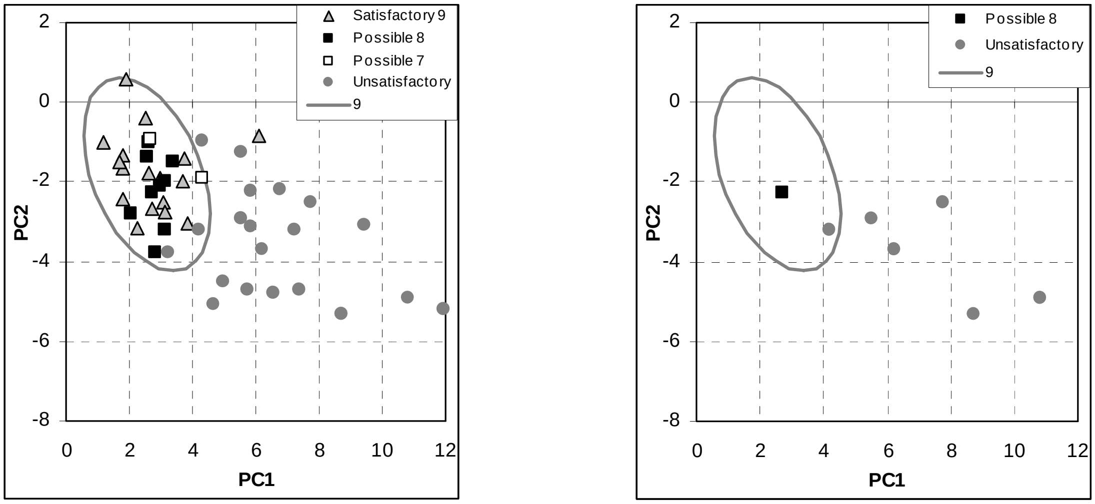
Varieties that were in the RL trials (winter and spring) for 2001 and 2002 (and including samples in NL2 for 2001) generally plotted within the boundary but there was a range of bread scores. For the NL1 winter 2002 harvest varieties, there were 8 varieties within the boundary, 5 varieties outside the boundary to the top right with satisfactory Spiral score (but unsatisfactory CBP score), consistent with the trend for weaker gluten, and 3 varieties outside with unsatisfactory scores. The most promising is the variety in the top left quadrant.

Relationships between PC plots (quality maps) and other quality measures – biscuit making varieties

SDS-dough peak time tended to increase from left to right, resistance tended to increase diagonally downward to the left (slope = 1.7) and extensibility tended to increase upwards, slightly diagonally and offset to the left (slope = -2.9).

Plots for the averages for biscuit making varieties, identified by overall biscuit making flour quality score, are shown in Figure Ga for all varieties and in Figure Gb for 2002 harvest NL1 winter varieties.

Figure G. Biscuit making flour quality score plots



a) All varieties

b) NL1 2002 harvest

A score of 9 is satisfactory overall. A ‘possible’ category (score of 8 or 7) denotes just below satisfactory for 1 or 2 of resistance, extensibility or SDS-dough peak time. The remainder are unsatisfactory. Also drawn is the statistically calculated boundary surrounding the points of score 9 (with one exception, which exhibited atypical Reomixer trace characteristics, omitted from the calculation). All the ‘possible’ points also plot within this area, with only two unsatisfactory averages plotting near the bottom of the area. Varieties that were in the RL trials for 2001 and 2002 (and including samples in NL2 for 2001) all plotted within the boundary except for Riband, which by current standards has gluten properties that are too weak. For the NL1 winter 2002 harvest varieties, only two plotted within the boundary and 5 plotted outside: these data confirm the finding of unsatisfactory quality that was suggested earlier by the SDS-dough peak time averages.

Use of whole grain

This work used white flour, as it was readily available in the RL and NL trials. A standard-dough trace currently requires knowledge of the Farinograph water absorption, which is routinely obtained in these trials.

In other circumstances (particularly for breeders) there may be insufficient white flour to obtain a water absorption value. NIR calibrations are available that will give an estimate of the value. The effect of the difference of this estimate from the value that would be obtained on the Farinograph is not known.

Both tests can use sieved ground grain. For standard-dough, the water addition is calculated from the ground grain moisture and protein contents as determined by NIR, negating the need for a Farinograph and thus making it more practical for breeders. Additional analyses are not needed for SDS-dough.

When using sieved ground grain, SDS-dough peak times are proportionally longer than from white flour: this needs to be taken into consideration when interpreting the data. For standard-dough, the torque-time traces are sufficiently dissimilar from those from white flour to require construction of separate varietal reference boundaries, although the locations on the map of the boundaries for a variety for the two materials are in the same general area. Reference data for sieved ground grain are currently more limited than for white flour.

Breeders’ assessment

Elsoms Seeds Ltd. and Monsanto UK Ltd. used a Reomixer loaned by Reologica Instruments AB to form an initial opinion on the suitability of the technique from the breeders’ perspective. Elsoms predominantly used sieved ground grain and found the results placed lines into similar categories as their current manual assessment of gluten and gave better discrimination than their existing tests for biscuit making lines. Monsanto only used standard-dough from white flour and found that, although the technique appears to offer some potential to predict ‘quality’ for breadmaking, there are significant drawbacks for them, including the need to use the Farinograph water absorption.

CONCLUSIONS

SDS-dough

The peak time provides a measure of dough strength. Although it is highly correlated with gel protein elastic modulus (G´) for which it is a possible replacement, it has value in its own right. Spiral loaf volume decreased as either SDS-dough peak time or G´ increased, with the correlation being higher for the peak time measurement. The measurement can be made on biscuit making flour (unlike G´), where the data showed that selection to the RL is favoured by a value at the higher end of the range for biscuit making varieties.

Standard-dough

Reduction of standard-dough torque-time traces to two principal component scores (PC1 and PC2) is an effective condensation of the information in the traces. Using these values as co-ordinates on a quality map (with centre at the origin) gives a plotted position that summarises the trace. Use of the quality map allows simultaneous assessment of a number of traces. Construction of boundaries enclosing traces of a particular reference characteristic (e.g. from single varieties or a quality attribute) enables additional comparisons.

The work showed that established **nabim** group 1 winter breadmaking varieties (Malacca, Hereward and Shamrock) had predominantly negative PC1 values and therefore tended to plot to the left of the y-axis: the newer group 1 variety Xi19 tended to plot to the right of the y-axis. **nabim** group 2 varieties had predominantly positive PC1 values and tended to plot to the right of the y-axis: the exception was Soissons which has strong gluten, the area for which is in the bottom left quadrant.

Trends in relationships with other quality measures were found on the map: these are indicative but not strong enough for predictive value. For breadmaking varieties, SDS-dough peak time and G´ increased with diagonal movement downward from right to left (slope = 1 and 0.7 respectively): Spiral loaf volume increased diagonally upwards from left to right (slope = 2.9). For biscuit making varieties, resistance increased diagonally downward to the left (slope = 1.7) and extensibility increased upwards from right to left (slope = - 2.9): SDS-dough peak time increased from right to left (slope = 0).

A region based on a bread score from averaged values was identified on the map lying diagonally downward from left to right and centred slightly downward to the left of the origin that provided useful bread quality information. Outside this region, varietal averages were unsatisfactory overall. However, although all satisfactory varietal averages plotted within this boundary, those with unsatisfactory scores also plotted inside this region but were confined to PC2 values less than zero.

A region based on a score from averaged values was identified on the map lying mainly just inside the bottom right quadrant that provided useful biscuit making flour quality information. All varieties (except Riband) that have been accepted for RL trials (established or newly promoted) plotted within this area.

IMPLICATIONS FOR LEVY PAYERS

- The Reomixer provides practical, rapid small-scale wheat protein quality measurements derived from dough mixing characteristics with the advantage of reduced capital equipment cost compared with an ultracentrifuge and an Extensograph. SDS-dough provides a dough strength measurement. Standard-dough and a quality map allows assessment of the mixing characteristics in relation to quality areas derived from individual reference varieties or a quality attribute.
- The technique is best suited to assessing the average performance of a variety (although it does have value for looking at individual samples). It is therefore of most use to breeders and in other varietal assessment studies (e.g. RL and NL studies and investigations by millers) where the technique would allow similar measurements by all concerned, facilitating direct comparison of values with improved understanding of quality requirements.
- With an understanding of what measurement values are preferred, the technique would enable breeders to better target varieties for National List testing. Similar testing on National List varieties would provide additional quality information for decisions regarding selection for the Recommended List trials, thus ensuring use of HGCA funds for testing more appropriate varieties.

3. INTRODUCTION

3.1. Background

The annual Recommended and National List trials provide valuable information relating to varietal quality. Part of these trials is the production of white flour from bread and biscuit making varieties and assessment of the quality for respective end-use. Direct assessment of gluten quality is limited for breadmaking varieties (apart from baking bread) to measurement of gel protein weight and elastic modulus (G´) and for biscuit making varieties to Extensograph resistance and extensibility measurements.

When defatted flour is extracted with sodium dodecyl sulphate (SDS) and ultracentrifuged, a gel layer is produced at the interface between the solid and the liquid[1]. This material is known as gel protein and has also been termed glutenin macropolymer[2]. It consists mainly of high molecular weight glutenins, which are only extractable from flour in the presence of reducing agents. Gel protein is viscoelastic and in an oscillating rheometer its viscous modulus (G") and elastic modulus (G´) can be measured. The elastic modulus has been related to breadmaking quality and can explain abnormal behaviour of weak and strong varieties[3]. A relatively high (> 40 Pa) elastic modulus is indicative of a strong gluten that may be unsuitable for a low energy mixing regime when producing bread.

Gel protein measurement currently requires the use of an ultracentrifuge and a sophisticated rheometer. The occurrence of these pieces of equipment in laboratories is limited by the expense and consequently gel protein measurement is only carried out in a few cereal research laboratories worldwide.

Extensograph measurement requires the use of a minimum of 300 g of white flour and uses expensive equipment that has high between-instrument variability[4].

Protein quality measurement using lower-cost accessible equipment and less material would enable plant breeders and end-users to perform the same tests, allowing direct comparison of protein quality measurements. In addition, plant breeders could use the technique for selection within their breeding programmes.

HGCA has previously sponsored a pilot study using a 2-g Mixograph[5]. This took 15 parameters from a torque-time trace and investigated the relationship with bread volume. A different equation was required for each site. Predicting volume for an unknown sample would therefore require knowledge of the growing location and equations would not be available for commercially grown samples. An equation with 10 variables was derived using data from 12 varieties averaged over 5 sites in order to reduce the site effect.

The ability to rapidly measure wheat and flour quality for a particular end-use without the time consuming requirement to produce the final product is a high-priority research need of the milling and baking industry.

Protein quality will play a major role in determining quality but as protein is not the only constituent, it is very unlikely that the ability to predict loaf volume will come from studies on protein alone. It is therefore not surprising that equations to predict loaf volume from data-sets with a small range of analyses have limited value.

Prior to the start of this project, studies carried out at the Campden & Chorleywood Research Association (CCFRA), sponsored by the Research Association's research programme[6] to screen new equipment for quality testing and by **nabim**[7]**,** has demonstrated the potential for using a Reomixer to provide protein quality information. The Reomixer is designed to be similar to a Mixograph, which is a planetary pin mixer that provides torque-time data while mixing dough, and is interfaced to a computer. It was being used to provide protein quality information from torque-time traces using two different dough recipes:-

1. SDS-dough (SDS is sodium dodecyl sulphate) where the recipe was flour and SDS solution.

   The peak time is a measure of protein strength.

2. Standard-dough where the recipe was flour, salt and water.

   The Reomixer software produces smoothed data from the torque-time trace in the form of a centre line together with an upper envelope, a lower envelope and envelope width lines. The quality information is held in any two of these lines as the other two can be derived from them: e.g. the envelope width is the difference between the upper and lower envelope lines and the centre line is their average.

   Visual examination showed that traces from the same variety were similar and were often characteristic of the variety.

   Assignment of the quality to a test sample by direct visual comparison of the whole trace with traces of known quality would be a difficult task because of the amount of information that would have to be reviewed.

   For the Mixograph (supplied by National Manufacturing Division, TMCO, Lincoln, USA) computerisation has allowed derivation of a number of parameters from the torque-time data that may be used to examine relationships with other quality attributes (e.g. loaf volume)[5]. The Reomixer software also produces a parameter set and was used to derive prediction equations with data from a limited set of flours from Swedish wheat[8].

   The prior work at CCFRA had taken data reduction a stage further by using equations derived from principal component analysis (PCA). Using PCA, experimental data for each sample are transformed into a series of uncorrelated numbers that together explain the variation in the data. This can result in considerable data reduction. Principal component weightings were derived from a calibration set and were used to calculate the principal component scores of subsequent torque-time traces. This results in calculated values that will not be entirely uncorrelated. The first two principal component scores were used as co-ordinates to plot on a ‘quality map’. Points from the same variety form a diffuse group on the plot. These groupings are not necessarily distinct, showing that some samples from different varieties can have similar characteristics (where overlap occurs). A boundary around the area of the map containing the points for a reference variety defines the region on the map where a test sample would have a torque-time profile that matches that variety.

The main output for a test sample is protein quality information as shown by the torque-time trace (reduced to two co-ordinates) in comparison with traces from established variety reference samples (as an area on the map). This comparison matches the torque-time profile but does not necessarily provide any further quality information such as loaf volume or extensibility.

3.2. Project objectives

The overall aim was to evaluate use of the Reomixer in providing protein quality information, particularly in relation to varietal testing over a number of sites in the Recommended and National List trials.

Specific objectives were:-

1. Quality maps would be used to compare varietal quality areas for Recommended List varieties over two harvests (2001 and 2002) and the protein quality of National List varieties would be assessed in relation to these reference areas.

   Note that for the 2002 harvest, there was a change in the RL testing procedure such that, for the established varieties, only the control varieties were tested for flour quality. The consequence is that there are limited data for establishing varietal reference areas for this harvest year.

2. Protein strength measurement in the presence of SDS would be used to:-

   Assess peak time measurements as an alternative to gel protein measurement by comparison of use (e.g. when considering loaf volume).

   Provide peak time measurements (as gluten strength) for biscuit varieties.

3. Additionally:-

   The information provided in 1 and 2 above would be compared and contrasted.

   The relationships with other flour quality data would be investigated; e.g. with loaf volume and Extensograph measurements.

   The methodology and errors would be documented.

3.3. Use of whole grain compared to pre-milled white flour

The assessment work described in this report has used white flour as it is readily available in the RL and NL trials. For mill intake, it is necessary to start from whole grain. Breeders may not have sufficient wheat to produce white flour and would also have a requirement to use whole grain. Methods for SDS-dough and standard-dough starting from whole grain have been developed at CCFRA with funding from **nabim**. **nabim** has agreed that these methods may be placed in the public domain.

Prior to the current work there were limited data available relating the SDS-dough peak time value obtained from white flour to the value obtained starting from whole grain. Additional data were collected and analysed in this work.

3.4. In-kind contributions

During the latter part of year 2 of the project a Reomixer was loaned for a few weeks to Elsoms Seeds Ltd. and to Monsanto UK Ltd. – Plant Breeding Activity by Reologica Instruments AB. The objective was for them to use the instrument with some of their breeding samples in order to form an initial opinion on the suitability of the technique from the breeder's perspective. Their assessments are given in Appendix C with comments in section 5.7.

4. MATERIALS AND METHODS

The study principally used white flour milled from wheat. As noted above, it is also possible to use the techniques developed starting from whole wheat grain. Details of using grain are included in the methods. Most quantities in the assays were weighed.

4.1. Reomixer

The apparatus used was a Reomixer supplied by Reologica Instruments AB, Scheelevägen 30, S-22363, Lund, Sweden. It is designed to be similar to a Mixograph, which has a planetary pin mixer action. The Reomixer has a removable bowl (for 10 g flour) that has 3 fixed pins and is located in a water jacket for constant temperature mixing. Mixing action is provided by 2 pairs of driven pins that are lowered into the bowl and are set rotating. The speed of rotation can be varied by the user. When dough is mixed in the apparatus, a twisting action is imparted to the bowl (a torque), the extent of which is recorded as a voltage by an accompanying computer. The primary output is a torque-time trace.

The instrument was calibrated such that 1.0 V output equals 220 g cm (0.0216 Nm). All torque values were recorded as a voltage figure, which was used in subsequent calculations.

4.2. Flours (white and sieved ground grain)

Samples analysed on the Reomixer were the white flours from the 2001 and 2002 harvests from the RL and NL wheat varieties that were also assessed at CCFRA for quality (except for two breadmaking varieties in the NL1 2002 trial). These flours were produced by Bühler milling (CCFRA method TES-CM-0001). Wheat samples were cleaned using a Carter-Day Dockage tester before conditioning to 16% moisture for breadmaking varieties and 15% moisture for biscuit making varieties. Mills were set to achieve flour yields and starch damage levels as close as possible to current commercial practice.

Selected wheats were used for a comparative study of SDS-dough peak time measurements (section 4.3.1) with white flour and sieved ground grain. When starting with grain, a representative sample (> 50 g) was ground on a KT 3100 mill with 0.8 mm mesh. The ground sample was mixed and allowed to cool and when mixing standard-dough, the protein and moisture content is determined by NIR (FTWG Method No. 14[4]). A representative portion was manually sieved through a 125 µm sieve to give more than 10.0 g of throughs for use with the Reomixer.

4.3. SDS-dough

4.3.1. White and sieved ground grain

Water from a water-bath at 30.0 ± 0.2 °C was circulated around the instrument.

White flour or sieved ground grain (10.0 ± 0.02 g) was weighed into a Reomixer bowl; the bowl was covered to prevent drying of the flour and was placed in the water-bath for 4 minutes to pre-warm the flour.

After pre-warming, a three-spoked well approximately 5 mm wide (between the pins) was made in the flour in the bowl. Sodium dodecyl sulphate (minimum purity 99%) solution (5% w/v, 10.0 g) was weighed into the well. The SDS solution was kept at 30 °C in the water bath.

The bowl with ingredients was placed in the Reomixer and a torque-time trace was recorded for 4 minutes at a speed of 93 ± 2 rpm. The time to reach peak torque (peak time) was measured from a smoothed trace after transfer of the raw data to a spreadsheet.

The method is fully documented as CCFRA method TES-CM-75.

4.4. Standard-dough

4.4.1. White flour

The total liquid weight required (g) is calculated from the 600 line Farinograph water absorption (WA) and is given by the formula:-

$$\text{Total liquid (g)} = \text{WA}(\%)/10 + 0.2$$

Water from a water-bath at 30.0 ± 0.2 °C was circulated around the instrument.

White flour (10.0 ± 0.02 g) was weighed into a Reomixer bowl; the bowl was covered to prevent drying of the flour and was placed in the water-bath for 7 minutes to pre-warm the flour.

After pre-warming, a three-spoked well approximately 5 mm wide (between the pins) was made in the flour in the bowl. Sodium chloride (AR) solution (5% w/v, 4.2 g) was weighed into the well (a salt level equivalent to 2% of the flour) and distilled water was added to the total liquid weight required. The sodium chloride solution and the distilled water were kept at 30 °C in the water bath.

The bowl with ingredients was placed in the Reomixer and a torque-time trace was recorded for 10 minutes at a speed of 93 ± 2 rpm.

The method is fully documented as CCFRA method TES-CM-74.

4.4.2. Sieved ground grain

This method was not used in these studies but is given here for completion.

The total liquid weight required (g) is calculated from the NIR protein and moisture values on the ground grain before sieving. The two values are entered into the Reomixer software and a water level is calculated. The total weight of liquid used in the assay is 0.3 g less than this instrument calculated figure.

Water from a water-bath at 30.0 ± 0.2 °C was circulated around the instrument.

Sieved ground grain (10.0 ± 0.02 g) was weighed into a Reomixer bowl; the bowl was covered to prevent drying and placed in the water-bath for 7 minutes to pre-warm the flour.

After pre-warming, a three-spoked well approximately 5 mm wide (between the pins) was made in the flour in the bowl. Sodium chloride solution (5% w/v, 4.2 g) was weighed into the well (a salt level equivalent to 2% of the flour). Ascorbic acid (AR) solution (1% w/v, 0.2 ml) was added (equivalent to 200 mg/kg) and distilled water was added to the total liquid weight required. The sodium chloride solution and the distilled water were kept at 30 °C in the water bath. The ascorbic acid solution was prepared daily and was kept on the bench and was protected from light by covering with aluminium foil.

The bowl with ingredients was placed in the Reomixer and a torque-time trace was recorded for 10 minutes at a speed of 83 ± 2 rpm.

The method is fully documented as CCFRA method TES-CM-73.

4.5. Method errors

Approximately every 10th sample assayed on the Reomixer was mixed in duplicate on the same day by the same operator to provide data for calculation of the ‘within-day’ standard deviation (a measure of the repeatability in the CCFRA laboratory).

The instrument was monitored on each day of use with a single measurement of a check-sample. These data were used to calculate a standard deviation, giving a measure of the day-to-day variation.

4.6. Additional flour analysis data

The flour analytical data were kindly provided from the RL and NL trials. In these trials the values were obtained using the Recommended List trials protocol.[9]

Results used were:-

1. Farinograph water absorption, FTWG method 04[4] using a 50 g bowl. The instrument records a torque-time trace while mixing flour and water. The water absorption is the water level, expressed as a percentage of the flour weight, that is required to centre the maximum of the torque-time trace on the 600 BU line.

2. NIR protein, FTWG method 14[4].

3. Gel protein elastic modulus (G´) based on CCFRA method TES-CM-0013. The elastic modulus of the gel layer that contains the SDS insoluble glutenin protein and which is formed after ultracentrifugation of a mixture of defatted flour and SDS solution is measured using a rheometer.

4. Bread volume (ml) (800g loaf) and texture score (1 – 10) based on CCFRA method WI-BCP-301 using a high-energy mixer (Morton) by the Chorleywood Bread Process (CBP). Duplicate bakes producing 4-piece, unlidded loaves were carried out. The recipe was 1680 g flour with water at the Farinograph water absorption level, 2 % salt, 1 % fat (Quartz, slip point ca. 45 °C), 2.5% compressed yeast, 100 ppm ascorbic acid and fungal *alpha*-amylase supplement to a total of 0.8 CU/g. Doughs were mixed to an energy input of 11 Wh/kg in a Morton mixer to a final temperature of 30.5 ± 1 °C.

Dough-pieces were scaled to 930 g and proved to a constant height of 11 cm at 43 °C and 80% relative humidity. Baking was in a direct gas-fired 12-tray reel oven for 30 min at 244 °C. After cooling overnight, loaf volume was measured by seed displacement. Loaf crumb was scored by a trained assessor. The average values for loaf volume and crumb score were calculated.

5. Bread volume (ml) (400g loaf) based on CCFRA method WI-BCP-302 using a low-energy mixer (Spiral). Single bakes producing single-piece, unlidded loaves were carried out. The recipe was 1400 g flour with water at the Farinograph water absorption level, 2 % salt, 1 % fat (Quartz, slip point ca. 45 °C), 2.5% compressed yeast, 100 ppm ascorbic acid and fungal *alpha*-amylase supplement to a total of 0.8 CU/g. Doughs were mixed using a two-speed Spiral no-time process for 2 min at the slower speed and 6 min at the higher speed to a final temperature of 30.5 ± 1 °C. Dough-pieces were scaled to 465 g and proved to a constant height of 10 cm at 43 °C and 80% relative humidity. Baking was in a direct gas-fired 12-tray reel oven for 25 min at 244 °C. After cooling overnight, loaf volume was measured by seed displacement. Loaf crumb score was not assessed.

4.7. Data analysis

Measured values for a variety were used either as individual results or as a varietal average for each harvest year. Where data have been identified for each trial year, e.g. NL1 or NL2, the points and data analysis do not include the reference variety data in those trials (only the RL data were used and plotted) as it is the test varieties that are of interest. Where overall average data for the year were used without reference to trials, the average values for Malacca do not include RL and NL Spring results.

On the basis of informed judgement, five standard-dough torque-time traces from breadmaking varieties were considered sufficiently anomalous to be excluded from calculations: their PC1 values were atypically high. A low protein sample of Riband gave an atypical SDS-dough trace and the peak time value was also excluded from calculations. Two flour samples (different varieties) had extensibility values very inconsistent with the measurements from other samples of the same variety in that year and were outliers in regression analyses: these extensibility values were also excluded.

4.7.1. Quality maps

For standard-dough (flour-salt-water), the torque time traces were exported into a spreadsheet and the first two principal component scores (PC1 and PC2) were calculated using equations with weightings derived at CCFRA on a different data-set before this work started. Because of the use of different data-sets, the calculated values will not necessarily be uncorrelated. Revised software for the Reomixer that directly calculates these scores should be available shortly.

A linear relationship between the scores and the flour protein content was found (section 5.3.2). Using this relationship, additional scores were calculated corrected to a fixed ‘as-is’ protein content (10.5% for breadmaking flours and 9.0% for biscuit making flours).

These pairs of scores were plotted as x, y co-ordinates on quality maps (one ‘as-is’ and one protein corrected). Points from the same variety generally plot in a characteristically positioned group on the map: grouping for a particular quality trait may also occur. Boundaries that define the area encompassing the points from a particular established variety or quality parameter are drawn on a map as required. These provide reference areas to which the plotted position of a test sample was compared.

There are two separate criteria for setting the position of the boundary:-

1. Comparing a test sample with the (whole) population of the quality grouping, e.g. the full range of protein contents for a variety. This is the more likely requirement when buying or selling wheat as an example of the variety population.

   The experimental results in the quality grouping (e.g. a single variety) for which a boundary is required are taken as representative[*] samples of this population. Statistical analysis is carried out to calculate the boundaries that encompass the population. The boundary can be set at the desired level of significance, e.g. at 95%, where 1 in 20 samples would plot outside, or at 99% (1 in 100 outside).

2. Direct comparison of test samples with control samples (e.g. a limited set of the variety) grown under similar regimes.

   This is the case in this study when comparing provisional varieties with established varieties grown on the same sites. The control sample results for a particular variety are the ‘whole population’ to which comparison is to be made. Here, the boundaries are required to relatively closely surround the experimental points and are not necessarily drawn to statistical criteria.

   Currently, an algorithm to draw these latter boundaries completely objectively is not available. It is possible to alter manually the values used in the equations that calculate the ellipses used for criterion 1 so that elliptical boundaries are constructed that appear approximately visually correct.

The starting point for the boundary was the ellipse bounding the 95% confidence interval assuming that the results for the samples for a particular quality parameter (e.g. variety) were part of a bivariate normal

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[*] The samples used must reasonably represent the whole population. If the whole population has a protein range from, e.g., 9.5% to 12.5% and the sample protein range is only, e.g. 10.3% to 11.5%, the resulting boundary is very likely to encompass too small an area. Alternatively the population to which comparison is to be made may be defined with a reduced protein content. In this case, the smaller boundary more correctly reflects the quality area for this newly defined population.

distribution. For varietal boundaries, the ellipse was subsequently modified manually to more closely surround the reference samples.

To investigate the relationships between the position on the quality map (as-is) and other quality measures (e.g. extensibility), all the points from samples (either individually or as averaged data) that had been assayed for the particular parameter (e.g. biscuit making varieties for extensibility) were plotted on a map. The range of values for the parameter was divided into bands and the samples within each band were identified by different markers in order to visualise possible regions of similar values. Multiple linear regression derived an equation between the parameter and the PC1 and PC2 values. The direction of this line was plotted on the map showing the trend.

For breadmaking varieties, the combination of measurements for CBP loaf volume, CPB loaf texture and Spiral loaf volume was investigated by assigning a score. Sets of criteria for 4 boundaries were set up. The test value was compared to the values in the boundaries and the score assigned was that for the relative value for the particular parameter. Loaf volume was compared to the average of the results for the control variety (Malacca for winter varieties and Paragon for spring varieties). CBP loaf texture score was on an absolute scale. The boundary values and scoring are shown in Table 1a, with the control variety volumes given in Table 1b.

For example, a 2001 harvest winter breadmaking variety with a CBP loaf volume of 3300 ml, a texture score of 6 and a Spiral loaf volume of 1530 ml would have a breadmaking score of 7 as the sum of 2 + 2 + 3 for the respective parameters.

Table 1a. Boundaries and scoring for breadmaking quality

Boundary values				**Scoring**	
Boundary	**CBP Text. (1-10)**	**CBP Vol. (ml)**	**Spiral Vol. (ml)**	**Relative value**	**Score**
1	8	Average + 100	Average + 50	≥1	4
2	6.5	Average – 100	Average – 50	≥2 - <1	3
3	6	Average – 200	Average – 100	≥3 - <2	2
4	5	Average – 300	Average – 150	≥4 - <3	1
				<4	0

Table 1b. Control variety loaf volume averages (ml)

	CBP loaf		Spiral loaf	
	2001	2002	2001	2002
Malacca	3448	3366	1562	1521
Paragon	3439	3493	1565	1584

The boundary values and scoring for biscuit making varieties are shown in Table 2.

Table 2. Biscuit making flour boundaries and scoring

Boundary values				**Scoring**	
Boundary	**Resistance (BU)**	**Extensibility (cm)**	**SDS-dough peak time (s)**	**Relative value**	**Score**
1	100	16	60	≥1	3
2	90	15	55	≥2 - <1	2
				<2	1

4.7.2. Additional analyses

The relationship between SDS peak time and other quality measures was investigated graphically and by regression analysis.

4.7.3. Comparison of SDS-dough peak time from white flour and sieved ground grain

Duplicate measurements were made on a selection of 14 samples for each harvest year and the relationship between the values for the two types of flour was investigated graphically and by regression analysis.

5. RESULTS AND DISCUSSION

5.1. Method errors

5.1.1. SDS-dough

The ‘within-day’ standard deviation was 2.6 s (n = 62).

The standard deviation for day-to-day variation was 3.7 s (n = 65).

5.1.2. Standard-dough

The ‘within-day’ standard deviation for PC1 was 0.33 and for PC2 was 0.25 (n = 53).

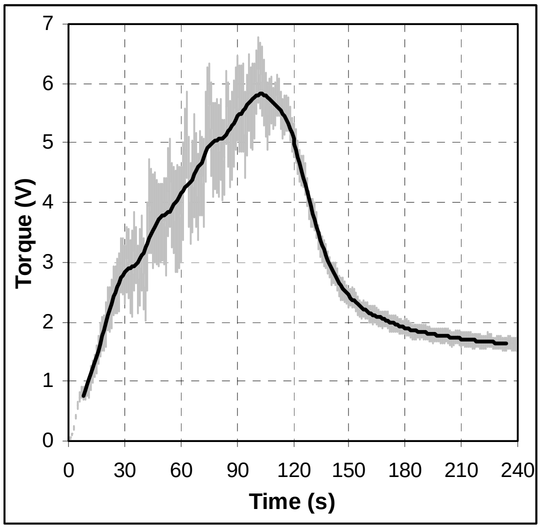
The standard deviation for day-to-day variation for PC1 was 0.46 and for PC2 was 0.31 (n = 79).

5.2. SDS-dough peak time and quality measures

5.2.1. Example torque-time trace

An example SDS-dough torque-time trace is given in Figure 1. There is dough development to a peak (of varying time and height) followed by rapid breakdown.

Figure 1. Example SDS-dough torque-time trace



5.2.2. Varietal averages

The varietal average values for SDS-dough peak time are included in the data given in Appendix B. The data in this appendix are ordered such that, when a variety has been tested in both harvest years, the results are in adjoining rows to facilitate comparison.

5.2.3. Breadmaking varieties

5.2.3.1. Relationship with gel protein elastic modulus

The relationship between gel protein elastic modulus (G´) and SDS-dough peak time for varietal averaged results is shown in Figure 2. Inspection of the graphs shows that the relationships are very similar for the two harvest years. The regression line for the relationship for the results for combined data for both years is shown as the dotted line. The equation of this line is:-

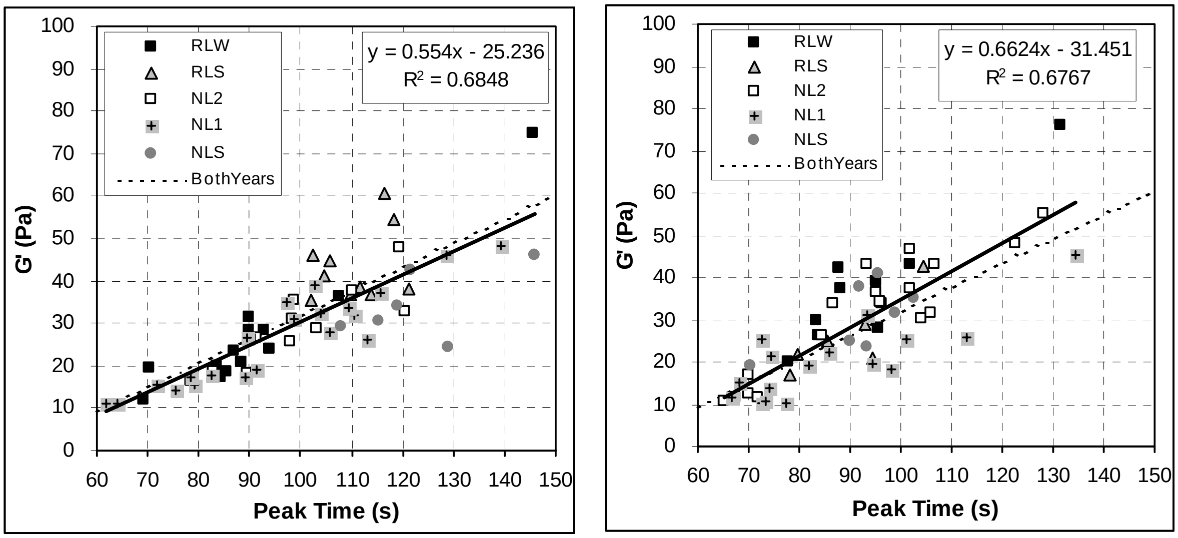
$$G' \text{ (Pa)} = 0.568 * \text{Peak time (s)} - 24.9 \quad (n = 119, r^2 = 0.65, \text{RSD} = 7.55 \text{ Pa})$$

For combined individual results for the two years (data not shown) the equation for the relationship is:-

$$G' \text{ (Pa)} = 0.554 * \text{Peak time (s)} - 23.0 \quad (n = 350, r^2 = 0.58, \text{RSD} = 9.64 \text{ Pa})$$

G´ is used as a measure of protein strength. The fact that there is a very significant relationship between peak time and G´ shows that it also is providing a strength measurement. G´ is measured on an extract from flour and is a direct measure of the high molecular weight glutenins. SDS-dough peak time is measured on whole dough. There will therefore be additional components affecting the result, thus the fact that the value of the squared correlation coefficient (r^2) is not near 1 is not unexpected. The residual error (given by the RSD) in the above equations is too large for precise estimation of G´: the equations could be used to estimate whether the G´ value is likely to be high or low. However, the SDS-dough peak time value should be viewed as a strength measurement in its own right.

Figure 2. Relationship between G' and SDS-dough peak time


a) 2001

b) 2002

5.2.3.2. Relationships with Spiral loaf volume

The relationship between Spiral loaf volume and SDS-dough peak time for varietal averaged results is shown in Figure 3. The regression line for the relationship for the results for combined data for both years is shown as the dotted line. The equation of this line is:-

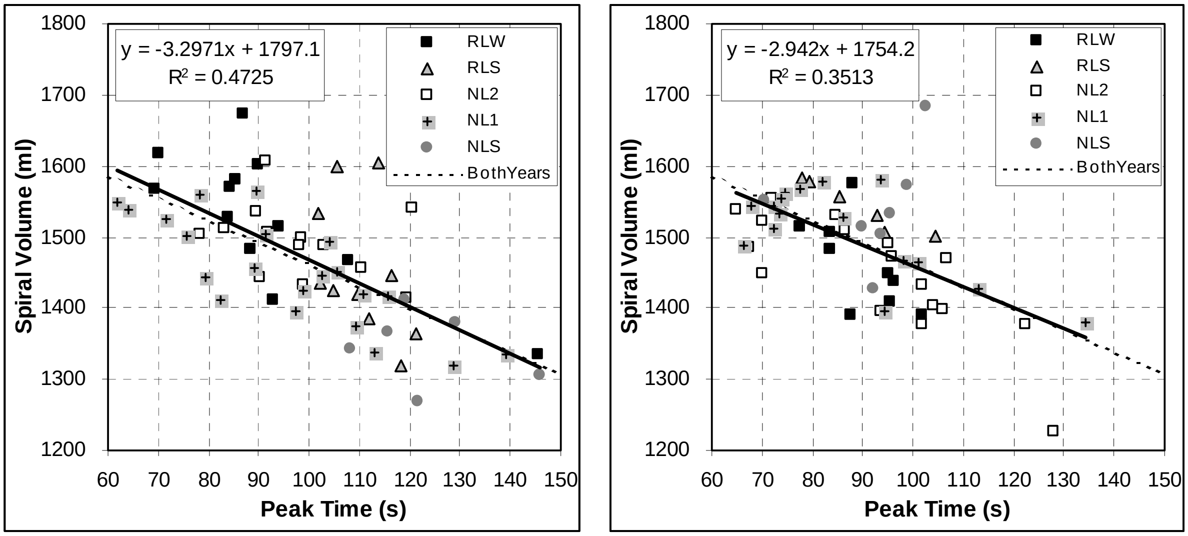
Spiral loaf volume (ml) = -3.086 * Peak time (s) + 1772 (n = 118, r^2 = 0.43, RSD = 63.8 ml)

For combined individual results for the two years (data not shown) the equation for the relationship is:-

Spiral loaf volume (ml) = -2.515 * Peak time (s) + 1719 (n = 348, r^2 = 0.26, RSD = 85.7 ml)

Figure 3. Relationship between Spiral loaf volume and SDS-dough peak time

a) 2001 b) 2002



Inspection of the graphs shows that the regression lines for the individual year data and for the combined data are very similar. The trend is for Spiral loaf volume to decrease as peak time increases.

The relationship between Spiral loaf volume and G´ for varietal averaged results is shown in Figure 4. The regression line for the relationship for the results for combined averaged data for both years is shown as the dotted line. The equation of this line is:-

Spiral loaf volume (ml) = -3.790 * G´ (Pa) + 1588 (n = 118, r^2 =0.30, RSD = 71.1 ml)

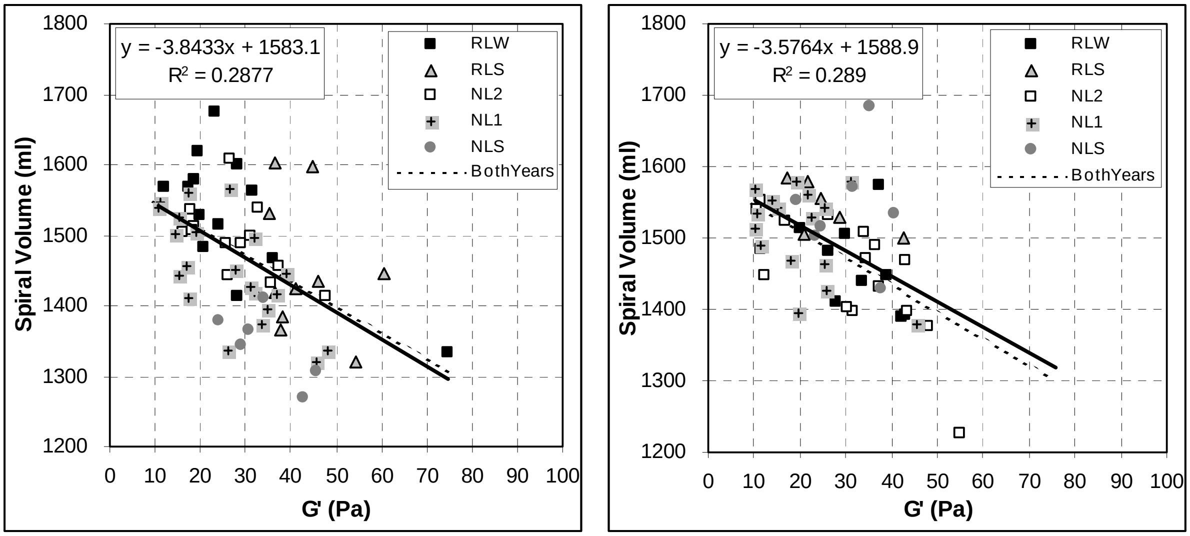
For combined individual results for the two years (data not shown) the equation for the relationship is:-

Spiral loaf volume (ml) = -2.847 * G´ (Pa) + 1563 (n = 348, r^2 =0.17, RSD = 90.9 ml)

Inspection of the graphs shows that the regression lines for the individual year data and for the combined data are very similar. The trend is for Spiral loaf volume to decrease as G´ increases.

The residual standard deviation for SDS-dough peak time, 64 ml, is smaller than for G´, 71 ml. This shows that the peak time measurement (on whole flour) is a better dough strength measure than G´ (on an extract) in this context and reinforces its use in its own right.

Figure 4. Relationship between Spiral loaf volume and G´



a) 2001

b) 2002

5.2.3.3. Relationships with CBP loaf volume

The relationship between either SDS-dough peak time or G´ with CBP loaf volume was poor. Summary data for SDS-dough peak time are given in Table 3 and that for G´ are given in Table 4. For SDS-dough peak time, relationships significant at the 5% level were found but the squared (multiple) correlation coefficient values were less than 0.25 and the residual standard deviations were all above 100 ml. For G´, only the relationship for 2002 was significant, but again the squared multiple correlation coefficient value was poor and the residual standard deviation was high.

Table 3. Summary data for the relationship between CBP loaf volume and SDS-dough peak time (averaged varietal data)

Year	Relationship	Number	R squared	RSD (ml)
2001	Linear	63	0.08	104
2002	Quadratic	55	0.22	108
Combined	Quadratic	118	0.09	109

Table 4. Summary data for the relationship between CBP loaf volume and G´ (averaged varietal data)

Year	Relationship	Number	R squared	RSD (ml)
2001	Not significant	63	0.02	
2002	Quadratic	55	0.14	113
Combined	Not significant	118	0.00	

Although specific relationships were not found, the SDS-dough peak time value will provide a useful screen for weak and very strong gluten wheats that are unlikely to be suitable for the CBP process.

5.2.4. Biscuit making varieties

5.2.4.1. Peak time values

Gel protein measurements are not made on biscuit making varieties because there is insufficient quantity: therefore comparison cannot be made. The average value for each variety is shown in ascending order grouped by trial in Table 5a for the 2001 harvest and in Table 5b for the 2002 harvest. The order of the varieties is only indicative, as the standard errors of the means are relatively large. The acceptance of NL2 varieties into the RL is shown in the last column of each table.

Table 5. Varietal average SDS-dough peak time values

a) 2001 harvest

Trial	Variety	Peak Time (s)	SD	n	SEM	2002 status
NL1	Colonel	50	11.2	3	6.5	
NL1	NSL WW47	55	3.2	3	1.9	
NL1	CEB 98057	56	4.5	3	2.6	
NL1	NSL WW50	57	8.1	3	4.7	
NL1	NFC 10034	58	6.4	2	4.5	
NL1	Dart	60	5.0	3	2.9	
NL1	NSL WW48	62	5.6	3	3.2	
NL1	CWW 00/4	63	7.4	3	4.3	
NL1	Nijinsky	64	10.1	3	5.8	
NL1	Dick	67	5.5	3	3.2	
NL1	SEMC 29	80	7.8	3	4.5	
NL2	CWW 99/43	53	10.5	3	6.1	
NL2	CPBT W77	56	6.1	3	3.5	
NL2	Harbour	59	12.5	3	7.2	
NL2	CWW 99/45	63	10.6	3	6.1	
NL2	CPBT W75	66	7.6	3	4.4	
NL2	CPBT W79	67	13.1	3	7.6	
NL2	Robigus	69	12.5	3	7.2	RL
NL2	Arran	70	15.3	3	8.8	RL
NL2	Wizard	73	13.2	3	7.6	RL
NL2	Goodwood	78	13.6	3	7.8	RL
RL	Riband	57	5.7	3	3.3	RL
RL	Consort	65	5.8	5	2.6	RL
RL*	Claire	71	10.4	11	3.1	RL
RL	Deben	74	8.2	5	3.7	RL

b) 2002 harvest

Trial	Variety	Peak Time (s)	SD	n	SEM	2003 status
NL1	PBI 01/0045	33	7.5	3	4.3	
NL1	NFC 10109	46	2.3	3	1.3	
NL1	CPBT W95	47	6.8	3	3.9	
NL1	CPBT W96	52	3.5	3	2.0	
NL1	CEB 99080	53	1.0	3	0.6	
NL1	NSL WW56	59	9.7	3	5.6	
NL1	A39-01	60	5.7	3	3.3	
NL2	Colonel	51	5.5	3	3.2	
NL2	NSL WW47	54	0.0	3	0.0	
NL2	Nijinsky	61	8.2	3	4.7	RL
NL2	Dick	61	3.5	3	2.0	RL
NL2	CEB 98057	61	2.9	3	1.7	
NL2	NSL WW50	62	2.5	3	1.5	
NL2	Dart	62	5.5	3	3.2	RL
NL2	NSL WW48	62	13.0	3	7.5	
NL2	CWW 00/4	64	8.5	3	4.9	
NL2	SEMC 29	67	6.4	3	3.7	
RL	Robigus	62	4.3	5	1.9	RL
RL*	Claire	65	5.0	11	1.5	RL
RL	Arran	67	4.3	5	1.9	RL
RL	Wizard	68	7.0	5	3.1	RL
RL	Goodwood	72	4.8	5	2.2	RL

SD = standard deviaton, n = number, SEM = standard error of the mean (SD/$\sqrt{n}$).
* Mean for Claire includes NL2 and NL1 measurements.

The four varieties promoted to RL for 2002 had mean peak times of at least 69 s in 2001. The 3 varieties promoted to RL for 2003 had peak time values of at least 61 s in 2002 (they also had values of at least 60 s in 2001). This indicates that selection for the RL is favouring the stronger varieties and that an average value of at least 60 s is required, but not all varieties with a value over 60 s will necessarily be selected. In 2002, five of the seven varieties in NL1 had mean values of 53 s or less, with the lowest mean being 33 s. This suggests a low probability of acceptance. Data such as this, if obtained when considering varieties for trial testing, would be discouraging.

5.2.4.2. Relationships with resistance and extensibility

The correlation between SDS-dough peak time and either Extensograph resistance or extensibility was low. Summary data are shown in Table 6.

Table 6. Summary data for the relationship between SDS-dough peak time and Extensograph parameters (averaged variety data)

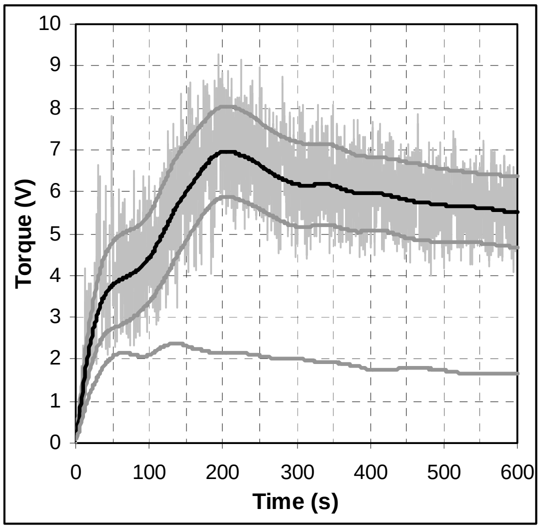
	number	r^2	RSD
Resistance	48	0.12	24 (BU)
Extensibility	48	0.18	1.4 (cm)

5.3. Standard-dough, quality maps and quality measures

5.3.1. Example torque-time trace

An example standard-dough torque-time trace together with the software calculated smoothed centre (in black) and envelope lines (in grey) is given in Figure 5. Some varieties have a characteristic shape, for example, as shown by the trace ‘Towards bottom left’ in Figure 10, which typifies Soissons.

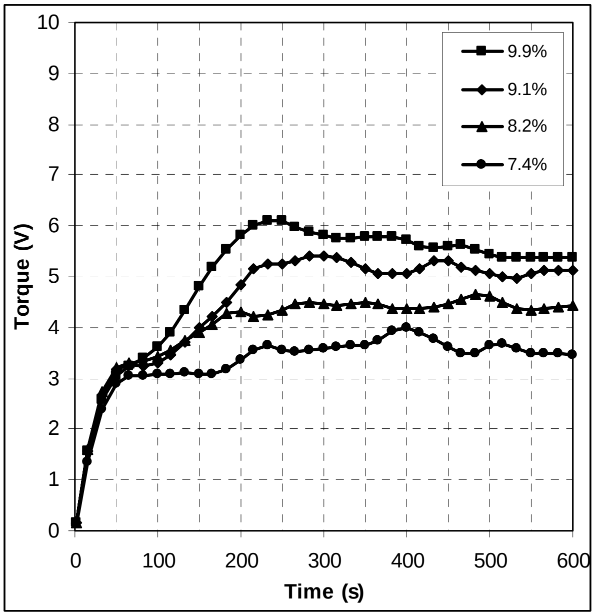
Figure 5. Example standard-dough torque-time trace



5.3.2. Effect of protein on principal component scores

When standard-dough torque time traces are compared for the same variety at decreasing protein content, there is a tendency for the peak height to decrease and the peak time to increase. This is perhaps counter-intuitive, where the probable expectation is that higher protein samples would take longer to develop. For a higher protein sample of the same variety, energy is more readily transferred to the dough such that it develops earlier. The effect of protein is illustrated for the variety Claire in Figure 6.

Figure 6. Effect of protein on standard-dough torque-time traces (centre line) for Claire

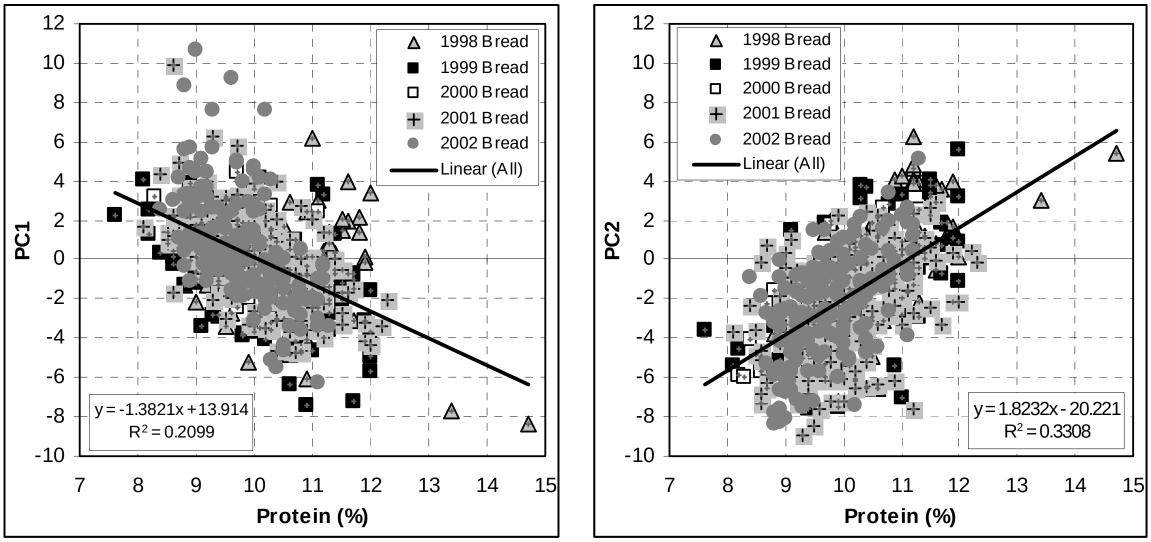


This phenomenon results in a relationship between the principal component scores and protein content. This has been examined separately for breadmaking and biscuit making varieties. The overall effect of protein level on principal component scores for breadmaking varieties is shown in Figure 7 and for biscuit making varieties in Figure 8.

The data include measurements made at CCFRA prior to this work, in order to make the relationship as robust as possible. There is considerable scatter about the line-of-best-fit due in part to the following:-

- Individual varieties have slopes that are similar but not identical to the overall slope: if it were important, a specific slope could be calculated.
- The relationships are approximate so there is variation about the line.
- Additionally, the general position of the points for some varieties may be offset from the overall line for PC1, PC2 or both.

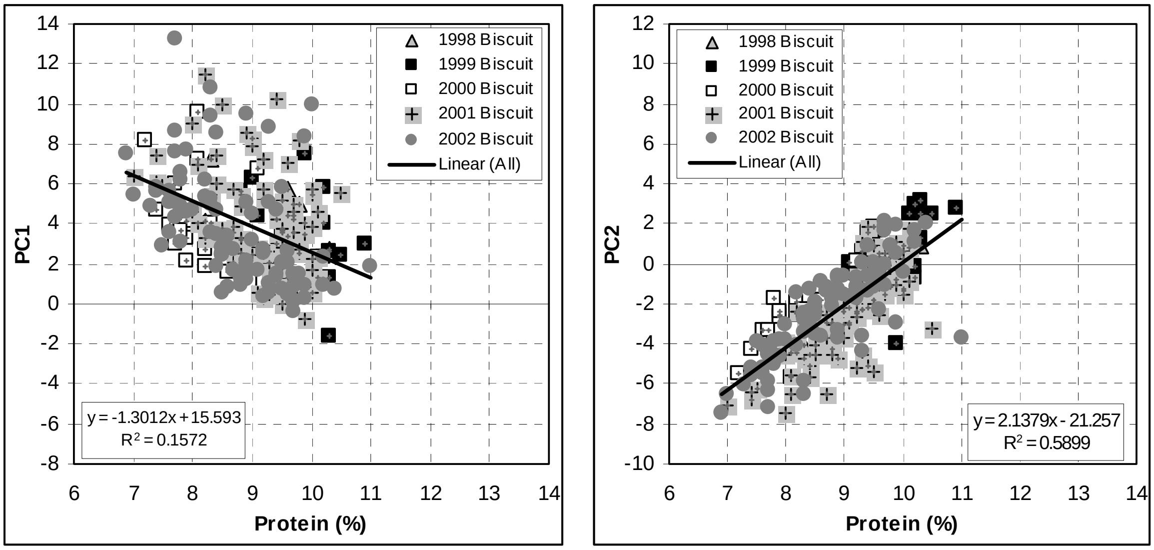
Figure 7. Effect of protein on breadmaking variety principal component scores



a) PC1

b) PC2

Figure 8. Effect of protein on biscuit making variety principal component scores



a) PC1

b) PC2

It may be useful to compare varieties at constant protein, e.g. when considering breeding lines. However, it is only meaningful if a variety is capable of achieving the reference protein content: particular care should be taken if the natural protein content of a variety is low. In this work, correction to an ‘as-is’ white flour protein content of 10.5% for breadmaking varieties and 9.0% for biscuit making varieties has been used.

The appropriate slope, shown in Table 7 is used to correct the ‘as-is’ value to a fixed protein content (section 4.7.1). A change in calculated slopes was observed when adding the 2002 harvest data. As information has already been published using the slopes including data up to the 2001 harvest[10], these data have not been recalculated with the revised slopes, as the difference in protein corrected values would be relatively small. Corrections for the 2002 harvest use the revised values.

Table 7. Slopes for protein correction of principal component scores

		Up to and including 2001		Up to and including 2002	
Flour	Reference Protein	Slope for PC1	Slope for PC2	Slope for PC1	Slope for PC2
Bread	10.5	-1.13	1.75	-1.38	1.82
Biscuit	9.0	-1.23	2.19	-1.30	2.14

The equation for correction is given by:

$$PC_{corr} = (P_{ref} - P) * S + PC_{as\text{-}is}$$

Where:-

PC_{corr} is the corrected value (of PC1 or PC2)

P_{ref} is the reference protein value for the type of flour

P is the ‘as-is’ protein content of the flour

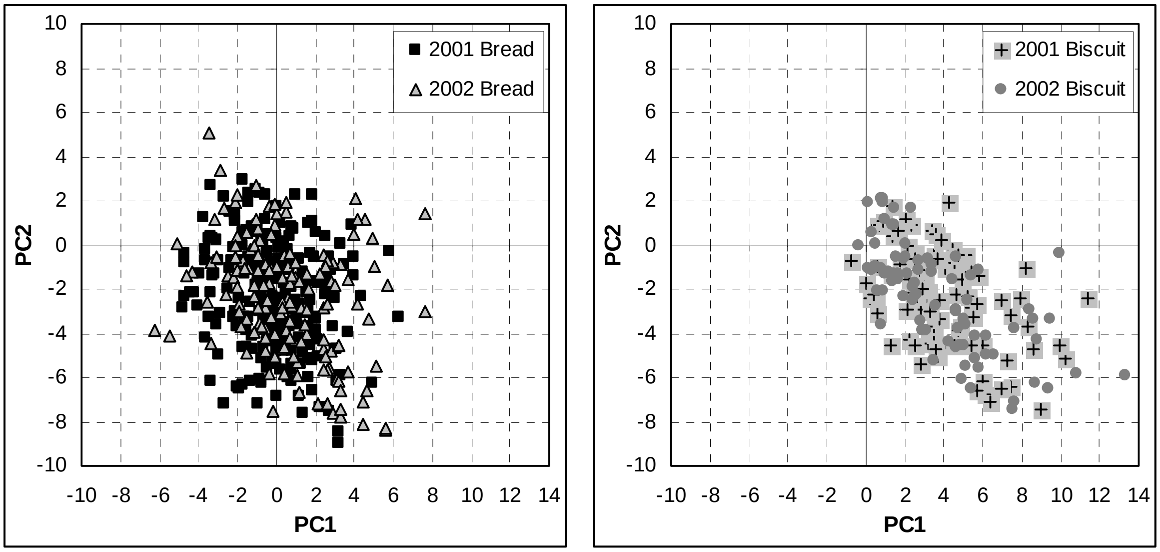
S is the appropriate slope

$PC_{as\text{-}is}$ is the originally calculated principal component score

5.3.3. Exploring the quality map

All the points for the traces taken during the course of this work (excluding anomalies) are shown in Figure 9a for breadmaking varieties and in Figure 9b for biscuit making varieties, with identification of the two harvest years. Although excessive for any more than general interpretation, they illustrate the potential of condensing the data. Consider the problems involved in attempting to compare so many individual traces to determine their range. With the data held in a spreadsheet database with filtering active, more meaningful sub-sets can be quickly viewed.

Figure 9. Quality map plot of the 2001 - 2002 harvest bread and biscuit variety data


a) Breadmaking
b) Biscuit making

The nature of the traces at various positions on the map is illustrated in Figure 10. Points have been selected towards the top-left, bottom-left, bottom-right and in the centre of the quality map. It can be seen that there are no points in the top-right of Figure 9a and Figure 9b (the legends are not hiding any points) so a point on the diagonal in that direction has been taken.

The map covers the complete range of trace shapes expected, as summarised in Table 8, and is therefore universally applicable. In the top-left, the trace rises rapidly to a high peak and remains relatively high (trace characteristics are high – high). In the bottom-left the trace starts low with a delayed rise to a high second half (the trace is low – high). In the bottom-right the trace is low throughout (low – low). Towards the top-right there is rapid rise and more breakdown. A theoretical curve for the top-right (not shown) indicates rapid rise and rapid breakdown (high – low). Wheat with claimed breadmaking potential is unlikely to have this latter trace shape and therefore would not be expected to be submitted for list trials, hence the lack of a real example in this study. In the centre, both the initial and final trace heights are in middle positions (middle – middle).

Figure 10. Illustration of traces at various map positions (upper = centre line; lower = envelope width)

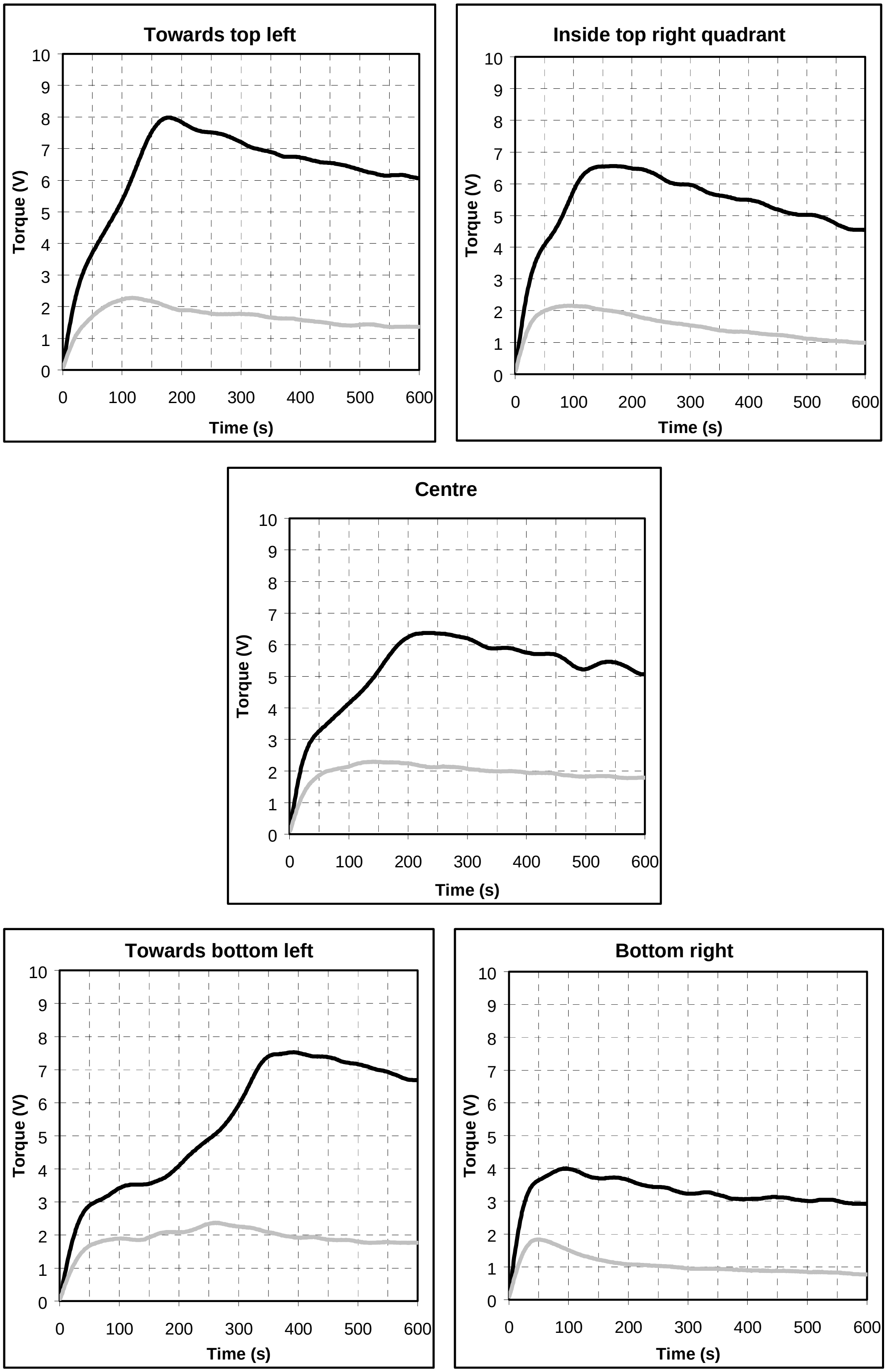


Table 8. Trace characteristics at various map positions (given as the first half followed by the second half)

Map Position	Left	Right
Top	High - High	High - Low
Bottom	Low - High	Low - Low

5.3.4. Established variety reference boundaries

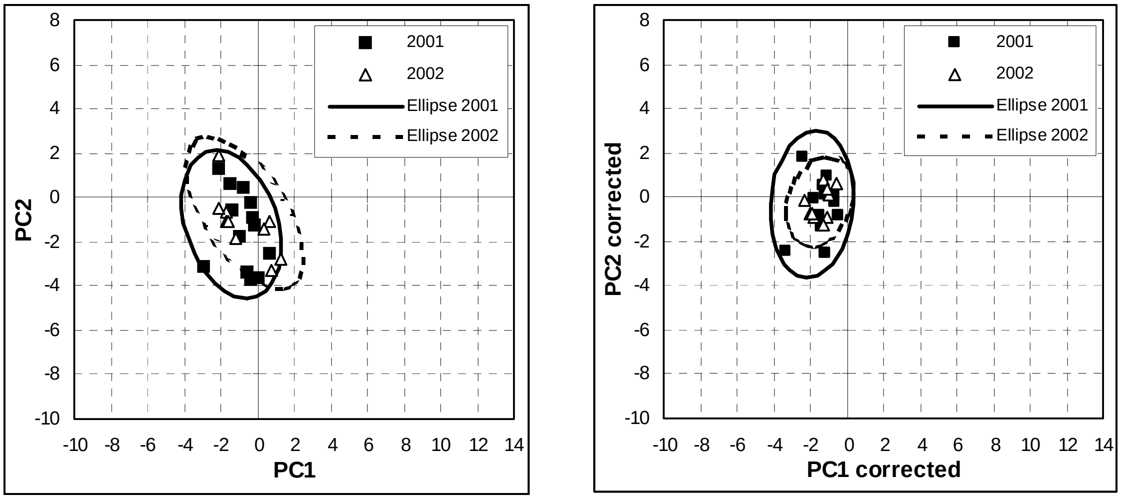
In 2001, all the established varieties were tested for quality in the RL trials and were assayed in this work. In 2002, there was an RL policy change such that for established varieties only control varieties were tested. This meant that, apart from control varieties, no other established varieties were assayed in this work except for two samples of Soissons.

Example reference boundaries, ‘as-is’ and protein corrected are shown for Malacca in Figure 11. The complete set of reference boundaries is given in Appendix A.

5.3.4.1. RL winter breadmaking varieties

Malacca plots mainly to the left of the y-axis (PC1 = 0). The ‘as-is’ boundaries are very similar for the two harvest years. Protein correction for 2002 produced a smaller area than in 2001.

Figure 11. Example points and boundaries for Malacca



a) Malacca ‘as-is’

b) Malacca ‘protein corrected’

Option plots mainly to the right of the y-axis, diagonally down to the right of Malacca. The majority of the samples had very similar grouping for the two years. In 2002, there were two samples that mapped diagonally upward to the left from this grouping: one other sample was excluded as anomalous.

Soissons plots in a curved area towards the bottom left of the map. In 2001, the variation in traces was larger than had previously been measured. The boundary is drawn as two overlapping ellipses as an oval would encompass an area in part of which Soissons samples would not be expected to plot. The two 2002 samples were insufficient to establish an area for that year: the points only are shown on the plot.

Hereward (2001 only) plots just in the top left quadrant and extending into the bottom left quadrant, overlapping with the top left area for Malacca.

Rialto (2001 only) gave a large range of traces resulting in a large area mainly in the top left corner of the bottom right quadrant.

Shamrock (2001 only) plotted in a vertically oriented area just to the left of the y-axis mainly in the bottom left quadrant.

The Charger area (2001 only) straddled the y-axis with PC2 values below zero.

The established **nabim** group 1 varieties (Malacca, Hereward and Shamrock) had PC1 values that were mainly less than zero and therefore tended to plot to the left of the y-axis. The newer group 1 variety Xi19, with a tendency to lower protein content, plotted mainly to the right of the y-axis. The **nabim** group 2 varieties (Option, Rialto and Charger) had PC1 values that were mainly greater than zero and therefore tended to plot to the right of the y-axis. Soissons (**nabim** group 2) plotted to the left of the y-axis but is in a region of the map showing strong gluten characteristics (section 5.4.1.2).

5.3.4.2. RL winter biscuit making varieties

The biscuit making varieties have ‘as-is’ areas that are very elongated in the direction corresponding to that from top-left to bottom-right as a result of varying protein content. The areas are considerably reduced after protein correction.

Claire plots around the diagonal downward to the right from the origin. The ‘as-is’ areas were very similar for the two harvest years. The corrected area for 2002 was smaller than that for 2001 but the latter completely overlaps the area for 2002.

The area for Consort (2001 only) is very similar to that for Claire, but does not extend quite so far towards the bottom left. This indicates that some samples of Claire are stronger than samples of Consort. This is consistent with their relative positions in Table 5a.

Riband (2001 only) plots to the right of Claire and Consort, indicating weaker gluten.

5.3.4.3. RL spring breadmaking varieties

The bulk of the Paragon samples plotted just inside the top-left quadrant (similar to Hereward). However, in 2002 there were two samples (of lower protein content) that plotted diagonally downwards to the right, producing a larger area than for 2001. After protein correction, all samples plotted in a relatively small region.

Chablis plotted mainly below Paragon and slightly more to the left with some overlap. Like Paragon there were two lower protein samples in 2002.

Imp (NL control only in 2002) plotted below Paragon and to the right of Chablis, effectively completing a triangle of areas.

5.3.4.4. Test sample dough mixing quality characteristics

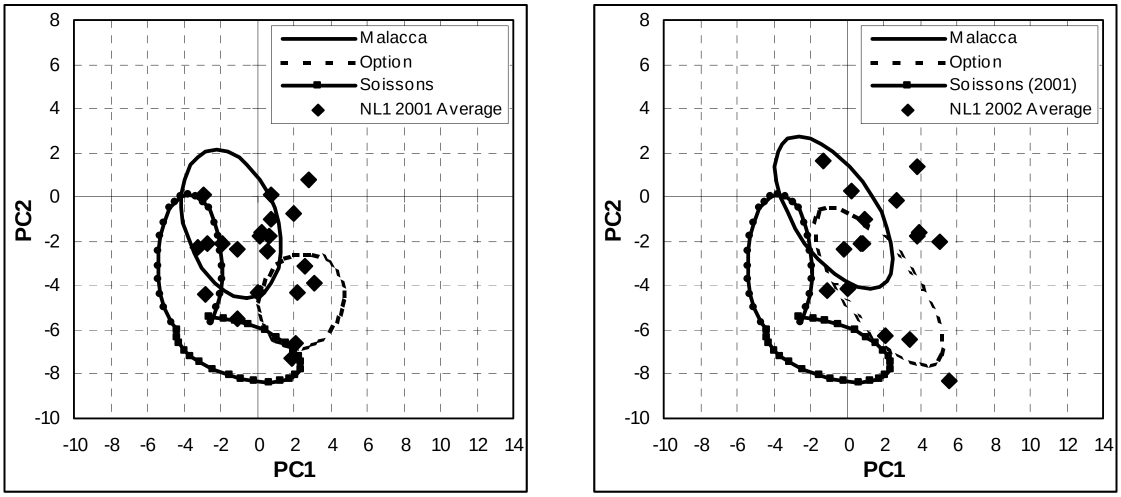
The varietal average uncorrected and corrected principal component scores are included in the data given in Appendix B. The data in this appendix are ordered such that, when a variety has been tested in both harvest years, the results are in adjoining rows to facilitate comparison.

It is impractical in this report to provide an identified plotted position on a quality map for each varietal average. Using the average values in Appendix B and the reference boundaries given in Appendix A, readers may determine the relationship to the reference areas for the varieties of specific interest to themselves. The reference areas are constructed from individual values whereas the plotted positions are from averaged values. Therefore, where the average value plots within the boundary but near the edge it is likely that some individual samples of that variety plotted outside the boundary.

Additional reference to breadmaking score and biscuit making flour score quality areas (derived from averaged data) may be made with the boundary data in section 5.4.1.5 and section 5.4.2.4 respectively.

As an illustration, the ‘as-is’ quality maps for the NL1 winter bread varieties are shown in Figure 12a for the 2001 harvest and in Figure 12b for the 2002 harvest (without individual variety identification).

Figure 12. Position of NL varieties



a) NL1 winter 2001 harvest

b) NL1 winter 2002 harvest

In 2001, there were several varieties with PC1 values less than zero (more likely to be **nabim** group 1), although only one is near the top left quadrant. There are two varieties low down to the right with positive PC1 in an area of poor loaf volume (section 5.4.1.5) and with trace characteristics of later peak development and with lower peak height (possibly stronger gluten). There are two varieties outside to the right of the Malacca area, which is characteristic of good Spiral loaf volume but poor CBP loaf volume (section 5.4.1.5). One variety plotted near the junction of the two Soissons ellipses, showing stronger gluten characteristics.

In 2002, the varietal averages had predominantly positive PC1 values. Of the varieties with a negative PC1 value (more likely to be **nabim** group 1), only one plotted in the top left quadrant. There are three varieties low down to the right with positive PC1 in an area of poor loaf volume (section 5.4.1.5) and with trace characteristics of later peak development and with lower peak height (possibly stronger gluten). There are five varieties outside to the right of the Malacca area which is characteristic of good Spiral loaf volume but poor CBP loaf volume (section 5.4.1.5).

5.4. Relationships between PC plots (quality maps) and other quality measures.

5.4.1. Breadmaking varieties

Diagonal relationships from bottom left towards the top right with G´, SDS-dough peak time and Spiral loaf volume were found as detailed below. These relationships are not sufficiently good for prediction purposes but indicate that protein strength is high towards the bottom left (as shown by Soissons) and decreases moving upwards in the direction of the diagonal.

5.4.1.1. Gel protein elastic modulus (G´)

The relationship with G´ for averaged data is shown in Figure 13. Inspection of the plot shows the higher G´ values towards the bottom left with decreasing values moving diagonally upwards to the right.

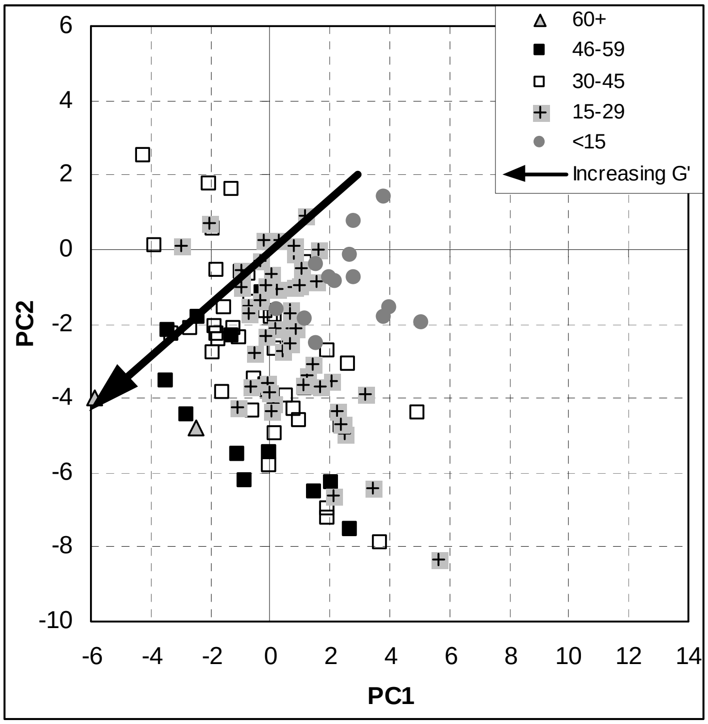
Regression analysis gives the equation:-

$$G´ \text{ (Pa)} = - 4.258 * PC1 - 2.982 * PC2 + 23.24$$

$$(n = 120, R^2 = 0.52, RSD = 8.87 \text{ Pa}, \text{Slope} = 0.70)$$

For individual results, n=381, R^2 = 0.40, RSD = 11.7 Pa, Slope = 0.78

Figure 13. Relationship between principal component scores and G' (Pa) (average values)



5.4.1.2. SDS-dough peak time

The relationship with SDS-dough peak time for averaged data is shown in Figure 14. Similarly to G´, the higher peak time values are towards the bottom left with decreasing values moving diagonally upwards towards the right. This is consistent with the relationship between the two parameters.

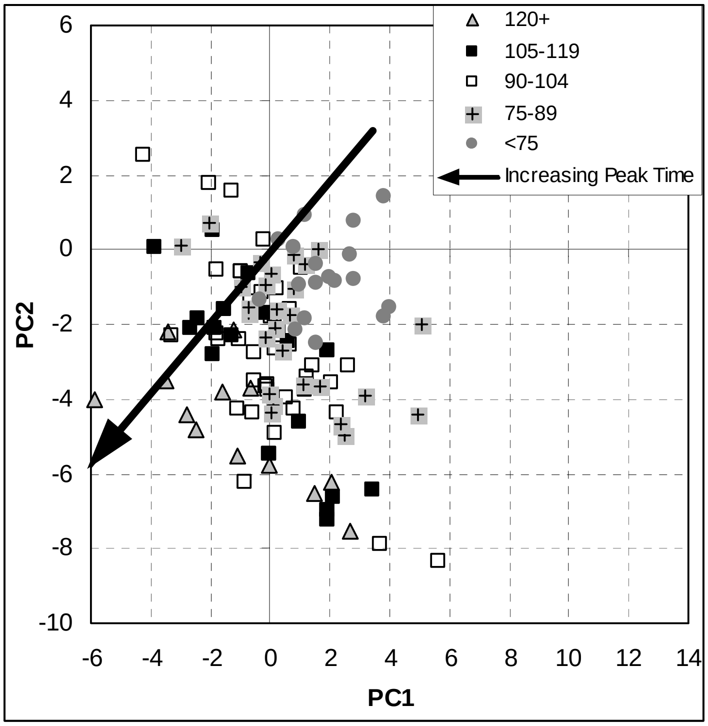
Regression analysis gives the equation:-

Peak time (s) = – 5.521 * PC1 – 5.363 * PC2 + 84.08

(n = 120, R^2 = 0.56, RSD = 12.2 s, slope = 0.97)

For individual results, n = 381, R^2 = 0.51, RSD = 14.3 s and slope = 1.01.

Figure 14. Relationship between principal component scores and SDS-dough peak time (s) (average values)



5.4.1.3. Spiral loaf volume

The relationship with Spiral loaf volume for averaged data is shown in Figure 15. Lower volumes are towards the bottom of the plot with increasing volume moving upwards at a slight diagonal to the right. This effect is to be expected because of the relationship between Spiral loaf volume and both G´ and SDS-dough peak time (section 5.2.3.2).

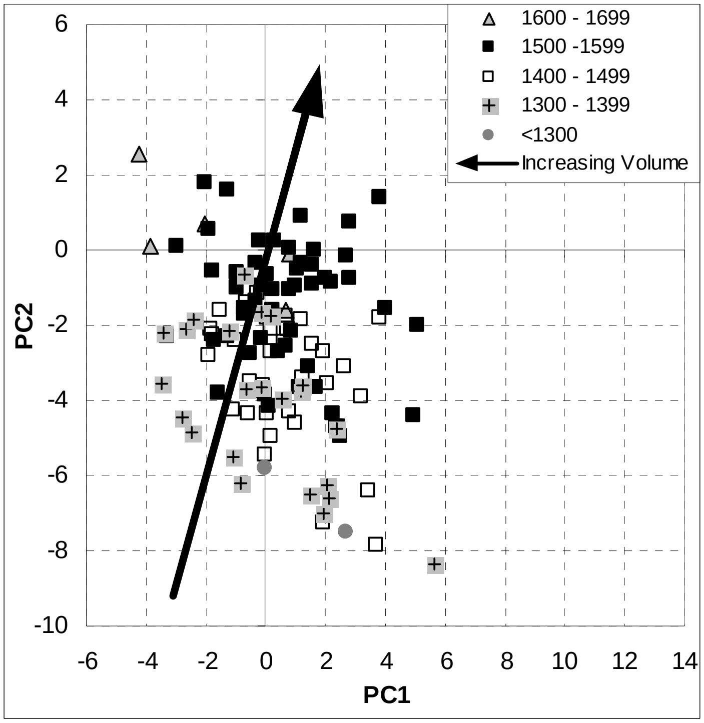
Regression analysis gives the equation:-

Spiral loaf volume (ml) = 9.687 * PC1 + 28.52 * PC2 + 1546

(n = 119, R^2 = 0.50, RSD = 59.9 ml, slope = 2.94)

For individual results, n = 379. R^2 = 0.27, RSD = 84 ml and slope = 4.5

Figure 15. Relationship between principal component scores and Spiral loaf volume (ml) (average values)



5.4.1.4. CBP loaf volume

For CBP loaf volume and texture, the relationships are not of much value. Summary data are given in Table 9.

Table 9. Summary data for the relationshiop between principal component scores and CBP loaf volume and texture

Parameter	Average	Number	R^2	RSD	Slope
Volume	Yes	119	0.19	105 ml	-0.81
Volume	No	379	0.11	138 ml	-0.21
Texture	Yes	119	0.28	0.69 score	-0.04
Texture	No	379	0.23	0.86 score	0.03

There was a tendency for higher values moving from right to left (in a slight diagonal upward direction for loaf volume). This is consistent with established **nabim** group 1 varieties tending to plot at PC1 values less than zero and with Hereward plotting mainly just inside the top left quadrant.

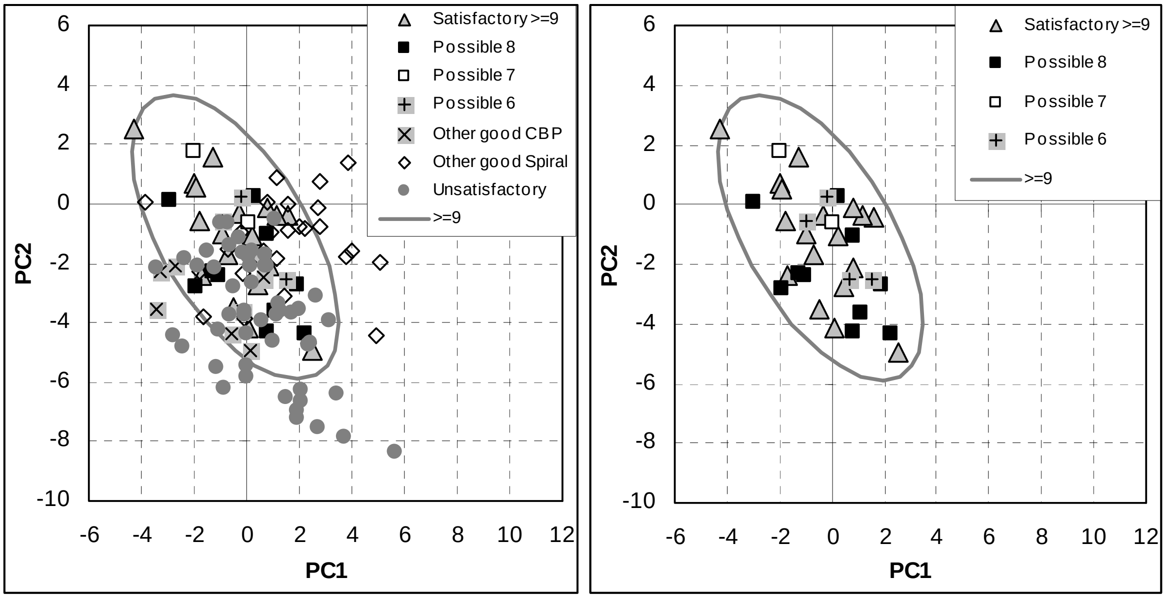
5.4.1.5. Combined bread score

Using the scoring system outlined in section 4.7.1 and Table 1, each breadmaking variety for each year was assigned a combined score for CBP loaf volume, CBP loaf texture and Spiral loaf volume from the averaged values. Satisfactory quality in each category is a score of 3. Satisfactory overall quality is a value of 9 as the sum of a score of 3 in each category. There were no scores of 9 achieved as the sum of 4+3+2 (which would not be satisfactory overall). When the score in a category is 2 then the overall score may be 8, 7 or 6 giving rise to three 'possible' categories. For the remaining samples, some may have satisfactory CBP loaf performance (a score of 3 + 3 for CBP loaf characteristics) with poor Spiral loaf performance and some may have satisfactory Spiral loaf performance (a score of 3 for Spiral loaf volume) with poor CBP loaf performance. This leaves varieties with both unsatisfactory CBP and Spiral loaf performance.

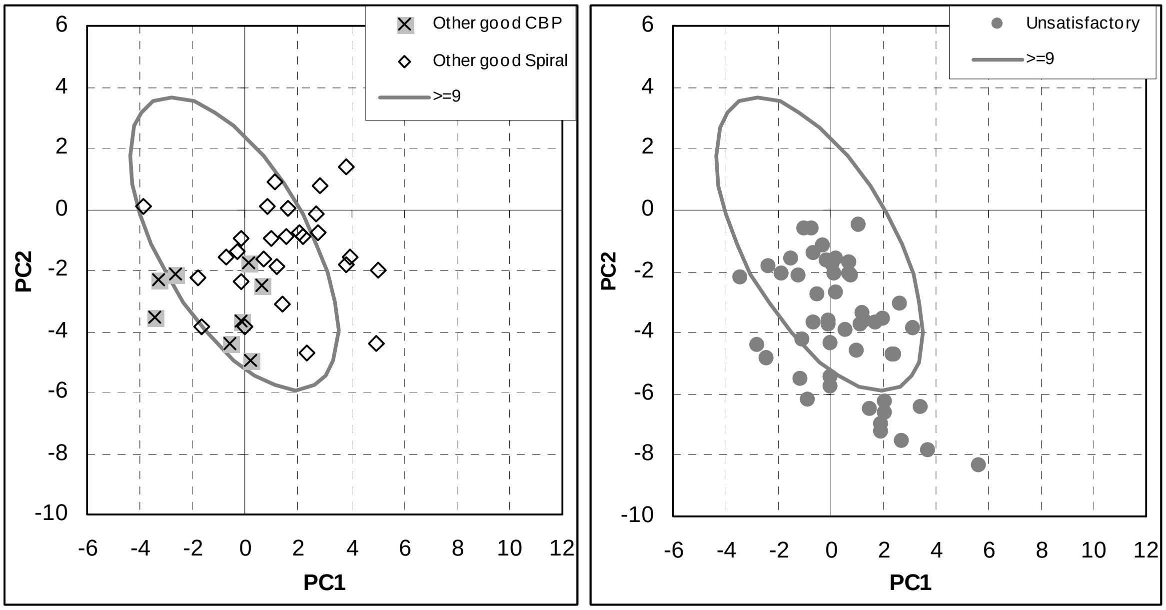
Figure 16 shows the positions of the averaged values on the quality map identified by score characterisation. Figure 16a shows all the data plotted on one graph. Figure 16b shows the sample averages with the satisfactory and three 'possible' categories. Figure 16c shows the remaining samples with satisfactory ('other good') CBP or Spiral loaf performance and Figure 16d shows those samples with unsatisfactory performance. On all graphs, the boundary defining the area where bread quality score was 9 or above has been plotted.

The plots show that the area defining where samples are satisfactory (>=9) is not exclusive for this category. Examples of all categories may plot within the boundary. The unsatisfactory varieties all had average PC2 values that were less than zero. All samples that plotted outside the boundary were not in the satisfactory overall or 'possible' categories. When they were satisfactory for CBP baking but unsatisfactory for Spiral baking, there were some varietal averages that plotted outside towards the bottom left: this is the direction for stronger gluten varieties (Figure 14). Where the quality is for Spiral baking only, then some varietal averages plotted outside towards the top right: this is the direction for weaker gluten varieties (Figure 14) with lower SDS-dough peak times: a higher Spiral loaf volume would be expected (Figure 3).

Figure 16. Quality map relationship with bread quality, coded by score with boundaries.


a) All categories

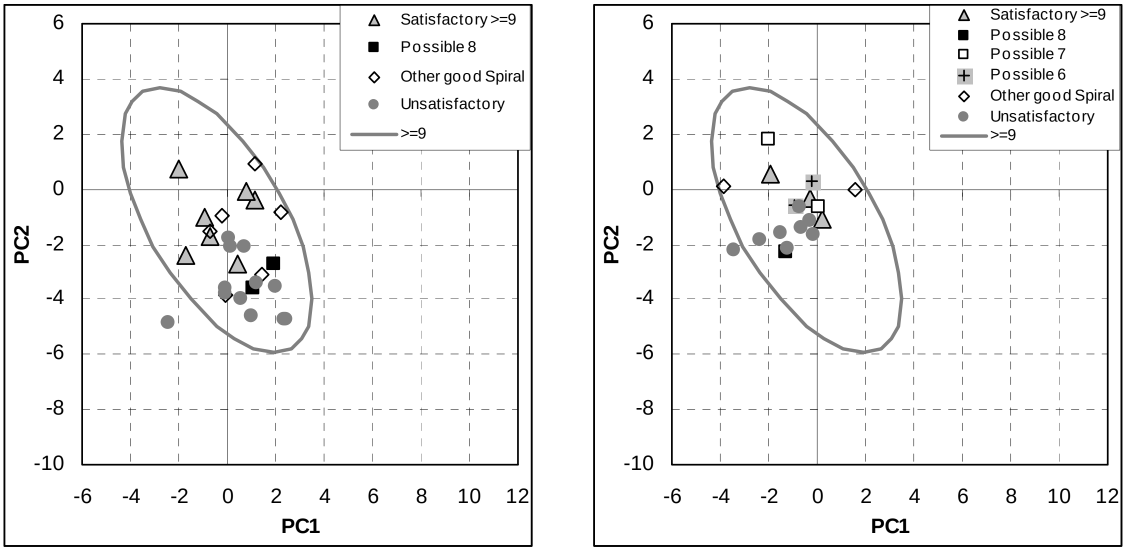
b) Satisfactory and 'possible'


c) Satisfactory CBP and satisfactory Spiral

d) Unsatisfactory

Figure 17 shows the averaged positions (separately by year) and bread quality score for those samples tested that were in the RL trials for 2001 and 2002 (including NL2 values for 2001): these range from fully recommended to newly promoted varieties. For RL winter, only one varietal sample (Soissons 2001) is outside the boundary although the scores are not all satisfactory. For RL spring, the one variety outside the boundary is Chablis (2001) and again there is a range of scores.

Figure 17. Quality map relationship with bread score for RL varieties

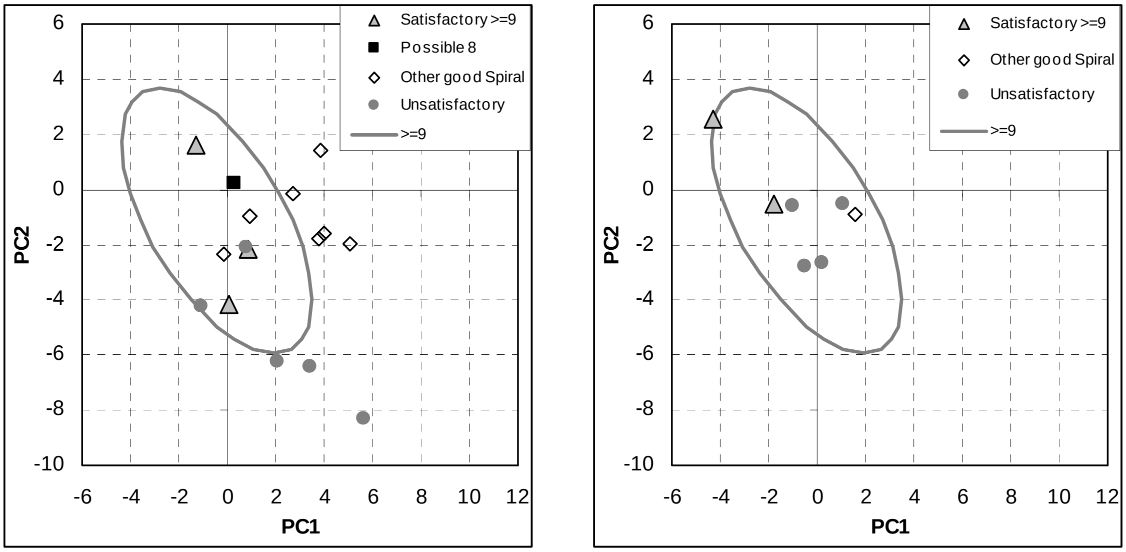

a) RL Winter

b) RL Spring

Figure 18a shows the positions and bread quality scores for the NL1 winter varieties for the 2002 harvest. There are 8 varieties within the boundary, 5 varieties outside the boundary with good Spiral score (but poor CBP score) and 3 varieties with poor scores. The most promising is the variety in the top left quadrant.

Figure 18b shows the positions and bread quality scores for the NL spring varieties (years 1 and 2) for the 2002 harvest. All 7 varieties are within the boundary, again with a promising variety in the top left quadrant.

Figure 18. Quality map relationship with bread score for NL 2002 varieties


a) NL1 Winter

b) NL Spring

5.4.2. Biscuit making varieties

5.4.2.1. SDS-dough peak time

The relationship with SDS-dough peak time for averaged data is shown in Figure 19. Regression analysis gives the equation:-

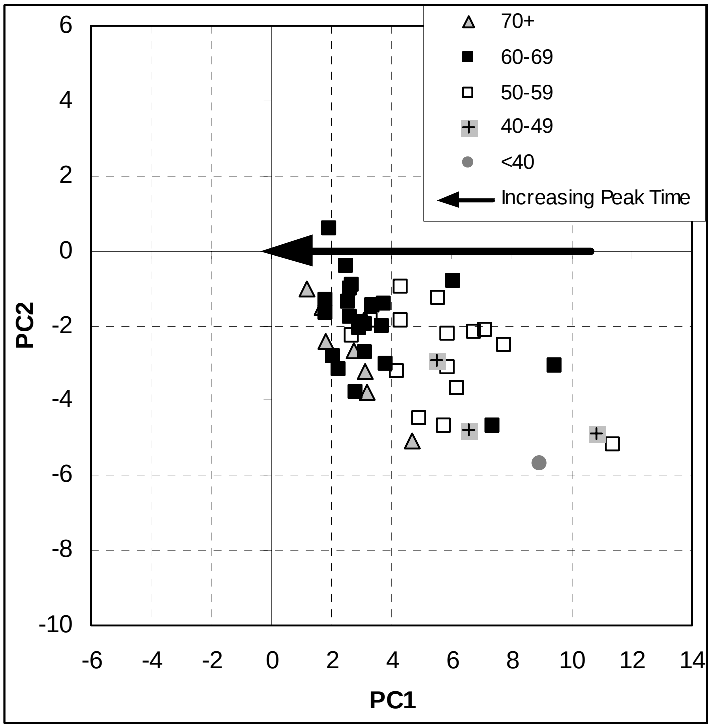
$$\text{Peak time (s)} = -2.033 * PC1 - 0.0083 * PC2 + 70.17$$

$$(n = 48, R^2 = 0.34, RSD = 7.1\ s, slope = 0.004)$$

This gives an increase in peak time moving from right to left.

For individual results, n = 171, R^2 = 0.31, RSD = 8.9 s, slope = 0.48. This is again in a direction from right to left but with a slight downward slope.

Figure 19. Relationship between principal component scores and SDS-dough peak time (s) (average data)



5.4.2.2. Resistance

The relationship with Extensograph resistance is shown in Figure 20. Regression analysis gives the equation:-

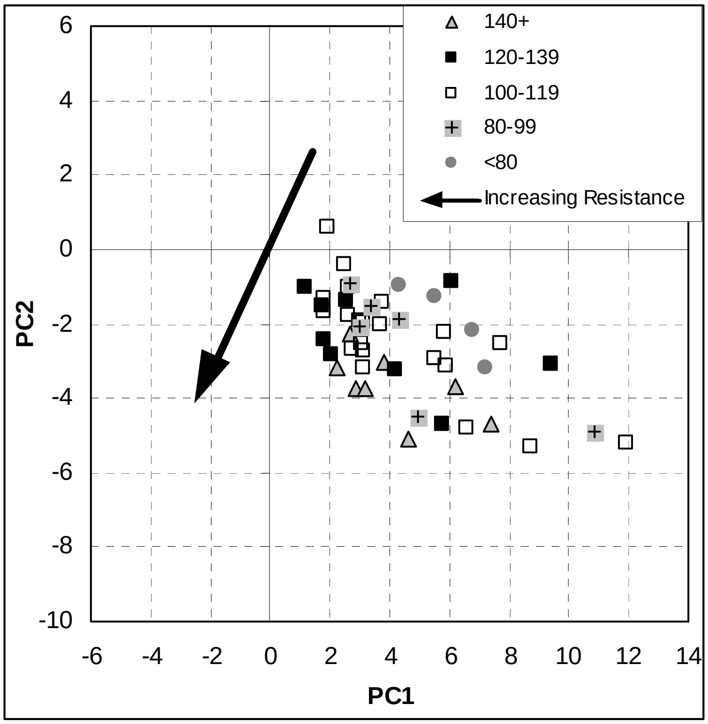
$$\text{Resistance (BU)} = -6.873 * \text{PC1} - 11.90 * \text{PC2} + 115.4$$

$$(n = 48, R^2 = 0.35, \text{RSD} = 20.6 \text{ BU, slope} = 1.73)$$

This shows a trend of increased resistance in a diagonal from upper right to lower left.

For individual results, n=169, $R^2 = 0.31$, RSD = 24.9 BU, slope = 1.54.

Figure 20. Relationship between averaged principal component scores and resistance (BU)



5.4.2.3. Extensibility

The relationship with Extensograph extensibility is shown in Figure 21. Regression analysis gives the equation:-

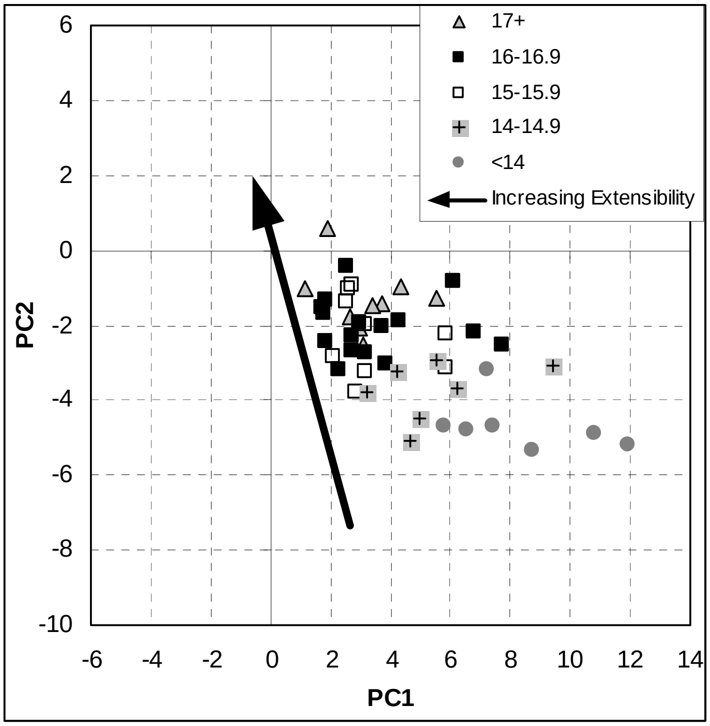
Extensibility (cm) = -0.234 * PC1 + 0.681 * PC2 + 18.45

(n = 48, R^2 = 0.75, RSD = 0.82 cm, slope = -2.90)

With such a relatively high value of the squared multiple correlation coefficient (R^2), this shows a very definite trend of increased extensibility in almost a vertical direction.

For individual results, n = 169, R^2 = 0.65, RSD = 1.4 cm, slope = -5.46. This again shows a definite upward trend.

Figure 21. Relationship between averaged principal component scores and extensibility



The diagonal upward to the left is the direction of the effect of increasing protein on the plotted position. This suggests a link between extensibility and protein. Analysis of the data-set confirmed this. For the averaged data, the relationship was:-

Extensibility (cm) = 2.334 * Protein (%) - 5.109

(n = 48, r^2 = 0.34, RSD = 1.31 cm)

and for individual results the relationship was:-

$$\text{Extensibility (cm)} = 1.897 * \text{Protein (\%)} - 1.048$$

$$(n = 169, r^2 = 0.43, \text{RSD} = 1.78 \text{ cm})$$

However, examination of the values of the squared correlation coefficient (r^2) and the residual standard deviation shows that the relationship with the Reomixer data is much the stronger.

5.4.2.4. Biscuit making flour score

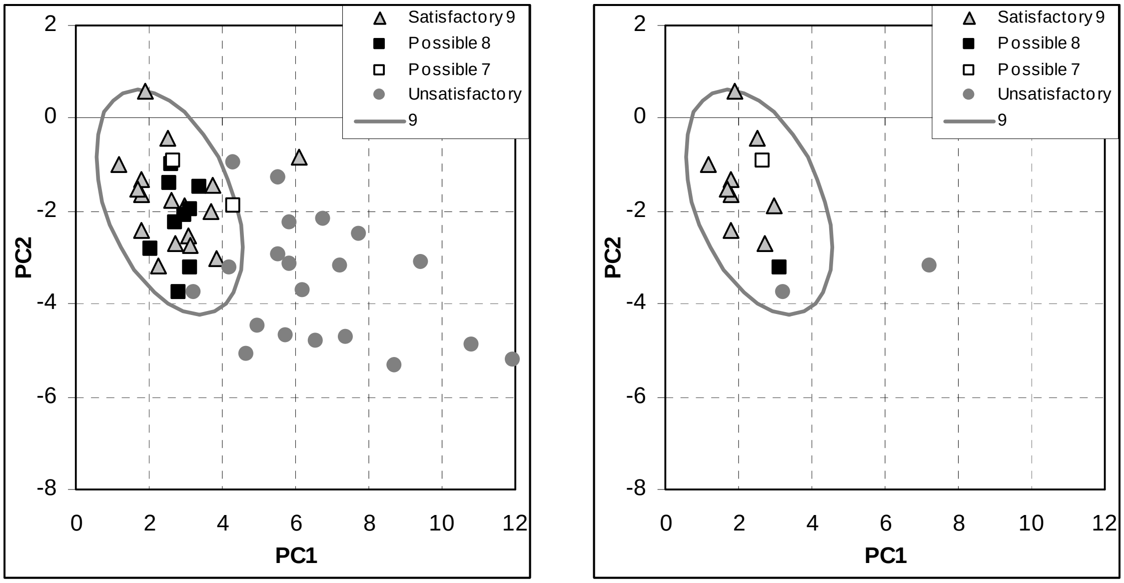
Using the scoring system outlined in section 4.7.1 and Table 2, each biscuit making variety for each year was assigned a combined score for extensibility, resistance and SDS-dough peak time from the averaged values. Satisfactory quality in each category is a score of 3. Satisfactory overall quality is a value of 9 as the sum of a score of 3 in each category. When the score in a category is 2 then the overall score may be 8, 7 or 6, giving rise to three ‘possible’ categories (in practice, there were not ‘possible 6’ combined averages). The remaining samples will have unsatisfactory quality.

Figure 22 shows the positions of the averaged values on the quality map identified by score characterisation. Figure 22a shows all the data on one plot. Figure 22b shows all the data from averages where the variety was in the 2001 and/or 2002 harvest RL trials (including NL2 data for 2001). Figure 22c shows the data for the 2001 harvest NL1 varieties and Figure 22d shows the data for the 2002 harvest NL1 varieties. On all graphs, the boundary defining the area where the biscuit quality score was 9 has been plotted. The point with score of 9 and plotting at co-ordinates 6.1, -0.8 was excluded from the boundary calculation. It is not consistent with the rest of the data and inspection of the raw trace data shows that for two of the three traces there was considerable breakdown in the later stages of mixing that would have produced high PC1 values.

Figure 22. Quality map relationship with biscuit flour quality

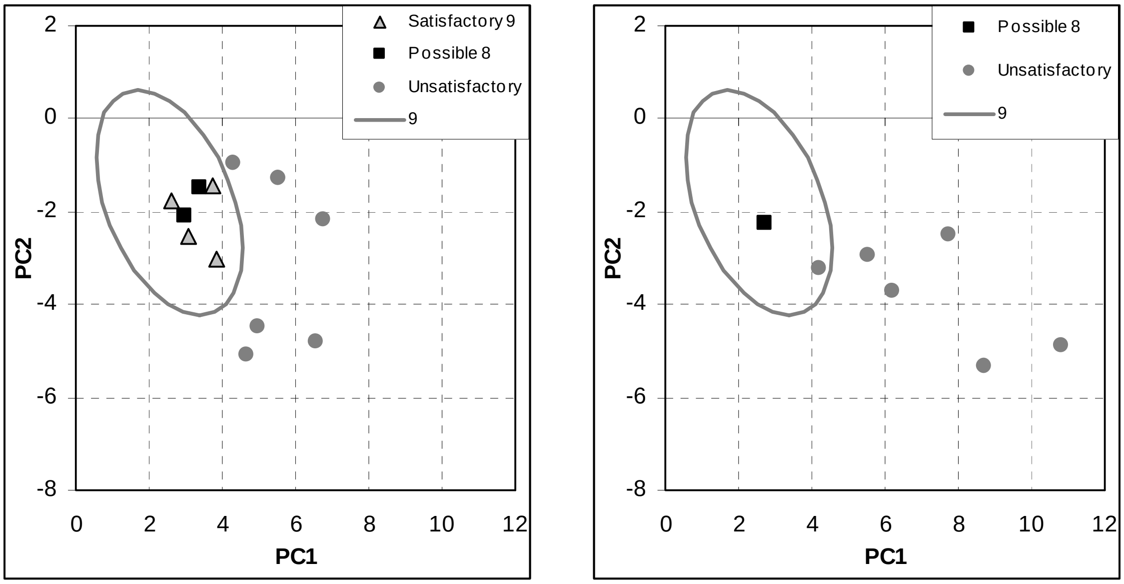
a) All data

b) RL (including corresponding NL2 2001)



c) NL1 2001

d) NL1 2002



All the ‘possible’ points also plotted within this area with only two unsatisfactory points plotting near the bottom. All varieties in the RL trials (except Riband, which by current standards has too weak a gluten) plotted within the boundary. For the NL1 winter 2002 harvest varieties, only two plotted within the boundary and there were five plotting outside: these results confirm the finding of unsatisfactory quality suggested earlier by the SDS-dough peak time averages (section 5.2.4.1). Thus a varietal average plotting in this region has a higher probability of being acceptable for RL trials.

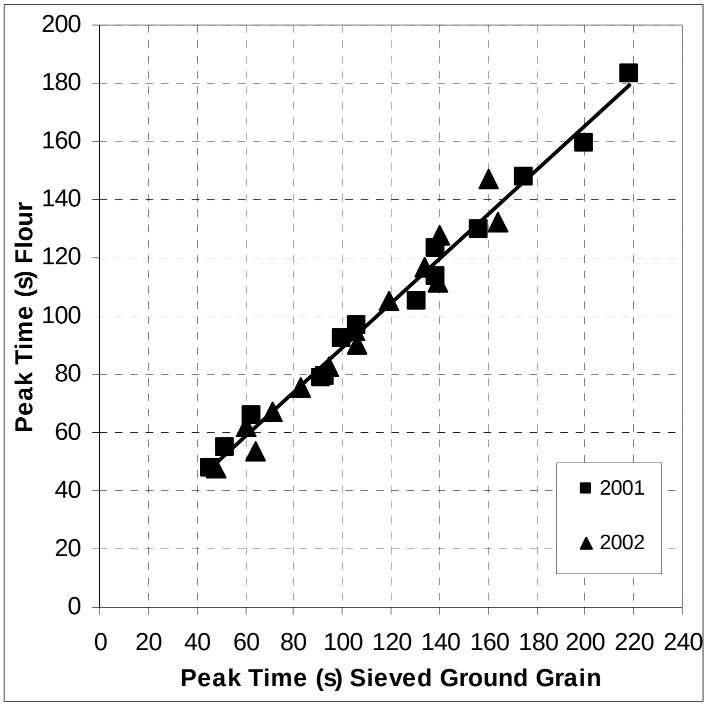
5.5. Comparison of SDS-dough peak time from white flour and sieved ground grain

The relationship between the SDS-dough peak time from white flour and the corresponding value obtained starting from whole grain is shown in Figure 23.

The equation of this line is:-

$$\text{Peak time (s) (flour)} = 0.766 * \text{Peak time (s) (sieved ground grain)} + 12.2 \quad (r^2 = 0.98)$$

Figure 23. Relationship between SDS-dough peak time for white flour and sieved ground grain



The corresponding values are very similar at lower peak times values, so within the errors of the relationship the indicated critical value of 60 s (section 5.2.4.1) for biscuit making flour is the same for the two materials. As the dough strength increases, the values for sieved ground grain are proportionally higher than those from white flour.

5.6. Comparison of SDS-dough and standard-dough

The quality information from SDS-dough is a single peak time value that is evaluated as a number on a single scale and provides a measure of dough strength (the higher the number the higher the dough strength). For breadmaking varieties, it is reasonably correlated with gel protein elastic modulus (G´). The trend was for Spiral loaf volume to decrease as peak time (and G´) increases. For CBP loaves, the relationship was poor and was virtually of no value (similar to G´). Unlike G´, SDS-dough peak time has the advantage that it can be measured for biscuit making varieties where the indication is that selection to the RL is favouring the relatively stronger varieties. The correlation with Extensograph resistance and extensibility was low and had no predictive value.

The quality information from standard-dough is a torque-time trace and its two principal component scores (that can also be corrected to a constant protein level). These data require more interpretation than is required for SDS-dough. The trace provides information on dough development and stability. The principal component scores are a condensation of this information and are plotted on a quality map, the position representing the trace characteristics, with the considerable advantage that several traces can be assessed on one plot. Use can be taken further, where the position of a sample may be compared with reference areas constructed from established varieties, thus directly matching dough-mixing characteristics. Additionally, the positions may be compared with a quality area derived from other parameters. For breadmaking varieties, trends relating the position on the quality map to G´, SDS-dough peak time and Spiral loaf volume were identified. A bread score has been calculated from CBP loaf volume and texture and Spiral loaf volume and an area has been identified outside which an unsatisfactory score is likely (inside the boundary does not guarantee a good score). For biscuit making varieties, trends relating the position on the quality map to SDS-dough peak time and Extensograph resistance and extensibility have been identified. A biscuit flour score has been calculated from resistance, extensibility and SDS-dough peak time and an area has been identified on the quality map inside which there is a high likelihood of the required characteristics.

To obtain an SDS-dough trace requires 10 g flour and 10 g SDS solution without any other flour analysis, whereas a standard-dough trace from white flour currently requires knowledge of the Farinograph water absorption. For RL and NL testing, this value is routinely obtained: in other circumstances (particularly for breeders) there may be insufficient white flour to obtain a water absorption value. NIR calibrations for water absorption are available that will give an estimate of the value. The effect of the difference of this estimate from the value that would be obtained on the Farinograph is not known.

Methods are available to carry out both tests on sieved ground grain. There is no change in the subsequent protocol for SDS-dough. For standard-dough, the water addition is calculated from the ground grain moisture and protein contents as determined by NIR: therefore the test can be carried out with less material. However, the grinding and sieving approximately double the overall time for each test (single determination).

This work has been carried out with a single instrument and as with all machines there will be differences between them. Some preliminary work has been carried out with a second instrument at CCFRA (unpublished data). For SDS-dough, there is likely to be a small proportional change in the value: this difference would blur any absolute boundaries (e.g. for minimum biscuit flour strength) but the relative position of samples is unlikely to be changed, with strength classifications being similar. For standard-dough, the torque-time traces are likely to show small differences with resultant differences in calculated principal component scores. Boundaries around reference areas produced on one instrument would not strictly be directly transferable to a second instrument for some areas of the quality map: caution would need to be exercised in interpretation in the regions near the boundaries.

When starting from wheat, SDS-dough peak times are similar at lower values but are proportionally longer than from white flour at higher values: this needs to be taken into consideration when interpreting the data. For standard-dough from sieved ground grain, the torque-time traces are sufficiently dissimilar from those from white flour to require construction of separate reference boundaries. The location on the map of the boundaries for a variety for the two materials are in the same general area.

SDS-dough provides a dough strength measure that is an alternative to gel protein elastic modulus (G´). Standard-dough provides summary information relating to the dough mixing characteristics, many of which may be compared together on a quality map. The position on the plot is characteristic of the trace profile: if direct comparison with reference areas is needed, then these boundaries require additional work for their construction.

5.7. Breeders' assessments

Their reports are given in Appendix C.

5.7.1. Elsoms Seeds Ltd.

Elsoms Seeds Ltd. assessed both SDS-dough and standard-dough using predominantly sieved ground grain. They found that the practicalities of running the Reomixer compared with their current in-house gluten wash-out testing were no different as the most time consuming part of both is the grinding and sieving. Using single SDS-dough tests would enable them to do slightly more tests in one day than a combined test of SDS-sedimentation and gluten wash-out.

They found a steep learning curve with the data-handling option as provided by CCFRA and consider it should be more user-friendly. This option enabled collation of 24 traces and thumbnail plots of 12 per page after transfer of Reomixer data to a spreadsheet. A blank worksheet enabling plotting of up to 24 differently identified traces (as PC1 and PC2 values) on an 'as-is' and protein corrected 'quality map' was also supplied.

Their conclusion was that they felt that the Reomixer gave significantly better predictions of bread making quality over the SDS sedimentation volume. When compared with their manual assessment of gluten, it was placing lines in similar categories, i.e. too tough, too weak or potential breadmaking.

When assessing potential for biscuit making the Reomixer gave better discrimination between varieties than their existing tests.

5.7.2. Monsanto UK Ltd.

Monsanto only reported assessment of standard-dough from white flour. With a check sample provided by CCFRA, they found that the overall variability in PC1 and PC2 values was similar to that given in section 5.1.2. Where test samples were assayed in duplicate they found a high correlation between the replicate values for PC1 and PC2: data are also provided for peak time, peak height and area to peak (values not used in this work).

When assessing breeding samples, they found that the better the baking quality, the more the samples tended to the top left quartile of the quality map. To be sure about the reliability of this prediction they would need more samples with quality data and more environmental variation with material from different sites and seasons. Their finding is consistent with the data in this report.

Their conclusion is that the Reomixer appears to offer some potential to predict ‘quality’ for bread-making, using as little as 10g white flour and within about 15 minutes. However, for them, there are significant drawbacks to the method that has been developed so far. These were having to use the Farinograph water absorption for which Bühler milled flour will be required and maintaining the temperature of the solutions and flours at 30 °C; they also found that the mixer bowl is not easy to clean between samples because of its small size.

Author’s comment. As noted in section 5.6, a method is available using sieved ground grain that does not require a Farinograph water absorption. The reason for using 30 °C is because dough final temperature after mixing for baking is usually around this figure and so that the test can be carried out without problems of high laboratory temperature most of the year. A larger size bowl would require more sample.

6. CONCLUSIONS

6.1. SDS-dough

SDS-dough peak time provides a measure of dough strength. It is highly correlated with gel protein elastic modulus (G´) for which it is a possible replacement. However, it has value in its own right. Spiral loaf volume decreased as either SDS-dough peak time or G´ increased, with the correlation being higher for the peak time measurement, thus showing it to be a better measure in this context. The measurement has the advantage that it can be made on biscuit making flour (unlike G´), where the data showed that selection to the RL is favoured by a value at the higher end of the range for biscuit making varieties (relatively stronger dough).

No meaningful relationships were found with CBP loaf volume and Extensograph resistance and extensibility.

6.2. Standard-dough and quality maps

Reduction of standard-dough torque-time traces to two principal component scores (PC1 and PC2) is an effective condensation of the information in the traces. Using these values as co-ordinates on a quality map (with centre at the origin) gives a plotted position that summarises the trace characteristics of dough development, peak height, peak time and breakdown. Use of the quality map allows simultaneous assessment of a number of traces. Construction of boundaries enclosing traces of a particular reference characteristic (e.g. from single varieties or a quality attribute) enables additional comparison to be made.

The established **nabim** group 1 winter breadmaking varieties (Malacca, Hereward and Shamrock) had PC1 values that were mainly less than zero and therefore tended to plot to the left of the y-axis. The newer group 1 variety Xi19, with a tendency to lower protein content, plotted mainly to the right of the y-axis. The **nabim** group 2 varieties (Option, Rialto and Charger) had PC1 values that were mainly greater than zero and therefore tended to plot to the right of the y-axis. Soissons (**nabim** group 2) plotted to the left of the y-axis but, as expected, is in a region of the map showing strong gluten characteristics.

For established spring breadmaking varieties, Paragon (**nabim** group 1) plotted mainly to the left of the y-axis and straddled the x-axis. Chablis (**nabim** group 2) plotted mainly inside the lower left quadrant downwards and slightly to the left of Paragon.

Biscuit making varieties plotted mainly in the lower right quadrant with Claire (**nabim** group 3) plotting in the upper right of this region (to the right of and below the origin).

Trends in relationships with other quality measures were found on the map: these are indicative but are not strong enough for predictive value. For breadmaking varieties, SDS-dough peak time and G´ increased with diagonal movement downward from right to left (slope = 1 and 0.7 respectively): Spiral loaf volume increased diagonally upward from left to right (slope = 2.9). For biscuit making varieties, resistance increased diagonally downward to the left (slope = 1.7) and extensibility increased upwards from right to left (slope = -2.9): SDS-dough peak time increased from right to left (slope = 0).

A region was identified on the map lying diagonally downward from left to right and centred slightly downward to the left of the origin that provided useful bread quality information. An overall bread score from varietal average loaf volume and texture data (separately for each year) giving categories of ‘satisfactory’, ‘possible’ and ‘unsatisfactory’ was calculated. Inside this region, all ‘satisfactory’ samples plotted (by definition) together with all the ‘possible’ category samples. Outside this region, samples were ‘unsatisfactory’ overall. Varietal averages with unsatisfactory scores also plotted inside this region but were confined to PC2 values less than zero: there were no unsatisfactory samples in this region where it was in the upper left quadrant. Nearly all RL varieties plotted within this region indicating that a variety plotting outside is much less likely to be acceptable.

A region was identified on the map lying predominantly just inside the bottom right quadrant that provided useful biscuit making flour quality information. An overall score was calculated from varietal average resistance, extensibility and SDS-dough peak time data (separately for each year) giving ‘satisfactory’, ‘possible’ and ‘unsatisfactory’ categories. All ‘satisfactory’ and ‘possible’ category samples plotted inside this region. The majority of the ‘unsatisfactory’ category samples plotted outside the region: the two samples out of twenty that plotted in the region were near the bottom.

7. IMPLICATIONS FOR LEVY PAYERS

- The Reomixer provides practical, rapid small-scale wheat protein quality measurements derived from dough mixing characteristics.

  Using SDS-dough gives a dough strength measurement. For breadmaking varieties, it enables assessment for weak (less likely to be suitable for CBP bread) and strong gluten (less likely to be suitable for Spiral bread with extra-strong varieties also being unsuitable for CBP bread). For biscuit making varieties, it enables screening for relatively stronger dough (more likely to be acceptable).

  Using standard-dough and a quality map allows assessment of the mixing characteristics in relation to quality areas derived from individual reference varieties or a quality attribute. The quality map surface covers the expected range of trace profiles and the plotted position of a test sample summarises the dough mixing characteristics. This enables rapid comparison of a number of samples at the same time.

- The technique is best suited to assessing the average performance of a variety (although it does have value for looking at individual samples). It is therefore of most use to breeders and in other varietal assessment studies (e.g. RL and NL studies and investigations by millers) where the technique would allow similar measurements by all concerned facilitating direct comparison of values with improved understanding of quality requirements.

- With an understanding of what measurement values are preferred, the technique enables breeders to better target varieties for National List testing. Similar testing on National List varieties would provide additional information for decisions regarding selection for the Recommended List trials, thus ensuring use of HGCA funds for testing more appropriate varieties.

- The equipment has the advantage of reduced capital equipment cost compared to an ultracentrifuge plus rheometer and an Extensograph.

8. ACKNOWLEDGEMENTS

Grateful thanks are extended to the following:-

The technicians in the Cereals and Milling Department of CCFRA who carried out the Reomixer assays: in particular, Paula Stabler, Neil Buck, Andrew Keene, Joanne Pratt and Janet Insoll. David Evans, who provided statistical advice, particularly for the equations to calculate the bounding ellipses.

The flour and loaf analytical values were obtained in the Recommended and National List quality evaluations. The Recommended List analytical data are available on the HGCA Recommended List Database, which can be consulted at www.hgca.com.

The British Society of Plant Breeders Ltd. for use of the National List samples and data.

Elsoms Seeds Ltd. and Monsanto UK Ltd. for their assessment from the breeders' perspective.

Reologica Instruments AB for loan of a Reomixer for use by the breeders.

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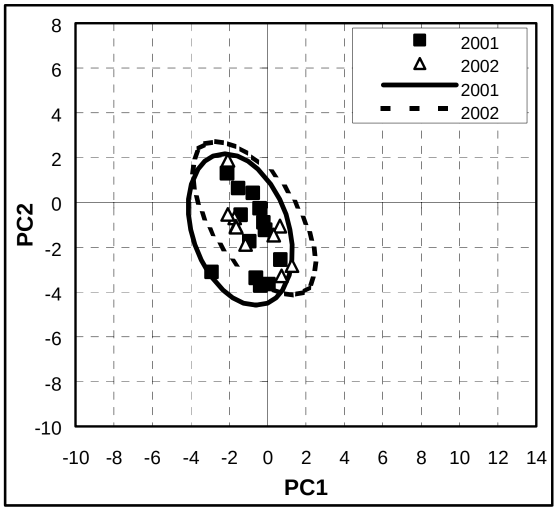
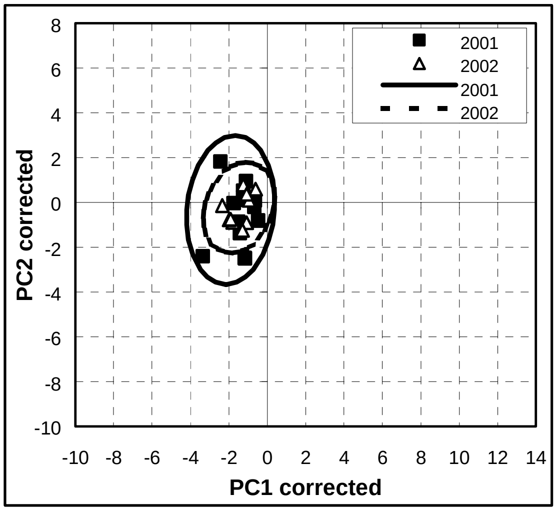
APPENDIX A. REFERENCE VARIETY QUALITY MAPS

Reference variety quality maps showing individual sample points and surrounding boundaries.

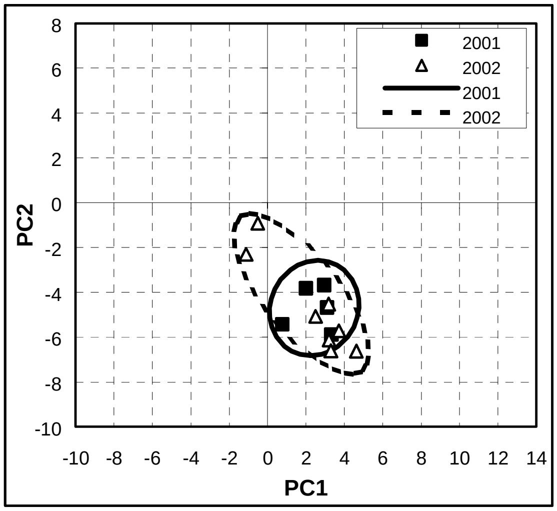
Malacca, as-is



Malacca, corrected



Option, as-is



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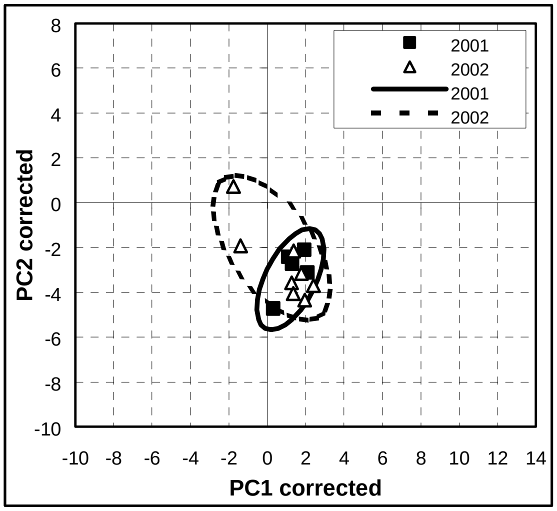
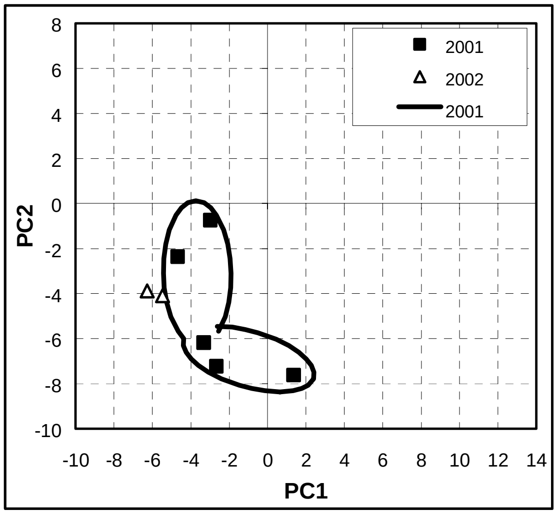
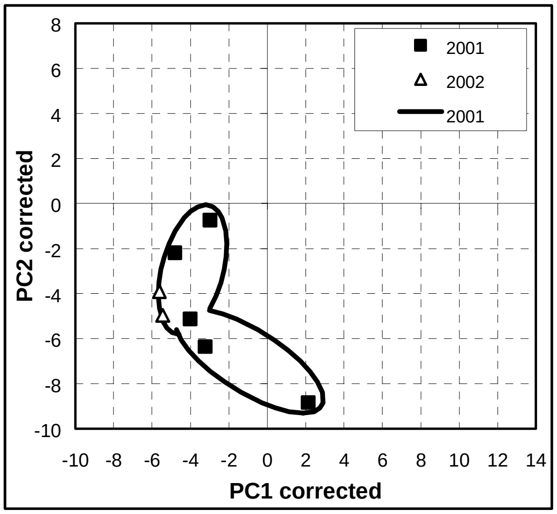


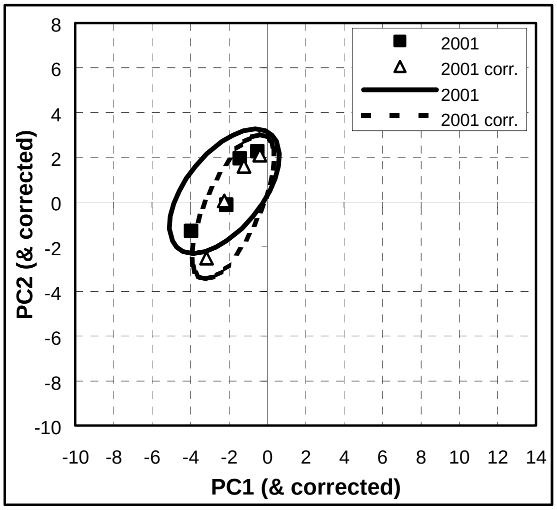
Soissons, as-is



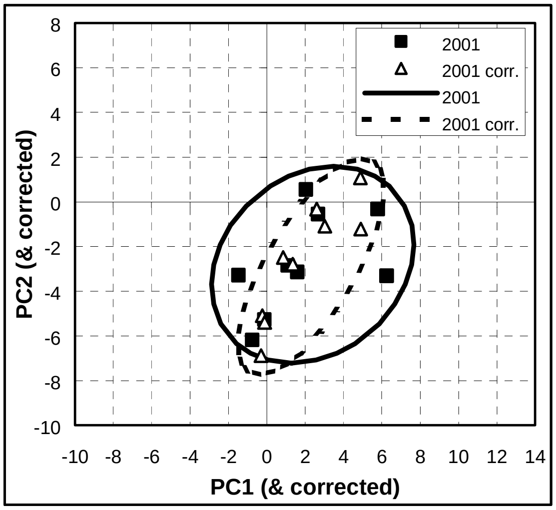
Soissons, corrected



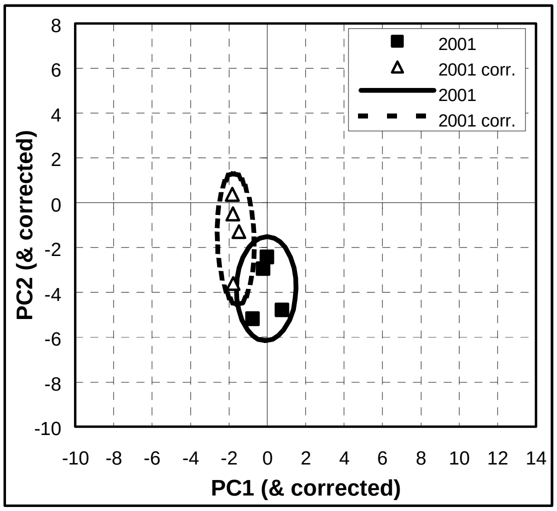
Hereward, as-is and corrected, 2001 only



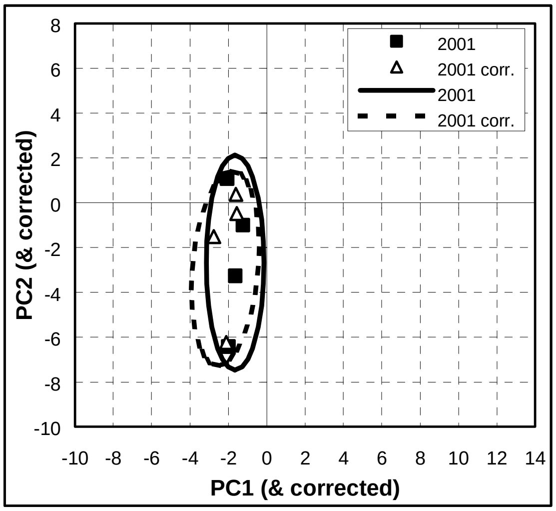
Rialto, as-is and corrected, 2001 only



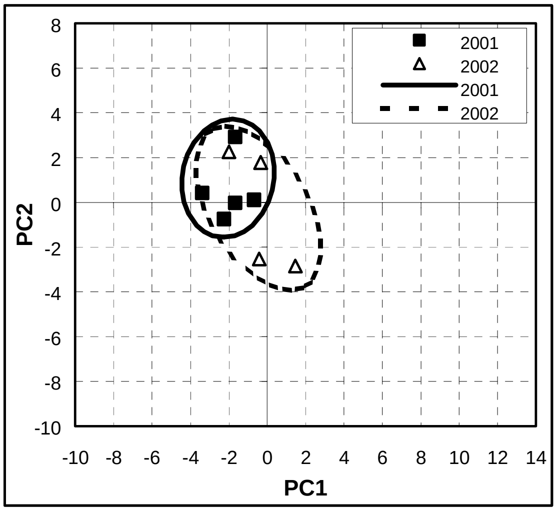
Charger, as-is and corrected, 2001 only



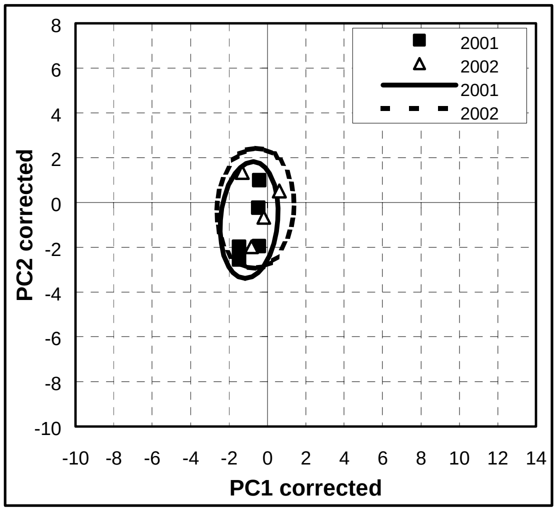
Shamrock, as-is and corrected, 2001 only



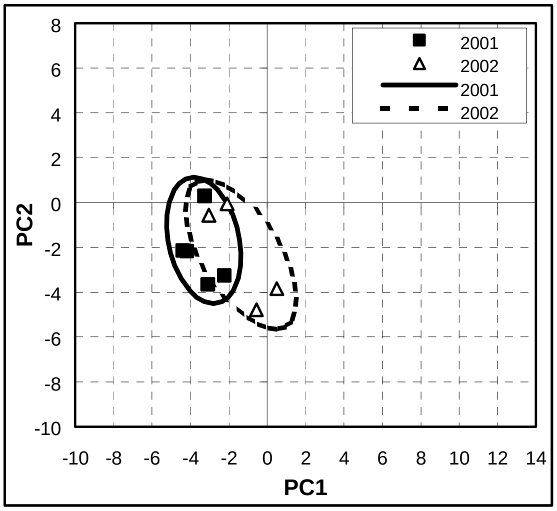
Paragon, as-is



Paragon, corrected



Chablis, as-is



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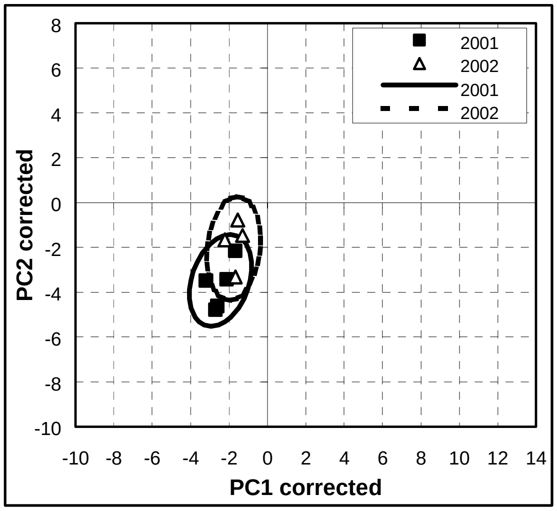
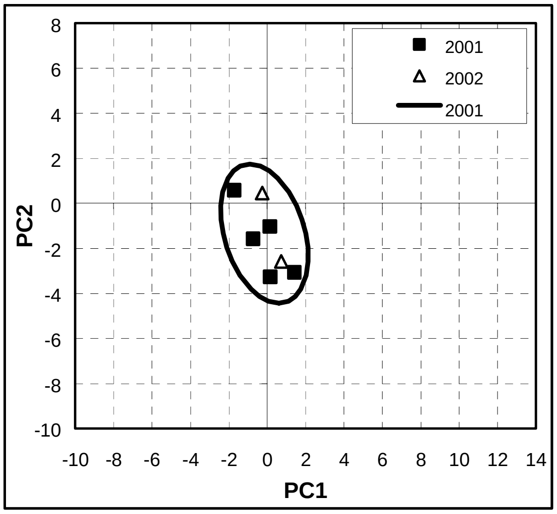
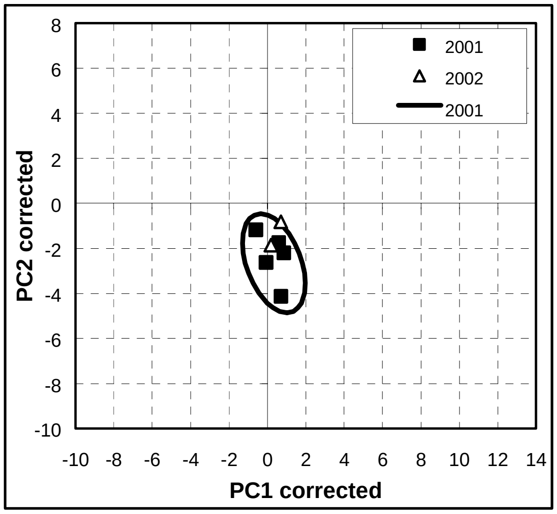
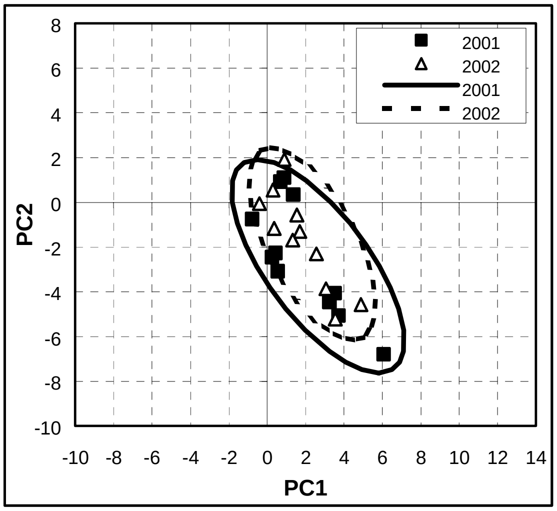


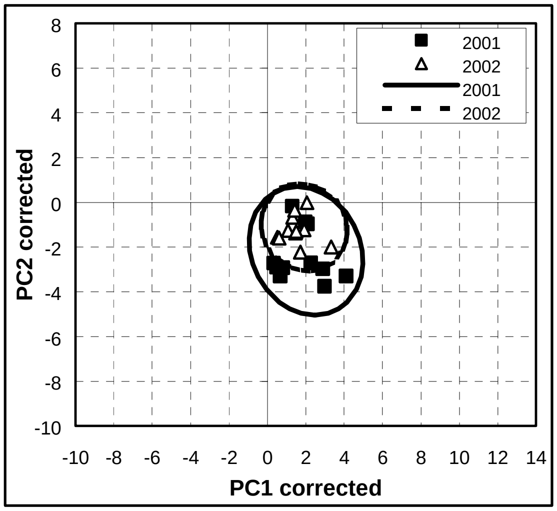
Imp, as-is

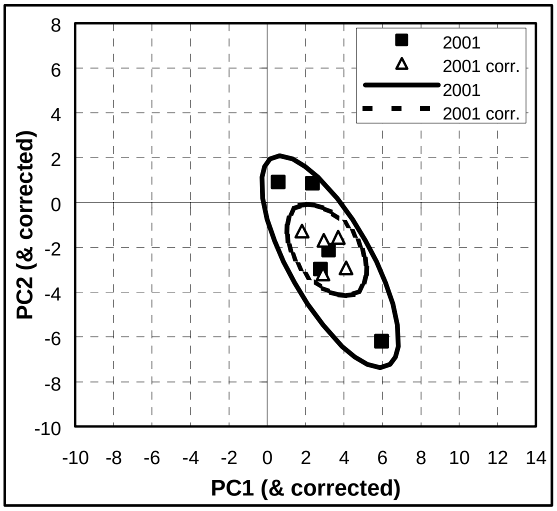


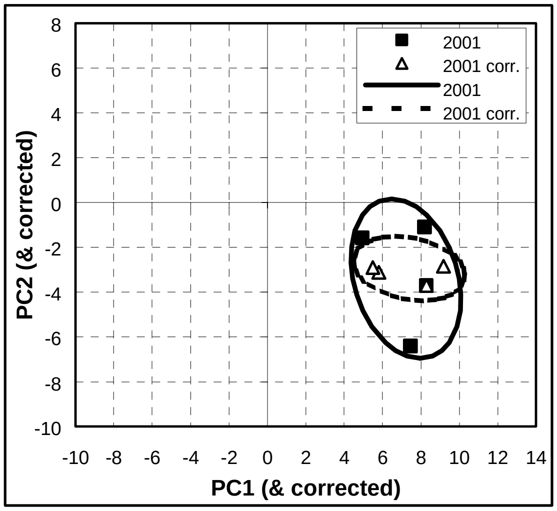
Imp, corrected




Claire, as-is


Claire, corrected


Consort, as-is and corrected, 2001 only


Riband, as-is and corrected, 2001 only

APPENDIX B. YEARLY VARIETAL AVERAGE REOMIXER DATA

Breadmaking RLW 2001 and 2002 and NL2 2001 varieties. Varieties tested in both years followed by varieties tested in one year only.

			Peak Time (s)		PC1		PC2		PC1 corr		PC2 corr		
Year	Trial(s)	Variety	**Mean**	SD	**Mean**	SD	**Mean**	SD	**Mean**	SD	**Mean**	SD	n
2002	RLW	Chardonnay	**82**	15.7	**0.4**	1.8	**-2.7**	2.0	**-0.5**	1.8	**-1.5**	1.9	4
2001	NL2	Chardonnay	**89**	14.6	**1.1**	1.2	**-3.6**	2.2	**-0.3**	1.1	**-1.4**	1.7	3
2002	RLW	Einstein	**83**	19.6	**-0.7**	1.6	**-1.5**	2.6	**-2.1**	1.1	**0.3**	1.6	5
2001	NL2	Einstein	**90**	15.0	**-0.1**	0.6	**-3.6**	3.1	**-1.3**	0.9	**-1.7**	2.5	3
2002	R&NLW	Malacca	**81**	9.2	**-1.0**	1.2	**-1.0**	1.4	**-1.5**	0.6	**-0.3**	0.7	9
2001	R&NLW	Malacca	**85**	7.7	**-0.7**	1.0	**-1.7**	1.7	**-1.4**	0.8	**-0.7**	1.5	11
2002	R&NLW	Option	**89**	11.0	**2.4**	2.1	**-4.7**	2.1	**0.9**	1.6	**-2.8**	1.7	8
2001	RLW	Option	**93**	11.1	**2.4**	1.1	**-4.7**	1.0	**1.3**	0.7	**-3.0**	1.0	5
2002	RLW	Scorpion 25	**95**	12.5	**0.0**	3.7	**-1.8**	1.5	**-0.9**	3.1	**-0.5**	1.5	5
2001	NL2	Scorpion 25	**103**	21.5	**1.2**	0.9	**-3.4**	2.7	**-0.3**	0.7	**-1.1**	3.0	3
2002	RLW	Soissons	**132**	4.9	**-5.9**	0.6	**-4.0**	0.2	**-5.5**	0.1	**-4.4**	0.8	2
2001	RLW	Soissons	**146**	19.6	**-2.5**	2.3	**-4.8**	3.1	**-2.6**	2.7	**-4.7**	3.2	5
2002	RLW	Solstice	**88**	10.3	**1.2**	2.8	**-0.4**	2.1	**0.3**	2.4	**0.8**	1.0	5
2001	RLW	Solstice	**90**	14.1	**0.8**	2.5	**-0.1**	0.8	**0.2**	2.1	**0.8**	1.3	5
2002	RLW	Tellus	**102**	16.1	**0.5**	3.1	**-4.0**	2.3	**-0.3**	2.5	**-2.9**	2.0	5
2001	NL2	Tellus	**110**	19.0	**1.0**	0.6	**-4.6**	2.3	**0.0**	0.3	**-3.0**	1.8	3
2002	RLW	Warlock 24	**103**	4.8	**-0.1**	2.2	**-3.8**	1.8	**-1.0**	1.1	**-2.6**	0.6	4
2001	NL2	Warlock 24	**98**	21.0	**2.0**	2.0	**-3.6**	2.0	**0.7**	1.6	**-1.5**	2.3	3
2002	RLW	Xi19	**96**	15.2	**0.7**	2.9	**-2.1**	2.2	**0.0**	2.0	**-1.1**	1.6	5
2001	RLW	Xi19	**94**	14.5	**1.4**	1.2	**-3.1**	1.4	**0.0**	1.3	**-0.9**	1.4	5
2001	RLW	Charger	**84**	7.4	**-0.1**	0.6	**-3.8**	1.4	**-1.7**	0.2	**-1.3**	1.7	4
2001	RLW	Chatsworth	**88**	6.0	**0.1**	1.0	**-2.1**	1.6	**-0.8**	0.7	**-0.7**	1.0	5
2001	RLW	Fender	**85**	9.9	**-0.2**	0.8	**-1.0**	2.2	**-0.7**	0.8	**-0.1**	1.4	5
2001	RLW	Hereward	**87**	11.6	**-2.0**	1.5	**0.7**	1.7	**-1.8**	1.2	**0.3**	2.1	4
2001	RLW	Macro	**69**	6.5	**2.2**	1.5	**-0.9**	1.3	**0.6**	1.0	**1.6**	1.1	5
2001	RLW	Phlebas	**71**	12.1	**1.1**	0.6	**0.9**	1.2	**-0.1**	1.2	**2.9**	1.2	3
2001	R&NLW	Rialto	**111**	19.7	**1.9**	2.7	**-2.7**	2.2	**1.9**	2.1	**-2.7**	2.6	9
2001	RLW	Shamrock	**90**	15.7	**-1.7**	0.4	**-2.4**	3.2	**-2.0**	0.6	**-2.0**	3.0	4
2001	NL2	CWW 99/8	**83**	13.1	**2.3**	0.6	**-4.7**	2.1	**0.6**	1.1	**-1.9**	1.4	3
2001	NL2	CWW 99/15	**120**	18.0	**-1.6**	0.3	**-3.8**	2.8	**-3.1**	0.7	**-1.5**	2.6	3
2001	NL2	CWW 99/16	**98**	18.6	**0.8**	0.8	**-4.3**	2.0	**0.0**	0.8	**-3.1**	1.8	3
2001	NL2	CWW 99/51	**78**	14.6	**1.7**	0.6	**-3.7**	1.8	**0.2**	0.9	**-1.4**	1.5	3
2001	NL2	ECO 22	**91**	14.6	**0.7**	0.5	**-1.6**	1.7	**-0.5**	0.4	**0.3**	2.4	3
2001	NL2	Fronty	**99**	17.8	**-0.6**	0.3	**-4.4**	1.9	**-1.2**	0.4	**-3.4**	1.9	3
2001	NL2	NSL WW35	**119**	14.5	**0.0**	1.2	**-5.5**	1.4	**-1.2**	0.9	**-3.6**	1.1	3
2001	NL2	PR21R60	**92**	17.6	**0.7**	0.8	**-2.5**	1.7	**-0.2**	1.0	**-1.1**	1.7	3

SD = standard deviation, n = number

RLS and NLS for 2001 and 2002. Varieties tested in both years followed by varieties tested in one year only.

			Peak Time (s)		PC1		PC2		PC1 corr		PC2 corr		
Year	Trial(s)	Variety	**Mean**	SD	**Mean**	SD	**Mean**	SD	**Mean**	SD	**Mean**	SD	n
2001	RLS	Ambient	**105**	8.2	**-0.7**	1.2	**-1.4**	1.6	**-0.7**	1.1	**-1.3**	1.2	4
2002	RLS	Ambient	**78**	2.8	**1.6**	2.4	**0.0**	1.2	**0.1**	1.4	**2.0**	0.1	2
2001	RLS	Ashby	**121**	14.4	**-1.2**	1.6	**-2.1**	1.7	**-0.8**	1.4	**-2.7**	1.3	4
2002	RLS	Ashby	**95**	10.6	**-0.2**	3.7	**0.3**	4.4	**-0.4**	2.9	**0.4**	3.3	2
2002	R&NLS	Chablis	**107**	7.7	**-1.3**	1.6	**-2.3**	2.4	**-1.7**	0.4	**-1.8**	1.1	4
2001	R&NLS	Chablis	**126**	13.8	**-3.4**	0.9	**-2.2**	1.5	**-2.5**	0.6	**-3.7**	1.1	5
2002	NLS	Imp	**102**	2.1	**0.2**	0.7	**-1.1**	2.1	**0.4**	0.4	**-1.3**	0.7	2
2001	R&NLS	Imp	**110**	5.8	**-0.1**	1.2	**-1.7**	1.6	**0.3**	0.6	**-2.4**	1.1	5
2002	R&NLS	Paragon	**84**	5.6	**-0.3**	1.4	**-0.3**	2.7	**-0.4**	0.8	**-0.2**	1.4	4
2001	R&NLS	Paragon	**108**	8.3	**-1.9**	1.0	**0.5**	1.4	**-0.8**	0.6	**-1.1**	1.5	5
2002	RLS	Tybalt	**93**	7.1	**-0.9**	2.4	**-0.6**	3.1	**-1.6**	1.1	**0.3**	1.3	2
2001	NLS	Tybalt	**119**	2.8	**-1.5**	1.0	**-1.6**	2.1	**-1.7**	0.4	**-1.2**	0.1	2
2002	RLS	Wallace	**86**	3.5	**0.0**	1.3	**-0.6**	1.2	**-1.3**	0.3	**1.2**	0.1	2
2001	RLS	Wallace	**118**	8.0	**-2.4**	1.6	**-1.8**	1.4	**-1.7**	1.6	**-2.9**	1.0	4
2001	RLS	Alder	**112**	8.5	**-0.7**	0.3	**-0.6**	1.5	**0.2**	0.5	**-2.0**	1.6	4
2001	RLS	Morph	**102**	7.0	**-2.0**	1.1	**1.8**	1.1	**-1.3**	1.1	**0.6**	0.7	4
2001	RLS	Shiraz	**114**	13.7	**-3.9**	0.6	**0.1**	2.4	**-3.4**	0.9	**-0.7**	2.1	4
2001	RLS	Status	**102**	8.6	**-0.3**	2.1	**-1.1**	1.2	**0.1**	1.8	**-1.8**	0.8	4
2002	NLS	CPBT W92	**94**	4.9	**-0.5**	0.7	**-2.8**	3.3	**-2.0**	0.2	**-0.9**	2.6	2
2001	NLS	CPBT W92	**129**	2.8	**-0.7**	1.0	**-3.7**	1.6	**-1.4**	0.1	**-2.6**	0.0	2
2002	NLS	CPBT W93	**92**	7.1	**0.2**	0.7	**-2.7**	2.2	**-1.7**	0.2	**-0.2**	1.5	2
2001	NLS	CPBT W93	**122**	9.2	**0.0**	1.7	**-5.8**	1.5	**-1.4**	0.6	**-3.7**	0.2	2
2002	NLS	NSL SW9	**90**	12.7	**1.0**	0.7	**-0.5**	3.5	**0.6**	0.5	**0.1**	1.8	2
2001	NLS	NSL SW9	**108**	2.8	**1.3**	1.1	**-3.6**	0.4	**0.7**	1.7	**-2.8**	0.5	2
2002	NLS	CPBT W100	**96**	7.8	**-1.0**	1.3	**-0.6**	3.4	**-1.7**	1.8	**0.4**	2.8	2
2002	NLS	NSL SW10	**99**	8.5	**-1.8**	1.1	**-0.6**	2.4	**-1.5**	2.1	**-0.9**	1.1	2
2002	NLS	Roy	**71**	26.2	**1.6**	3.6	**-0.9**	2.8	**0.8**	3.9	**0.1**	2.5	2
2002	NLS	Vinjett	**103**	21.9	**-4.3**	1.2	**2.5**	3.6	**-3.9**	2.2	**2.0**	2.3	2
2001	NLS	CPBT W82	**146**	9.9	**1.5**	1.1	**-6.5**	1.2	**0.3**	0.2	**-4.6**	0.8	2
2001	NLS	NSL SW8	**116**	2.1	**1.1**	0.8	**-3.7**	1.1	**0.2**	0.2	**-2.3**	0.1	2

Breadmaking NL2 2002 and NL1 2001 where varieties were tested in both years

			Peak Time (s)		PC1		PC2		PC1 corr		PC2 corr		
Year	Trial	Variety	**Mean**	SD	**Mean**	SD	**Mean**	SD	**Mean**	SD	**Mean**	SD	n
2002	NL2	21R42	**96**	5.7	**-1.8**	0.3	**-2.3**	1.5	**-2.5**	0.3	**-1.3**	0.7	2
2001	NL1	21R42	**111**	22.3	**-1.9**	1.4	**-2.1**	2.2	**-2.6**	1.3	**-1.0**	2.2	3
2002	NL2	Bentley	**102**	7.1	**3.7**	1.0	**-7.9**	0.3	**1.6**	1.1	**-5.0**	0.5	2
2001	NL1	Bentley	**116**	21.4	**1.9**	1.7	**-7.2**	1.8	**0.5**	1.8	**-5.0**	2.0	3
2002	NL2	Caphorn	**123**	3.5	**-3.5**	0.1	**-3.5**	1.3	**-3.2**	0.1	**-3.9**	1.1	2
2001	NL1	Caphorn	**139**	24.0	**-2.8**	1.7	**-4.4**	3.5	**-2.8**	1.5	**-4.4**	3.2	3
2002	NL2	CEB 98179	**65**	1.4	**2.8**	0.2	**-0.8**	0.0	**1.5**	0.8	**0.9**	0.8	2
2001	NL1	CEB 98179	**64**	7.9	**2.0**	1.4	**-0.7**	0.9	**1.0**	1.4	**0.8**	0.6	3
2002	NL2	CPBT W83	**107**	4.9	**-1.9**	0.1	**-2.8**	1.3	**-2.6**	0.2	**-1.9**	0.8	2
2001	NL1	CPBT W83	**109**	13.0	**-2.7**	0.8	**-2.1**	3.1	**-3.2**	0.8	**-1.4**	2.6	3
2002	NL2	CWW 00/2	**106**	4.2	**1.9**	1.0	**-7.0**	0.4	**0.0**	1.3	**-4.5**	0.7	2
2001	NL1	CWW 00/2	**113**	17.1	**2.1**	1.5	**-6.6**	2.4	**1.0**	1.6	**-4.9**	2.6	3
2002	NL2	CWW 00/7	**87**	2.1	**4.9**	0.3	**-4.4**	1.5	**3.6**	0.6	**-2.7**	0.3	2
2001	NL1	CWW 00/7	**99**	16.4	**2.6**	1.6	**-3.1**	1.7	**2.2**	1.6	**-2.4**	1.0	3
2002	NL2	CWW 00/22	**68**	2.1	**1.2**	0.7	**-1.9**	0.2	**-0.2**	0.5	**0.0**	0.1	2
2001	NL1	CWW 00/22	**76**	8.5	**0.2**	0.8	**-1.6**	1.8	**-1.2**	0.3	**0.6**	0.9	3
2002	NL2	CWW 00/36	**70**	5.7	**1.5**	0.0	**-2.5**	1.6	**0.8**	0.1	**-1.5**	1.8	2
2001	NL1	CWW 00/36	**79**	9.3	**0.7**	0.4	**-1.7**	2.2	**-0.1**	1.0	**-0.6**	1.8	3
2002	NL2	DSV 90425/353	**102**	4.2	**-0.8**	1.0	**-6.2**	1.9	**-2.3**	0.7	**-4.3**	1.5	2
2001	NL1	DSV 90425/353	**103**	11.2	**-3.3**	0.2	**-2.3**	2.6	**-4.0**	0.2	**-1.2**	2.0	3
2002	NL2	HADM 21502-94	**94**	6.4	**-0.1**	0.5	**-3.6**	0.8	**-1.5**	0.8	**-1.9**	0.4	2
2001	NL1	HADM 21502-94	**97**	11.1	**0.2**	0.9	**-1.8**	0.9	**-0.9**	0.7	**-0.1**	0.6	3
2002	NL2	Mayfair	**85**	2.1	**2.5**	0.2	**-5.0**	1.0	**1.4**	0.4	**-3.5**	0.2	2
2001	NL1	Mayfair	**91**	13.3	**2.2**	0.8	**-4.3**	2.4	**1.4**	0.8	**-3.1**	2.4	3
2002	NL2	NFC 10006	**72**	0.0	**1.6**	1.3	**-0.4**	0.0	**0.7**	1.5	**0.7**	0.3	2
2001	NL1	NFC 10006	**78**	10.8	**0.8**	0.9	**-1.0**	1.9	**-0.2**	0.4	**0.6**	1.4	3
2002	NL2	NORD 00/318	**95**	2.8	**-0.5**	0.3	**-3.5**	0.3	**-1.2**	1.1	**-2.6**	0.7	2
2001	NL1	NORD 00/318	**104**	18.1	**-1.1**	1.1	**-2.4**	1.5	**-1.4**	0.9	**-1.9**	1.7	3
2002	NL2	NSL WW44	**104**	4.2	**0.2**	0.4	**-4.9**	1.3	**-1.4**	0.7	**-2.8**	0.1	2
2001	NL1	NSL WW44	**106**	21.0	**0.6**	0.3	**-2.5**	2.3	**-0.4**	0.4	**-1.0**	1.9	3
2002	NL2	Smuggler	**128**	1.4	**2.7**	0.8	**-7.5**	0.4	**0.8**	0.1	**-5.1**	0.5	2
2001	NL1	Smuggler	**129**	20.6	**-1.1**	0.8	**-5.5**	1.8	**-2.1**	0.8	**-4.1**	1.9	3

Breadmaking NL2 2002 and NL1 2002 and 2001 where varieties were tested for one year only

			Peak Time (s)		PC1		PC2		PC1 corr		PC2 corr		
Year	Trial	Variety	**Mean**	SD	**Mean**	SD	**Mean**	SD	**Mean**	SD	**Mean**	SD	n
2002	NL2	SUR.HD.199/5	**70**	4.2	**-0.3**	0.1	**-1.4**	0.5	**-1.9**	0.4	**0.7**	0.1	2
2002	NL1	40497 AT21	**73**	2.1	**0.8**	0.1	**-2.1**	1.8	**-1.2**	0.4	**0.5**	1.4	2
2002	NL1	CPBT W94	**67**	0.7	**3.8**	1.7	**-1.8**	1.2	**2.1**	2.5	**0.4**	0.2	2
2002	NL1	CPBT W98	**135**	7.8	**2.1**	1.7	**-6.2**	1.7	**1.6**	1.8	**-5.6**	1.8	2
2002	NL1	DSV 121/01	**68**	1.4	**1.0**	3.0	**-1.0**	1.2	**-1.5**	2.7	**2.2**	0.9	2
2002	NL1	IPF5	**78**	4.9	**5.1**	3.6	**-2.0**	1.5	**2.8**	4.5	**1.0**	2.6	2
2002	NL1	LD 232	**95**	2.1	**5.6**	0.0	**-8.3**	0.1	**3.4**	0.1	**-5.3**	0.1	2
2002	NL1	NSL WW55	**113**	7.1	**3.4**	1.4	**-6.4**	1.0	**1.9**	1.0	**-4.4**	0.5	2
2002	NL1	NSL WW58	**101**	9.9	**0.8**	0.6	**-2.1**	0.6	**-0.4**	0.6	**-0.7**	0.6	2
2002	NL1	PBI 00/35	**98**	2.8	**-1.1**	1.1	**-4.3**	2.3	**-2.8**	0.1	**-2.1**	1.0	2
2002	NL1	PBI 01/0073	**82**	1.4	**-0.2**	0.7	**-2.3**	0.7	**-1.0**	0.3	**-1.3**	0.6	2
2002	NL1	PBI 01/0074	**75**	10.6	**0.3**	0.3	**0.2**	1.7	**-0.4**	0.7	**1.2**	3.0	2
2002	NL1	PBI 01/0091	**73**	13.4	**2.7**	2.7	**-0.1**	1.8	**1.7**	3.1	**1.2**	1.1	2
2002	NL1	PBI 01/0096	**74**	3.5	**3.8**	5.3	**1.4**	0.1	**3.1**	5.8	**2.4**	0.7	2
2002	NL1	PI-W-10-99	**74**	0.0	**4.0**	2.4	**-1.6**	0.4	**2.5**	2.2	**0.4**	0.1	2
2002	NL1	UN98-16-1	**94**	3.5	**-1.3**	0.3	**1.6**	1.5	**-0.8**	0.9	**1.0**	0.7	2
2002	NL1	WW9043	**86**	4.2	**0.1**	1.7	**-4.2**	0.3	**-1.8**	1.6	**-1.7**	0.1	2
2001	NL1	A35-00	**62**	9.5	**2.8**	1.6	**0.7**	1.6	**2.1**	1.1	**1.8**	0.3	3
2001	NL1	CPBT W84	**90**	11.9	**-3.0**	1.9	**0.1**	2.1	**-3.0**	1.7	**0.1**	2.2	3
2001	NL1	CPBT W85	**82**	10.0	**0.0**	1.5	**-4.3**	0.6	**-1.3**	1.1	**-2.2**	1.2	3
2001	NL1	CPBT W86	**72**	11.1	**0.8**	1.7	**0.1**	1.5	**0.3**	1.4	**0.9**	1.1	3
2001	NL1	LW92W49-1	**89**	11.1	**3.2**	1.6	**-3.9**	2.1	**2.1**	0.7	**-2.2**	1.3	3

Biscuit making RL 2002 and 2001 and NL2 2001. Varieties tested in both years followed by varieties tested in one year only.

			Peak Time (s)		PC1		PC2		PC1 corr		PC2 corr		
Year	Trial(s)	Variety	**Mean**	SD	**Mean**	SD	**Mean**	SD	**Mean**	SD	**Mean**	SD	n
2002	RLW	Arran	**67**	4.3	**1.8**	1.3	**-1.3**	1.9	**1.6**	0.7	**-1.0**	0.9	5
2001	NL2	Arran	**70**	15.3	**3.1**	1.7	**-3.2**	2.4	**3.0**	1.3	**-3.1**	1.9	3
2002	R&NL	Claire	**65**	5.0	**1.8**	1.6	**-1.7**	2.2	**1.5**	0.8	**-1.2**	0.7	11
2001	R&NL	Claire	**71**	10.4	**1.8**	2.0	**-2.4**	2.6	**1.8**	1.2	**-2.4**	1.2	11
2002	RLW	Goodwood	**72**	4.8	**1.7**	0.9	**-1.5**	1.7	**1.9**	0.4	**-1.9**	0.4	5
2001	NL2	Goodwood	**78**	13.6	**2.7**	0.8	**-2.7**	2.2	**2.7**	0.9	**-2.6**	0.6	3
2002	RLW	Robigus	**62**	4.3	**2.5**	1.9	**-0.4**	2.2	**2.5**	1.8	**-0.5**	0.8	5
2001	NL2	Robigus	**69**	12.5	**2.7**	2.5	**-0.9**	2.0	**2.6**	1.9	**-0.8**	1.1	3
2002	RLW	Wizard	**68**	7.0	**1.9**	1.0	**0.6**	1.4	**2.5**	0.5	**-0.4**	0.5	5
2001	NL2	Wizard	**73**	13.2	**1.2**	1.0	**-1.0**	2.4	**1.7**	1.0	**-2.0**	1.1	3
2001	RLW	Consort	**65**	5.8	**3.0**	1.9	**-1.9**	3.0	**3.1**	0.9	**-2.1**	0.9	5
2001	RLW	Deben	**74**	8.2	**3.2**	2.3	**-3.8**	2.3	**2.5**	1.2	**-2.4**	0.3	5
2001	RLW	Riband	**57**	5.7	**7.2**	1.6	**-3.2**	2.4	**7.2**	1.8	**-3.1**	0.4	4*
2001	NL2	CPBT W75	**66**	7.6	**9.4**	5.0	**-3.1**	2.2	**9.5**	3.9	**-3.2**	0.6	3
2001	NL2	CPBT W77	**56**	6.1	**11.4**	3.5	**-5.2**	0.5	**11.3**	3.1	**-5.0**	0.9	3
2001	NL2	CPBT W79	**67**	13.1	**6.1**	4.7	**-0.8**	2.4	**6.0**	4.0	**-0.7**	1.7	3
2001	NL2	CWW 99/43	**53**	10.5	**5.9**	1.2	**-3.1**	1.3	**6.0**	1.5	**-3.4**	0.4	3
2001	NL2	CWW 99/45	**63**	10.6	**2.6**	1.2	**-1.0**	1.5	**3.1**	1.3	**-1.9**	0.8	3
2001	NL2	Harbour	**59**	12.5	**4.3**	1.1	**-1.9**	1.8	**4.3**	1.3	**-1.8**	0.3	3

*n = 3 for peak time

Biscuit making NL2 2002 and NL1 2001 and 2002. Varieties tested in both years followed by varieties tested in one year only.

			Peak Time (s)		PC1		PC2		PC1 corr		PC2 corr		
Year	Trial	Variety	**Mean**	SD	**Mean**	SD	**Mean**	SD	**Mean**	SD	**Mean**	SD	n
2002	NL2	CEB 98057	**61**	2.9	**3.7**	1.8	**-2.0**	2.8	**3.1**	0.4	**-0.9**	0.9	3
2001	NL1	CEB 98057	**56**	4.5	**6.8**	2.8	**-2.2**	2.1	**7.3**	1.9	**-3.0**	0.8	3
2002	NL2	Colonel	**51**	5.5	**5.8**	1.5	**-4.7**	2.4	**4.5**	0.6	**-2.7**	0.9	3
2001	NL1	Colonel	**50**	11.2	**6.6**	2.1	**-4.8**	2.6	**6.1**	1.4	**-4.1**	1.2	3
2002	NL2	CWW 00/4	**64**	8.5	**2.8**	2.2	**-3.8**	1.6	**2.3**	1.8	**-2.9**	0.6	3
2001	NL1	CWW 00/4	**63**	7.4	**3.8**	3.0	**-3.0**	3.2	**4.2**	2.8	**-3.8**	2.1	3
2002	NL2	Dart	**62**	5.5	**2.1**	2.5	**-2.8**	2.8	**1.6**	0.9	**-2.0**	0.8	3
2001	NL1	Dart	**60**	5.0	**2.6**	0.8	**-1.8**	1.8	**3.1**	0.4	**-2.6**	1.3	3
2002	NL2	Dick	**61**	3.5	**3.1**	2.3	**-2.7**	2.5	**2.6**	1.0	**-1.8**	0.6	3
2001	NL1	Dick	**67**	5.5	**3.7**	1.1	**-1.4**	2.1	**4.3**	0.5	**-2.4**	1.2	3
2002	NL2	Nijinsky	**61**	8.2	**2.6**	1.5	**-1.4**	2.7	**2.3**	0.4	**-1.0**	0.6	3
2001	NL1	Nijinsky	**64**	10.1	**3.4**	0.8	**-1.5**	1.5	**3.7**	1.3	**-2.0**	0.1	3
2002	NL2	NSL WW47	**54**	0.0	**5.8**	1.6	**-2.2**	1.3	**5.0**	1.1	**-0.9**	1.0	3
2001	NL1	NSL WW47	**55**	3.2	**5.5**	1.6	**-1.3**	1.7	**5.7**	0.8	**-1.6**	0.3	3
2002	NL2	NSL WW48	**62**	13.0	**2.3**	2.7	**-3.2**	2.9	**1.6**	1.1	**-2.0**	0.3	3
2001	NL1	NSL WW48	**62**	5.6	**3.0**	0.7	**-2.1**	1.4	**3.0**	0.2	**-2.1**	1.0	3
2002	NL2	NSL WW50	**62**	2.5	**3.1**	1.4	**-2.0**	2.3	**3.0**	0.2	**-1.8**	0.6	3
2001	NL1	NSL WW50	**57**	8.1	**3.3**	0.4	**-1.9**	1.2	**3.6**	0.7	**-2.5**	0.7	3
2002	NL2	SEMC 29	**67**	6.4	**7.4**	2.2	**-4.7**	2.1	**6.9**	2.1	**-3.9**	0.7	3
2001	NL1	SEMC 29	**80**	7.8	**4.7**	1.6	**-5.1**	1.7	**5.4**	2.0	**-6.3**	0.4	3
2001	NL1	CPBT W87	**59**	12.9	**5.0**	2.5	**-4.5**	1.9	**4.6**	2.3	**-3.8**	0.7	3
2001	NL1	NFC 10034	**58**	6.4	**4.3**	0.4	**-1.0**	0.2	**5.6**	0.5	**-3.2**	0.1	2
2002	NL1	A39-01	**60**	5.7	**2.7**	2.1	**-2.3**	2.0	**1.8**	1.4	**-0.7**	0.1	3
2002	NL1	CEB 99080	**53**	1.0	**7.7**	2.7	**-2.5**	1.8	**7.5**	3.9	**-2.1**	0.4	3
2002	NL1	CPBT W95	**47**	6.8	**10.8**	2.5	**-4.9**	1.7	**10.3**	1.1	**-4.1**	0.9	3
2002	NL1	CPBT W96	**52**	3.5	**6.2**	0.4	**-3.7**	2.2	**5.4**	0.9	**-2.3**	0.1	3
2002	NL1	NFC 10109	**46**	2.3	**5.5**	0.8	**-2.9**	2.1	**4.7**	0.8	**-1.6**	0.7	3
2002	NL1	NSL WW56	**59**	9.7	**4.2**	1.5	**-3.2**	1.4	**3.4**	0.7	**-1.9**	0.2	3
2002	NL1	PBI 01/0045	**33**	7.5	**9.0**	0.4	**-5.7**	1.2	**8.2**	1.1	**-4.5**	0.9	3

APPENDIX C. BREEDERS' ASSESSMENTS

ELSOMS SEEDS LTD

INTRODUCTION

The objective of the testing carried out at Elsoms Seeds was to evaluate the Reomixer as an instrument for testing wheat lines from our breeding programme for their protein quality. To this end samples of white flour of standard wheat varieties, provided by CCFRA, were run and compared with the same wheat samples ground on our Retsch mill and sieved over a 125 micron sieve. This was to enable us to calibrate our method of obtaining flour with the standard white flour from which the experimental procedures were established.

In addition, 96 samples from our breeding programme were run to compare the Reomixer traces with the standard tests for protein quality that we use to screen lines from our breeding programme. We currently use SDS sedimentation volume to indicate whether a variety has protein quality where it may be a potential bread or biscuit making variety: we then manually assess the gluten to establish if the gluten is too tough to be of practical use for breadmaking purposes.

ASSESSMENT

After being trained on the Reomixer we were able to achieve 18 runs a day using the standard-dough method and 22 runs a day using the SDS-dough method. This compares with 20 samples a day using our standard in-house method of assessing protein quality. To support the quality objectives of our programme we are required to assess up to 200 samples a year.

Comparing the time to evaluate the SDS-dough method results with the combined tests of the SDS sedimentation and gluten wash-out tests that Elsoms carry out, we found that the single SDS-dough method would enable us to do more tests in one day as one gluten wash-out test alone can take 20 minutes. We found the practicalities of running the Reomixer tests compared to our own in-house tests were no different, as the most time consuming part of any of the tests is the grinding and sieving.

The traces from the Reomixer gave an individual visual picture of the protein quality. For comparison of samples, we found the quality map of plotted PC1 and PC2 data very useful.

The method of handling the data was the most difficult aspect in the study. Once the Reomixer trace had been produced and stored there are several stages in copying files and converting the data into a suitable format to give the principal component plots and traces to identify the quality group to which the samples belong. It was felt that confidence of interpreting the data would come with experience with the test. The procedures for converting the Reomixer traces into a format for interpretation would need streamlining to make them more user-friendly.

CONCLUSION

We felt that the Reomixer gave significantly better predictions of bread making quality over the SDS sedimentation volume. When compared with our manual assessment of gluten, it was placing lines in similar categories i.e. too tough, too weak or potential breadmaking. When assessing potential for biscuit making the Reomixer gave better discrimination between varieties than our existing tests.

MONSANTO UK LTD

INTRODUCTION

A Reomixer was obtained on loan from CCFRA between 20 May and 9 July 2003. The instrument was provided for us to evaluate its ease of use and to investigate how it performed when predicting wheat quality as described in HGCA project 2531, especially when assessing novel wheat genotypes from the Monsanto breeding programme.

MATERIALS AND METHODS

CCFRA provided a day of training in the use of the Reomixer and the spreadsheet software used to collate and plot data.

Standard-dough was mixed on the Reomixer following the draft method provided by CCFRA entitled ‘Recording of mixing traces on the Reomixer from a white flour dough with salt (amended for Reomixer 32 Software, version 0.93)’. SDS-dough, and using sieved ground wheat for both tests was not investigated.

A check sample (CM/920734/10181) supplied by CCFRA was run at least once every day the Reomixer was used.

Material from the 2002 harvest was analysed on the Reomixer. Samples were selected to try to provide a range in quality with hard and soft milling texture and varying protein levels, based on routine quality assays already completed on this material. Two named varieties from this trial were included, Malacca (**nabim** group 1) and Rialto (**nabim** group 2).

PC1 versus PC2 data were plotted for all the samples analysed by the Reomixer using Excel spreadsheets supplied by CCFRA. These data were then extracted from them and re-plotted in another Excel spreadsheet where we have been able to combine all the samples from each trial tested (the CCFRA spreadsheet limits the samples to 24).

RESULTS AND DISCUSSION

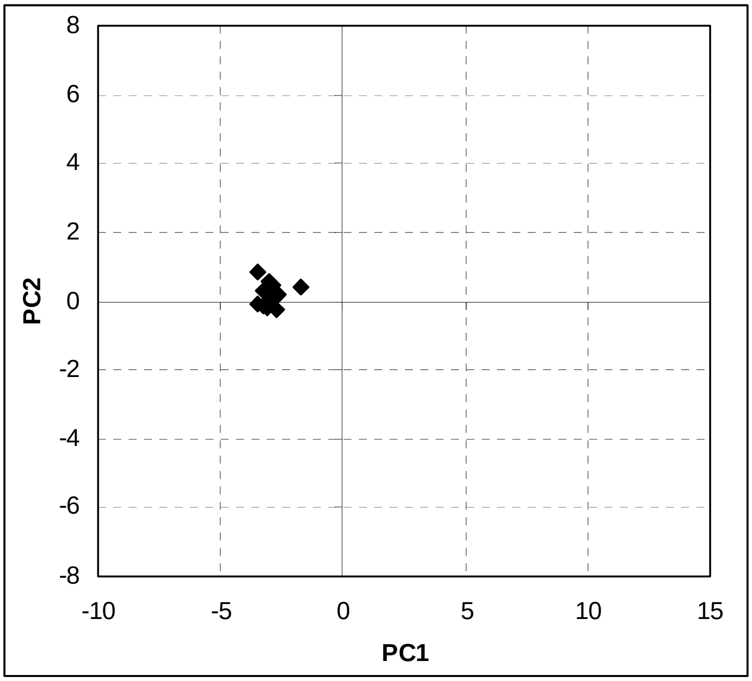
Consistency of Check Results

The peak time, peak height, area to peak and calculated PC1 and PC2 values for the check sample are shown in Table I. A plot of the PC1 and PC2 values is shown in Figure I. The latter shows a good, close grouping and no sign of any trend with date of analysis, indicating no problems with the instrument or analysis.

Table I. Check sample values

Sample ID	Date	Peak Time (min)	Peak Height (V)	Area to Peak (min V)	PC1	PC2
1	11-Jun	5.28	6.73	26.39	-3.48	0.82
2	11-Jun	5.60	6.46	27.32	-2.97	-0.10
3	11-Jun	4.58	6.65	20.45	-2.69	-0.25
4	11-Jun	4.67	6.69	21.98	-3.03	0.56
5	11-Jun	6.20	6.55	31.17	-3.07	-0.20
6	12-Jun	4.47	6.75	20.49	-2.84	0.49
7	12-Jun	5.72	6.77	27.87	-3.25	-0.11
8	16-Jun	5.23	6.79	25.24	-2.96	0.14
9	17-Jun	5.63	6.64	28.02	-2.62	0.20
10	23-Jun	4.87	6.73	22.42	-3.49	-0.08
11	24-Jun	5.18	6.60	25.38	-1.75	0.42
12	26-Jun	5.22	6.67	25.37	-2.83	0.28
13	02-Jul	5.25	6.81	25.55	-3.24	0.29
Mean		5.22	6.68	25.20	-2.94	0.19
Std Dev		0.49	0.10	3.16	0.49	0.33

Figure I . Plot of check sample PC1 and PC2 values

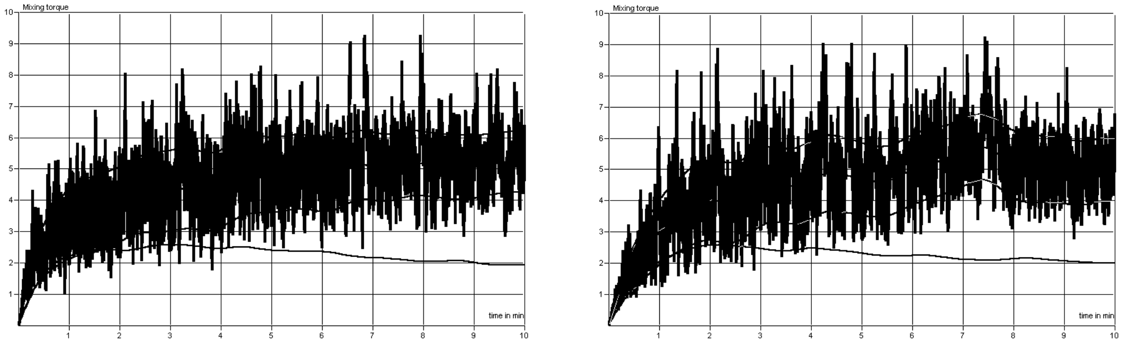


Replication of Samples from Job 1

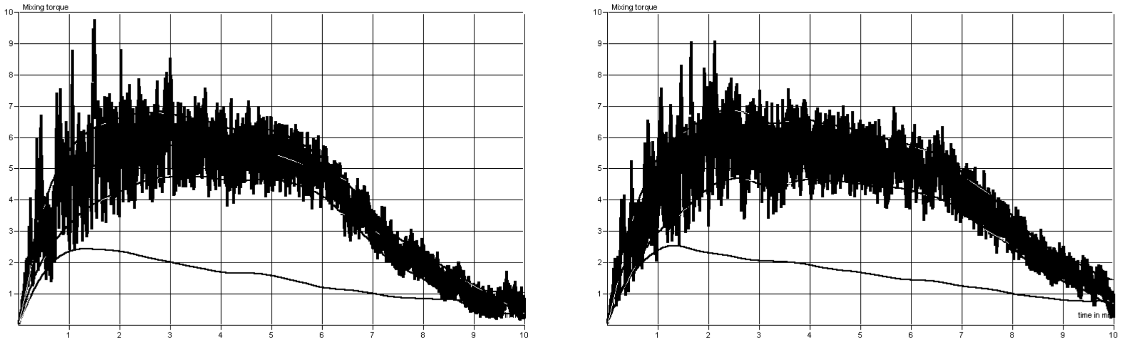
Job 1 samples were replicated and the duplicate graphs were consistently similar, though not identical. Two examples are given in Figure II:

Figure II. Reomixer trace replication

Job 1-1a 1b



Job 1-19a 19b



Replication values for peak time, peak height and area to peak are given in Table II. Replication for peak height was good but there was more variation for peak time and area to peak, particularly at longer peak times (e.g. samples 1 and 4).

Replication values for PC1 and PC2 are given in Table III. The replication was very consistent.

Table II. Trace parameter replication data for Job 1

	Peak Time (min)			Peak Height (V)			Area to Peak (min V)		
Sample ID	Rep 1	Rep 2	Mean	Rep 1	Rep 2	Mean	Rep 1	Rep 2	Mean
1	9.98	7.37	8.68	5.24	5.71	5.48	44.06	30.83	37.45
2	4.65	5.87	5.26	6.11	6.08	6.10	19.52	27.34	23.43
3	4.52	3.60	4.06	6.45	6.40	6.43	21.16	15.88	18.52
4	6.65	9.98	8.32	5.63	5.32	5.48	29.24	45.64	37.44
5	5.63	5.30	5.47	5.71	5.80	5.76	23.11	22.85	22.98
6	6.02	5.82	5.92	5.76	5.82	5.79	24.89	22.82	23.86
7	4.57	3.13	3.85	6.21	6.36	6.29	22.13	14.40	18.27
8	3.63	3.45	3.54	6.71	6.37	6.54	16.58	15.13	15.86
9	4.62	4.07	4.35	5.68	5.80	5.74	19.14	15.84	17.49
10	2.58	3.35	2.97	6.61	6.61	6.61	10.90	15.49	13.20
11	4.42	3.80	4.11	6.47	6.27	6.37	20.46	17.34	18.90
12	4.58	5.03	4.81	6.00	5.77	5.89	19.32	21.90	20.61
13	6.45	6.83	6.64	5.71	5.78	5.75	27.05	29.82	28.44
14	5.30	5.33	5.32	6.71	6.52	6.62	25.80	26.01	25.91
15	5.22	4.92	5.07	6.37	6.42	6.40	23.36	21.60	22.48
16	5.22	4.98	5.10	6.63	6.39	6.51	24.10	21.73	22.92
17	4.07	3.72	3.90	6.45	6.29	6.37	17.51	14.60	16.06
18	3.37	3.73	3.55	4.61	4.43	4.52	11.47	12.47	11.97
19	2.80	2.53	2.67	5.75	5.76	5.76	12.21	10.33	11.27
20	2.62	2.27	2.45	4.84	4.70	4.77	9.69	8.03	8.86
21	2.55	4.15	3.35	5.04	4.82	4.93	9.24	16.42	12.83
22	1.88	2.17	2.03	4.86	4.77	4.82	6.45	7.60	7.03
23	5.15	5.22	5.19	6.09	5.95	6.02	22.98	22.76	22.87
Mean	4.63	4.64	4.64	5.90	5.83	5.87	20.02	19.86	19.94
Correlation Reps			0.80			0.96			0.76

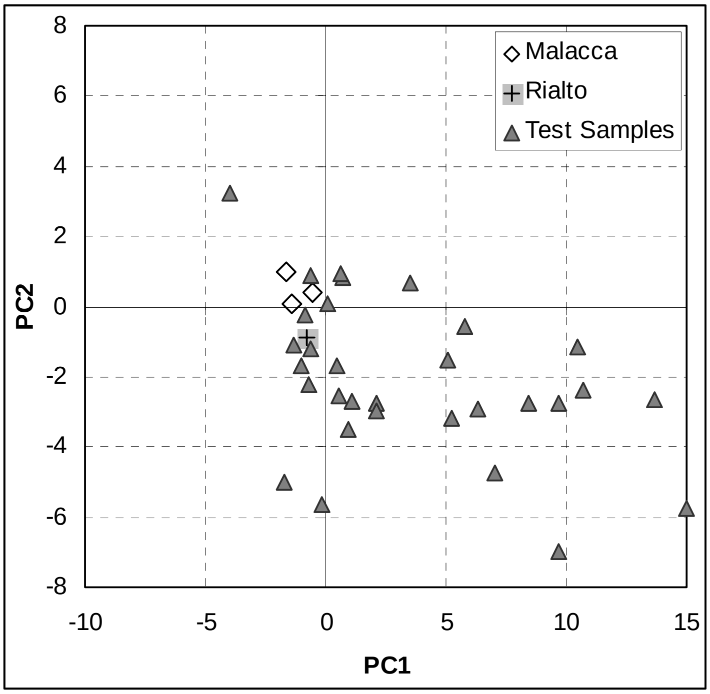
Table III. Replication data for PC1 and PC2 for Job 1

	PC1			PC2		
Sample ID	Rep 1	Rep 2	Mean	Rep 1	Rep 2	Mean
1	0.77	0.62	0.70	-3.64	-3.60	-3.62
2	-2.06	-1.53	-1.80	-1.07	-0.90	-0.99
3	-1.19	-0.72	-0.96	0.65	0.81	0.73
4	-0.43	0.18	-0.13	-2.63	-2.81	-2.72
5	-1.16	-1.36	-1.26	-2.47	-1.43	-1.95
6	-1.07	-1.51	-1.29	-2.83	-3.08	-2.96
7	-0.79	-0.61	-0.70	0.99	1.60	1.30
8	-2.00	-2.11	-2.06	1.58	1.01	1.30
9	0.64	0.40	0.52	-1.48	-1.55	-1.52
10	-0.72	-2.21	-1.47	1.71	1.90	1.81
11	-1.86	-0.96	-1.41	0.76	1.08	0.92
12	-0.52	-0.31	-0.42	-1.16	-1.38	-1.27
13	0.04	-1.10	-0.53	-3.34	-2.92	0.21
14	-3.38	-2.66	-3.02	0.52	0.66	0.59
15	-2.38	-2.08	-2.23	-1.03	-0.92	-0.98
16	-3.53	-3.00	-3.27	-0.23	-0.64	-0.44
17	-1.58	-0.97	-1.28	0.27	-0.17	0.05
18	5.83	5.64	5.74	-3.73	-4.49	-4.11
19	11.83	9.06	10.45	0.88	0.60	0.74
20	5.56	6.11	5.84	-3.16	-3.31	-3.24
21	3.68	3.86	3.77	-2.38	-2.71	-2.55
22	8.05	9.14	8.60	-2.68	-2.78	-2.73
23	-1.03	-1.61	-1.32	-0.96	-1.22	-1.09
Mean	0.55	0.53	0.54	-0.82	-1.14	-0.98
Correlation Reps			0.98			0.98

Analysis of breeding samples

The plotted position of the breeding samples together with the controls is shown in Figure III. We found that the better the baking quality, the more the samples tended to the top left quartile of the chart.

Figure III. Test sample plot



CONCLUSIONS

The Reomixer is a little slow for our needs at an analysis time of 10 minutes for standard-dough. We found use of the instrument to be involved and complicated; all the reagents and the instrument need time to adjust to 30 ºC before any analysis can start and flours have to be equilibrated to 30 ºC in the water bath before a run. The plus point is that the mixing bowl is held at 30 ºC so room temperature would not be an issue.

At present the Reomixer at CCFRA has only been assessed using water absorption values derived from the Farinograph (white flour standard-dough method), and CCFRA is not aware that anyone has used predicted water absorption values with this method. The use of Farinograph water absorption values would not be practical for our routine use since we need a system that will work satisfactorily using predicted water values, without the need to run the samples through the Farinograph.

To be sure about the reliability of this prediction of baking quality we would need more samples with quality data and more environmental variation with material from different sites and seasons. The correlation of the plot of the PC1 versus PC2 derived from the torque-time trace with various quality parameters would need to be studied in more detail since we have only had a quick comparison of a few of the sample plots with a limited number of quality components.

The Reomixer appears to offer some potential to predict ‘quality’ for bread-making using as little as 10g white flour and within about 15 minutes. But there are significant drawbacks to the method that has been developed so far: having to use the Farinograph water absorption for which Bühler milled flour will be required, maintaining the temperature of the solutions and flours plus the mixer bowl is not easy to clean between samples because of its small size. This is not a system we will be adopting at this stage for screening bread wheats.