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The analysis of the NSW wheat variety database. II. Variance component estimation

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Abstract The efficiency of various trialling systems for wheat variety evaluation in New South Wales (NSW) is considered. This involved the estimation of the variance components due to genotype, genotype-by-year, genotype-by-location and genotype-by-year-by-location. It is shown that there is a significant reduction in the magnitude of these variance components by the inclusion of the interaction of genotype maturity, winter habit and aluminium tolerance with environment.

Key words Genotype-by-environment interaction · REML · Variance components

Introduction

In the previous paper (Cullis et al. 1995) a database for wheat variety trialling in southern and central NSW was described. The first stage in the process of estimating the magnitude of the sources of variation in these data involved modelling the trial error variance. This modelling, which was reported in the first paper, showed that there have been significant effects on trial error variance due to the year of trialling and location of trial.

In considering the estimation of the variance components due to genotype, genotype-by-year (G.Y), genotype-by-location (G.L) and genotype-by-year-by-location (G.Y.L) we firstly need to address the identification of known or explainable genotype by environment interactions. Classical or standard variance component estimation in genotype-by-environment data has usually only considered a partition of the total interaction variance into genotype-by-year, genotype-by-location and genotype-by-year-by-location. This approach was used by Patterson et al. (1977), Talbot (1984), Brennan et al. (1981), Brennan and Byth (1979) and Thomson and Cunningham (1979). There is no attempt to explain the interactions and thus reduce the size of the unexplainable interaction variances. A reduction in unexplainable interaction variance will result in a reduction in the number of trials required to achieve the same accuracy (Patterson et al. 1977).

Other common approaches to the analysis of genotype-by-environment data usually attempt to explain the genotype-by-environment interaction. The AMMI model (Gauch 1988; Kempton 1984) is one such approach. This method is useful as it helps to elucidate the nature of the interactions. Zobel et al. (1988) analyse a set of data with 7 soybean genotypes sown at a total of 35 environments. This represented only a small fraction of the total data set as the AMMI model requires that the data be balanced. The analysis demonstrated that the major source of genotype-by-environment interaction was due to the interaction of genotype maturity with trial location (see Fig. 1 of Zobel et al. 1988).

Another approach to the analysis of genotype-by-environment data used extensively in Australia is pattern and ordination analysis. Basford (1982) uses three-way multidimensional scaling to analyse the soybean data of Mungomery et al. (1974). There were a total of 58 genotypes sown at 8 environments, and six attributes were measured. Close inspection of Fig. 1 in Basford (1982) suggests that the grouping of genotypes is due to maturity. This conclusion is reinforced by a re-analysis of the same data by Krooneberg and Basford (1989). In that paper three-mode principal component analysis (PCA) is used and similar groupings of the genotypes emerge (see Fig. 1 of Krooneberg and Basford 1989).

Our approach to the estimation of the variance components is therefore aimed at combining the essential features of each of these approaches. The focus of this analysis is to determine the most efficient trialling system for wheat variety evaluation in southern New South

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Wales (NSW), which requires the estimation of the variance components. It is imperative, however, that we first consider partitioning the genotype-by-environment interaction into the explainable and unexplainable. Several key genotype traits are available for this purpose. These include maturity, winter habit, disease resistance and aluminium tolerance. Unfortunately, there is little site-specific data from which we can further elucidate the interactions.

Thus, the present paper consists of five main sections. We describe the database in the section on experiment means. In the next section we determine the explainable genotype-by-environments interactions. We do not use the AMMI or pattern analyses for this preliminary analysis as the data is highly unbalanced with only a small subset of genotypes occurring in all years. We then develop a model which accounts for the explainable genotype-by-environment interactions and compare the estimates of the variance components from this extended model with those from the standard model, which ignores the explainable genotype-by-environment effects. We conclude the paper with a comparison of the efficiency of hypothetical trialling systems.

Description of experiment means

For each of the 1071 experiments, the mean yield of a genotype was included if that genotype was present in at least 2 years of testing. This resulted in 16 552 experiment means representing 107 genotypes being included in the final database, at an average of approximately 15 means per trial. Table 1 presents the genotype name, its winter habit (W; 1 = spring and 2 = winter), maturity score [M; mean of Zadoks (Zadoks et al. 1974) taken at a subset of sites when the genotype with the latest maturity is past the flagleaf emergence and the genotype with the earliest maturity has not commenced grain filling], aluminium tolerance rating (A; 1 = susceptible to 2 = tolerant) and stripe rust tolerance rating (YR; 1 = tolerant, 2 = susceptible and 3 = susceptible after 1986–1987). Ideally, ear emergence data would have been recorded for each experiment for each genotype in order to predict genotype yield response to the environment. However this data was only available for a very limited number of experiments. Instead, two measures of maturity were deemed necessary to account for the different responses of ear emergence to sowing date for winter and spring types. (Fig. 1, Pugsley 1973). The maturity score was assessed from experiments sown in mid-May and therefore did not adequately predict ear emergence across the range of sowing dates in this data. Prior to analysis, all data was rigorously checked and cross-referenced. This checking resulted in the deletion of a small number of clearly anomalous yield values.

The nature of the current trialling system requires that genotypes change from year to year. Table 2 presents the matrix of common genotypes. Of the 107 genotypes included in the study only 12 were in common between 1982 and 1991; approximately one-half were trialled in any 1 year.

Identification of explainable genotype-by-environment interactions

There is a significant range in maturity within both the spring and winter types. Patterson et al. (1977) estimated separate components of variance for spring and winter wheats. The climate in the UK precludes the inclusion of both types in the same experiment. Experiments conducted in NSW often include a mixture of both spring and winter wheats and genotypes with a range of maturity. The genotypes are grouped into two series, namely those suitable for an early sowing (slower maturing, 1 April–15 May) and those suitable for mid-season sowing (faster maturing, 15 May–July). A small number of genotypes have intermediate maturity and so can be included in either series. However, the variation in seasonal conditions may not allow for the early sown experiments to be sown by 15 May. It is a common farmer practice to still sow genotypes from series 1 after 15 May and so the two series are amalgamated and sown in the one experiment. If the sowing date exceeds 15 June then the genotypes in series 1 are not sown. The result is that most locations have two experiments each year, with a small number of genotypes in common. In some years and at some locations there is only one experiment with a larger set of genotypes with a wider range of maturities. Because of this complexity and to avoid making arbitrary decisions, the data was not split according to sowing date or maturity.

Two other factors which may contribute to genotype-by-environment interaction are differential disease resistance and differential acidity tolerance mainly through aluminium tolerance (Scott and Fisher 1989). Several significant epidemics of stripe rust occurred during the period 1982–1991, and several commercial genotypes suffered significant yield losses in some experiments during these epidemics due to changes in races of stripe rust. There has been an increased awareness of the importance of genetic tolerance to aluminium as soil pH declines in southern NSW (Scott and Fisher 1989). Prediction of yield response to aluminium in the field is difficult, particularly without reliable and adequate data on soil pH.

Separate analyses of the means from each experiment were conducted to assess the significance of these factors and how their effects may have varied with location, sowing date and year of planting. In these analyses, the data from the *i*th experiment was weighted by

$$w_i = \frac{r_i \bar{s}^2}{\hat{s}_i^2}$$

where r_i is the replication in the *i*th experiment, $\bar{s}^2 = 0.08715$ is the pooled plot error variance and $\hat{s}_i^2$ is

Table 1 Genotype list for the NSW wheat variety trial data set (*A* aluminum, *W* winter, *M* maturity, *YR* stripe rust tolerance)

Number	Name	A	W	M	YR	Number	Name	A	W	M	YR
1	Banks	1	1	55	1	55	M5108	2	1	52	1
2	Batavia	1	1	52	1	56	M5111	1	1	57	1
3	BD159	2	1	54	1	57	M5184	1	2	51	1
4	Comet	2	1	57	1	58	M5218	1	1	52	1
5	Condor	1	1	55	1	59	Matong	2	1	49	1
6	Cook	1	1	59	1	60	Meering	1	1	55	1
7	Corella	1	1	58	3	61	Meteor	2	1	54	1
8	Cranbrook	2	1	60	1	62	Millewa	2	1	60	3
9	Diaz	1	1	55	1	63	Minto	1	1	58	1
10	Dollarbird	2	1	58	1	64	Miskle	1	1	52	1
11	Eagle	1	1	58	1	65	Olympic	2	1	50	1
12	Egret	1	1	54	2	66	Osprey	1	2	52	1
13	F79-2597	1	1	61	1	67	Owlet	1	2	45	1
14	Flinders	1	1	55	1	68	Oxley	1	1	55	1
15	Gatcher	1	1	62	1	69	Perouse	1	1	52	1
16	Harrier	1	1	49	2	70	QT3604	1	1	54	1
17	Hartog	2	1	58	1	71	QT8104	1	1	55	1
18	Janz	1	1	55	1	72	Quarrion	1	2	51	1
19	K1056	2	1	55	1	73	Rosella	1	2	48	1
20	K1091-1	1	1	56	1	74	Shrike	1	2	53	1
21	K1179	2	1	60	1	75	Skua	1	1	55	1
22	K1182	1	1	60	1	76	Songlen	1	1	58	1
23	K1939	2	1	56	1	77	Sun110S	1	1	59	1
24	K2018	2	1	57	1	78	Sun129A	2	1	59	1
25	K2036	1	1	57	1	79	Sun134C	2	1	54	1
26	K2620	2	1	57	1	80	Sun139A	1	2	53	1
27	K2626	2	1	57	1	81	Sun155C	1	1	56	1
28	K2806	1	1	54	1	82	Sun89D	1	1	55	1
29	K2926-1	1	1	56	1	83	Sunbird	1	1	56	1
30	Kiata	1	1	57	1	84	Sunbri	1	2	49	1
31	King	1	2	52	2	85	Sunco	1	1	53	1
32	Kite	1	1	53	1	86	Sundor	1	1	56	1
33	Lark	1	1	55	1	87	Suneca	2	1	52	1
34	Lillimur	2	1	54	1	88	Sunelg	1	1	53	1
35	M2255	1	2	49	1	89	Sunfield	2	1	60	1
36	M2369	1	2	48	2	90	Sunkota	2	1	50	1
37	M2479	1	1	49	2	91	Sunstar	1	1	56	1
38	M2483	1	1	49	1	92	T860799	2	1	63	1
39	M3029	1	1	55	1	93	Takari	1	1	58	1
40	M3087	1	2	52	1	94	Vasco	1	1	56	1
41	M3117	1	1	55	1	95	Vulcan	1	1	57	1
42	M3344	1	2	48	1	96	Wilgoyne	1	1	62	1
43	M3345	2	2	48	1	97	WW1006	1	2	54	1
44	M3458	1	1	55	1	98	WW1145	1	1	57	1
45	M3730	1	1	55	1	99	WW1203	1	1	58	1
46	M3844	1	2	51	1	100	WW725	1	1	47	1
47	M4287	1	1	55	1	101	WW728	1	1	55	1
48	M4308	1	2	52	1	102	WW729	1	1	57	1
49	M4312	1	2	52	1	103	WW731	2	1	55	1
50	M4513	1	1	54	1	104	WW766	1	1	52	1
51	M4965	1	1	58	1	105	WW809	1	1	56	1
52	M5060	2	2	53	1	106	WW879	2	1	54	1
53	M5075	1	1	52	1	107	WW925	1	2	51	1
54	M5100	1	1	55	1						

the plot error variance predicted from the model described in the first paper. Table 3 presents the cumulative relative frequencies of the probability of the variance ratios for each of the four factors, maturity, winter, stripe rust and aluminium tolerance, from each experiment. Not all the effects were estimable for all experiments. These results demonstrate the importance of these factors, particularly maturity and winter habit, in explaining genotype-by-environment interaction.

Figure 1 presents the yield response to maturity and winter habit for four experiments in which the absolute value of the *t*-statistic for the regression coefficient exceeded 4. Figure 2 presents the plots of the *t*-statistic for maturity and winter habit against the sowing date of the experiment in Julian days (1 = April 1). These figures reflect the broad advantage that winter types and the slower (lower Zadoks score) maturing genotypes have in early sown experiments. These figures also demonstrate

Table 2 Matrix of genotype numbers ($n = 107$). Diagonal terms are the number of genotypes tested each year; off-diagonal terms are the number of common genotypes

1982	1983	1984	1985	1986	1987	1988	1989	1990	1991
32									
32	40								
28	35	44							
23	31	39	46						
22	30	37	44	53					
21	28	33	40	48	60				
16	21	25	30	36	47	54			
15	20	20	24	28	37	44	55		
14	19	20	25	28	34	35	43	60	
12	17	18	22	24	30	31	37	50	52

Table 3 Cumulative relative frequencies of the probability of the variance ratios from the analysis of the means from each experiment

	>0.0 & $\leqslant 0.001$	>0.001 & $\leqslant 0.010$	>0.010 & $\leqslant 0.050$	>0.050 & $\leqslant 0.100$	>0.100 & $\leqslant 1.0$	n
M[a]	0.05	0.08	0.17	0.23	1.00	1071
W	0.02	0.05	0.10	0.16	1.00	985
A	0.03	0.07	0.14	0.19	1.00	1014
YR	0.01	0.02	0.07	0.12	1.00	577

[a] See Table 1 for definitions

the unpredictable nature of the interaction of maturity, winter habit and environment. We note that the inclusion of the 2 winter-type genotypes in experiment 465 sown on 23/8 was inappropriate, and thus those data were deleted from subsequent analyses.

Figure 3 presents the plots of yield against maturity for four experiments in which the effects of stripe rust resistance were highly significant. Table 3 indicates that the effect of stripe rust was the least important of the four factors although the interaction can be large (Fig. 3). Data relating to the susceptible genotypes could have been deleted from the database but this option appeared unsatisfactory. There were many experiments where no stripe rust was present and due to changes in stripe rust races, some genotypes were resistant in some experiments and susceptible in others. Each experiment which presented evidence for a stripe rust effect was carefully examined and those offending means deleted. A total of 33 genotype means from 18 experiments was deleted.

Figure 4 presents the plots of yield against maturity for four experiments which had a significant (positive) response to aluminium. Table 3 indicates that this interaction effect was quite large. Some experiments were specifically located in areas with a soil acidity problem in order to examine the yield benefit of aluminium tolerance. However, the aluminium tolerance response

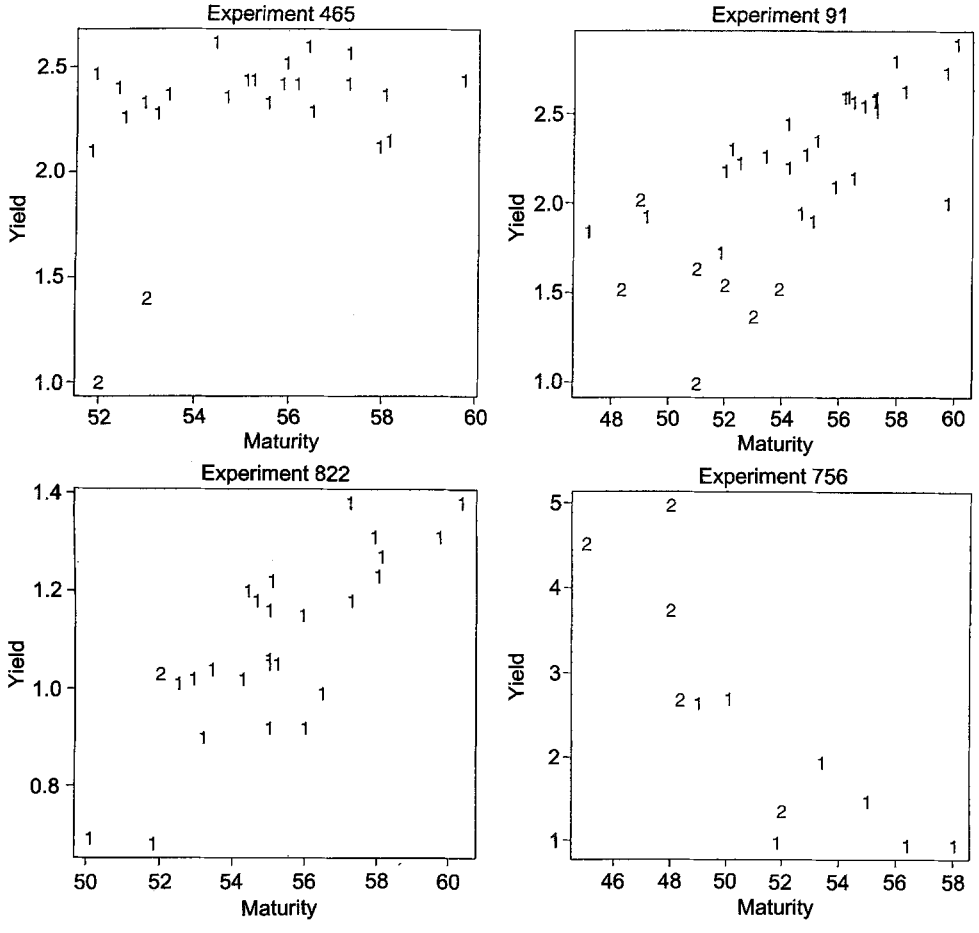


Fig. 1 Examples of the effects of maturity and winter habit on yield. *1* Spring wheat, *2* winter wheat

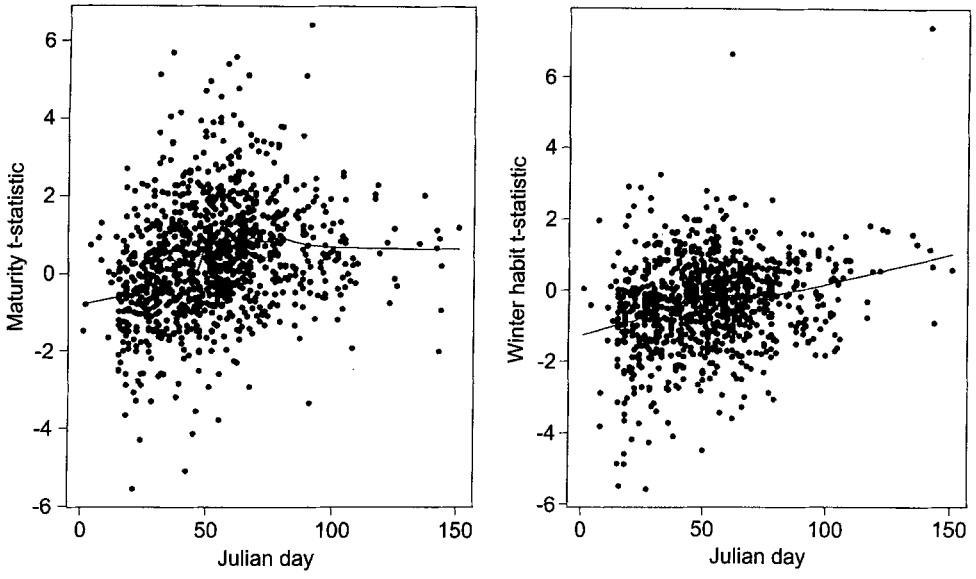


Fig. 2 Plots of the *t*-statistics for maturity and winter habit

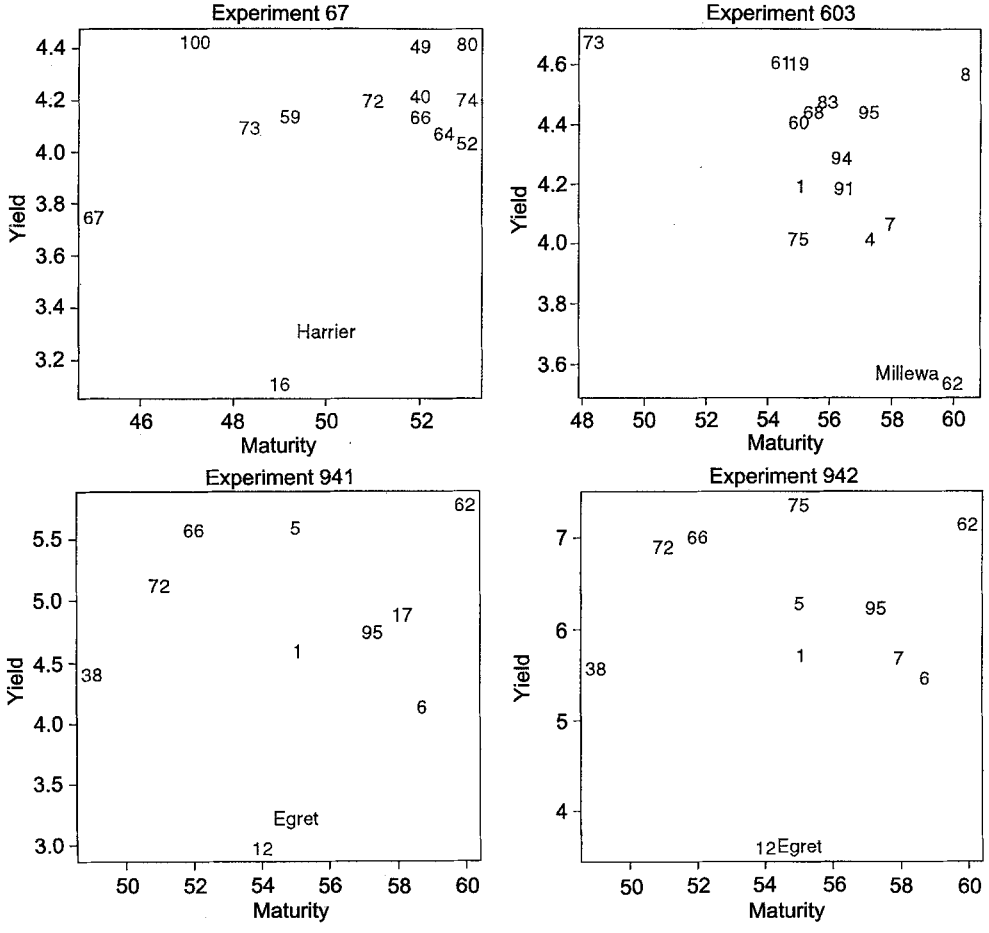


Fig. 3 Plot of yield against maturity for four experiments affected by stripe rust with stripe rust-susceptible genotypes indicated

was often significant for experiments sown in other locations. Soil pH data confirmed that some of the sites were acid. Site pH data was not available for all sites. This response may not have been only a result of aluminium tolerance but could also have been attributable to other genotype differences such as early vigour. The aluminium effects were in general positive and were larger for experiments sown at locations with a history of soil acidity. Figure 5 presents the boxplots of the *t*-statistic for aluminium tolerance for each of the 60 locations. There was substantial variation both within and between locations.

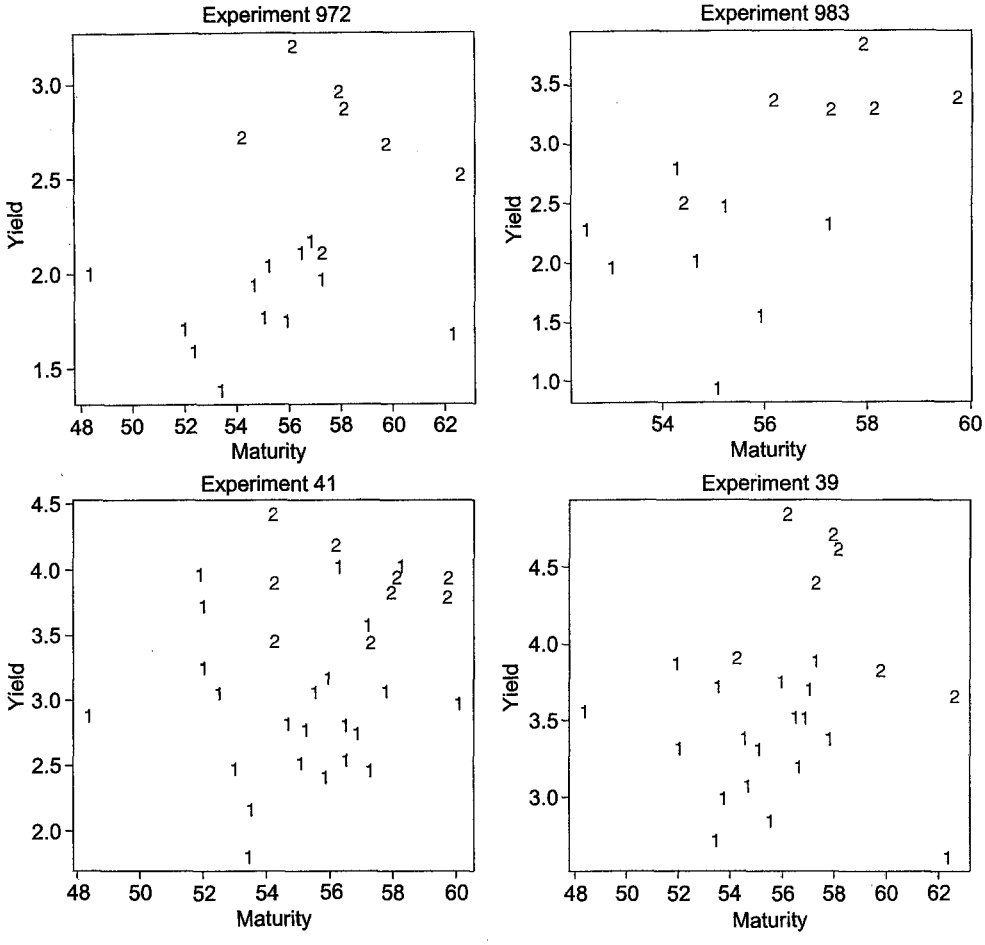


Fig. 4 Plot of yield against maturity for four experiments affected by aluminum toxicity. *1* Susceptible, *2* tolerant to aluminum

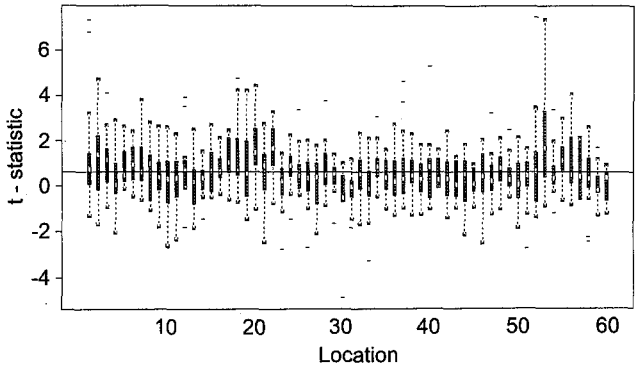


Fig. 5 Plot of *t*-statistics of aluminum for each location

Variance component estimation

Statistical methods

Williams et al. (1992) suggest that a two-stage analysis of genotype-by-environment data has some advantages. Patterson et al. (1977), Talbot (1984) and many others all use this two-stage approach when analysing genotype-by-environment data. This analysis is statistically inefficient in the context of variance component estimation, as genotype effects are conditionally fixed for each experiment in the first stage, but then taken as random in the second stage. Clearly, if each experiment is analysed by an orthogonal procedure such as randomized block analysis then there is essentially no difference between either a two-stage or one-stage analysis. This is not the case, however, for spatial and incomplete block analyses of trial data. In the past computational ease seems to have been the main reason for this approach, although Williams et al. (1992) present other reasons. As only experiment means were readily available we therefore proceeded with this approach.

The conventional approach for the analysis of non-orthogonal genotype-by-year-by-location data is to divide the total variance into components according to the three-way classification (Patterson et al. 1977; Brennan et al. 1981; Brennan and Shepherd 1985; Talbot 1984; Thomson and Cunningham 1979). With that approach, additional factors such as maturity and winter habit are not accounted for. If genotypes are considered to be random then these additional effects need to be included as covariates in all models. We present results from two separate analyses of this data. Firstly, we proceeded with the model used by Patterson et al. (1977). Subsequently, this model will be referred to as the standard model. In this model we also included the effects of genotype maturity (M), genotype winter habit (W), and genotype aluminium tolerance (A) as fixed effects. In the extended model, additional fixed effects for the interaction of sowing date (t) and M and t and W, as well as additional random effects for the interactions of A, W and M with location, year and experiment, were included. Table 4 presents the schematic ANOVA representation of the terms included in the standard and extended models. Terms were deleted from the extended model if the REML estimate of the component of variance (associated with that term) was less than zero. Since there was often more than one experiment at each location in each year, the genotype-by-year-by-location term in the analysis of the experiment means includes both the genotype-by-year-by-location component and the genotype-by-experiment variance components.

All analyses were conducted in either Splus (Becker et al. 1988) or in a FORTRAN program written by Arthur Gilmour. This program

Table 4 Schematic ANOVA representation of the two models used to estimate the components of variance

Source		*df* or number of Effects	Fixed/random (F = Fixed, R = Random)	Standard model	Extended model
Experiment(Ex)		1 070	F	X	X
	Year(Y)				
	Location(L)				
	Y.L				
	Sowing date (*t*)				
Genotype(G)		107	R	X	X
	Maturity(M)	1	F	X	X
	Winter(W)	1	F	X	X
	Aluminium(A)	1	F	X	X
t.M		1	F	–	X
t.W		1	F	–	X
G.Y		496	R	X	X
	M.Y	10	R	–	X
	W.Y	10	R	–	X
	A.Y	10	R	–	X
G.L		3 872	R	X	X
	M.L	60	R	–	X
	W.L	60	R	–	X
	A.L	60	R	–	X
G.Y.L		16 552	R	X	X
	M.Ex	1071	R	–	X
	W.Ex	1002	R	–	X
	A.Ex	1040	R	–	X

obtains the REML (Patterson and Thompson 1971) estimates of variance components for large unbalanced genotype-by-environment data. It uses the algorithm described by Gilmour et al. (1996) and so is very computer-efficient. Copies are available from the fourth author on request.

Results and discussion

Estimates of the variance components for both models are given in Table 5. The variance components for genotype-by-year and genotype-by-location and experiment have all been reduced. The plot error variance component remains the largest variance component. The reduction in all variance components by the inclusion of these factors has important ramifications in the calculation of the relative accuracy of various trialling systems, which will be discussed in the following sections.

Table 6 presents the estimates of the three genotype effects (M, W and A) and the interaction of M and W with sowing date. There is a significant yield advantage to those genotypes with tolerance to aluminium. Since there were only 3 locations (18, 22 and 53) with a history of aluminium toxicity, this result suggests that soil acidity is a widespread problem. There are strong interactions of both genotype maturity and winter habit with sowing date. There is an overall advantage to the quicker maturing genotypes, and this advantage increases the later the sowing date. For example, for 2 genotypes with a difference of 10 zadoks units (this is equivalent to about 10 days of difference in heading in mid-October in southern and central NSW), there is a

Table 5 Estimated components of variance $(t/ha)^2$

	Standard model	Extended model
G	0.02281	0.02224
M.Y	–	0.02665
W.Y	–	0
A.Y	–	0
G.Y	0.00984	0.00664
M.L	–	0.00204
W.L	–	0.00578
A.L	–	0.00917
G.L	0.00829	0.00536
M.Ex	–	0.10472
W.Ex	–	0.04352
A.Ex	–	0.02884
G.Y.L	0.05346	0.03375
Plot error	0.08715	0.08715

The units for M.Y., M.L. and M.Ex components are $(t/ha)^2$. $(Zadoks/10)^{-2}$

Table 6 Estimates of the fixed effects for the extended model

Term	Estimate	Standard error
M	0.1047	0.0755
W	0.0882	0.0501
A	0.1573	0.0393
M.t	0.0994	0.0179
W.t	−0.0869	0.0129

yield advantage to the quicker maturing genotype of 0.01, 0.11 and 0.20 t ha^{-1} for sowing dates of 15 April, 15 May and 15 June, respectively. The effects of winter habit and its interaction with sowing date are also quite significant. For example, the yield advantage of a winter wheat compared to a spring wheat (of similar maturity and aluminium tolerance) is 0.17, 0.09 and 0 t ha^{-1} for sowing dates of 15 April, 15 May and 15 June, respectively.

Table 7 presents the best linear unbiased predictor (BLUP) of the breeding value (EBV), the estimated specific effect (ESV) and the sum of these effects for the 107 genotypes in this study. The EBV is the genotype effect adjusted for M, W and A, while the ESV is the sum of the specific effects of M, W and A and the estimate of the interaction effects of M and W with sowing date at the mean sowing date for each genotype. The results show that the benefit of selecting for specific characteris-

Table 7 Genotype effects for the NSW wheat variety trial data set

Name	Number	EBV	ESV	Effect	Name	Number	EBV	ESV	Effect
Banks	1	−0.091	0.078	−0.013	M5108	55	−0.275	0.186	−0.089
Batavia	2	0.114	0.030	0.144	M5111	56	0.096	0.110	0.206
BD159	3	0.150	0.215	0.365	M5184	57	0.030	0.112	0.142
Comet	4	0.122	0.275	0.398	M5218	58	0.047	0.031	0.078
Condor	5	0.056	0.074	0.130	Matong	59	0.095	0.151	0.247
Cook	6	−0.159	0.136	−0.023	Meering	60	0.169	0.061	0.231
Corella	7	0.038	0.110	0.148	Meteor	61	0.190	0.223	0.414
Cranbrook	8	0.095	0.318	0.413	Millewa	62	−0.046	0.303	0.256
Diaz	9	0.061	0.089	0.150	Minto	63	0.065	0.112	0.177
Dollarbird	10	−0.014	0.285	0.271	Miskle	64	0.072	0.035	0.107
Eagle	11	−0.180	0.164	−0.016	Olympic	65	−0.258	0.157	−0.101
Egret	12	−0.126	0.049	−0.077	Osprey	66	0.011	0.096	0.107
F79-2597	13	−0.047	0.173	0.126	Owlet	67	−0.383	0.076	−0.307
Flinders	14	−0.194	0.073	−0.122	Oxley	68	0.120	0.082	0.202
Gatcher	15	−0.240	0.244	0.004	Perouse	69	0.064	0.041	0.105
Harrier	16	−0.072	−0.011	−0.083	QT3604	70	−0.036	0.064	0.028
Hartog	17	−0.007	0.297	0.290	QT8104	71	0.002	0.085	0.087
Janz	18	0.237	0.085	0.322	Quarrion	72	−0.190	0.090	−0.100
K1056	19	0.166	0.221	0.387	Rosella	73	0.193	0.066	0.259
K1091-1	20	0.009	0.097	0.106	Shrike	74	−0.083	0.125	0.042
K1179	21	−0.052	0.296	0.245	Skua	75	−0.049	0.080	0.031
K1182	22	0.031	0.144	0.175	Songlen	76	−0.304	0.161	−0.143
K1939	23	0.100	0.257	0.357	Sun110S	77	0.272	0.183	0.455
K2018	24	−0.091	0.267	0.176	Sun129A	78	0.201	0.347	0.548
K2036	25	0.322	0.101	0.424	Sun134C	79	−0.061	0.217	0.155
K2620	26	0.057	0.266	0.322	Sun139A	80	0.009	0.147	0.156
K2626	27	−0.067	0.263	0.195	Sun155C	81	0.145	0.106	0.252
K2806	28	−0.099	0.050	−0.049	Sun89D	82	−0.058	0.087	0.029
K2926-1	29	0.015	0.094	0.109	Sunbird	83	0.097	0.096	0.193
Kiata	30	0.213	0.103	0.316	Sunbri	84	−0.047	0.107	0.060
King	31	−0.066	0.097	0.031	Sunco	85	0.056	0.049	0.105
Kite	32	−0.183	0.048	−0.135	Sundor	86	−0.028	0.099	0.071
Lark	33	0.055	0.074	0.129	Suneca	87	−0.193	0.185	−0.008
Lillimur	34	−0.030	0.221	0.190	Sunelg	88	−0.118	0.052	−0.066
M2255	35	0.020	0.121	0.141	Sunfield	89	−0.046	0.321	0.275
M2369	36	0.025	0.109	0.134	Sunkota	90	−0.168	0.159	−0.010
M2479	37	−0.031	−0.010	−0.041	Sunstar	91	0.043	0.107	0.150
M2483	38	−0.169	−0.011	−0.181	T860799	92	−0.226	0.383	0.156
M3029	39	−0.135	0.074	−0.061	Takari	93	−0.070	0.140	0.070
M3087	40	0.066	0.117	0.184	Vasco	94	0.116	0.097	0.213
M3117	41	0.047	0.075	0.122	Vulcan	95	0.156	0.118	0.274
M3344	42	0.227	0.052	0.279	Wilgoyne	96	−0.261	0.201	−0.060
M3345	43	0.206	0.209	0.415	WW1006	97	0.044	0.142	0.186
M3458	44	0.004	0.079	0.083	WW1145	98	0.020	0.090	0.110
M3730	45	−0.105	0.078	−0.028	WW1203	99	0.167	0.127	0.294
M3844	46	0.051	0.086	0.137	WW725	100	0.203	−0.020	0.184
M4287	47	0.001	0.067	0.067	WW728	101	0.191	0.076	0.267
M4308	48	−0.064	0.121	0.057	WW729	102	−0.155	0.096	−0.060
M4312	49	−0.009	0.137	0.128	WW731	103	0.058	0.224	0.283
M4513	50	−0.057	0.050	−0.007	WW766	104	0.164	0.030	0.193
M4965	51	0.003	0.110	0.114	WW809	105	−0.138	0.086	−0.053
M5060	52	0.076	0.303	0.379	WW879	106	0.018	0.222	0.240
M5075	53	−0.133	0.017	−0.115	WW925	107	−0.115	0.120	0.005
M5100	54	0.048	0.070	0.118					

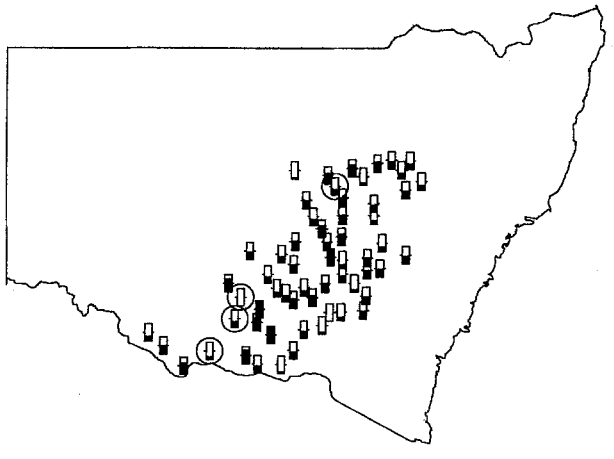
tics (ESV) that relate to genotype performance is large compared to the benefit from selecting for inherent yielding ability (EBV). The genotypes with the most desirable set of characteristics have a yield advantage of about 0.25 t ha^{-1}. Since EBV and ESV are largely uncorrelated for these data an additional improvement of 0.20 t ha^{-1} could be achieved by combining the best inherent yielding ability (EBV) with the most desirable set of specific characteristics within this current material. These specific characters are all simply inherited, so that this would be a simple and relatively inexpensive breeding objective in a plant breeding programme.

A recommendation to plant breeders from this work is that they should more carefully define the set of phenological and adaptation characteristics that are optimum in each target environment and select for those characteristics before commencing the expensive process of grain yield evaluation. Plant breeders have tended to do this, but an additional advantage could be achieved by being more rigorous in its implementation. The optimum combination of these characteristics may differ for each target environment. The results provide some information on the optimum combination of winter habit, maturity and aluminium tolerance that is desired for each target environment. However, it would be preferable to have an independent physiological basis to guide breeders and these data provide additional guidance in targeting specific environments.

The BLUPs for the interaction effects of M, W and A with location are presented in Figs. 6, 7 and 8. These effects are presented geographically by thermometers that gauge the relative magnitude of each effect. An empty thermometer represents the largest negative effect, whilst a full thermometer represents the largest positive effect.

The effects of maturity are shown in Fig. 6. The irrigated locations are circled. There is a tendency for slower maturing (lower zadoks score) genotypes to perform better in higher rainfall and irrigated locations. There are some anomalies such as Nyngan (36) in the north-west where later maturing varieties have had an advantage. This could be a result of summer storms late in the season favouring later maturing varieties in some years.

Fig. 6 Geographic distribution of the maturity effects



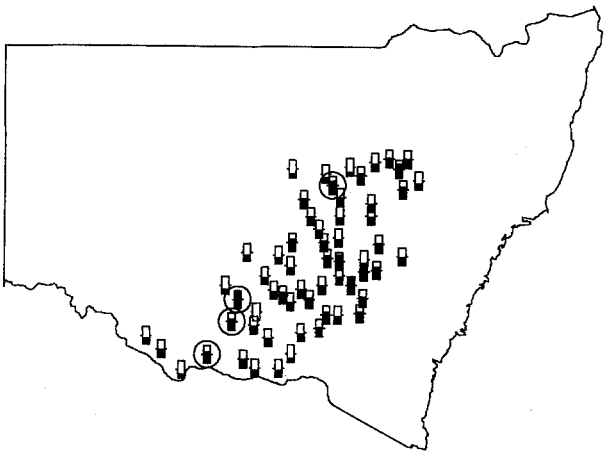


Fig. 7 Geographic distribution of the winter effects

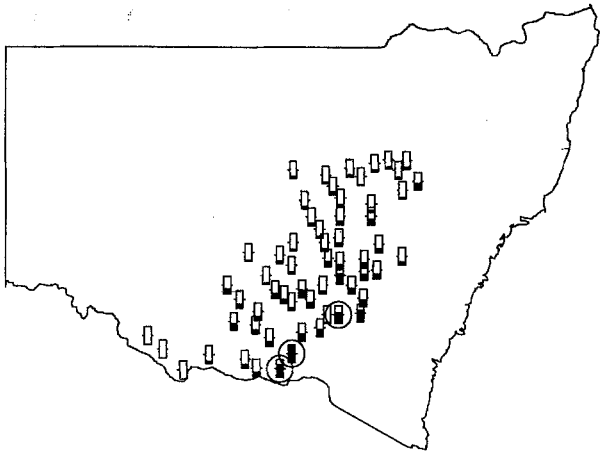


Fig. 8 Geographic distribution of the aluminum effects

The distribution of effects from winter habit (Fig. 7) is more difficult to explain. There is a tendency for winter habit to be of more benefit in the higher rainfall locations in the south-eastern wheat belt and in irrigated trials. The spread of sowing dates at each location will have an effect on the size of the winter effect. Reliable locations which can be sown on schedule will have a greater benefit from winter habit than locations where sowing is sometimes very late.

There is an interesting contrast between the irrigated location 9 (Murrumbidgee) and location 3 (Yanco) for both winter and maturity effects. Yanco is sown on a short fallow on a sandy soil and favours genotypes that mature quickly.

The aluminium effects as displayed in Fig. 8 are distributed largely as would be expected from the known distribution of acid soils. The most acid areas are

in the eastern section of the wheat belt. The only location in this area with a low A effect is Cootamundra 2, which was chosen specifically for its non-acid soil. The location in the north-east which shows a moderate A effect is located on a deep acid sand. There is no benefit of A tolerance in the alkaline soils along the Murray River, the southern border of NSW, but A tolerance is becoming more important in the irrigation areas north of the Murray.

Relative accuracy of trialling systems

To compare the relative accuracy of the current trialling system and some possible alternate trialling systems, we derived the acceptance probabilities (Patterson et al. 1977) for a range of systems. Our notation is consistent with the notation used by Patterson et al. It follows that

$$\hat{\delta} \sim N\left(\delta, 2V\left(\frac{100}{\mu}\right)^2\right) \quad (1)$$

where δ is the true percentage yield difference between the two genotypes, $\hat{\delta}$ is the estimate of δ obtained from trialling the genotypes in the same m experiments over n years. Each experiment is assumed to have r replicates. The formula for V is

$$\theta = \frac{\sigma^2_{gl}}{m} + \frac{\sigma^2_{gy}}{n} + \frac{\sigma^2_{gyl}}{mn} + \frac{\sigma^2_e}{rmn}$$

$$V = \frac{\theta}{1 + \frac{\theta}{\sigma^2_g}}$$

It can be shown that the formula for the variance between two unadjusted genotype means does not involve the additional variance components due to M.E, W.E and A.E. In practice genotypes will only be compared within a narrow range of maturity and with the same winter habit as it is biologically meaningless to compare adjusted genotype means.

The acceptance probability (α) is defined by the following equation

$$\alpha = P(\hat{\delta} > D)$$

where D is the critical percentage difference (CPD). When Eq. 1 is used, it follows that

$$\alpha = P\left(Z > \frac{D - \delta}{\frac{100}{\mu}\sqrt{2V}}\right)$$

$$= 1 - F\left(\frac{D - \delta}{\frac{100}{\mu}\sqrt{2V}}\right)$$

where Z denotes the standard normal deviate and $F(\,)$ its cumulative distribution function; hence,

$$\alpha = \alpha(V, D, \delta)$$

$$V = V(r, m, n, \sigma^2_x)$$

Thus, α is a function of V, D and δ and depends on r, m, n and σ^2_x through V. Table 8 presents the acceptance probabilities for a range of values of r, m and n. The values in part a of Table 8 are calculated using the variance components estimated from the standard model while those in part b are calculated using estimates of variance components using the extended model. Also, we set $D = 0$; that is, we accept the genotype if the observed difference is zero. However, the acceptance probabilities for other values of D can be obtained by using

$$\alpha(V,D,\delta) = \alpha(V,0,\delta - D)$$

The values chosen for m and n were those most likely to be of practical value. Changing the replication from 3 to 4 had little effect on the acceptance probability. The accuracy for $n = 2$ is always less than the accuracy for $n = 3$ within the range of m for (10,100). This result supports the need for more years of testing than 2, which is currently in place. The genotype-by-year interaction is larger than the genotype-by-location interaction and the 10 years included in this study are reasonably typical of those experienced in NSW.

Discussion

The acceptance probabilities presented in Table 8 are based on the analysis of the current database. Although this database represents the largest yet assembled in Australia, the estimates of the variance components are subject to sampling errors and are subject to changes in future populations of years and locations. We have already noted that there has been a reduction in plot error variance for the period 1982–1991 inclusive. Furthermore, plot error also varied significantly with location, and thus these probabilities must be interpreted with caution. We have assumed that we are sampling 'average' years and locations. Improvements in trial analysis, design and field technique will decrease plot error. Similarly, it has been indicated that the use of spatial analysis may reduce genotype-by-environment interaction. The impact of these changes may therefore require these estimates of variance components to be regularly updated.

Additionally, in both the standard and extended models, we assumed that the genotype-by-location, genotype-by-year and genotype-by-year-by-location interaction effects are homogeneous. This assumption requires validation, and preliminary investigations indicate this may not be true. For example, it may be

Table 8 The probability of accepting a genotype between the observed difference between it and the control is zero but the true difference ranges from −2.5% to 10% (*r* number of replicates, *m* number of locations, *n* number of years)

(a) Standard (r,m,n)	−5%	−2.5%	0%	2.5%	5.0%
(3,10,2)	0.098	0.259	0.5	0.741	0.902
(3,20,2)	0.076	0.237	0.5	0.763	0.924
(3,30,2)	0.067	0.227	0.5	0.773	0.933
(3,40,2)	0.062	0.221	0.5	0.779	0.938
(3,50,2)	0.059	0.217	0.5	0.783	0.941
(3,60,2)	0.057	0.215	0.5	0.785	0.943
(3,70,2)	0.055	0.213	0.5	0.787	0.945
(3,80,2)	0.054	0.211	0.5	0.789	0.946
(3,90,2)	0.053	0.210	0.5	0.790	0.947
(3,100,2)	0.053	0.209	0.5	0.791	0.947
(3,10,3)	0.070	0.230	0.5	0.770	0.930
(3,20,3)	0.048	0.203	0.5	0.797	0.952
(3,30,3)	0.040	0.191	0.5	0.809	0.960
(3,40,3)	0.036	0.184	0.5	0.816	0.964
(3,50,3)	0.033	0.179	0.5	0.821	0.967
(3,60,3)	0.031	0.176	0.5	0.824	0.969
(3,70,3)	0.030	0.174	0.5	0.826	0.970
(3,80,3)	0.029	0.172	0.5	0.828	0.971
(3,90,3)	0.028	0.171	0.5	0.829	0.972
(3,100,3)	0.028	0.169	0.5	0.831	0.972
(b) Extended (r,m,n)	−5%	−2.5%	0%	2.5%	5.0%
(3,10,2)	0.071	0.231	0.5	0.769	0.929
(3,20,2)	0.049	0.204	0.5	0.796	0.951
(3,30,2)	0.041	0.192	0.5	0.808	0.959
(3,40,2)	0.036	0.185	0.5	0.815	0.964
(3,50,2)	0.034	0.180	0.5	0.820	0.966
(3,60,2)	0.032	0.177	0.5	0.823	0.968
(3,70,2)	0.031	0.175	0.5	0.825	0.969
(3,80,2)	0.030	0.173	0.5	0.827	0.970
(3,90,2)	0.029	0.172	0.5	0.828	0.971
(3,100,2)	0.028	0.170	0.5	0.830	0.972
(3,10,3)	0.045	0.198	0.5	0.802	0.955
(3,20,3)	0.026	0.166	0.5	0.834	0.974
(3,30,3)	0.020	0.152	0.5	0.848	0.980
(3,40,3)	0.017	0.144	0.5	0.856	0.983
(3,50,3)	0.015	0.139	0.5	0.861	0.985
(3,60,3)	0.014	0.136	0.5	0.864	0.986
(3,70,3)	0.013	0.133	0.5	0.867	0.987
(3,80,3)	0.012	0.131	0.5	0.869	0.988
(3,90,3)	0.012	0.129	0.5	0.871	0.988
(3,100,3)	0.012	0.128	0.5	0.872	0.988

possible that the same effects of experiment mean on error variance exist for the genotype-by-environment variance components. Furthermore, locations may be chosen using those criteria developed by Williams et al. (1992) or Pederson and Rathjen (1981). This investigation would not invalidate the recommendations in this paper since there is interest in providing baseline information for comparisons between the economics of various trialling systems.

The importance of genotype maturity, winter habit and aluminium tolerance in reducing unexplained genotype-by-environment interactions in NSW is clear from the results of this work. This reduction significantly improves the accuracy of proposed trialling systems and therefore would imply that routine collection of this data be mandatory. Furthermore, it would be reasonable to expect that if additional experiment variables were collected in future, the accuracies quoted in this paper would be found to be conservative as the maturity score and aluminium tolerance ratings are surrogate data for actual ear emergence and soil pH. It should be a research priority to understand and measure the sources of genotype-by-environment interaction so these effects can be eliminated.

It is apparent that the current trialling system is in need of change. Reasonable accuracy can be achieved with as few as 30 or 40 experiments annually, with 3 years of multi-site experiments and basic genotype data. Even allowing for failure, the current system, which consists of approximately 100 experiments annually, appears difficult to justify on the grounds of statistical accuracy.

The significant genotype-by-location interaction requires further investigation. Genotype recommenda-

tions in NSW have historically been made on the basis of silo groups. In practice, however, there is very little difference between the recommended lists of genotypes between silo groups. The results from this study suggest that there may be a more meaningful partition of NSW based on genotype performance. A review of silo groups has been undertaken. This review included the major grain buyers and has recommended that the number of silo groups in NSW be reduced from six to two.

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