

## Paper 7

# RESPONSE OF GRAIN YIELD, PLANT HEIGHT AND KERNEL WEIGHT IN WINTER WHEAT TO DIFFERENT SELECTION METHODS

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### ABSTRACT

A method of handling segregating populations which combined the positive attributes of traditional pedigree and bulk methods was evaluated. Derived  $F_3$  lines from the pedigree, bulk, and modified bulk methods were obtained from three winter wheat crosses (*Triticum aestivum* em Thell). The effectiveness of the methods was measured in terms of plant height, and phenotypic selection for grain yield based on plant ideotype in early generations. Material was grown at three diverse experimental sites to evaluate levels of heterogeneity in relation to possible  $F_3$  line x environment interactions.

The modified bulk method was as effective as the pedigree method in establishing the desired semi-dwarf height. Selection methods used on different crosses and locations did not affect kernel weight.

The modified bulk method was superior for grain yield in only one cross when the  $F_3$  lines were averaged. However, when individual  $F_3$  lines were compared, a higher percentage was obtained from the modified bulk method for different crosses and locations.

Data suggests that to reduce the cultivar x environment interaction, a level of genetic heterogeneity within varieties must be maintained.

### KEYWORDS

Pedigree, bulk, modified bulk, stability, homogeneity, heterogeneity.

### INTRODUCTION

The pedigree and bulk methods of handling segregating populations have been used extensively in the breeding of self pollinated species.

The bulk procedure allows natural selection to operate on segregating populations. Individual plants are selected in  $F_2$ , and in later non-segregating populations. This method allows a large number of crosses to be evaluated and large population sizes to be maintained. Plants which are more competitive emerge as the material is more densely seeded. Progeny resulting from this method are those which were favoured by natural selection. In contrast, the pedigree

method involves phenotypic selection of individual plants in the  $F_2$  and in subsequent segregating generations. Detailed records are maintained for each progeny. A major disadvantage of the pedigree method is the limited number of crosses and/or population size that can be handled. Also, the individual plants are generally space planted, which discounts any effects of competition. The pedigree method is also expensive and time consuming. A proposed modified bulk method combines some of the desirable features of each of these methods.

A number of papers relating to the comparison of bulk and pedigree methods for breeding self pollinated species have been reviewed by Raeber and Weber (1953), Torrie (1958), Voight and Weber (1960), and Matsuo *et al.* (1960). Their conclusions may be illustrated by the findings of Palmer (1952), and Casali and Tigschellaar (1975). Palmer (1952) suggested that there is no clear evidence favouring either the pedigree or bulk method of breeding. He also concluded that where only a few genes of importance are segregating, or where speed is essential, the pedigree method is preferable. Where many genes are segregating, or where selection for recessive major genes is combined with polygenic selection, the bulk population method makes more economical use of available facilities.

Luedders *et al.* (1973) compared the bulk, pedigree, and early generation testing selection methods in soybeans. The latter method involved yield trial evaluations of phenotypically-selected plants in  $F_4$  and  $F_5$  generations. No differences were found between lines selected by the different methods for grain yield. Luedders *et al.* pointed out that visual selection is not an accurate way to discern differences in yield, and thus should only be applied when discarding the poorest lines.

Allard and Bradshaw (1964) defined a well buffered variety as one that can adjust its genotypic or phenotypic state in response to transient fluctuations in environment to give a high, stable, economic return for the population, place, and year. In genetically heterogeneous populations, buffering may result from interaction among different coexisting genotypes within the population, whereas genetically homogenous populations, such as pure line varieties, depend heavily on individual buffering.

Simmonds (1982) found that mixed populations are more stable in yield than their component lines. The work

of Finlay (1963) on barley (*Hordeum vulgare*) and Allard (1961) on lima beans (*Phaseolus lunatus*) showed that hybrid populations in self-pollinated species are often highly buffered. Finlay found that 45 F<sub>2</sub> barley crosses out-yielded their parents and were more stable in Australian environments. In lima beans, Allard found three unselected F<sub>4</sub> populations out-yielded their parents by an average of 7% in 16 environments.

The yield stability of barley was studied by Rasmusson (1968). The populations consisted of three distinct levels of genetically diverse homogeneous varieties, simple mechanical mixture, and complex mixture (bulk hybrids). They were evaluated in two locations for five years. As a group, the simple mixtures had slightly higher yields than varieties or complex mixtures. Varieties and simple mixtures were similar in stability but both were less stable than complex mixtures.

The objectives of this study were:

- To compare the efficiency of three methods of handling segregating populations: pedigree, bulk, and modified bulk.
- To test the effectiveness of different cycles of phenotypic selection on plant height and indirectly for kernel weight, and grain yield.
- To study the relationship between genetic diversity and stability in different environments.

## MATERIALS AND METHODS

Cross combinations of F<sub>2</sub> lines from three winter wheats included Yamhill/Druchamp (YMH/DRC), Yamhill/Daws (YMH/DWS), and Yamhill/Stephens (YMH/SPN). Druchamp and Yamhill are awnless, lower tillering, mid-tall cultivars which resulted from crosses between Vilmorin 27/Fleche d'Or and Heines VII Alba, respectively. Daws and Stephens are awned, high tillering, semi-dwarf cultivars obtained from crosses between C.I. 14484//C.I. 13645/P.I. 178383 and Nord Desprey/Pullman Selection 101, respectively. With the exception of Druchamp, the parents were developed in the Pacific Northwest of the US and are regarded as having a high grain yield potential. Druchamp is an introduction from France with a lower grain yield potential. The F<sub>2</sub> population from each cross consisted of 600 plants divided randomly into three equal sections of 200 plants to start the selection methods. Three different procedures were used for each cross:

- Pedigree method, where three cycles of visual selection were applied.
- Modified bulk method, where two cycles of visual selection were exercised.
- Non-selected bulk population, without visual selection.

### Pedigree method

Using the pedigree method, 25 F<sub>2</sub> plants were selected from a total population of 200 in 1981. Selection criteria included tillering capacity; large, fertile spikes; stiff straw; intermediate height; and visual selection of grain yield

potential. The progeny of these plants were space planted to select F<sub>3</sub> progenies. Twenty-five plants were selected in each F<sub>3</sub> population using the same selection criteria as previously noted. This represented the second cycle of selection. The resulting seed was planted in 1983 giving 25 rows of the F<sub>4</sub> generation. From each set of 25 rows the best eight rows were identified which represented the third selection cycle. These rows were harvested separately and F<sub>5</sub> seed was used for the replicated yield trial.

### Modified bulk method

To develop populations for the modified bulk method, a single spike was obtained from the most promising of the 200 F<sub>2</sub> plants in 1981. This represented the first cycle of selection. Eighty individual head rows per cross were planted for the F<sub>3</sub> generation. The phenotypically similar progeny rows were harvested and bulked to make the F<sub>4</sub> generation. Superior individual head rows were also maintained separately as elite lines. A total of 20 modified bulk selections were planted as F<sub>4</sub> and eight lines were chosen on phenotypic evaluation. The F<sub>5</sub> seed was used for replicated yield trials.

### Bulk method

A random sample of seed harvested from the 200 F<sub>2</sub> plants was used for a dense planting of the F<sub>3</sub> generation, and no further selection was made. The same procedure was followed in the F<sub>4</sub>, and a random sample of F<sub>5</sub> seed was chosen for the replicated yield trial. No selection took place in the F<sub>6</sub> population.

### Comparison of procedures

In 1985, a trial was sown with F<sub>5</sub> progeny of the three crosses to compare the pedigree, modified bulk, and bulk selection methods. This generation included eight lines each for the pedigree and the modified bulk methods, and one bulk population. They were planted in a replicated yield trial using a nested design arrangement of treatments. Methods were randomly assigned in each replication. Four replications were used for the analysis of grain yield, and three for kernel weight and plant height. Three environmentally-diverse locations were chosen in Oregon; they included Corvallis (1000 mm average annual rainfall), Arlington (250mm), and Pendleton (500 mm). The experimental unit consisted of six rows, 20 cm apart and 4.5 m long. The differences within methods, and between lines within methods, were analysed within each particular location and across locations.

Genetic variances for lines within methods were computed. The standard error of the variances were calculated using the formula proposed by Anderson and Bancroft (1952).

Estimates of genotype x environment interaction were obtained for two locations, Corvallis and Arlington. The stability across locations was computed using the technique of Plaisted and Peterson (1959).

Plant height represented a qualitatively inherited trait while the weight of 500 kernels and grain yield are regarded

**Table 1. Mean squares and coefficients of variation (cv.) for 500 kernel weight, plant height and yield<sup>1</sup> for the combined analysis.**

Sources of variation	Yamhill/Druchamp (YMH/DRC)			Yamhill/Daws (YMH/DWS)			Yamhill/Stephens (YMH/SPN)		
	500 kernel weight	Plant height	Yield	500 kernel weight	Plant height	Yield	500 kernel weight	Plant height	Yield
Locations	19.89	46495.60**	295.67**	79.00*	36075.00**	214.85**	45.89	39196.30**	109.02**
Reps/locs	13.50**	200.75**	12.78**	9.09**	171.38	5.94**	12.39	315.70	10.19**
Methods	1.89	174.92	2.34	0.26	4691.32**	2.49**	13.68	824.55**	4.34*
Pooled reps x methods	1.34	112.28**	0.78	1.53*	116.40	0.31	5.39**	16.33	1.01
Lines/methods	14.85**	579.98**	2.16*	27.26**	101.33	0.77	26.67**	1850.13**	0.79**
Methods x locs	1.41	122.73	0.96	8.79	337.25	1.63	3.30	116.10	0.46
Lines/methods x locs	2.30	181.28**	0.82	5.29**	129.26**	0.74**	4.60**	200.49**	0.33
Pooled exp. error	1.29**	35.50		1.49**	89.69		2.28**	50.90	
Pooled samp. error	0.62	42.29		0.69	69.16		0.56	52.22	
Pooled error			0.18			0.18			0.31
C.V.(%)	3.73	5.68	8.68	3.90	7.66	7.63	3.26	6.82	10.81

\*, \*\* Exceed F value at 5% and 1% probability level, respectively. <sup>1</sup>Grain yield obtained at Corvallis and Arlington only.

as being quantitatively inherited. Thus, a comparison of the effectiveness of each method could be evaluated in terms of the nature of inheritance of a specific trait. Total plot means were used to examine grain yield, while three 1 m row samples from each plot were obtained to measure plant height and 500 kernel weight.

## RESULTS

The mean squares and coefficients of variation for all characters for the combined analysis are presented in Table 1. Location differences were observed for all three crosses and all characters, except 500 kernel weight in YMH/DRC and YMH/SPN. Differences in YMH/DWS and YMH/SPN crosses for plant height and yield were noted. Lines within methods were significantly different for all three crosses and all characters, except for plant height and yield in the YMH/DWS cross. Differences were also found for lines/methods x locations. Coefficients of variation for all three characters were relatively low.

For plant height, differences between methods were noted for two of the three crosses studied, YMH/DWS and YMH/SPN (Table 2). Phenotypic selection notably reduced plant height in both crosses. Mean values for plant height involving the bulk method were higher than for the pedigree and modified bulk methods.

Mean values for grain yield involving the three methods of selection are presented in Table 2. The modified bulk method mean was higher than either the pedigree or bulk methods in the YMH/DWS cross. It was also superior to the pedigree method for improving mean value of yield in the YMH/SPN cross. When bulk and modified bulk

**Table 2. Means of F<sub>2</sub> lines in each cross method combination for three winter wheat crosses grown at three locations<sup>1</sup>.**

Cross	Method	Height (cm)	Yield (t/ha)
YMH/DRC	Pedigree	114.59	5.01
	Mod. bulk	114.72	4.64
	Bulk	118.59	5.03
LSD .05		NS	NS
YMH/DWS	Pedigree	99.53	5.51
	Mod. bulk	106.74	5.84
	Bulk	117.08	5.31
LSD .05		<sup>2</sup> 1.65 <sup>3</sup> 3.51	0.149 0.315
YMH/SPN	Pedigree	103.57	4.51
	Mod. bulk	105.59	5.52
	Bulk	112.13	5.42
LSD .05		<sup>2</sup> 1.45 <sup>3</sup> 3.07	0.387 0.821

<sup>1</sup> Grain yield obtained at Corvallis and Arlington only.

<sup>2</sup> LSD .05 is given for the comparison of ped. and m. bulk methods

<sup>3</sup> LSD .05 is given for the comparison of bulk and ped and m. bulk method

**Table 3. Estimates of relative contribution of F<sub>1</sub> lines within method to the mean lines by location interaction component of variance in two inter crosses grown at Corvallis and Arlington, Oregon, 1984.**

Method	Line	YMH/ DRC	Method	Line	YMH/ DWS
Pedigree	1	0.089	Pedigree	1	0.062
	2	0.066		2	0.097
	3	0.074		3	0.147
	4	0.299		4	0.305
	5	0.080		5	0.074
	6	0.384		6	0.122
	7	0.144		7	0.077
	8	0.410		8	0.335
	Mean	0.194		Mean	0.145
M. bulk	9 (E) <sup>2</sup>	0.068	M. bulk	9 (E)	0.061
	10 (E)	0.214		10 (E)	0.196
	11 (E)	0.060		11 (E)	0.106
	12 (E)	0.073		12	0.198
	13	0.032		13	0.069
	14	0.258		14	0.112
	15	0.024		15	0.201
	16	0.052		16	0.135
	Mean	0.098		Mean	0.135

<sup>1</sup> M. bulk (E) are lines selected from modified bulk method and referred to as elite lines.

methods were applied for this cross, no improvement was observed.

To assess yield stability of the lines for each method of selection, a study was conducted to determine possible genotype x environment interactions. Estimates of mean lines x location variance components are given in Table 3. YMH/DRC cross lines handled using the pedigree method, had the largest interaction component. The average relative contribution of the cross (0.194) was higher than the modified bulk mean (0.098). It appears that the modified bulk method generated lines which were less influenced by environmental effects. In the YMH/DWS cross, no clear evidence of the superiority of any one method for stability of yield was detected. Individual lines resulting from the YMH/DRC cross were not studied because the line x location interaction was not different between environments.

## DISCUSSION

### Evaluation of methods

Many breeders have tried to modify traditional ways of handling segregating populations. The modified bulk method was designed to combine the best attributes of the pedigree and bulk methods and to use limited resources more efficiently. The major apparent advantage, in

addition to the large number of crosses and population sizes which can be handled, is that individual F<sub>2</sub> can be selected for desired qualitatively inherited traits. F<sub>3</sub> populations are grown under a competitive densely-sown regime; the best rows can therefore be identified under the same conditions as a commercially produced crop. Enough seed is available by F<sub>4</sub> to develop replicated yield trials. Furthermore, interactions between selected lines and different environments can be obtained by growing the material as early as F<sub>3</sub> generation in different locations.

When methods within and between crosses were compared for plant height in different locations, the effectiveness of three cycles of selection employed with the pedigree method was apparent. This would be expected for qualitatively-inherited traits such as plant height. The greater plant height associated with the bulk method population suggests that natural selection favoured the taller plants and agrees with the hypothesis of Allard (1966) that competition in segregating populations eliminates poorest competitors. In this study, shorter plants in the unselected bulk populations could not compete for light and thus were disadvantaged.

When the overall mean values are considered for grain yield, phenotypic selection was effective; however the selection criteria followed by the modified bulk method was more effective than the pedigree method in both YMH/DWS and YMH/SPN crosses.

It appears that additional cycles of selection practiced with the pedigree system for either plant height or plant type and indirectly for grain yield may not be worthwhile. With the modified bulk method, one less cycle of selection was as effective in establishing the desired plant height, and was superior in identifying the highest yielding progeny. The question which should be raised is whether a broader genetic base or broader heterogeneity within the modified bulk-derived lines might have contributed to superior yield and apparent greater stability of yield.

### Relationship between genetic diversity and stability

The different selection methods for yield resulted in lines with different levels of genetic diversity. Progeny lines originating from the pedigree method, with three cycles of individual plant selection, were genetically uniform. The modified bulk method, with only two cycles of selection, produced more genetically diverse lines.

When the stability of yield is compared across locations in terms of genetic diversity within lines for the various methods, differences did exist between methods for the genotype x environment interaction. In the YMH/DRC cross, homogeneous lines from the pedigree method had the greatest variation between locations. No significant differences between lines from the different methods were observed in the YMH/DWS cross. However, lines from the pedigree method did contribute more to the genotype x environment (location) interaction.

Based on limited data, in terms of the number of crosses involved, the results support the modified bulk method of breeding. This method was effective in

stabilising the desired height level after two cycles of selection. A similar situation would be expected for most qualitatively-inherited traits. Solid seeding the F<sub>2</sub> head rows introduced competitive stress which placed progeny under conditions found in the commercial production of wheat. Also, by bulking phenotypically similar rows or individual rows in the F<sub>3</sub>, it is possible to achieve a degree of genetic heterogeneity for stability of yield.

The modified bulk method of breeding allows a large number of crosses to be evaluated and less promising populations discarded in early generations. Furthermore, large segregating populations can be handled, a crucial factor because the probability of finding plants which have the desired genetic combination to withstand the stresses incurred during the growing season is low.

A final advantage of the modified bulk method is that in developing countries, it would be a more efficient system, especially where resources are limited and there is often a lack of trained scientists.

## CONCLUSIONS

Differences in overall mean values between methods of handling segregating populations were detected for plant height and grain yield in YMH/DWS and YMH/SPN crosses. These differences were observed within and across locations. The level of genetic heterogeneity observed within lines resulting from the modified bulk method appears to produce lines with higher yields, and greater yield stability when their performance is evaluated in different locations. The modified bulk method appears to take advantage of the best attributes of the pedigree and bulk methods of breeding.

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