

Blanchability of peanut (*Arachis hypogaea* L.) kernels: early generation selection and genotype stability over three environments

A. W. Cruickshank^A, J. W. Tonks^A, and A. K. Kelly^B

^AQueensland Department of Primary Industries, PO Box 23, Kingaroy, Qld 4610, Australia.

^BQueensland Department of Primary Industries, PO Box 102, Toowoomba, Qld 4350, Australia.

Abstract. Blanching is the removal of testa from peanut kernel by heating followed by abrasion. Blanchability is the capacity to recover kernels with all the testa removed. This study investigated the response to early generation selection for blanchability and the stability of 22 breeding lines over 3 environments.

F₂-derived families with 'good' and 'poor' blanchability were selected. BLUPs for F_{4:5} lines from F₂ families were significantly correlated with the mean blanchability of F_{2:3} rows. The within-family variance was mostly in 3 of the poor blanching families. In all other families, variance among lines within families was smaller than the error variance. Early generation selection was effective.

In the 22 lines × 3 site experiment, there was a high genetic correlation common to each pair of sites, suggesting that differences in blanchability are repeatable. The expression of genetic variation was much greater at Coominya, with a 5-fold greater genetic variance than at Walkamin. All 3 environments in this experiment were irrigated. Interaction may have been greater with the inclusion of rainfed environments.

Parent selection could make an important contribution to breeding for improved blanchability. Environment may not substantially affect the rank of genotypes but may affect the capacity to detect differences.

Additional keywords: quality, aflatoxin, post-harvest, groundnut.

Introduction

Blanching is the removal of testa from peanut kernel by heating followed by abrasion. A large proportion of the peanut crop is sold to processors after blanching by shellers/blanchers. The costs associated with blanching are comparable with the costs of growing or shelling the crop (R. B. Hansen, pers. comm., 2000). Blanchability is the capacity to recover kernels with all the testa removed. Blanchability of a kernel lot is affected by genotype, kernel grade, and harvest date (Mozingo 1979), and by pre-treatment of kernels (Farouk *et al.* 1977).

Wright and Mozingo (1975) have published a sample blanching procedure. This procedure used a purpose-built machine. Peanut Company of Australia (PCA) compared the Wright and Mozingo (1975) procedure with a small-scale emulation of commercial blanching using an oven and a single abrasive blanching unit (M. J. Read, pers. comm., 1994). They found the use of the abrasive blancher to be superior as a predictor of commercial blanching results. Shokraii *et al.* (1985) found an association between the presence of a particular protein in kernel and poor blanchability. The association was not strong and is not in use as a selection tool.

The capacity to select for improved blanchability in a peanut breeding program is vital. This is particularly so if parents with other desirable traits have poor blanchability, e.g. the drought-resistant cultivar Streeton. This study investigated the response to early generation selection for blanchability, and the stability of the blanchability of 22 lines over 3 different environments.

Materials and methods

All blanching samples were mature kernels chosen by using split grading screens appropriate to each variety (32 by 7 mm or 32 by 5.5 mm). This was done to eliminate kernel maturity as a source of variation in blanchability. Blanching was done by heating all samples to 100°C for 35–40 min, allowing them to cool, then passing them over an Ashton abrasive-roller blanching unit using replicates, but not plot order from the field experiments. Blanched kernels and splits were grouped and the combined weight recorded as Blanched %. Part-blanched and unblanched kernels and splits were grouped and the weight recorded as Reject %.

Early generation selection experiment

Genetic material came from a group of 2-way crosses between high yielding Virginia lines (Table 1). In 1996–97, families derived from single F₂ plants were grown in the F₃ generation as unreplicated progeny rows. Routine selection for attractiveness/uniformity of pods

Table 1. Crosses used in selection experiment

Cross	Parents		F _{2,4} Rows tested	F _{2,4} Families selected		F _{4,6} Lines tested
	Female	Male		Good ^A	Bad ^B	
B235	Streeton	A166L17	10	2	1	27
B240	A46L10	VA-C92R	6	2	0	13
B245	VA-C92R	A46L10	12	8	0	70
B262	A166L17	Streeton	5	0	1	11
B263	A166L17	A46L10	6	0	0	0
B267	Southern R.	A46L10	4	0	0	0
B268	Southern R.	VA-C92R	3	0	1	11

^ABlanched % >85%. ^BBlanched % <75%.

and kernels was practiced. Two 300-g samples of F₄ kernels from the selected F_{2,3} rows and a companion plot of VA-C92R were taken and blanched. Means were formed from these 2 samples and within-plot variation was calculated, giving an indicative measure of variability. Twelve families with 'good' blanchability and 3 with 'poor' blanchability were selected. The remaining F₄ seed of selected families was planted in 1997–98 and 10–15 single plants selected per family.

In the 1998–99 season, 132 F_{4,5} lines were grown in 2 separate replicated experiments to compare their blanchability. The lines were allocated to experiments at either Redvale or Kairi so that all F₂-derived families were represented at both sites. The 2 trials had 6 check varieties in common: NC7, Streeton, Florunner, VA-C92R, Roberts, and Conder. These trials had single-row plots of approx. 5 m and 0.9 m apart, and were each planted as 2 replicates of 8 × 9 rectangular lattice designs. Samples of 200 g of mature kernels (i.e. F₆ kernels from F₅ plants) from each plot were blanched as described above.

Genotype × environment experiment

Kernel samples were taken from each plot of 3 regional variety trials: Coominya (southern Queensland), Emerald (central Queensland), and Walkamin (northern Queensland). The trials were designed as randomised complete block trials of 22 genotypes, where the Coominya trial had 4 replicates, and the Emerald and Walkamin trials had 3 replicates. Unit plots were 2 rows by approx. 5 m. Samples of 200 g of mature kernels from each plot were blanched as described above.

Statistical methods

A linear mixed model was fitted to the blanchability data for both the early generation and the genotype × environment experiment. The residual maximum likelihood (REML) procedure (Patterson and Thompson 1971) was used to estimate variance components for the random effects, and the model was fitted in S-plus using *samm* (Butler *et al.* 2002), which implements the average information algorithm of Gilmour *et al.* (1995). Best linear unbiased predictors (BLUPs) of the performance of random line were estimated across sites.

For the early generation trial, fixed effect terms were fitted for site, check (a factor specifying the 6 check lines), and the interaction between site and check. Random terms were fitted for the design factors of replicate and incomplete blocks within replicates at each site. The family structure was modelled by allowing for heterogeneous variances for families at each site, and a genetic correlation for families between sites. This model is termed the common correlation model in Smith *et al.* (2001). A random term was also included for lines within families, but due to the design, interactions between sites and lines within families could not be estimated.

The genotype by environment experiment was analysed using the standard multi-environment trial methodology of Smith *et al.* (2001). Specifically, a fixed effect was fitted for site, and random terms were fitted for replicates at each site. A common correlation model (Smith *et al.* 2001) was fitted to the site × genotype interaction.

Results

Early generation selection experiment

The total of Blanched and Reject material did not differ greatly between progenies (Table 2) and this is consistent with non-significance in other unpublished data. The Blanched % and Reject % have a strong inverse linear relationship, so only the Blanched % is considered here. Blanching measurements on the selected F_{2,4} kernel samples were different (Table 2). A number of progenies were lower in Blanched % than the check variety VA-C92R. Many were close in value to VA-C92R. The 3 lowest and the 12 highest were chosen for selection of F₄-derived lines.

BLUPs for F_{4,5} lines from F₂ families ranged from 64.2 for B268-p7 to 89.5 for B245-p26. These BLUPs were significantly correlated with the mean Blanched % of the F_{2,4} kernel samples ($r = 0.87$, $P < 0.0001$).

Most of the variance of Blanched % in the 2-site analysis was genotypic, with a genetic correlation at the family level between sites of 0.96. There was more variance within families than among families but the within-family variance was mostly in 3 families: B235-p31, B262-p6, and B268-p7 (Table 3). In all other families, variance among lines within families was smaller than the error variance. The within-family variances appear to be negatively correlated with

Table 2. Blanched F_{2,4} kernel samples as a percentage of original weight

	Blanched (%)	Reject (%)	Total (%) ^A
B245-p11 ^B	91.3	4.0	95.3
B240-p25 ^B	90.9	2.1	93.0
VA-C92R	90.5	2.1	92.6
B245-p32 ^B	90.0	2.8	92.8
B245-p5 ^B	89.9	2.9	92.8
B245-p42 ^B	89.9	2.4	92.3
B245-p14 ^B	89.4	3.2	92.6
B235-p5 ^B	89.1	4.4	93.5
B245-p16 ^B	89.1	4.0	93.1
B240-p9 ^B	88.7	3.9	92.6
B245-p26 ^B	88.5	4.1	92.6
B245-p1 ^B	88.5	4.0	92.5
B235-p29 ^B	86.6	6.9	93.5
B235-p31 ^C	70.7	22.4	93.1
B268-p7 ^C	61.8	31.4	93.2
B262-p6 ^C	51.4	43.0	94.4

^AWeight does not add up to 100 due to loss of moisture and skins.

^BProgenies classed as blanching well.

^CProgenies classed as blanching poorly.

Table 3. Predicted family means and within-family variance components from F_{4:6} experiments

Family	Predicted family means (BLUPS)	Redvale	Kairi
B235-p29	82.61	0.00	5.84
B235-p31	64.88	33.07	19.29
B235-p5	78.69	0.00	0.00
B240-p25	88.98	0.00	0.00
B240-p9	87.52	0.00	0.00
B245-p1	88.15	7.93	0.00
B245-p11	87.72	3.53	0.00
B245-p14	88.09	5.28	8.68
B245-p16	88.01	0.00	0.00
B245-p26	89.72	0.00	0.00
B245-p32	89.55	0.00	4.61
B245-p42	88.88	0.00	2.50
B245-p5	88.72	16.87	0.00
B262-p6	70.51	94.53	0.00
B268-p7	63.76	17.83	42.33

mean family F_{2,4} Blanched %, but they are confounded with line × site interaction so no clear inference can be made.

Genotype × environment experiment

Streeton, D45-p37-102, and 3 lines from the D28-p33 family all had consistently lower Blanched % than the best lines at each site (Table 4). Seven lines had mean Blanched % over the 3 sites of >90%.

Quite high genetic correlation (0.85) was evident across the 3 sites. The heterogeneous genetic and error variances estimated from the across-site analysis are summarised in Table 5.

Discussion

Early generation selection experiment

Early generation selection for Blanched % was very effective. From the 3 families selected for poor blanching, only one F_{4,5} line out of 29 performed acceptably. Of the 12 families selected for good blanchability, 10 produced uniformly good F_{4,5} lines. The other 2 families, B235-p5 and B235-p29, had uniform mean performances that were better than the poor blanching families but less than the best families and checks. The low within-family variance of better blanching families suggests that genes conferring better blanchability were fixed early in those families. Conversely, the more variable nature of the poor blanching families suggests genetic segregation within those families. The high proportion of F₂-derived families that were apparently fixed suggests that the trait is under oligogenic control.

Genotype × environment experiment

The high genetic correlation common to each pair of sites suggests that differences in blanchability are repeatable. The expression of genetic variation was much greater at Coominya, with a 5-fold greater genetic variance than at

Table 4. BLUPs of Blanched % of 22 lines across 3 sites

Line	Predicted value	Standard error
Conder	88.21	1.85
D1-p52-17	92.69	1.90
D1-p73-4	92.15	1.84
D13-p5-4	92.81	1.84
D28-p33-1	78.40	1.84
D28-p33-11	72.80	1.86
D28-p33-5	76.23	1.85
D28-p33-6	87.87	1.90
D28-p33-7	78.19	1.84
D28-p34-10	92.37	1.84
D28-p34-6	91.39	1.83
D34-p37-202	90.12	1.85
D45-p37-102	71.51	1.84
Florunner	88.84	1.91
Fla MDR98	84.35	1.84
N91026E	90.04	1.85
NC12C	90.16	1.85
NC7	87.97	1.85
Roberts	89.86	1.84
SO95R	88.41	1.85
Southern Runner	80.66	1.85
Streeton	79.18	1.84

Table 5. Variance components for Blanched % from the across-site analysis of 3 sites

Site	Mean	Genetic variance	Error variance
Coominya	81.30	111.68	33.80
Emerald	85.72	54.51	34.12
Walkamin	89.73	20.37	9.98
Genetic correlation common between each pair of sites	0.85		

Walkamin, and all 3 of these sites were irrigated. The common correlation may have been poorer with the inclusion of rainfed environments but this is not certain.

Breeding and selection for improved blanchability

There were clear differences among crosses in the frequency of desirable progenies. All the best progenies came from the reciprocal crosses of VA-C92R and A46L10. Careful parent selection could make an important contribution to breeding and selection for improved blanchability. This is consistent with the conclusions of Mzingo (1979), although he did not study segregating populations.

The choice of environment for selection may not substantially affect the rank of genotypes but may affect the capacity to detect differences. Although early generation selection will show a response, the testing of material over a range of environments prior to release or recommendation remains important.

The need for a significant quantity of seed from a progeny row for the blanchability test limits the possibility of single-plant selection for improved blanchability. Similarly, recurrent backcrossing would be impractical if $F_{2:3}$ rows were the test material to choose genotypes for crossing to the recurrent parent. The test used in these studies is ideal for integration into a pedigree-breeding program using plant-progeny rows.

References

- Butler DG, Cullis BR, Gilmour AR, Gogel BJ (2002) Sann reference manual. QDPI Technical Report.
- Farouk SM, Brusewitz GH, Paulsen MR (1977) Blanching of peanut kernels as affected by repeated rewetting–drying cycles. *Peanut Science* **4**, 63–66.
- Gilmour AR, Thompson R, Cullis BR (1995) AI, an efficient algorithm for REML estimation in linear mixed models. *Biometrics* **51**, 1440–1450.
- Mozingo RW (1979) Effects of genotype, digging date and grade on the blanchability of Virginia type peanuts. *Proceedings of the American Peanut Research and Education Association* **11**, 9–15.
- Patterson HD, Thompson R (1971) Recovery of interblock information when block sizes are unequal. *Biometrika* **31**, 100–109.
- Shokraii EH, Esen A, Mozingo RW (1985) Relation of a 36000 Dalton arachin subunit to blanchability in peanuts (*Arachis hypogaea* L.). *Journal of Agricultural and Food Chemistry* **33**, 1114–1116.
- Mith AB, Cullis BR, Thompson R (2001) Analysing variety by environment data using multiplicative models and adjustments for spatial trend. *Biometrics* **57**, 1138–1147.
- Wright FS, Mozingo RW (1975) Laboratory device for peanut skin removal. *Peanut Science* **2**, 11–15.

Manuscript received 26 July 2002, accepted 7 July 2003