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# Factor analysis of the functional properties of rice flours from mutant genotypes

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ABSTRACT

A set of 27 waxy rice genotypes and 52 rice genotypes with medium and high amylose contents were screened for various functional properties of flour. In this study, 68 genotypes containing various amylose contents (1.2–30.4%) were mutants of the rice variety TNG67 widely grown in Taiwan. The proximate composition, pasting, thermal and textural properties of rice flours were determined and analysed with factor analysis to assess the genetic differences. A wide variation in various functional properties was observed. Factor analysis indicated that four factors relating to amylose content, gel textural, gelatinization and protein content could explain 80% of the variability among 79 rice flours. Correlation studies and scatter diagrams also indicated the larger role of amylose with respect to protein and lipid in determining the rice flour quality. The present study can be used for readily identifying differences between rice genotypes for eating/cooking quality.



## 1. Introduction

Rice (*Oryza sativa* L.) is the staple food of over approximately one-half of the world's population. In Asia alone, more than 2000 million people obtain 60–70% of their calories from rice and its products. Rice production in Taiwan is estimated to be 1.2 million ton; people in Taiwan consume rice as boiled rice besides in processed products like noodles, crackers, cakes, desserts, and cookies. Starch is the main component of rice grain. Gelatinization, retrogradation and pasting characteristics of starch affect the quality of rice flour and hence rice products. These characteristics are dependent upon the ratio of amylose to amylopectin, chain length, degree of branching of amylopectin, lipid-complexed amylose, and chains and granule architecture, i.e. crystalline to amorphous area ratio (Tester, 1997).

The difference in the amylose content in rice varieties has been attributed to a single nucleotide polymorphism in an allele of the waxy gene encoding the granule bound starch synthase enzyme (Ayres et al., 1997). Juliano (1996) suggested that the cooking profile of rice obtained from Rapid Visco Analyzer (RVA) might be helpful for the evaluation of grain quality and the selection of lines with good quality in rice breeding. The mechanical properties of flour and starch gels are dependent upon the retrogradation tendency of starch molecules. Amylose has been reported to be responsible for retrogradation in gels stored for short time (Miles, Morris, Orford, & Ring, 1985).

The dynamic nature of the RVA curve has been exploited for studying the genetic basis of grains derived from populations developed from crosses between intermediate or high apparent amylose content (AAC) lines and low AAC lines (Chen, Bergman, Pinson, & Fjellstrom, 2008). Bao et al. (2000) and Wang et al. (2007) mapped the largest QTL for paste viscosity measurements to the waxy locus on rice chromosome six, which was also the major locus controlling AAC. Rice is diploid and easily transformable due to a relatively small genome (Rahman et al., 2007). Factor Analysis is one of the multivariate techniques to analyse large and complicated data. This technique is based on the extraction of 'latent factors' from several variables for comparison and interpretation of the data. Factor analysis has been used previously for predicting the rice eating quality (Champagne et al., 1999; Lyon et al., 1999; Tan & Corke, 2002).

A large pool of rice samples (79 genotypes) differing in their amylose contents were investigated for the viability of their flours by examination of their functional properties. Factor analysis was used to analyse the genetic similarities and differences in the functional properties of flours from the mutants and the parent genotype. The present study was focused on identifying predictive parameters for the rapid screening of rice genotypes for flour quality, suitable both for small and large scale use.

## 2. Materials and methods

### 2.1. Materials

Four Indica varieties of rice TCN1, TCS10, TCS17 and TS2, three Japonica TNG67, TK8 and TK16 and four waxy varieties namely

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TCW70, TKW1, TKW5 and TSW2 were obtained from Taichung District Agricultural Research and Extension Station (COA), Datsun, Chunghua, Taiwan. Sixty-eight genotypes of rice were sodium azide ($NaN_3$) induced mutants of TNG67, and were supplied by Agricultural Research Institute of Taiwan (COA), Wufong, Taichung, Taiwan. The polished rice were milled using Cyclotec 1093 sample mill (Tecator Co., Sweden) and passed over sieve with 0.5 mm pore size to get flour. Among these 68 mutant genotypes, 23 showed low amylose content, 42 showed medium and 3 showed high content of amylose in their flours.

### 2.2. Methods

#### 2.2.1. Proximate composition

Amylose content of rice flour was measured using AACC 61-03 (2000) method, and the total starch content in rice flours was determined by AACC 76-12 (2000) method using Megazyme Total Starch Assay Kit (Megazyme International Ireland Ltd., Wicklow, Ireland). Flour samples were also evaluated for their crude protein (N × 5.95) and lipid contents by using of AACC (2000) methods.

#### 2.2.2. Pasting properties

Pasting properties of rice flour gels were determined using Rapid Visco Analyzer (RVA 3D+, Newport Scientific Pvt. Ltd., Warriewood, Australia). Rice flour slurry (12% w/w, db) was prepared, and the temperature–time cycle included a heating step at 50 °C for 1 min, followed by heating at a rate of 12 °C/min to 95 °C, holding at 95 °C for 2.5 min, followed by cooling at the same rate to 50 °C and maintaining at 50 °C for 1.5 min. The paddle speed was kept at 960 rpm for the first 10 s and then kept constant at 160 rpm for the rest of the analysis. The parameters recorded were peak viscosity (PV), hot paste viscosity (HPV) (minimum viscosity at 95 °C), final viscosity (FV), breakdown (BD = PV − HPV), and setback (SB = FV − HPV). Breakdown ratio (BDR) and setback ratio (SBR) were defined as the ratios of BD to PV and SB to HPV, respectively. All measurements were done in triplicate.

#### 2.2.3. Thermal properties

Thermal properties of flour were determined by using a differential scanning calorimeter (DSC, model 2910, TA Instruments, Surrey, England). Flour sample (about 2.5 mg, db) was weighed in the sample pan, mixed with distilled water (flour:water = 1:3), and the pan was sealed hermetically. The samples were heated from 25 to 130 °C at 10 °C/min heating rate. The onset temperature ($T_o$), peak temperature ($T_p$), conclusion temperature ($T_c$), temperature range ($R = T_c - T_o$) and enthalpy change of gelatinization ($\Delta H_{gel}$) were recorded. Enthalpies were calculated on weight of flour on a dry basis.

The gelatinized samples were kept in pans at 4 °C for 7 days and rescanned in DSC using the same procedure described above for determining the retrogradation enthalpy change ($\Delta H_{ret}$) and percentage retrogradation (%$R$); the latter was taken as the ratio of $\Delta H_{ret}$ to the $\Delta H_{gel}$ multiplied by 100.

#### 2.2.4. Textural properties

The flour pastes (6 ml) prepared in RVA was sealed in plastic containers (21.5 mm id × 12.8 mm height) and stored at 4 °C for 7 days. The textural properties of rice flour gels were determined using a TA-XT2 texture analyser (Stable Microsystems, Surrey, UK). The gel was compressed at a speed of 1 mm/s, using a 5-kg load cell to a distance of 10 mm with a cylindrical plunger (12.5 mm diameter). The compression was repeated twice to generate a force time curve, from which hardness (height of the first peak) and springiness (ratio of the time elapsed between the end of first bite and the start of second bite) were determined.

The resilience was calculated as the area during the withdrawal of the first compression divided by the area of the first compression. The cohesiveness was calculated as the ratio of the area under the second peak to the area under the first peak (Bourne, 1978). The gumminess was determined by multiplying hardness and cohesiveness. The chewiness was derived from gumminess and springiness and was obtained by multiplying these two. Ten repeated measurements were performed for each sample and the average was taken.

#### 2.2.5. Statistical analysis

The data reported are averages of triplicate observations unless otherwise stated. Pearson correlation coefficients ($r$) for relationships between various flour properties were determined and the factor analysis with varimax rotation was performed.

## 3. Results and discussion

### 3.1. Proximate composition

Table 1 summarises the basic statistical parameters of the proximate composition of the rice flours studied. The amylose content in the flours ranged from 1.2% to 3.7%, 14.7% to 18.6% and 22.7% to 30.4% for 27 genotypes of low amylose content, 47 genotypes of medium amylose content and five genotypes of high amylose content, respectively. The amylose content in the flours of commercial varieties was within the range mentioned above. The amylose content in the starches isolated from rice was found to be higher by 9.5–46% than the corresponding amylose content of their flours. Wang et al. (2010) reported the amylose content between 18%

**Table 1**
Basic statistical parameters of the proximate composition of rice flours.

| Rice flour | Amylose (%, flour) | Amylose (%, starch)[a] | Total starch (%, db) | Crude protein (%, db) | Crude lipid (%, db) |
|---|---|---|---|---|---|
| *Low amylose content* | | | | | |
| TKW5 | 2.4 | 7.38 | 93.5 | 7.38 | 1.43 |
| TCW70 | 2.6 | 7.92 | 94.1 | 7.92 | 1.86 |
| TKW1 | 2.6 | 10.82 | 82.8 | 10.82 | 3.21 |
| TSW2 | 2.6 | 7.96 | 88.7 | 7.96 | 1.90 |
| Average[b] | 2.3 | 9.10 | 85.8 | 9.10 | 1.80 |
| SD | 0.6 | 1.98 | 3.2 | 1.98 | 0.77 |
| Min | 1.2 | 6.30 | 80.9 | 6.30 | 0.07 |
| Max | 3.7 | 14.4 | 94.1 | 14.4 | 3.21 |
| CV (%) | 26.5 | 21.8 | 3.8 | 21.8 | 43.9 |
| *Medium amylose content* | | | | | |
| TCS10 | 16.7 | 7.69 | 88.5 | 7.69 | 1.85 |
| TK8 | 17.0 | 6.40 | 91.0 | 6.40 | 2.00 |
| TS2 | 17.2 | 7.41 | 90.2 | 7.41 | 1.31 |
| TNG67 | 17.7 | 9.80 | 80.3 | 9.80 | 0.99 |
| TK16 | 18.0 | 6.69 | 90.7 | 6.69 | 1.94 |
| Average | 16.8 | 9.24 | 85.8 | 9.24 | 0.97 |
| SD | 1.0 | 1.61 | 2.8 | 1.61 | 0.49 |
| Min | 14.7 | 6.40 | 79.6 | 6.40 | 0.05 |
| Max | 18.6 | 12.70 | 91.0 | 12.70 | 2.09 |
| CV (%) | 6.0 | 17.4 | 3.3 | 17.4 | 50.6 |
| *High amylose content* | | | | | |
| TCN1 | 30.2 | 8.55 | 87.6 | 8.55 | 1.31 |
| TCS17 | 30.4 | 9.03 | 87.8 | 9.03 | 1.97 |
| Average | 27.0 | 9.80 | 86.5 | 9.80 | 1.00 |
| SD | 3.3 | 1.92 | 2.1 | 1.92 | 0.71 |
| Min | 22.7 | 8.55 | 82.9 | 8.55 | 0.16 |
| Max | 30.4 | 13.18 | 87.8 | 13.18 | 1.97 |
| CV (%) | 12.1 | 19.8 | 2.4 | 19.8 | 67.7 |

[a] Amylose content (%) was calculated from total starch for basis.
[b] Average under various headings of low, medium and high amylose contents is mean of values of 27, 47 and 5 genotypes (mutants and named varieties), respectively. Similar holds for other statistical parameters. SD, Min, Max, and CV stand for standard deviation, minimum, maximum and coefficient of variation, respectively.