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Title: A Comparison of Selected Analyses for Estimating Environmental

Variation in Early Generations and Advanced Lines of

Wheat (Triticum aestivum L. em thell).

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Warren E. Kronstad

This investigation was motivated by the introduction of the new
nearest neighbour analyses which reportedly provided a better control
of soil gradients than conventional experimental mthods.

Three nearest neighbour analyses and six other analyses were
compared with the completely randomized design or the randomized
complete block design in reducing the experimental error.

In F1 and F2 generations none of the analyses when compared with
randomized complete block design provided a better control of error for
plant height evaluation. For grain yield modest increases in efficiency
were observed in weighted nearest neighbour analysis in F1 generation
(116%) and F2 generation (109%) at Rugg Farm when compared to
randomized complete block design (100%). Iterated nearest neighbour
analysis (108%) and moving mean covariance analysis (109%) also showed
increases in efficiency for the evaluation of F2 generation at Rugg
Farm over randomized complete block design.

Moving mean covariance analysis appeared more consistent in
reducing error for the evaluation of F5 lines in unreplicated yield
trials with the efficiency ranging from 122 to 212% when compared to

completely randomized design (100%). Recently proposed weighted nearest neighbour analysis proved to be more efficient at Sherman Station, which was the most variable of the experimental sites. Augmented design was more efficient at Rugg Farm site where blocks matched field patterns.

In the evaluation of 32 advanced selection replicated yield trials, the highest average efficiency was recorded for iterated nearest neighbour analysis (128%) and weighted nearest neighbour analyis (122%).

Iterated nearest neighbour analysis, weighted nearest neighbour analysis, moving mean covariance analysis and weighted Papadakis method proved useful in the evaluation of advanced selection trials particularly in trials with correlation of adjacent plot residuals were greater than 0.4 and in trials where entries number was greater than 40.

A Comparison of Selected Analyses for
Estimating Environmental Variation in
Early Generations and Advanced Lines of
Wheat (Triticum aestivum L. em thell)

by

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IN DEDICATION

to my son Mohisn Hasan Noor Khan

who passed away January, 11 1984.

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INTRODUCTION

Concerns are being expressed among plant breeders that an

increasingly larger portion of their resources are being used to

maintain current levels of productivity. As yield levels have gone up

in species like wheat, breeders have been forced to seek genotypes with

smaller increments of increase. This requires a greater degree of

precision in identifying superior genetic combinations in all phases of

a plant breeding programme. The three critical phases where an

assessment of the nature of variation is crucial are; a) the F1 and

early segregating generations, c) individual F5 lines which are nearly

homozygous and c) advanced selections grown in replicated yield trials.

The F1 and early segregating generations are crucial in terms of

determining the nature and amount of genetic variation associated with

quantitatively inherited traits as the expression of such traits is

more difficult because polygenes are involved with a large

environmental influence. This situation is further complicated in self

pollinated species as a breeder can use only the additive portion of

the total genetic variability. The non-additive genetic variation which

is associated with heterozygosity is lost by a factor of 1/2 each

generation of selfing. Therefore an accurate assessment of true nature

of the genetic variation is critical for effective selection. Selection

for qualitatively inherited traits like plant height or maturity

present no problems as few genes are involved and the genetic variation

is discontinuous with limited environment interaction.

Through the use of various biometrical models applied to the F1 populations estimates of the nature of gene action controlling a trait is obtained. Unfortunately a large environmental component frequently masks the true genetic components, making such assessment difficult.

For grain yield selection must be delayed until some degree of homozygosity is reached usually by the F5 generation. Breeders must as a consequence evaluate hundreds of F5 lines. Effective selection from such a large number of F5's is a problem since economic constraints and limited seed supplies per line do not permit the use of replicated yield trials. Thus, the risk of inappropriate ranking due to masking effect of environmental factors associated with various abiotic gradients are high. Check plots are routinely used for comparison to identify high yielding lines but the use of such a procedure has been questioned.

A randomized complete block design is frequently used for the evaluation of advanced selections of wheat. Unfortunately abiotic gradients in the field may not match the assumption that systematic effects are the same for all units in a block. However, randomization and ease of analysis often were thought to justify the use of this design. Therefore, the potential for obtaining higher estimate of the error and obtaining inaccurate treatment means could lead to erroneous conclusions.

Results from uniformity field trials suggested that frequently the randomized complete block design does not provide for an adequate approximation of the underlying patterns of variation. Other

statistical techniques involve the evaluation of each plot relative to the performance of its neighbors. The blocking technique coupled with the use of randomization as with the randomized complete block designs attempts to exclude the correlation among neighboring plots whereas the techniques involving neighboring plots takes advantage of this correlation. Nevertheless, the later approach has been ignored due to the time required in making calculations.

Due to wide spread use of electronic computers, computational convenience is no longer a consideration. As a consequence there has been a renewed interest in the use of neighboring plot analyses to account for the plot to plot positional effects in the field. As a result many new and more sophisticated analyses have been developed for both the unreplicated and replicated yield trials. However, concerns regarding the soundness of the mathematical theory behind these analysis is open to question. This is particularly true the number of degrees of freedom associated with experimental error is unknown.

The objective of this investigation was to determine the utility of selected analyses when employed to different phases of a wheat breeding program. These include space planted F1 and solid seeded F2 populations, relatively homozygous F5 lines in unreplicated yield trials, and advanced selections grown in replicated yield trials. Data were obtained over a four year period from four experimental sites and analyzed employing eleven different analyses.

REVIEW OF LITERATURE

As yield levels have increased for the major food crops, plant breeders have become increasingly more concerned with the identification and evaluation of superior progenies. This is especially true for quantitatively inherited traits such as grain yield in self pollinating species like wheat. Selection for such traits is made difficult, especially in early generations, since their expression is influenced by the total genetic variability present of which the non-additive portion is subsequently lost through selfing. Also, quantitatively inherited traits are influenced by various environmental factors including genotype x environment interactions. If the breeder could obtain a reliable estimate of the environmental effects a more precise determination of the genetic potential, including the predominant type of gene action, could be obtained. As a result more efficient breeding systems could be developed for the selection of quantitatively inherited traits.

A related problem facing the breeders of self pollinated species is the evaluation of several hundred lines, each of which is relatively genetically homogenous by the F5 generation. Due to limited seed supplies, such lines have to be tested in unreplicated trials with check cultivars frequently used to estimate the environmental influences. However, there is a danger of inappropriate adjustment if the check cultivars do not detect true environmental differences (Yates, 1936; Baker and Mckenzie, 1967). As adequate quantity of seed supplies become available in F6 and in subsequent generations, advanced

lines are usually tested using a randomized complete block design with three or four replications. If blocking is effective in removing environmental variation, the experimental error provides a good estimate of the random variation and theoretically there is no environmental bias in estimating the performance of an advanced line. However, if blocking fails to match the patterns of field variation, the experimental error will become inflated. This could result in poor genotypes appearing more desirable due to positive environmental effects and vice versa (Keuls and Sieben, 1955). Recently, several new analyses have been proposed to better estimate the environmental influence for unreplicated and replicated yield trials.

The literature review will concentrate on investigations pertaining to: a) classical block designs, b) check plot designs, c) augmented designs, d) moving mean analyses, and e) nearest neighbour analyses and their empirical comparison in wheat and selected crop species.

a) Classical Block Designs.

Today the most commonly employed experimental designs used in plant breeding are the result of field research conducted by R. A. Fisher and his associates. Fisher (1925) laid down three basic principles of experimental designs which include: a) replication, b) randomization, and c) blocking. Replication refers to the number of different plots in which a cultivar is sown and provides an estimate of experimental error. Randomization reduces the chances of the cultivar mean value and estimate of experimental error of being biased. Furthermore, randomization has made it possible to measure the relative

efficiencies of different experimental designs (Yates, 1950). Yates (1950) considered that randomization was the initial fundamental step in the development of field designs for comparisons among treatment means. Blocking (or local control) is a method of reducing the environmental variance of a difference between cultivar means. (Fisher, 1925; Yates, 1936). This approach is successful in reducing experimental error provided the environmental variation is small among plots within each block and greater between blocks.

A randomized complete block design has several advantages. The analysis is simple. In lengthy operations, such as planting and harvesting, one block can be completed before another is begun. Several workers can also take observations simultaneously. However, some investigators consider that block designs have some limitations in their application to field trials. The main concern is that blocks cannot be arranged to match patterns of variation in the field. Also plots within a block often differ in response which result in inflated experimental errors (Richey, 1926; Barker and Briggs, 1950; Hoyle and Baker, 1961; Wilkinson et al., 1983). According to Greenberg (1953), it is impractical to expect randomization to cancel the full impact of all causes of field variation from plot to plot within a block. Randomization will ordinarily remove the bias, but not the accompanying variability produced by the plot to plot variation within a block.

Block designs make an indirect approach in controlling soil variation by dividing the experimental area under test into smaller blocks. However, soil variation is usually continuous in nature (Wilkinson et al., 1983; Schwarzbach, 1984; Shorter and Butler, 1986;

Buker and Alvey, 1986). Correlations between residuals (deviation of a cultivar yield on a given plot from its mean) of cultivar yield on a plot and fertility levels were established by Riddle and Baker (1944). They indicated that if such associations exist, soil productivity biases exist in cultivar performance. It was also concluded that a bias is inherent in any large scale experiment that imposes an inflexible design upon a soil whose fertility may fluctuate markedly within short distances. Hoyle and Baker (1961) view the soil as a complex manifestation of nature that seldom conforms to simple and rigid mathematical models that are easily analyzed by routine techniques. Blocking can do more harm then good if inappropriately used (Pearce, 1980).

b) Check Plot Designs.

Early in agricultural research, breeders began to use systematically distributed check plots in field trials. With the advent of block designs, check plot designs were no longer used in replicated trials. However, check plot designs are still widely used to correct for fertility gradients in preliminary testing of large number of lines where limited seed supplies exists. The performance of a genotype is expressed as a difference between its performance and the adjacent check plots or as a percentage of the check plots.

In wheat yield trials significant correlations were reported between the productivity of adjacent plots, however the correlations in productivity of adjacent plots decreased rapidly as the distance between plots increased (Wiebe, 1935; Garber et al.,1962; Briggs and Shebeski, 1968). In the presence of high correlations between adjacent

plot yields, check plot adjustment was successful in reducing environmental influence in aforementioned studies.

Two replications were used to test F3 lines for grain yield in wheat (Knott, 1972). Thatcher, a spring wheat was used as the check and was seeded in every fifth row. Yields of each F3 line were expressed in three ways: a) the plot weight was expressed as a percentage of the mean of nearest two check plots, b) as a percentage of the replicate mean, and c) as a moving mean of nearest seven plots, excluding the control plots, but including the plot being considered. The coefficients of variation obtained were 17.5, 20.6, and 15.1 percent for the three methods, respectively. The efficiency of check plot design was tested in evaluation of 1560 F5 generation lines of winter wheat at Plant Breeding Institute Cambridge in unreplicated plots (Besag and Kempton, 1986). Every sixth plot was represented alternately by the cultivars Bounty or Maris Huntsman in the experiment. When selection was based on unadjusted yields, the highest 10 percent of the lines came almost wholly from that area of the field with the highest fertility. When a fertility index based on weighted mean values of six neighboring check plots was used to adjust the yield of the lines, the top ten percent of the lines then came from different parts of the field.

Serious statistical objections to the use of percent of checks and difference from checks to adjust yields for soil variation were pointed out by Yates (1936). He showed that such procedures almost always over-adjust plot yields which could result in a marked reduction in statistical efficiency. Yates also suggested that if checks are used,

then yield adjustment should be accomplished through the analysis of covariance procedures developed by Fisher (1932). The adjustment factor estimated by analysis of covariance is determined so experimental errors are minimized. Baker and McKenzie (1967) tested Yates suggestion using both theoretical and experimental approaches. Inappropriate adjustments were found in 27 of the 45 theoretical tests when yields were adjusted using checks without the analysis of covariance. The experimental evidence was compatible with the theoretical conclusions. In their experimental approach, results of a barley experiment showed that the loss in efficiency was 98 percent in check plot adjustment and only 0.05 percent in check plot covariance adjustment. Analysis of variance of a barley yield trial gave a error mean square (EMS) of 42076. Yield expressed as a deviation of mean of two adjacent checks gave an EMS of 37622. Error mean square was 36072 when yield was expressed as covariance of mean of nearest two check plots. They concluded that check plots should not be used in place of replication. If replications are limited due to a shortage of seed, an attempt should be made to use analysis of covariance as suggested by Yates (1936).

c) Augmented Designs.

To circumvent the difficulties arising from unreplicated experiments, Federer (1956, 1961) proposed a class of designs called 'Augmented Designs'. The basic idea is to repeat check cultivars several times in any standard classical block design. Each replication of the check cultivar is embedded in a block and the advanced lines are assigned to the remaining plots. Estimates of block effects or

experimental error is obtained using only check cultivars.

A modified augmented design (MAD) to test advanced lines without replication was proposed by Lin and Poushinsky (1983). Their approach mimics a split plot arrangement where the whole plot can be laid out in any standard design, but the arrangement of subplots is always 3 x 3 with the center plot used as a check. The shape of a subplot is square or nearly square, so that the distance between the center plot and its corresponding eight test plots is relatively uniform. The number of check plots under this design is approximately 13-17% of the total. Modified augmented design was compared with check plot adjustment method and the covariance of check plot method in a simulation study (Lin et al. 1983). Twelve hypothetical soil fertility maps were generated representing various fertility patterns with 144 lines and four check cultivars used to obtain estimate of environmental variation by different methods. All methods were more efficient than check plots analyzed using completely randomized design (CRD). Average efficiencies relative to CRD were 227.49, 222.88 and 232.57% for MAD, check plot design and check plot covariance analysis, respectively. Modified augmented design was the best when soil variation occurred in one or two directions but, the check plot covariance analysis was superior when variation was multi-direction. Check plot design was least satisfactory.

Sahagun-Castellanos (1985) evaluated 1158 F5 Oat lines in four environments. These lines were derived from two oat crosses contributing an equal number of 529 lines and evaluated in an augmented design field arrangement. Each block contained 28 plots which

accommodated five check cultivars and 23 lines. The yield evaluation
methods were: a) checks analyzed using CRD, b) Augmented design, and c)
block effects estimated using the mean of the 23 lines in a block and
plot value adjusted by subtracting the corresponding block effect.
Average gain at the 10% selection intensity in two populations was 8.1,
7.1 and 7.1% in the three methods, respectively. These results showed
no striking differences in the methods employed.

c) Moving Mean Analyses.

An alternative to randomized complete block design (RCBD) was
proposed by Richey (1924). He suggested a moving mean method to adjust
plot yields to remove the effect of correlated soil variation. Richey's
method consisted of obtaining indexes of field productivity based upon
the production of small groups of contiguous plots. These indexes (I)
are the ratios of the sum of the actual yield of a cultivar on a given
plot and its two neighbours divided by the sum of the overall trial
mean yield of the respective three cultivars. The second step was to
obtain actual percentage yields on a plot basis which are ratios 'A' of
the actual yield of a cultivar on a given plot over the mean yield of a
respective cultivar in the experiment. A regression of 'A' on 'I' is
performed to obtain estimated values '$\hat{A}$'. The correction of treatment
yield is obtained by the equation: Corrected yield = Observed yield/ $\hat{A}$.
Finally corrected yields are subjected to an analysis for a completely
random design to obtain an estimate of experimental error. Richey
(1924) applied the moving mean method to an experiment involving 11
maize cultivars with checks planted in alternate rows. He obtained
26.75 percent less EMS than for a completely randomized design. In

another report Richey (1926) compared the moving mean method with an RCBD in an eight cultivar barley trial previously presented by Student (1923). Richey obtained 12.5 percent less EMS as compare to the RCBD analysis. Bryan (1933) made a comparison between Richey's moving mean method and RCBD using data from three maize uniformity trials. In each trial application of moving mean resulted in a decrease in EMS. Average reduction over RCBD was 35.96%. To achieve equal precision by the two methods, RCBD would require from seven to 14 replications as compared with six for the moving mean analysis.

Several researchers have tried various combinations of moving mean methods for unreplicated and replicated yield trials. Townley-Smith and Hurd (1973) studied thirteen wheat trials to evaluate yield of common and durum wheats. The yield of 13 trials were expressed in three different ways: a) the plot as measured and analyzed using RCBD, b) the plot weight adjusted by subtracting the mean of two to 20 adjacent plots (moving mean analysis) and, c) in five trials yields were adjusted by subtracting the mean of a number of closest check plots. Moving mean analysis was superior to RCBD in all thirteen trials. The average EMS in 13 trials was 2386 for the moving mean analysis as compared to 3296 in RCBD. On the basis of only five trials where checks plots were included, the magnitude of EMS was 3543, 2620, and 4007 for the three methods, respectively. The efficiency of applying a moving mean analysis was compared with RCBD in 59 forage grass trials by Lawrence and Townley-Smith (1975). Moving means comprised two to 24 plots which were subtracted from the actual yields to obtain adjusted yields. In 55 of the 59 trials, the moving mean analysis gave a lower

EMS than RCBD and was equal in the remaining four trials. Magnitude of average EMS of 59 trials was 127139 in moving mean analysis and 264163 in RCBD. The optimum number of adjacent plots to include in the moving mean varied widely from test to test, as well as from year to year for the same test.

Mak et al. (1978) compared: a) check plot design (CPD), b) check plot covariance analysis (CPCA), c) moving mean analysis (MMA), and d) moving mean covariance analysis (MMCA) with RCBD in a single row, space planted barley yield trial. The coefficients of variation were 28.04, 23.49, 23.54, 23.40 and 23.54 percent for CPD, CPCA, MMA, MMCA and RCBD, respectively. In a second barley experiment, a lattice design (LD) was also included in the comparison. The coefficients of variation in CPD, CPCA, MMA, MMCA, LD and RCBD were 17.30, 14.75, 16.88, 14.65, 15.74 and 18.25%, respectively. Rosielle (1980) evaluated 81 wheat lines grown in two experimental design field arrangements with four replications at seven locations in Western Australia. The two experimental designs were a partially balanced 9 x 9 lattice square (LD) and a check plot design. The check plot design (CPD) consisted of a randomized complete block design in which a check cultivar 'Gamenya' was planted between every third test plot. The efficiency of moving mean covariance analysis was compared with LD and RCBD in 9 x 9 lattice square field arrangement and with CPCA and RCBD in check plot design field arrangement. In the first trial, mean coefficients of variation for the seven locations were 19.8, 17.0 and 17.5% for RCBD, LD and MMCA, respectively. In the second experiment mean coefficients of variation were 21.4, 15.8 and 17.0 percent for RCBD, CPCA and MMCA,

respectively.

Moving mean covariance analysis was applied by Mareck (1981) to evaluate segregating barley populations. Grain yield was measured on S1 and F3 lines grown in unreplicated 0.7 square meter, two-row plots at two locations. In a subsequent year, grain yield was also measured in S1 and F3 bulk progenies in unreplicated 6.0 square meter plots at three locations. Check plots were replicated in the experiment and subjected to standard analysis of variance (CRD) to determine environmental variation. Moving mean configurations were comprised of four to 12 adjacent plots and were used as a covariable in an analysis of covariance. The application of MMCA resulted in a reduction of EMS between 0 at Holmes Farm and 80 percent at Redmond site when compared to CRD depending on the experimental site.

e) Nearest Neighbour Analyses.

The first nearest neighbor model was suggested by Papadakis (1937). In this method the residual for each plot is obtained by subtracting cultivar yield on a given plot from the mean of all plots planted with the same cultivar. Means of the residuals of two adjacent plots are used as independent covariates for the plot in question in an analyses of covarince. In a trial employing five wheat cultivars, Papadakis (1937) obtained a 57% reduction in EMS when compared to RCBD. In a wheat uniformity yield trial with 13 cultivars and five blocks, the magnitude of EMS was 52% less than RCBD analysis (Papadakis, 1970).

Bartlett (1938) applied Papadakis method to cotton experiments grown at Tukh and Mahallet Roh locations in Egypt. Both experiments were previously analyzed using RCBD. Using Papadakis method, the

coefficient of variation for Mahallet Roh location was reduced to 8.6 from 12.0%. Coefficient of variation at the Tukh site was reduced to 7.0 from 8.9%. Bartlett concluded that a close correlation between neighboring plots could be largely eliminated by the Papadakis method. He recommended that two degrees of freedom should be allowed for the regression coefficient instead of the usual one. Bartlett noted that although the calculations required were simple, but they were far still too laborious to be practical. With modern computers these limitations may no longer apply (Yates, 1970).

A covariance technique using neighbouring plot residuals to reduce experimental error was proposed by Buker et al. (1972). A co-variable for each plot observation is obtained by averaging two or more neighboring plot residuals (deviation of the yield of a cultivar on a given plot from mean yield of that cultivar in a experiment). An analysis of covariance is then performed to determine EMS and adjust treatment means. Based on the magnitude of EMS, covariance technique appeared to be 50 to 75 percent more efficient 'than the randomized complete block design. This method of analysis was later called Productivity Covariance Analysis (PCA) by Buker and Alvey (1979). The results of 655 maize cultivar experiments were averaged and they found that the magnitude of EMS was less in PCA than in RCBD in 61% of the trials. In a recent report, Buker et al. (1986) provided a comparison of PCA and RCBD in 1407 maize cultivar performance trials conducted during the period of 1972 to 1982. The error mean square was 36% less in PCA relative to RCBD analysis in 1407 maize trials. Buker et al. (1986) also indicated that their method is basically not different from

Papadakis method (1937).

Papadakis method was re-examined by Bartlett (1978) on theoretical grounds. The conclusions were: a) Papadakis method is available for randomized block design as a possible ancillary device for improving the accuracy of treatment comparisons, b) the gain in efficiency over orthodox randomized block analysis can be appreciable when the number of cultivars is large, and c) the gain can be increased by iterating the analysis. Bartlett further suggested that the minimum number of replications should be three, otherwise the cultivar adjustment of plot values is likely adversely to affect the neighboring plot adjustment.

Pearce (1978) recalculated the results from 56 maize fertilizer trials conducted during 1969 over 11 sites in the West Indies. Each trial was analyzed using CRD to obtain the base coefficient of variations of the site. These base coefficients of variation were then used to compare the efficiency of RCBD and three configurations of Papadakis method in comparison to CRD. Average reduction in coefficient of variation was 8.33% in RCBD and 10.67 to 12.67% in three configurations of Papadakis method. In a subsequent study, the results of 33 experiments conducted in Africa and West Indies on maize, groudnuts, and cowpeas were recalculated by different analyses (Pearce, 1980). The coefficient of variation obtained from CRD analysis was used to compare efficiency of RCBD and four neighboring models based on Papadakis method. Average reduction over CRD in coefficient of variation were 8.2% in RCBD and 6.8 to 14.8% in four neighboring models.

Kempton and Howes (1981) investigated the environmental variation

in 163 wheat and barley performance trials carried out between 1975 and 1978. Approximately half of these trials were conducted at Plant Breeding Institute and the remainder at other sites in the United Kingdom. Each trial was analyzed by CRD to obtain an estimate of the base coefficient of variation. Average reduction in 163 trials in coefficient of variation was 9.8 and 23.30% in RCBD and Papadakis method, respectively. Kempton and Howes (1981), used data from uniformity trials and superimposed a dummy cultivar response, and then adjusted for covariance of neighboring plot residuals. They found that the reduction in estimate of error variance reflected the increased accuracy of the estimates of cultivar means.

A new nearest neighbour analysis, later named Waite nearest neighbour analysis (Waite NNA) was proposed by Wilkinson et al. (1983). This method was described as the ˜moving block' analogue of classical ˜fixed-block' methods. The yield of each plot is divided into three components: a) a true genotypic effect, b) an approximately linear local trend effect, and c) a local plot error. Each plot observation is adjusted by subtracting from it the mean of the two neighboring plot observations, thereby forming a nearest-neighbor comparison of treatment effects. The efficiency of the Waite NNA is largely independent of the physical layout of the replications of the trial. A ninety cultivar barley yield trial with three replications conducted at Bondleigh, Australia was analyzed using Waite NNA and RCBD (Wilkinson et al., 1983). The magnitude of EMS was 41.33 percent less in Waite NNA than that obtained in an randomized complete block analysis. Wilkinson (1984) applied Waite NNA to the International spring wheat yield trial

conducted at El Batan in Mexico. This was a 50 cultivar trial with three replications. The coefficient of variation obtained from the RCBD was 29% and 14% as determined by the Waite NNA. Wilkinson (1984) admitted that if there is no soil fertility gradient patterns within the trial, Waite NNA may result in a significant loss in precision. He suggested that when the Waite NNA proves ineffective, a RCBD should be used. Similar views were expressed by Kempton (1984) for all nearest neighbour analyses.

Waite nearest neighbour analysis was compared with RCBD in a nineteen cultivar barley trial grown at two locations in New Zealand (Wynn-Williams, 1984). At the Mitcham location, the coefficient of variation values were 5.7 and 5.4% for RCBD and Waite NNA, respectively. At Swannanoa, the coefficient of variation values were 5.0% for RCBD and 5.5% using the Waite NNA.

Nearest neighbour analyses are more effective when there are at least three replications and more than 40 plots in the experiment (Blaird, 1984). Also there should be reasonable correlations (r) between neighboring plot residuals. Blaird recommended use of Waite NNA only if r is greater than 0.4 when three or four replications are used. Blaird warned that a loss in accuracy can occur with the use of Waite NNA when there is no correlation between adjacent plot residuals.

Schwarzbach (1984) developed a new iterative nearest neighbor analysis (I-NNA). Iterated nearest neighbour analysis is suited for any kind of experimental design with replicated plots, including irregular designs with different numbers of replications per cultivar, or plots per block and designs with missing plots. Seven official trials

conducted by Austrian Federal Institute of Agriculture and Seed testing were analyzed by I-NNA, lattice design and RCBD (Schwarzbach, 1984). The average error mean square of seven trials were 16.74, 20.88 and 49.41 using I-NNA, lattice design (LD) and RCBD, respectively. In a subsequent study the efficiency of I-NNA was compared with LD and RCBD in ten simulation yield trials (Schwarzbach and Horn, 1985). Each trial consisted of thirty six cultivars tested using six replications. When compared to RCBD, the application of I-NNA and LD resulted in a 26.98 and 17.44% reduction in EMS, respectively. The same simulation trials were also analyzed by weighted nearest neighbor analysis (W-NNA), and a mean reduction of 28.57% percent in EMS relative to RCBD was obtained (Schwarzbach, 1985).

Weighted nearest neighbor analysis (W-NNA) is flexible and can be used for analysis of unreplicated trials where some check cultivars are replicated. Schwarzbach and Betzwar (1985) compared W-NNA with check plot design in a simulation trial. There were 121 entries in the trial with a check cultivar occupying every fifth row. Check plot design and W-NNA, resulted in 30.29, 44.24% reduction in EMS when compared to CRD, respectively.

Effects of moving mean covariance adjustment on EMS control was examined in nine peanut trials (Shorter and Butler, 1986). Two to fourteen adjacent plots were used in two types of moving mean covariate: one based on adjacent plot yields (MMCA) and a second based on adjacent plot residuals. The reduction in error was demonstrated by both covariates when compared to RCBD and was 26% using MMCA and 23% with the residual covariance adjustment on the average of nine trials.

Generally the greatest reduction in EMS occurred when six to eight adjacent plots were used.

In the future, grain yields of wheat and most of the major food crops will be secured by smaller increments of increase. Present techniques used for determining yield in cereals apparently are not refined to detect real yield differences if they are only in the magnitude of about 10% (Fowler and Heyne, 1955). Plant breeders will have to use more precise analyses to obtain more reliable genetic estimates in early generations and isolate the more productive wheat selections in unreplicated and replicated yield trials.

There is very little evidence concerning the usefulness of augmented designs or recently proposed weighted nearest neighbor analysis in the evaluation of large cultivar unreplicated trials. It has been indicated that soil fertility gradients are not sufficiently obvious in the field to allow meaningful blocking. In fact, application of RCBD was unsatisfactory in some investigations particularly when blocks did not match patterns of soil variation. In the past methods such as Ricehy's moving mean, and Papadakis method were proposed as alternatives to RCBD, they were not generally used. Recently there has been a great resurgence of interest in the use of Papadakis method in the analysis of field experiments, particularly following a publication of Bartlett (1978). This renewed interest have resulted in the development of new analyses such as Waite NNA (Wilkinson et al. 1983), I-NNA (Schwarzbach, 1984), W-NNA (Schwarzbach and Betzwar, 1985), autonormal model (Besag, 1983), least square smoothing (Green et al. 1985) and linear variance model (Williams, 1986). These innovations in

experimental designs merit detailed comparison with conventional randomized complete block design and previously proposed moving mean and Papadakis methods.

MATERIAL AND METHODS

This study was conducted to evaluate the efficiency of different analyses in estimating environmental variation in three phases of a plant breeding program. The phases involved: a) evaluation of spaced planted non segregating F1 and solid seeded segregating F2 populations, b) evaluation of F5 lines grown in unreplicated trials, and c) evaluation of advanced selections tested in replicated trials. The objective of this study was accomplished using data of 38 wheat trials; three each for phases a and b, and 32 for phase c and covering four testing years.

Experimental sites included: a) Hyslop Agronomy and Holmes Farms near Corvallis, Oregon b) Sherman Branch Experimental Station near Moro, Oregon, and c) Rugg Farm east of Pendleton, Oregon. At Hyslop Agronomy and Holmes Farms the soil type is a fine silty, mixed mesic Aquultic Argixeroll. The soil type at Sherman station and Rugg farm is coarse silty mixed mesic and typic Haploxeroll. Details of the cultural practices employed at each site are provided in Appendix Table 1. A summary of climatic data for the four experimental sites over a period of four years is presented in Appendix Table 2.

a. Evaluation of F1 and F2 populations.

a.1. <u>Genetic material</u>.

Crosses involving five winter wheat cultivars 'Stephens', 'Yamhill', 'Malcolm', 'Aurora' and 'Jackmar' were made during 1984 at Hyslop Agronomy Farm. Pedigrees and description of these five parents are given in Appendix Table 3. During the fall of 1984, five parents

and the ten hybrids were planted at Rugg Farm in a randomized complete block design with four replications (noted as Trial A). Each plot consisted of a single row 5 m long. The spacing between plants and rows was 30 cm. Data were recorded on 15 plants in the center of each row for plant height, a qualitatively inherited trait and grain yield, a quantitatively inherited trait. Plant height was measured in centimeters from ground level to the tip of the spike, excluding awns if present. Grain yield was recorded in grams from the yield of individual plants. The mean value of 15 plants from each row was used as the plot value in statistical analysis for both traits.

During 1985, five parents and 10 F2 populations were planted in a randomized complete block design with four replications at Hyslop Agronomy Farm (noted as Trial B) and at the Rugg farm (noted as Trial C). The experimental unit consisted of two row plots five meters long with an inter row spacing of 30 cm. All plots in Trial B and Trial C were seeded by hand at the rate of 400 seed per row. Plant height was measured on the main tillers at maturity, as previously noted. The mean of 10 observations was used to represent the plant height of each plot. At maturity, two rows at Rugg Farm and one row at Hyslop Agronomy Farm were harvested, threshed and weighed in gms to obtain the grain yield. Grain yields per plot was then converted to kilograms per hectare (Kg/Ha).

A single solid seeded row of barley was grown 30 centimeters from the edge of each range to serve as a border in three trials grown at Hyslop Agronomy and Rugg Farms.

a.2. Analyses used to determine environmental

variation in early generation trials.

Grain yield and plant height data obtained from three trials were analyzed with six analyses to estimate environmental variation.

a.2.1. Randomized complete block design (RCBD).

The error mean square obtained from RCBD was used as the basis of comparison of analyses.

a.2.2. Moving mean covariance analysis (MMCA).

The mean of a number of adjacent plots, excluding the plot in question was regarded as a moving mean. Six configuration of moving means were calculated using two to 12 adjacent plots. Moving means were calculated using an equal number of plots on each side of the plot in question, except at the end of the blocks where the appropriate number of plots nearest the border were used. For example, with eight adjacent plots the moving mean for the second plot from the end of the block would involve the last plot from the end plus seven plots on the other side. The moving mean for each plot were used as the independent covariate in an analysis of covariance structured in RCBD to adjust plot values and obtain adjusted error mean square. The most promising combination of neighboring plots based on lowest estimate of EMS was chosen for determining efficiency of MMCA.

a.2.3. Productivity covariance analysis (PCA).

A productivity map of the nursery was developed by calculating the deviation of each plot observation from its overall treatment mean,

$$d = Y_{ij} - \overline{Yi}.$$

where,   d = deviation of the plot yield,

(noted as residual),

Yij = cultivar yield on a given plot.

$\overline{Yi}.$ = The mean of a cultivar in a trial.

An independent variable (X) was generated for each plot by averaging the residuals of four nearest plots, two on both sides but not including the plot itself (1 1 0 1 1). This variable (X) was used as the productivity index of the experimental area. Standard analysis of covariance structured in randomized complete block design with the productivity index as the independent variable and plot observations as the dependent variable was used to obtain adjusted EMS.

a.2.4. Weighted nearest neighbour analysis (W-NNA).

The procedure is provided in Schwarzbach and Betzwar (1985).

a.2.5. Iterated nearest neighbour analysis (I-NNA).

The algorithm is given in Schwarzbach (1984). A computer programme version 20 written in Basic for W-NNA and I-NNA was used to carry out analyses.

a.2.6. Waite nearest neighbour analysis (Waite NNA).

The details of the calculations are complex and are not covered in this text. A computer program was used to carry out the analyses (Wilkinson et al., 1983).

a.3. Combining ability analysis.

Magnitude of General and Specific Combing Ability were calculated in Trial A to C on mean values obtained from different analyses for grain yield and plant height. However, combining ability analysis was performed only on genotypic values obtained from those analyses which recorded a reduction in error as compared to RCBD. These analysis

followed Model I, Method 2 as proposed by Griffing (1956). Model I was used because the parents represented a selected group of cultivars.

b. Evaluation of F5 lines in unreplicated yield trials.

b.1. Experimental material.

Two hundred soft white winter wheat F5 lines along with three check cultivars were evaluated for grain yield using six different analyses. Lines and check cultivars (Stephens, Hill 81 and Malcolm) were planted in augmented design field arrangement as proposed by Federer (1956, 1961). Experimental sites were Hyslop Farm, Sherman Branch Experiment Station, and Rugg Farm. The experimental areas were divided into nine blocks. Each block contained 26 plots which accommodated three check cultivars and 23 F5 lines. The exceptions were block two and five containing 22 F5 lines, and block nine containing only 18 F5 lines. Check cultivars and lines were randomized within each of the nine blocks (total entries=227). The plot size harvested was 6.5 m^2 at each location.

b.2. Analyses used to determine environmental variation in F5 lines

unreplicated grain yield trials.

Grain yield was analyzed using the six analyses to obtain environmental variation.

b.2.1. Completely randomized design (CRD).

Error mean square obtained using CRD analysis was used to compare efficiency of analyses.

b.2.2. Augmented design (AD).

Analysis of augmented design was completed in three steps as proposed by Federer (1956, 1961). Check cultivars were analyzed using

randomized complete block design to obtain estimate of EMS. Then, an adjustment factor (rj) for each block was computed by subtracting block means based only on check cultivars from the grand mean of the checks. Finally, F5 line yields were adjusted based on respective block adjustment factor with the equation.

$$Y = Yij - rj$$

where   Y = Yield of the ith new selection.

                Yij = Adjusted yield of the ith new selection.

                rj = Block adjustment factor.

b.2.3. Moving mean analysis (MMA).

Six configurations of the moving means were constructed as described previously. The grain yields of 227 entries were adjusted by subtracting the respective moving means. Check cultivars adjusted yields were analyzed using CRD to obtain an estimate of EMS at each location. The analysis with the lowest EMS was chosen to compute relative efficiency of MMA.

b.2.4. Moving mean covariance analysis (MMCA).

Grain yield of replicated check cultivars were analyzed at each location in an analysis of covariance to estimate EMS for six configuration of moving mean. Moving means used as covariable were constructed as described previously. The covariance analysis with the lowest EMS was chosen in each location to obtain relative efficiency of MMCA. Grain yield of 227 entries was then adjusted at each location with the following formula:

$$Y(A) = Y - b(MM - \overline{MM})$$

where; Y(A) = the adjusted grain yield,

$$Y \quad = \quad \text{the actual grain yield of a given entry,}$$

$$MM \quad = \quad \text{the moving mean covariable for a given plot, and}$$

$$\overline{MM} \quad = \quad \text{the average moving mean covariable.}$$

$$b \quad = \quad \text{regression coefficient}$$

b.2.5. Weighted moving mean covariance analysis (WMMCA).

Moving mean for each plot was constructed assigning more weight to closer plots (1 2 4 8 0 8 4 2 1). Zero represents plots for which a moving mean is generated, while digits represent the weight placed on adjacent plots. Standard analysis of covariance was performed on check cultivars to obtain an estimate of EMS, and grain yields of 227 entries were adjusted as previously described.

b.2.6. Weighted Nearest Neighbour Analysis (W-NNA)

b.3. Combined analysis over locations.

Combined analysis across locations was performed using mean values obtained from each of the six analyses using following form of analysis of variance:

Source of variation	Degrees of freedom	Mean square
Location	1-1	
Genotype	g-1	MS(g)
Genotype x Location	(1-1)(g-1)	MS(ge)

c. Evaluation of advanced selections in replicated yield trials.

c.1. Experimental material.

In this study environmental variation was investigated for grain yield using 10 analyses in 32 advanced selection replicated trials carried between 1981 and 1986 (noted as trial 1 to 32 in Appendix Table 4). These trials were established at Hyslop Agronomy and Holmes Farms, Sherman Branch Experiment Station, and Rugg Farm. All 32 trials were sown in a randomized complete block design with three or four replications. Information regarding number of entries, year of trial, and replication per trial is provided in Appendix Table 4. Plot size (six rows) was six m^2 in trial 1 to 30, and 1.86 m^2 for trial 31 and 32 (two rows). Trials numbered 31 and 32 were planted with the randomization with partial nearest neighbour balance (Wilkinson et al., 1983). A restriction was placed on the randomization so that no two cultivars occurred as neighbours more than once in four replications.

c.2. Analyses used to determine environmental variation

in 32 advanced selection replicated yield trials.

c.2.1. Completely randomized design (CRD).

Each of the 32 trial were analyzed using CRD to obtain maximum estimate of environmental variation.

c.2.2. Randomized complete block design (RCBD).

The EMS obtained from RCBD was used to compute the efficiency of analyses.

c.2.3. Moving mean covariance analysis (MMCA).

Six configurations of moving mean using two to 12 plots were used as covariables in an analysis of covariance to determine EMS for 32

yield trials. The exceptions were 13 of the 32 trials (marked with * in Appendix Table 4) which had only two to eight plots in a range.

c.2.4. Productivity covariance analysis (PCA).

c.2.5. Weighted nearest neighbour analysis (W-NNA).

c.2.6. Iterated nearest neighbour analysis (I-NNA).

c.2.7. Waite nearest neighbour analysis (Waite NNA).

c.2.8. Moving mean analysis (MMA)

Six configurations of moving means were constructed as described previously. Plot values were adjusted by subtracting the moving means. The adjusted values were subjected to RCBD analysis to determine EMS. The moving mean showing least EMS was chosen to compare with other analyses. The moving means for 13 of the 32 trials were comprised of two to eight plots as indicated previously.

c.2.9. Weighted moving mean covariance analysis (WMMCA).

The weighted moving mean comprised of eight adjacent plots was formed, putting more weight on the nearest plots (1 2 4 8 0 8 4 2 1). Analysis of covariance was applied using weighted moving mean as the independent covariate and using the corresponding plot observation as the dependent variable to obtain estimate of EMS.

c.2.10. Weighted Papadakis Method (WPM).

The weighted residual mean using adjacent eight plot residual was constructed putting more weight on the nearest plot (1 2 4 8 0 8 4 2 1). The weighted residual mean was used as the covariable in analysis of covariance to obtain an estimate of adjusted EMS.

Data management

All conventional statistical analyses for completely randomized

design and randomized complete block design were performed using Mstat 4.C statistical package. Data of 38 trials were transferred from Leading Edge PC to Cyber model, Control data computer using datalink programme. A computer programme written in Statistical Interactive Programming System was used to analyze unreplicated trial for augmented design analysis. A moving mean programme in fortran written by Mareck (1981) was modified to construct six configurations of moving means and a weighted moving mean. Residuals for each plot were obtained using 'R' option in the Statistical Interactive Programming System (Rowe and Brenne, 1982). The moving mean programme was used to calculate the mean residual of four adjacent plots for PCA and the weighted residual mean for WPM analysis. Analysis of covariance of plot yield with moving plot means, weighted mean, four plot residual mean, and weighted residual mean were performed using BMDP covariance analysis programme on the main frame computing facility to obtain EMS for MMCA, WMMCA, PCA and WPM.

RESULTS

Results are presented in three sections. Each relates to one of the three major phases of a wheat breeding program where statistical analyses are used to determine the genetic worth of potential new cultivars. The first section deals with a comparison of six analyses in estimating environmental variation in space planted F1 and solid seeded F2 populations. Six analyses are compared in the second section for efficiency in evaluating the performance of F5 genetically new uniform lines in unreplicated yield trials. In the final section, nine analyses are compared for precision in controlling environmental variation in 32 replicated yield trials involving advanced selections.

a) Evaluation of F1 and F2 populations.

Three early generation populations (Trial A, B and C) were used to estimate environmental variation involving plant height and grain yield. Trial A involved the evaluation of 10 F1 space planted populations and their five parents grown at Rugg Farm during 1984-85. Ten F2 populations and five parents were tested at Hyslop Agronomy Farm during 1985-86 (Trial B). Results of Trial C reveal the performance of the same five parental cultivars and 10 F2 populations when grown at Rugg Farm during 1985-86.

Efficiencies of moving mean covariance analysis (MMCA), productivity covariance analysis (PCA), weighted nearest neighbour analysis (W-NNA), iterated nearest neighbour analysis (I-NNA), and Waite nearest neighbour analysis (Waite NNA) were compared with randomized complete block design (RCBD) in reducing environmental

variation in trials A, B and C. The error mean square (EMS) obtained from the six analyses was used as the basis of comparison. The ratio of EMS from RCBD to EMS from MMCA, PCA, W-NNA, I-NNA or Waite NNA, provided an indication of the efficiency of the five analyses. Error mean squares, coefficients of variation and relative efficiencies obtained via six analyses for plant height and grain yield in three trials are provided in Tables 1 to 6.

The coefficient of variation in RCBD was 2.9% for plant height in Trial A. Only MMCA (102%) showed higher efficiency over RCBD (Table 1). For grain yield in Trial A, MMCA (109%) and W-NNA (116%) were more efficient in reducing EMS (Table 2). The coefficient of variation for grain yield in RCBD was 9.0% in Trial A.

Only small increases in efficiency over RCBD with the application of MMCA and PCA were obtained for plant height in Trial B (Table 3). The coefficient of variation for plant height was 4.1% in RCBD which increased in Weighted NNA, I-NNA and Waite NNA. In Trial B, only PCA (107%) demonstrated a superiority over RCBD as reflected in a lower coefficient of variation and higher relative efficiency involving grain yield (Table 4). Moving mean covariance analysis was only slightly better than RCBD. The coefficient of variation in RCBD was 8.9% and increased in W-NNA, I-NNA and Waite NNA.

The coefficient of variation was 2.8% in randomized complete block design for plant height in Trial C (Table 5). Superiority of MMCA and PCA over RCBD in reducing EMS was slight for plant height in Trial C (Table 5), while W-NNA, I-NNA and Waite NNA proved ineffective. Weighted nearest neighbour analysis and I-NNA were more efficient

Table 1. Error mean square, coefficient of variation and
relative efficiency of six analyses in evaluation
of plant height (cm) of five parents and 10 F1's
planted at Rugg Farm during 1984-85 (Trial A).

No	Analysis	EMS	CV (%)	RE #
1	RCBD[1]	4.0	2.9	100
2	MMCA[2]	3.9	2.8	102
3	PCA[3]	4.1	2.9	98
4	W-NNA[4]	4.8	3.1	84
5.	I-NNA[5]	4.7	3.1	86
6	Waite NNA[6]	4.5	3.0	90

EMS = Error mean square.
CV = Coefficient of variation.
1 Randomized complete block design (considered 100% efficient).
2 Moving mean covariance analysis.
3 Productivity covariance analysis.
4 Weighted nearest neighbour analysis.
5 Iterated nearest neighbour analysis.
6 Waite nearest neighbour analysis.
Relative efficiency = EMS (RCBD)* 100/EMS (analysis 2, 3,..or 6)

Table 2. Error mean square, coefficient of variation and
relative efficiency of six analyses in evaluation
of grain yield (gm/plant) of five parents and
10 F1's planted at Rugg Farm during 1984-85 (Trial A).

No	Analysis	EMS	CV (%)	RE #
1	RCBD[1]	15.2	9.0	100
2	MMCA[2]	14.0	8.6	109
3	PCA[3]	15.5	9.1	98
4	W-NNA[4]	13.1	8.4	116
5	I-NNA[5]	14.9	8.9	102
6	Waite NNA[6]	18.0	9.8	85

EMS = Error mean square.
CV = Coefficient of variation
1 Randomized complete block design (considered as 100% efficient).
2 Moving mean covariance analysis.
3 Productivity covariance analysis.
4 Weighted nearest neighbour analysis.
5 Iterated nearest neighbour analysis.
6 Waite nearest neighbour analysis.
Relative efficiency = EMS (RCBD) * 100/ EMS (analysis 2,3,.. or 6).

Table 3. Error mean square, coefficient of variation and relative
efficiency of six analyses in evaluation of plant height
(cm) of five parents and 10 F2 populations planted at
Hyslop Agronomy Farm during 1985-86 (Trial B).

No	Analysis	EMS	CV (%)	RE #
1	RCBD[1]	26.7	4.1	100
2	MMCA[2]	26.5	4.1	101
3	PCA[3]	26.3	4.1	102
4	W-NNA[4]	30.3	4.4	88
5	I-NNA[5]	37.7	4.9	71
6	Waite NNA[6]	40.8	5.1	65

EMS = Error mean square.
CV = Coefficient of variation.
1 Randomized complete block design (considered as 100% efficient)
2 Moving mean covariance analysis.
3 Productivity covariance analysis.
4 Weighted nearest neighbour analysis.
5 Iterated nearest neighbour analysis.
6 Waite nearest neighbour analysis.
Relative efficiency = EMS (RCBD)*100/EMS (analysis 2,3,..or 6).

Table 4. Error mean square, coefficient of variation and relative
efficiency of six analyses in evaluation of grain yield
(Kg/Ha) of five parents and 10 F2 populations planted
at Hyslop Agronomy Farm during 1985-86 (Trial B).

No	Analysis	EMS	CV (%)	RE #
1	RCBD[1]	314310	8.9	100
2	MMCA[2]	307669	8.8	102
3	PCA[3]	293060	8.6	107
4	W-NNA[4]	332355	9.2	95
5	I-NNA[5]	416352	10.3	75
6	Waite NNA[6]	519091	11.4	61

EMS = Error mean square.
CV = Coefficient of variation.
1 Randomized complete block design (considered as 100% efficient).
2 Moving mean covariance analysis.
3 Productivity covariance analysis.
4 Weighted nearest neighbour analysis.
5 Iterated nearest neighbour analysis.
6 Waite nearest neighbour analysis.
Relative efficiency = EMS (RCBD)*100/ EMS (analysis 2,3,..or 6).

Table 5. Error mean square, coefficient of variation and relative efficiency of six analyses in evaluation of plant height (cm) of five parents and 10 F2 populations planted at Rugg Farm during 1985-86 (Trial C).

No	Analysis	EMS	CV (%)	RE #
1	RCBD[1]	8.6	2.8	100
2	MMCA[2]	8.5	2.8	101
3	PCA[3]	8.3	2.8	103
4	W-NNA[4]	9.1	2.9	94
5	I-NNA[5]	9.2	2.9	94
6	Waite NNA[6]	10.3	3.1	83

EMS = Error mean square.
CV = Coefficient of variation.
1 Randomized complete block design (considered as 100% efficient).
2 Moving mean covariance analysis.
3 Productivity covariance analysis.
4 Weighted nearest neighbour analysis.
5 Iterated nearest neighbour analysis.
6 Waite nearest neighbour analysis.
Relative efficiency = EMS (RCBD)* 100/ EMS (analysis 2,3..or 6).

Table 6. Error mean square, coefficient of variation and relative
efficiency of six analyses in evaluation of grain yield
(Kg/Ha) of five parents and 10 F2 populations at
Rugg Farm during 1985-86 (Trial C).

NO	Analysis	EMS	CV (%)	RE #
1	RCBD[1]	390152	13.1	100
2	MMCA[2]	382523	13.0	102
3	PCA[3]	379988	12.9	103
4	W-NNA[4]	359471	12.6	109
5	I-NNA[5]	362161	12.6	108
6	Waite NNA[6]	442220	13.9	88

EMS = Error mean square.
CV = Coefficient of variation.
1 Randomized complete block design (considered as 100% efficient).
2 Moving mean covariance analysis.
3 Productivity covariance analysis.
4 Weighted nearest neighbour analysis.
5 Iterated nearest neighbour analysis.
6 Waite nearest neighbour analysis.
Relative efficiency = EMS (RCBD)*100/EMS (analysis 2,3,..or 6).

in Trial C (Table 6) for grain yield. A slight reduction in EMS also resulted with the application of MMCA and PCA. The coefficient of variation for grain yield was 13.1% in RCBD, while only Waite NNA having a higher coefficient of variation compared to RCBD.

The magnitude of regression coefficient in PCA and MMCA may indicate the presence of nature of variation in the experimental area. The regression coefficient was negative for plant height following MMCA and PCA in all three trials. (Appendix Table 5). The exception was PCA in Trial A, where the regression coefficient was almost zero. Largest reduction in EMS shown in Table 1, 3 and 5 was obtained in moving mean covariance analysis with moving means comprised of 10 plots in all three trials.

The regression coefficient was negative in Trial A and B for grain yield in MMCA and PCA, while being positive but non-significant in Trial C for both analyses. Largest reduction in EMS was obtained in MMCA with moving means comprised of ten plots in Trial A (Table 2), eight plots in Trial B (Table 4) and six plots in Trial C (Table 6) for grain yield.

Mean values of the parents, F1,s and F2 populations for the grain yield and plant height obtained via RCBD, MMCA, PCA, W-NNA, I-NNA and Waite NNA in Trials A, B and C are presented in Appendix Table 6 - 11. There were significant differences in genotypes in three trials for plant height and grain yield following different analyses (Appendix Table 12). Combining Ability Analyses using Griffing (1956) method 2 model I, was performed on the results for plant height and grain yield in five analyses which showed a reduction in EMS when compared to RCBD.

Estimates of General (GCA) and Specific Combining Ability (SCA) and their ratios are provided in Tables 7 - 12. Significant GCA estimates were found in all three trials for grain yield and plant height. Specific combining ability effects were significant for grain yield in Trial A (Table 8) and for plant height in all three trials (Table 7, 9 and 11).

For plant height in Trial A (Table 7) the estimate of GCA and SCA were lower for MMCA when compared to RCBD, while ratio of GCA/SCA was higher for MMCA. For grain yield in Trial A, estimates of GCA and ratios of GCA/SCA increased in W-NNA and I-NNA when compared to RCBD (Table 8). Estimates of GCA and SCA, and the ratio of GCA/SCA decreased in MMCA when compared to RCBD.

For plant height, the GCA and SCA estimate was lower in PCA and in MMCA when compared to RCBD (Table 9). However, the ratio of GCA/SCA was higher in PCA compared to RCBD. Higher estimate of specific combining ability was obtained in MMCA and PCA for grain yield in Trial B (Table 10). Estimate of GCA in PCA was higher than RCBD. The ratios of GCA/SCA were lower than RCBD in both MMCA and PCA involving grain yield in Trial B (Table 10).

Productivity covariance analysis (PCA) showed higher estimate of GCA and ratio of GCA/SCA as compare to RCBD. Estimates of GCA, SCA and ratio of GCA/SCA were lower in MMCA for plant height in Trial C (Table 11). The magnitude of GCA and SCA estimates and ratio of GCA/SCA were higher in all four analyses for grain yield when compared with RCBD in Trial C (Table 12). The exception was MMCA which recorded lower ratio of GCS/SCA.

Table 7. Observed mean square for general (GCA) and specific
(SCA) combining ability estimates for plant height in
Trial A using means obtained via two analyses of five
parents and 10 F1's planted at Rugg Farm during 1984-85.

No	Analysis	Mean squares			GCA/ SCA
		GCA	SCA	Error	
1.	RCBD[1]	75.44**	18.29**	2.59	4.12
2.	MMCA[2]	72.20**	16.71**	1.00	4.32

** Significant at .01 level of probability.
1 Randomized complete block design.
2 Moving mean covariance analysis.

Table 8. Observed mean squares for general (GCA) and specific
(SCA) combining ability estimates for grain yield
in Trial A using means obtained via four analyses
of five parents and 10 F1's planted at Rugg
Farm during 1984-85.

No	Analysis	Mean squares		Error	GCA/ SCA
		GCA	SCA		
1.	RCBD[1]	131.78**	38.51**	3.81	3.42
2.	MMCA[2]	110.95**	35.65**	3.50	3.11
3.	W-NNA[3]	133.86**	38.51**	3.28	3.48
4.	I-NNA[4]	136.70**	38.47**	3.72	3.55

** Significant at the .01 level of probability.
1 Randomized complete block design.
2 Moving mean covariance analysis.
3 Weighted nearest neighbour analysis.
4 Iterated nearest neighbour analysis.

Table 9. Observed mean squares for general (GCA) and specific (SCA) combining ability estimates for plant height in Trial B using means obtained via three analyses of five parents and 10 F2 populations planted at Hyslop Agronomy Farm during 1985-86.

No	Analysis	Mean squares			
		GCA	SCA	Error	GCA/SCA
1	RCBD[1]	157.79**	23.11**	6.63	6.83
2	MMCA[2]	139.16**	22.09**	6.63	6.30
3	PCA[3]	155.32**	17.88**	6.57	8.69

** Significant at the .01 level of probability.
1 Randomized complete block design.
2 Moving mean covariance analysis.
3 Productivity covariance analysis.

Table 10. Observed mean squares for general (GCA) and specific (SCA) combining ability estimates for grain yield in Trial B using means obtained via three analyses of five parents and 10 F2 populations planted at Hyslop Agronomy Farm during 1985-86.

NO	Analysis	Mean squares			
		GCA	SCA	Error	GCA/SCA
1.	RCBD[1]	3458136**	118181	78577	29.26
2.	MMCA[2]	3116950**	161506	76917	19.29
3.	PCA[3]	3598191**	148297	73265	24.26

** Significant at .01 level of probability.
1 Randomized complete block design.
2 Moving mean covariance analysis.
3 Productivity covariance analysis.

Table 11. Observed mean square for general (GCA) and specific (SCA) combining ability estimates for plant height in Trial C using means obtained via three analyses of five parents and 10 F2 crosses planted at Rugg Farm during 1985-86.

No	Analysis	Mean squares			GCA/ SCA
		GCA	SCA	Error	
1	RCBD[1]	137.69**	19.42**	2.14	7.09
2	MMCA[2]	121.67**	18.94**	2.12	6.42
3	PCA[3]	141.16**	19.04**	2.08	7.41

** Significant at the .01 level of probability.
1 Randomized complete block design.
2 Moving mean covariance analysis.
3 Productivity covariance analysis.

Table 12. Observed mean squares for general (GCA) and specific (SCA) combining ability estimates for grain yield in Trial C using means obtained via five analyses of five parents and 10 F2 crosses planted at Rugg Farm during 1985-86.

NO	Analysis	Mean squares			GCA/ SCA
		GCA	SCA	Error	
1	RCBD[1]	2045473**	548675	393524	3.72
2	MMCA[2]	2228643**	731841	385829	3.05
3	PCA[3]	2102691**	560580	383272	3.75
4	W-NNA[4]	2181878**	552214	362577	3.95
5	I-NNA[5]	3404307**	691863	365291	4.92

** Significant at .01 level of probability.
1 Randomized complete block design.
2 Moving mean covariance analysis.
3 Productivity covariance analysis.
4 Weighted nearest neighbour analysis.
5 Iterated nearest neighbour analysis.

b) Evaluation of F5 lines in unreplicated yield trials

Results in this section relate to the evaluation of 200 F5 lines

and three check cultivars (replicated in nine blocks) for grain yield

when grown at Hyslop Agronomy Farm, Sherman Station and Rugg Farm

during 1985-86. Augmented design (AD), moving mean analysis (MMA),

moving mean covariance analysis (MMCA), weighted moving mean covariance

analysis (WMMCA) and weighted nearest neighbour analysis (W-NNA) were

employed in an attempt to reduce experimental error (EMS). The estimate

of error mean squares obatined via six analyses in three trials are

provided in Appendix Table 13. The ratio of EMS from CRD to the EMS of

AD, MMA, MMCA, WMMCA or W-NNA in percentage provides an indication of

the efficiency of the five analyses. Completely randomized design is

regarded as 100% in efficiency.

b.1. Hyslop Agronomy Farm Trial.

b.1.1 Relative efficiency of analyses.

Efficiencies of the five analyses are presented in Table 13.

Moving mean covariance analysis (MMCA) appeared most efficient (122%),

while W-NNA least efficient (72%) when compared to CRD. A reduction in

EMS was observed with moving mean covariables in MMCA comprising two to

eight plots. However, greatest reduction in EMS for MMCA occurred with

a moving mean composed of the nearest two plots (Appendix Table 15).

The regression coefficient, b=0.41* (Appendix Table 16), was used to

adjust the grain yield of entries.

Moving mean analysis and WMMCA were similar (116%) in efficiency,

and slightly better than AD (111%). The regression coefficient, b=0.67*

(Appendix Table 16), was used to adjust the grain yield of entries in

WMMCA. The greatest reduction in error was obtained in MMA using moving mean of six plots (Appendix Table 15).

b.1.2. Variability at Hyslop Agronomy Farm.

The yield of each plot as a percentage of trial mean is presented in the field plan shown in Table 14. There are no patterns of high yielding plots as lines yielding more than trial mean are scattered over the experimental area. However, there are some small clusters of low and high yielding F5 lines. The coefficient of variation obtained from CRD was only 11% at this site. Block effects were non-significant in AD suggesting little variation between blocks (Appendix Table 16). The applicationn of W-NNA also did not indicate yield trends in the experimental area (Appendix Figure 1).

The correlation (r) of average of checks used to adjust performance of 200 F5 lines in a specific block was almost zero (r=-0.02). The correlation of moving means with the corresponding plot values employing MMA, MMCA and WMMCA were, r=0.34, r=0.32 and r=0.36, respectively (Appendix Table 16).

b.1.3. Effect on ranking of 200 F5 lines and three check cultivars

using six analyses.

As noted in Table 15 Stephens (entry 3) was present in the top 40 high yielding entries in all six analyses. Malcolm (entry 20) appeared in this group only in CRD and W-NNA and Hill 81 (entry 7) did not appear in the top 40 of the six analysis. Twenty seven lines ranked above Stephens in CRD, MMCA and W-NNA (Table 15). The number of lines surpassing Stephens in AD, MMA and WMMCA were 36, 12 and 21, respectively. Entry 4 was the top yielding F5 line in all six analyses.

Table 13. Relative efficiency of six analyses in evaluation
of 200 F5 lines and three check cultivars in
unreplicated grain yield trial grown at Hyslop
Agronomy Farm during 1985-86.

No.	Analysis	RE 1/
1.	Completely randomized design (CRD).2/	100
2.	Augmented design (AD).	111
3.	Moving mean analysis (MMA).	116
4.	Moving mean covariance analysis (MMCA).	122
5.	Weighted moving mean covariance analysis (WMMCA).	116
6.	Weighted nearest neighbour analysis (W-NNA).	72

1/ Relative efficiency = EMS (CRD) * 100/
                                    EMS (analysis 2,3,..or 6)
2/ Coefficient of variation = 11%.

48

Table 14. Grain yield of 200 F5 lines and three checks expressed
as a percentage of trial mean in field map in F5 line
unreplicated yield trial grown at Hyslop Agronomy Farm
during 1985-86.

			Blocks					
9	8	7	6	5	4	3	2	1
70	111	108	60	87	117b	134	117	120
123	103	107c	89	117	110	86	119	128
107	103b	112	99	84	92	113	94	129a
135	87	80	110	85	112	82	122	151
140c	102	116	131a	104	105	98	116	128
112	102	98	93	101	91	108	110c	69
77	101	72	92	86	60	102	92	106b
77	105a	115	111	107	71	112	119	92
75	72	100	98	115	97	118c	68	88
64	79	78	79	124a	92	118	123	122
75	82	82	101	127	91	112	109	132
86	96	78	124b	113	76	92	83	128
78	88	74	110	108	116	92	126a	134
99b	96	95	110	77	107c	118	109	111
95	96	97	86	132	122	112b	121	102
82	84	98a	112	107c	138	102	71	106
112a	104	106	90	104	117	83	128	102
105	111	110	98	97	126	109	81	90
87	132	81	105	82	82	95	87b	93
98	131	128	108	114	92	108	76	98c
87	127	84	108	93	129a	80	92	94
-	86c	88	76	126	71	87	97	91
-	90	86b	97	83	80	83	83	85
-	70	67	91	89b	72	115a	104	103
-	114	63	92	80	85	96	110	91
-	111	102	121c	-	87	108	-	85

a Stephens
b Hill 81
c Malcolm

Table 15. Entry numbers of the top 40 high yielding entries
amongst 200 F5 lines and three check cultivars
emerged from six analyses in unreplicated yield trial
grown at Hyslop Agronomy Farm during 1985-86.

Rank	CRD1/	AD2/	MMA3/	MMCA4/	WMMCA5/	W-NNA6/
1	4	4	4	4	4	4
2	89	176	36	36	36	89
3	212	120	127	120	53	212
4	13	190	53	53	120	13
5	53	13	120	176	127	53
6	190	189	176	127	176	190
7	11	11	212	89	89	11
8	120	36	89	210	212	120
9	189	115	106	45	43	189
10	12	89	164	43	164	12
11	5	127	43	13	106	5
12	2	53	38	212	13	2
13	36	161	3	87	45	36
14	115	212	190	38	190	115
15	188	164	11	5	210	188
16	127	12	66	190	87	127
17	87	5	28	106	38	87
18	176	188	161	11	11	176
19	210	2	72	164	5	210
20	43	43	188	161	161	43
21	10	159	96	49	189	10
22	49	49	189	125	3	49
23	90	38	13	55	115	90
24	38	174	125	115	125	38
25	1	45	182	92	49	1
26	45	51	45	189	66	45
27	51	10	210	10	182	51
28	3 7/	157	101	3	188	3
29	62	106	5	184	92	62
30	66	52	100	2	10	66
31	88	1	153	51	55	88
32	52	173	159	66	12	52
33	106	48	115	182	101	106
34	161	113	103	141	51	161
35	48	87	49	188	141	48
36	92	125	12	12	28	92
37	164	3	62	159	72	164
38	113	116	78	52	149	113
39	20 8/	210	165	183	2	20
40	125	182	87	149	184	125

1/ Completely randomized design. 2/ Augmented design 3/ Moving
mean analysis. 4/ Moving mean covariance analysis. 5/ Weighted
moving mean covariance analysis. 6/ Weighted nearest neighbour
analysis. 7/ Check cultivar Stephens. 8/ Check cultivar Malcolm

The top yielding lines were almost the same in six analyses.
However, change in position was noticed. For example line 12 was 10th
in CRD and W-NNA, 12th in AD, 36th in MMA and MMCA, and 32nd in MMCA.

b.2. Sherman Station trial.

b.2.1. Relative efficiency of analyses.

An efficiency of 536% was achieved with the application of W-NNA
at the Sherman Station for grain yield (Table 16). Application of AD
resulted in relative efficiency of 82% compared to CRD. The
efficiencies of MMA (156%), MMCA (150%) and WMMCA (151%) were similar.
All the six configurations of moving means employed in MMA and MMCA
demonstrated reduction in EMS when compared to CRD (Appendix Table 14
and 15). However, maximum reduction in EMS was obtained with the moving
mean comprised of eight plots in both analyses. The regression
coefficient, b=0.57* (Appendix Table 16) was used to adjust plot yields
in MMCA. In WMMCA, b=0.43*, was used to adjust plot yields for
fertility trends in the field. The correlation of F5 lines and average
of checks in AD was only, r=0.06.

b.2.2. Variability at Sherman Station.

The yields of each plot in CRD as a percentage of the trial mean
is presented in Table 17. There is an obvious yield trend running
diagonaly across the field. Application of W-NNA also showed the
fertility gradients in the field (Appendix Figure 2). A coefficient of
variation of 11% was obtained from CRD at the Sherman site (Table 16).
The F-value for blocks was only 0.5 in AD which suggests no difference
in performance of check cultivars from block to block (Appendix Table
16). The weighting factor, W=0.72, was used to adjust plot yield for

Table 16. Relative efficiency of six analyses in evaluation of
200 F5 lines and three check cultivars in unreplicated
grain yield trial grown at Sherman Station
during 1985-86.

No.	Analysis	RE 1/
1.	Completely randomized design (CRD). 2/	100
2.	Augmented design (AD).	82
3.	Moving mean analysis (MMA).	156
4.	Moving mean covariance analysis (MMCA).	150
5.	Weighted moving mean covariance analysis (WMMCA).	151
6.	Weighted nearest neighbour analysis (W-NNA).	536

1/ Relative efficiency = EMS (CRD) * 100/
EMS (analysis 2,3,..,or 6)
2/ Coefficient of variation = 11%.

Table 17. Grain yield of 200 F5 lines and three checks expressed as a percentage of trial mean in field map in F5 line unreplicated yeild trial grown at Sherman Station during 1985-86.

Blocks								
9	8	7	6	5	4	3	2	1
96	99	69	92	86	117b	100	117	87
99	94	106c	95	99	107	116	114	114
100	105b	120	111	109	112	104	93	121a
122	83	94	83	106	122	125	111	103
103c	83	96	99a	116	115	84	101	108
88	93	112	96	118	101	104	105c	119
105	80	104	111	125	98	103	53	121b
82	108a	102	116	135	102	93	103	93
63	89	123	96	110	92	103c	99	88
89	114	79	108	134a	88	103	92	118
94	100	62	116	101	103	92	97	117
109	86	92	134b	105	95	97	102	112
86	106	106	107	91	71	95	106a	61
106b	118	98	116	93	126c	100	102	117
94	86	100	94	112	137	102b	86	69
74	95	124a	104	115c	117	103	58	122
98a	100	95	84	94	99	105	120	80
96	143	103	76	104	109	131	85	60
101	117	115	90	90	96	109	112b	107
56	104	116	101	114	99	113	92	114c
101	119	111	90	88	105a	105	109	66
-	133c	93	95	89	114	83	114	47
-	107	92b	92	82	79	106	82	77
-	110	105	79	98b	115	123a	96	88
-	63	64	86	60	79	95	104	88
-	113	116	106c	-	120	94	-	74

a   Stephens
b   Hill 81
c   Malcolm

fertility gradients in W-NNA.

b.2.3. Effect on ranking of 200 F5 lines and three check cultivars

with the application of five analyses.

None of the three commercial cultivars appeared in the top 40
high yielding entries using CRD (Table 18). However, both Stephens
(entry 3) and Malcolm (entry 20) were among the top 40 generated by the
other five analyses and occupied different positions in different
analyses. Stephens ranked higher than Malcolm in AD and W-NNA; however,
the opposite was true for MMA, MMCA and WMMCA. Stephens occupied the
33rd position in AD and WMMCA and 31st in MMA. Stephens was 37th among
the top 40 in W-NNA. The number of lines showing changes in position of
more than ± 5 in ranking were 20, 17, 12, 15 and 16 in AD, MMA, MMCA,
WMMCA and W-NNA, respectively. Entry 191 was first in five of the six
analyses while the entry four found highest yielding at Hyslop Agronomy
Farm was not in the top 40 entries in any analysis at Sherman Station.

b.3. Rugg Farm Trial.

b.3.1. Relative efficiency of analyses.

The highest efficiency (212%) was recorded with the application
of AD and MMCA when compared to CRD (Table 19). The moving mean
analysis and WMMCA also exhibited a decrease in the experimental error,
with an efficiency of 185 and 167%, respectively. Weighted nearest
neighbour analysis revealed an efficiency similar to CRD (100%). All
six configurations of moving means used in MMA showed a decrease in EMS
when compared with CRD (Appendix Table 14). The decrease in error was
much higher in the moving means comprised of six to 12 plots compared

Table 18. Entry numbers of the top 40 high yielding amongst 200 F5 lines and three check cultivars emerged from six analyses in unreplicated yield trial grown at Sherman Station during 1985-86.

Rank	CRD1/	AD2/	MMA3/	MMCA4/	WMMCA5/	W-NNA6/
1	191	191	90	191	191	191
2	90	70	191	90	90	70
3	112	90	16	70	16	182
4	70	212	212	16	70	90
5	111	112	165	112	112	212
6	56	56	70	212	165	56
7	165	165	19	165	36	79
8	101	159	36	56	56	159
9	16	36	14	36	14	112
10	212	111	56	14	212	165
11	159	52	220	79	159	52
12	79	176	79	159	79	36
13	36	182	112	101	182	176
14	188	175	52	19	195	16
15	6	54	159	52	101	154
16	10	51	11	11	10	180
17	195	220	125	10	81	177
18	110	31	101	220	125	101
19	14	101	199	182	52	81
20	52	162	51	125	111	83
21	11	177	182	195	199	54
22	89	79	20	111	11	51
23	182	72	10	199	83	125
24	176	16	81	51	19	195
25	146	188	195	54	31	199
26	149	49	54	81	54	111
27	54	146	177	143	6	175
28	143	149	31	89	149	14
29	109	143	12	20	20	49
30	190	195	83	83	143	149
31	100	215	3	6	154	10
32	81	110	143	31	12	162
33	175	3 7/	49	188	3	31
34	2	32	120	176	176	11
35	51	89	154	3	51	150
36	83	20 8/	89	149	220	220
37	199	6	215	12	188	3
38	31	10	137	177	183	6
39	125	190	176	120	2	100
40	72	109	149	49	100	20

1/ Completely randomized design. 2/ Augmented design. 3/ Moving mean analysis 4/ Moving mean covariance analysis. 5/ Weighted moving mean covariance analysis. 6/ Weighted nearest neighbour analysis. 7/ Check cultivar Stephens.8/ Check cultivar Malcolm.

Table 19. Relative efficiency of six analyses in evaluation
of 200 F5 lines and three check cultivars in
unreplicated grain yield trial grown at Rugg Farm
during 1985-86.

No.	Analysis	RE 1/
1.	Completely randomized design (CRD).2/	100
2.	Augmented design (AD).	212
3.	Moving mean analysis (MMA).	185
4.	Moving mean covariance analysis (MMCA).	212
5.	Weighted moving mean covariance analysis (WMMCA).	167
6.	Weighted nearest neighbour analysis (W-NNA).	100

1/ Relative efficiency = EMS (CRD) * 100 /
                                            EMS (analysis 2,3,..,or 6).
2/ Coefficient of variation = 10%.

to moving means comprised of two to four plots. The greatest reduction

in EMS was demonstrated with the moving mean comprised of eight plots.

In MMCA, a similar pattern was observed among six configurations of

moving means (Appendix Table 15).

b.3.2. Variability at Rugg Farm.

The coefficient of variation obtained from CRD was 10% (Table

19). There is tendency of more high yielding F5 lines coming from some

blocks (Table 20). In blocks four and six particularly, the number of

F5 lines showing more than 100% yield relative to the trial mean was

low compared to other blocks. More high yielding F5 lines were in

blocks one, five and nine. Application of AD showed significant block

to block differences at Rugg Farm. Application of W-NNA, however, did

not reflect yield trends at Rugg Farm (Appendix Figure 3). Correlation

of average of the checks yield and F5 lines in respective blocks was

0.24 (Appendix Table 16). The correlation of moving means with the

respective plot yields was also 0.24 in MMA and MMCA. The correlation

of weighted means in WMMCA was 0.28 with the respective plot yields.

b.3.3. Effect on ranking of 200 F5 lines and three checks with

the application of five analyses.

In contrast to results found at Hyslop Agronomy Farm and Sherman

Station site, all three checks were among the top 40 entries emerging

from the six analyses, except MMA where Hill 81 (entry 7) was not

present (Table 21). Malcolm (entry 20) ranked higher than Stephens

(entry 3) in all analyses.

At the Rugg site 34 F5 lines demonstrated higher yields than

Stephens in AD. Twenty seven lines were superior to Stephens based on

Table 20. Grain yield of 200 F5 lines and three checks expressed as a percentage of trial mean in field map in F5 line unreplicated yield trial grown at Rugg Farm during 1985-86.

Blocks								
9	8	7	6	5	4	3	2	1
85	90	97	88	98	97b	86	92	117
89	85	110c	104	93	89	78	59	105
97	91b	99	101	106	99	95	97	117a
110	83	92	95	104	103	103	93	87
112c	91	92	85a	104	98	99	70	103
103	98	106	84	99	99	101	111c	102
108	101	90	82	114	103	93	97	120b
96	110a	102	92	116	87	100	108	95
94	93	111	89	116	98	112c	91	104
109	101	101	87	112a	94	114	102	107
104	91	114	104b	110	89	106	106	104
96	96	74	85	109	77	99	105a	93
128b	100	100	101	95	104c	105	109	95
101	87	111	87	112	105	107b	91	93
100	103	111a	115	113c	100	102	62	98
124a	104	98	106	99	96	107	107	108
112	119	89	90	103	98	106	84	63
120	103	113	109	101	89	107	103b	104
100	104	106	115	102	85	122	108	123c
113	97	116	97	106	101a	99	108	115
-	122c	116	97	108	103	96	110	105
-	102	113b	90	89	89	82	97	96
-	83	82	92	107b	87	124a	109	114
-	96	76	87	94	84	100	110	106
-	102	102	95c	-	101	99	-	103

a Stephens
b Hill 81
c Malcolm

Table 21. Entry numbers of the top 40 high yielding entries amongst
200 F5 lines and three check cultivars emerged from six
analyses in unreplicated yield trial grown at
Rugg Farm during 1985-86.

Rank	CRD1/	AD2/	MMA3/	MMCA4/	WMMCA5/	W-NNA6/
1	72	141	72	72	72	72
2	228	137	12	191	191	228
3	191	138	191	178	141	191
4	1	140	178	12	12	1
5	178	155	177	177	137	178
6	113	191	141	141	228	113
7	12	146	137	137	36	12
8	177	154	155	113	167	177
9	21	143	39	1	1	21
10	141	72	167	228	178	141
11	24	113	20	167	24	24
12	137	90	113	21	17	137
13	112	178	146	24	20	112
14	220	177	21	20	39	220
15	62	135	120	120	21	62
16	167	28	165	220	220	167
17	175	136	24	62	177	175
18	231	112	1	39	113	231
19	120	31	212	165	175	120
20	227	101	45	212	120	227
21	20 8/	39	220	112	118	20
22	171	29	154	171	62	171
23	165	98	90	3	171	165
24	115	167	62	155	112	115
25	28	83	3	45 ·	3	28
26	212	153	83	138	165	212
27	3 7/	20	36	28	212	3
28	31	32	171	115	28	31
29	138	175	33	17	45	138
30	39	120	138	146	138	39
31	29	45	228	175	155	29
32	118	33	17	36	115	118
33	32	79	79	33	127	32
34	127	36	28	31	146	127
35	17	3	127	90	162	17
36	215	89	31	29	7	215
37	45	42	115	127	29	45
38	33	115	29	118	31	33
39	69	62	112	83	215	69
40	7 9/	171	7	7	231	7

1/ Completely randomized design. 2/ Augmented design. 3/ Moving mean
analysis. 4/ Moving mean covariance analysis. 5/ Weighted moving mean
covariance analysis. 6/ Weighted nearest neighbour analysis. 7/ Check
cultivar Stephens.8/Check cultivar Malcolm 9/ Check cultivar Hill 81.

CRD and W-NNA analysis. Twenty four F5 lines outperformed Stephens in

MMA and WMMCA, while 22 were higher yielding in MMCA. The number of

entries appearing in the top 40, which did not appear in CRD, were 13

in AD, seven in MMA and five each in MMCA and WMMCA. Deviation in

position of more than $\pm$ 5 relative to CRD was found in 18 of the

entries in AD and MMA, 10 in MMCA and 15 in WMMCA. The most obvious

change in ranking by analysis was Row 138. It was 29th in CRD and 3rd

with the application of AD, while in all other analyses Row 138 was

below 20 in the ranking. Entry 72 ranked first in five of the six

analyses. As at Sherman site entry 191 again ranked high at the Rugg

site. Most of the F5 lines yielding higher than Stephens at Hyslop Farm

did not appear in any analysis above Stephen at Rugg Farm. The highest

yielding line (entry 4) did not appear in top 40 at Rugg Farm.

b.4. Combined analysis of three locations.

b.4.1. Effect of five analyses on genotype x environment

    (G x E) estimate.

Two way analyses were performed using mean values obtained from

six analyses. Estimate of G x E increased 26% with the application of

AD when compared to CRD (Table 22). A slight increase (4%) in G x E was

also noticed in W-NNA. Decreases in G x E were 12, 11 and 9% in WMMCA,

MMA and MMCA, respectively. Entry 191 and 212 appear to be the most

consistent in terms of high ranking across locations and analysis.

b.4.2. Effect on ranking over location with the application

    of six analyses.

Only Stephens and Malcolm appeared in the top 40 entries for all

analyses (Table 23). However, all three check cultivars were in the top

40 of WMMCA. Stephens ranked higher than Malcolm in all six analyses.
The number of F5 lines outperforming Stephens were 15, 12, 7, 11, 8 and
14 in CRD, AD, MMA, MMCA, WMMCA and W-NNA, respectively.

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Table 22. Effect of adjusted grain yield by five analyses as
compare to actual grain yield obtained using
completely randomized design on genotype x location
mean square (G x E MS) for 200 F5 lines and three
check cultivars grown at three locations.

No	Analysis	G x L MS
1	Completely randomized design (CRD).	217749
2	Augmented design (AD).	273325 (-26%) 1/
3	Moving mean analysis (MMA).	194561 (11%)
4	Moving mean covariance analysis (MMCA).	198159 (9%)
5	Weighted moving mean covariance analysis (WMMCA).	192106 (12%)
6	Weighted nearest neighbour analysis (W-NNA).	226372 (-4%)

1/ Reduction in G x L MS when compared to CRD is presented
in parenthesis. Negative value shows increase in G x L MS.

Table 23. Entry numbers of the top 40 high yielding entries on the basis of average performance of 200 F5 lines and three checks at three locations in six analyses during 1985-86.

Rank	CRD1/	AD2/	MMA3/	MMCA4/	WMMCA5/	W-NNA6/
1	191	191	36	36	36	212
2	212	36	212	212	212	191
3	90	176	120	120	191	12
4	12	90	165	191	120	36
5	120	120	90	90	90	90
6	112	212	191	176	72	120
7	36	112	12	89	176	176
8	89	89	3	12	12	11
9	11	190	72	72	3	89
10	190	165	89	45	165	112
11	10	159	176	112	45	70
12	2	45	127	3	89	72
13	176	3	20	70	112	10
14	72	113	137	11	182	62
15	70	188	101	10	70	3
16	3 7/	141	220	165	141	190
17	113	12	11	20	20	2
18	188	115	70	141	10	20
19	5	20	45	101	101	45
20	115	72	24	127	11	5
21	20 8/	189	141	125	127	101
22	4	28	125	182	125	159
23	189	101	182	190	159	4
24	62	70	159	159	16	182
25	101	49	28	2	137	165
26	165	164	164	62	87	125
27	87	182	62	137	28	127
28	141	52	16	16	62	87
29	45	143	49	49	190	113
30	159	87	79	87	49	66
31	125	39	39	5	52	189
32	1	137	199	143	143	49
33	28	11	154	52	199	188
34	127	31	52	164	220	115
35	143	162	10	113	31	52
36	137	62	31	199	164	28
37	183	43	19	220	5	141
38	16	10	112	31	79	39
39	49	125	143	28	149	227
40	109	177	100	115	7 9/	137

1/ Completely randomized design 2/ Augmented design. 3/ Moving mean analysis. 4/ Moving mean covariance analysis. 5/ Weighted moving mean covariance analysis. 6/ Weighted nearest neighbour analysis. 7/ Check cultivar Stephens. 8/ Check cultivar Malcolm 9/ Check cultivar Hill 81.

c. Evaluation of advanced selections in replicated yield trials.

Results presented in this section compare eight analyses with a randomized complete block design (RCBD) in estimating environmental variation in 32 replicated yield trials (noted as 1 to 32 in Appendix Table 4). These trials were grown at three environmentally diverse sites in Oregon over a four year period. Estimate of error mean square (EMS) obtained for the nine analyses and the EMS obtained for CRD for 32 yield trials are presented in Appendix Table 17. However, in this section the EMS obtained from RCBD was considered as 100% and the relative efficiency was determined as a ratio of EMS from RCBD to the EMS of other analyses. A relative efficiency greater than 100 indicates a reduction in EMS and increase in efficiency over RCBD (Appendix Table 18).

On the average of 32 trials, I-NNA (128%) was most efficient while Waite NNA (99%) and MMA (96%) were less than 100% in efficiency as compared to RCBD (Table 24). The average efficiencies of MMCA (114%), PCA (113%), WMMCA (111%) and WPM (114%) were similar. Nevertheless, these four analyses were less variable when compared to I-NNA, W-NNA and Waite NNA as can be observed from table 24 when the ranges and standard deviations are considered. The large variability in efficiency of the eight analyses across the different trials indicated that none were always superior to RCBD. To explore this, comparison of eight analyses with RCBD is considered as follows: 1) level of environmental variability, 2) size of the trial based on number of entries, 3) effectiveness of blocking, 4) correlation of adjacent plot residuals, and 5) location of the trials.

Table 24. Mean, range and standard deviation in relative efficiency
of eight analyses based on randomized complete block design
being 100% in efficiency in 32 replicated yield trials.

Analysis	Relative Efficiency (%)			
	Mean	Range		Standard deviation
RCBD 1/	100	-		-
MMCA 2/	114	98 -	173	15.2
PCA 3/	113	98 -	174	18.0
W-NNA 4/	122	80 -	223	36.2
I-NNA 5/	128	52 -	243	46.5
Waite NNA 6/	99*	69 -	175	31.0
MMA 7/	96	62 -	166	19.5
WMMCA 8/	111	97 -	171	16.1
WPM 9/	114	98 -	173	19.8

* Average of 22 trials.
1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.
7/ Moving mean analysis.
8/ Weighted moving mean covariance analysis.
9/ Weighted Papadakis Method.

c.1. <u>Level of environmental variability in 32 trials.</u>

The coefficient of variation obtained from completely randomized design (CRD) is considered a good measure of maximum environmental variability at a trial site. Each trial was analyzed using CRD in 32 trials and the resulting coefficient of variation was considered as the base value for comparison (Appendix Table 19). Based on the magnitude of CV values, the 32 trials were divided into three groups reflecting the level of environmetal variability, nine trials were in the low group (CV<10), 16 were in the medium group (CV>10 to CV<15) and seven trials were in the high group (CV>15).

c.1.1. <u>Efficiency of eight analyses in low variability trials.</u>

When the average efficiency of eight analyses in nine trials with low base coefficient of variation were evaluated, most were more efficient than RCBD (Table 25). The exception was Waite NNA (98%). When compared to other analyses the highest efficiency was recorded for I-NNA (129%) followed by W-NNA (125%). However, the results of I-NNA and W-NNA were more variable in efficiency on an individual trial basis. The average efficiency of PCA and WMMCA were similar (113%) and lower than MMCA (118%).

c.1.2. <u>Efficiency of analyses in 16 medium variability trials.</u>

Iterated nearest neighbour analysis (126%) was the most efficient of the eight analyses when the average of 16 trials are considered (Table 26). While MMA (95%) was the only analysis less efficient than RCBD. The average efficiency of MMCA, PCA and WPM were similar. When eight analyses were compared on an individual trial basis, it was found that MMCA, PCA, WMMCA and WPM were less variable in efficiency with the

Table 25. Relative efficiency based on the error mean squares
         of eight analyses when compared to randomized complete
         block design in nine replicated yield trials with a
         coefficient of variation less than and equal to 10 in
         completely randomized design.

Trial	RCBD 1/	MMCA 2/	PCA 3/	W-NNA 4/	I-NNA 5/	WAITE NNA 6/	MMA 7/	WMMCA 8/	WPM 9/
2	100	115	106	124	132	100	105	118	112
3	100	117	101	91	62	76	80	113	100
5	100	116	98	99	88	- 10/	81	101	98
6	100	101	99	100	101	79	94	99	100
14	100	173	154	223	243	-	166	171	164
16	100	116	127	119	115	86	113	112	122
23	100	102	107	123	136	116	78	101	112
26	100	125	124	134	167	122	115	102	120
30	100	101	99	109	121	105	90	101	105
Minimum RE 11/		101	98	91	62	76	78	99	98
Maximum RE		173	154	223	243	122	166	171	164
Average RE		**118**	**113**	**125**	**129**	**98**	**102**	**113**	**115**

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.
7/ Moving mean analysis.
8/ Weighted moving mean covariance analysis.
9/ Weighted Papadakis method.
10/ Unequal plots per range in a replication.
11/ Relative Efficiency = Error mean square (RCBD)*100/
                          Error mean square (analysis 2,3, .,or 9).

Table 26. Relative efficiency based on error mean squares of
eight analyses when compared to randomized complete
block design in 16 replicated yield trials with
coefficient of variation greater than 10 and less
than 15 in completely randomized design.

Trial	RCBD 1/	MMCA 2/	PCA 3/	W-NNA 4/	I-NNA 5/	WAITE NNA 6/	MMA 7/	WMMCA 8/	WPM 9/
7	100	135	133	175	190	- 10/	136	136	151
8	100	103	99	100	92	-	88	100	100
9	100	118	133	157	185	154	103	115	139
10	100	100	101	110	98	86	89	99	101
12	100	109	109	118	129	-	108	107	110
17	100	101	102	89	89	73	86	100	100
18	100	111	104	90	95	-	78	99	100
19	100	110	104	109	115	79	92	106	103
21	100	109	112	116	131	117	69	107	110
22	100	109	103	103	89	65	101	103	101
24	100	112	102	91	99	73	104	102	99
25	100	125	128	167	188	156	111	126	137
27	100	102	104	80	85	-	62	101	100
28	100	127	174	220	238	175	105	124	173
31	100	139	111	134	142	134	95	125	112
32	100	131	98	88	52	81	87	147	99

Minimum RE 11/		101	98	80	52	73	62	99	99
Maximum RE		139	174	220	238	175	136	147	173
Average RE		**115**	**114**	**122**	**126**	**108**	**95**	**112**	**115**

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.
7/ Moving mean analysis.
8/ Weighted moving mean covariance analysis.
9/ Weighted Papadakis method.
10/ Unequal plots per range in a replication.
11/ Relative Efficiency = Error mean square (RCBD)*100/
                          Error mean square (analysis 2,3,..,or 9).

greatest variability observed for the I-NNA.

c.1.3. Efficiency of analyses in seven high variability trials.

The average efficiency of eight analyses when compared to RCBD are presented in Table 27. Iterated nearest neighbour analysis appeared to be the most efficient followed by W-NNA and WPM with relative efficiencies of 128, 120 and 112%, respectively. Only the Waite NNA (74%) and MMA (92%) were less efficient than RCBD. When individual trials were considered the W-NNA and I-NNA showed the greatest range. However, in maximum efficiency I-NNA and W-NNA are far superior than other six analyses.

When the three levels of variability are considered in terms of the overall average efficiency, the four analyses MMCA, PCA, WMMCA and WPM tended to be more efficient in low and medium level of variability. Iterated nearest neighbour analysis and W-NNA were more efficient in all three levels of variability.

c.2 Efficiency of analyses based on number of entries.

The number of entries ranged from 18 to 90 in 32 trials (Appendix Table 4). Twenty one trials with entries ranging from 18 to 33 were identified as small size trials, while the remaining 11 trials with 48 to 90 entries were noted as large size trials.

c.2.1. Effectiveness of analyses in 21 yield trials with

18 to 33 entries.

Results pertaining to average efficiency of eight analyses with 33 or less entries are presented in Table 28. With the exception of Waite NNA (92%) and MMA (92%), all analyses were effective in reducing EMS when compared to RCBD. The efficiency of MMCA (112%), PCA (108%),

Table 27. Relative efficiency based on the error mean squares of
eight analyses when compared to randomized complete block
design in seven replicated yield trials with coefficient
of variation greater than 15 in completely randomized design.

Trial	RCBD 1/	MMCA 2/	PCA 3/	W-NNA 4/	I-NNA 5/	WAITE NNA 6/	MMA 7/	WMMCA 8/	WPM 9/
1	100	101	105	107	109	78	81	100	108
4	100	112	126	173	177	- 10/	89	110	134
11	100	118	118	138	161	-	110	113	125
13	100	106	119	127	154	-	96	102	115
15	100	98	100	93	87	69	86	97	101
20	100	105	100	109	112	78	95	105	103
29	100	105	99	92	99	70	90	103	99
Minimum	RE11/	98	99	92	87	69	81	97	99
Maximum	RE	118	126	173	177	78	110	113	134
Average	**RE**	**106**	**110**	**120**	**128**	**74**	**92**	**104**	**112**

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.
7/ Moving mean analysis.
8/ Weighted moving mean covariance analysis.
9/ Weighted Papadakis method.
10/ Unequal plots per range in a replication.
11/ Relative Efficiency = Error mean square (RCBD)*100/
                          Error mean square (analysis 2,3, .,or 9).

Table 28. Relative efficiency based on the error mean squares of eight analyses when compared to the randomized complete block design in 21 replicated yield trials with entries 18 to 33.

Trial	RCBD 1/	MMCA 2/	PCA 3/	W-NNA 4/	I-NNA 5/	WAITE NNA 6/	MMA 7/	WMMCA 8/	WPM 9/
1	100	101	105	107	109	78	81	100	108
2	100	115	106	124	132	100	105	118	112
3	100	117	101	91	62	76	80	113	100
4	100	112	126	173	177	- 10/	89	110	134
5	100	116	98	99	88	-	81	101	98
6	100	101	99	100	101	79	94	99	100
7	100	135	133	175	190	-	136	136	151
8	100	103	99	100	92	-	88	100	100
9	100	118	133	157	185	154	103	115	139
10	100	100	101	110	98	86	89	99	101
15	100	98	100	93	87	69	86	97	101
16	100	116	127	119	115	86	113	112	122
17	100	101	102	89	89	73	86	100	100
18	100	111	104	90	95	-	78	99	100
19	100	110	104	109	115	79	92	106	103
20	100	105	100	109	112	78	95	105	103
21	100	109	112	116	131	117	69	107	110
22	100	109	103	103	89	65	101	103	101
23	100	102	107	123	136	116	78	101	112
31	100	139	111	134	142	134	95	125	112
32	100	131	98	88	52	81	87	147	99
Minimum RE 11/		98	98	88	52	65	69	97	98
Maximum RE		139	133	175	190	154	136	147	151
Average RE		**112**	**108**	**115**	**114**	**92**	**92**	**109**	**110**

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.
7/ Moving mean analysis.
8/ Weighted moving mean covariance analysis.
9/ Weighted Papadakis method.
10/ Unequal plots per range in a replication.
11/ Relative Efficiency = Error mean square (RCBD)*100 / Error mean squa re (analysis 2,3, .,.or 9).

WMMCA (109%), and WPM (111%) were similar. Considerable variation was observed among analyses when the individual trials are compared. The range was noted for the I-NNA (52 to 190%). Highest average efficiency was displayed using I-NNA (115%) and W-NNA (114%).

c.2.2. Efficiencies of analyses in 11 trials with 48 to 90 entries.

The results of 11 yield trials with entries ranging from 48 to 90 are presented in Table 29. All the eight analyses appeared better than RCBD based on their average efficiency. In contrast to results shown in Table 29, all the eight analyses were much more efficient to RCBD in reducing error. The average efficiency of I-NNA (153%) and W-NNA (136%) were more pronounced when compared to MMCA (118%), PCA (121%), WMMCA 121%) and WPM (122%). With the exception of trials 24, 27, and 29, the eight analyses were consistently superior to RCBD in reducing EMS in large size trials. For example efficiency of I-NNA was 94% in above noted three trials as compare to 175% in the remaining eight trials. Weighted Papadakis method (122%) was superior to moving moving mean covariance analysis (114%).

c.3. Efficiencies of analyses in relation to effectiveness of blocking.

The effectiveness of blocking was determined based on significance of the F-ratio as determined in RCBD analysis. If the F-ratio was significant, blocks were considered effective in reducing EMS. In 24 of the 32 trials block effects were found to be significant (Appendix Table 20).

c.3.1. Efficiency of analyses in eight trials with

non-significant block effects.

The average efficiency of 10 trials are shown in Table 30. Six of

Table 29. Relative efficiency based on the error mean squares
of eight analyses when compared to the randomized
complete block design in 11 replicated yield trials with
entries 48 to 90.

Trial	RCBD	MMCA	PCA	W-NNA	I-NNA	WAITE	MMA	WMMCA	WPM
	1/	2/	3/	4/	5/	NNA 6/	7/	8/	9/
11	100	118	118	138	161	- 10/	110	113	125
12	100	109	109	118	129	-	108	107	110
13	100	106	119	127	154	-	96	102	115
14	100	173	154	223	243	-	166	171	164
24	100	112	102	91	99	73	104	102	99
25	100	125	128	167	188	156	111	126	137
26	100	125	124	134	167	122	115	102	120
27	100	102	104	80	85	-	62	101	100
28	100	127	174	220	238	175	105	124	173
29	100	105	99	92	99	70	90	103	99
30	100	101	99	109	121	105	90	101	105
Minimum RE 11/	101	99	80	85	70	62	101	99
Maximum RE	173	174	223	243	175	166	171	173
Average RE	**118**	**121**	**136**	**153**	**117**	**105**	**114**	**122**

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.
7/ Moving mean analysis.
8/ Weighted moving mean covariance analysis.
9/ Weighted Papadakis method.
10/ Unequal plots per range in a replication.
11/ Relative efficiency = Error mean square (RCBD)*100 /
                          Error mean square (analysis 2,3,..,or 9).

the analyses were more efficient than RCBD in controlling environmental variation. The exceptions were Waite NNA (96%) and MMA (93%). In trials 25 and 26, all eight analyses were highly efficient. For example, the average efficiency of I-NNA was 177% and that of MMCA 125% in these two trials.

In the remaining six trials (3, 5, 10, 15, 18, 22), coefficients of variations were similar for CRD and RCBD (Appendix Table 19). Based on the average of six trials the coefficient of variation was 11.7% in both CRD and RCBD. Moving mean covariance analysis (113%) was most efficient followed by W-NNA (111%). The average efficiency of PCA and WPM were the same (107%). Consistently, lower than 100% efficiency was recorded in these six trials for I-NNA and Waite NNA. Such patterns were also indicated for MMA with one exception in Trial 22.

c.3.2. Efficiency of analyses in 24 trials with significant

   block effects.

Although blocking in each of the 24 trials was effective, plot to plot variation was still present as indicated by more than 100% average efficiency of six of the eight analyses (Table 31). The two exceptions were Waite NNA (100%) and MMA (97%); however, this outcome did not prevail when individual trials were examined. Moving mean covariance analysis, PCA, W-NNA, I-NNA, WMMCA and WPM consistently showed a higher efficiency when compare to RCBD in 14 of the 24 trials (marked with * in Table 31). The average efficiency of I-NNA in 14 trials (marked with * in Table 31) was 160% compared to 96% in the remaining trials. Similarly the efficiency of MMCA was 121% in 14 trials (marked with * in Table 32) compared to 106% in the remaining 10 trials.

Table 30. Relative efficiency based on error mean squares of eight
analyses when compared to randomized complete block design
in eight replicated yield trials when blocking was
ineffective.

Trial	RCBD	MMCA	PCA	W-NNA	I-NNA	WAITE	MMA	WMMCA	WPM
	1/	2/	3/	4/	5/	NNA 6/	7/	8/	9/
3	100	117	101	91	62	76	80	113	100
5	100	116	98	99	88	- 10/	81	101	98
10	100	100	101	110	98	86	89	99	101
15	100	98	100	93	87	69	86	97	101
18	100	111	104	90	95	-	78	99	100
22	100	109	103	103	89	65	101	103	101
25	100	125	128	167	188	156	111	126	137
26	100	125	124	134	167	122	115	102	120
Minimum RE 11/		98	98	80	62	65	78	97	98
Maximum RE		125	128	167	188	156	115	126	137
Average RE		**113**	**107**	**111**	**109**	**96**	**93**	**105**	**107**

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.
7/ Moving mean analysis.
8/ Weighted moving mean covariance analysis.
9/ Weighted Papadakis method.
10/ Unequal plots per range in a replication.
11/ Relative Efficiency = Error mean square (RCBD)*100 /
                                    Error mean square (analysis 2,3, .,or 9)

Table 31. Relative efficiency based on the error mean squares
of eight analyses when compared to randomized complete
block design in 24 replicated yield trials when block
effects were significant.

Trial	RCBD 1/	MMCA 2/	PCA 3/	W-NNA 4/	I-NNA 5/	WAITE NNA 6/	MMA 7/	WMMCA 8/	WPM 9/
1	100	101	105	107	109	78	81	100	108
2*	100	115	106	124	132	100	105	118	112
4*	100	112	126	173	177	- 10/	89	110	134
6	100	101	99	100	101	79	94	99	100
7*	100	135	133	175	190	-	136	136	151
8	100	103	99	100	92	-	88	100	100
9*	100	118	133	157	185	154	103	115	139
11*	100	118	118	138	161	-	110	113	125
12*	100	109	109	118	129	-	108	107	110
13*	100	106	119	127	154	-	96	102	115
14*	100	173	154	223	243	-	166	171	164
16*	100	116	127	119	115	86	113	112	122
17	100	101	102	89	89	73	86	100	100
19*	100	110	104	109	115	79	92	106	103
20	100	105	100	109	112	78	95	105	103
21*	100	109	112	116	131	117	69	107	110
23*	100	102	107	123	136	116	78	101	112
24	100	112	102	91	99	73	104	102	99
27	100	102	104	80	85	-	62	101	100
28*	100	127	174	220	238	175	105	124	173
29	100	105	99	92	99	70	90	103	99
30	100	101	99	109	121	105	90	101	105
31*	100	139	111	134	142	134	95	125	112
32	100	131	98	88	52	81	87	147	99

Minimum RE10/		101	99	76	52	70	69	99	99
Maximum RE		173	174	223	243	175	166	171	173
Average RE		**115**	**114**	**126**	**134**	**100**	**97**	**113**	**116**

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.
7/ Moving mean analysis.
8/ Weighted moving mean covariance analysis.
9/ Weighted Papadakis method.
10/ Unequal plots per range in a replication.
11/ Relative Efficiency = Error mean square (RCBD)*100/
                                 Error mean square (analysis 2,.,or 9).

c.4. <u>Efficiency of analyses in relation to correlation of</u>

   <u>of adjacent plot residuals.</u>

Thirty two trials were categorized into low, medium and high

groups based on the values of correlation of adjacent plot residuals.

Correlation of adjacent plot residuals (henceforth noted as r) was

determined from the plot residual and mean of its adjacent two plot

residuals. The r values for 32 trials are given in Appendix Table 20.

c.4.1. <u>Efficiency of analyses in seven trials with lower r values.</u>

Trials with non-significant r values were considered together in

this group. On the basis of average efficiency, none of the eight

analyses showed more than a 5% advantage over RCBD (Table 32). The only

exception was MMCA (107%). The average efficiencies of W-NNA (98%), I-

NNA (89%), Waite NNA (75%) and MMA (87%) were less than 100%. Also,

with few exceptions, these analyses were consistently less precise when

compared to RCBD. Such low efficiencies were not found for MMCA (107%),

PCA (101%), WMMCA (102%) and WPM (100%).

There was little difference in RCBD and CRD at low r values as

evidenced by a comparison of the coefficients of variation for CRD and

RCBD (Appendix Table 19). The average coefficient of variation in six

trials with low r was 11.4% for CRD and 11.1% for RCBD. The regression

coefficient was significantly greater than zero in two trials in MMCA

and one in PCA (marked with * in Table 33). With the exception of

trial 18, the value of W (weighting factor), in W-NNA was less than 0.5

in all trials (Appendix Table 21).

c.4.2. <u>Efficiency of analyses with medium r values.</u>

Nine trials with significant correlation of adjacent plot

residuals, but with r<0.4 were placed into the medium group. With the increase in r, there was also an increase in efficiency of analyses judged from maximum and average efficiency of eight analyses shown in Table 33. Moving mean covariance analysis (111%) and weighted moving mean covariance analysis (108%) were more efficient compared to recently proposed analyses such as W-NNA (102%), I-NNA (104%) and Waite NNA (84%). Also MMCA and WMMCA showed higher efficiencies than Papadakis methods such as PCA (105%) and WPM (104%).

Moving mean covariance analysis appeared superior to all other analyses at low and medium levels of adjacent plot correlation. The results were most variable for I-NNA followed by Waite NNA, MMA and W-NNA. On the other hand results were more consistent for MMCA from trial to trial.

The regression coefficient was significantly greater than zero in four of the nine trials in PCA and MMCA (trials marked with * in Table 33). In WMMCA and WPM, the regression coefficient was significantly greater than zero in two trials. The weighting factor (W) in W-NNA was less than 0.5 in all the trials (Appendix Table 21).

c.4.3. Efficiency of eight analyses with r≥0.4.

In 16 trials with correlation of adjacent plot residuals ≥ 0.4, the efficiency of eight analyses was greater (Table 34). This is apparent from the comparison of results shown in Tables 32, 33 and 34. All the eight analyses surpassed RCBD in average efficiencies. Two of the recently proposed analyses; W-NNA (144%) and I-NNA (158%) were far higher in efficiency compared to previously proposed analyses such as MMCA (119%), PCA (122%), MMA (102%), WMMCA (117%) and WPM (126%).

Table 32. Relative efficiency based on the error mean squares of
eight analyses when compared to the randomized complete
block design in seven replicated yield trials when
correlation of adjacent plot residuals are non significant.

Trial	RCBD 1/	MMCA 2/	PCA 3/	W-NNA 4/	I-NNA 5/	WAITE NNA6/	MMA 7/	WMMCA 8/	WPM 9/
3	100	117	101	91	62	76	80	113	100
5	100	116	98	99	88	-10/	81	101	98
6	100	101	99	100	101	79	94	99	100
10	100	100	101	111	98	86	89	100	101
15	100	98	100	93	87	69	86	97	101
18	100	111*	104*	90	95	-	78	99	100
22	100	109*	103	103	89	65	101	103	101
Minimum RE 11/		98	97	90	62	65	78	97	98
Maximum RE		117	104	111	101	86	101	113	101
Average RE		**107**	**101**	**98**	**89**	**75**	**87**	**102**	**100**

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.
7/ Moving mean analysis.
8/ Weighted moving mean covariance analysis.
9/ Weighted Papadakis method.
10/ Unequal plots per range in a replication.
11/ Relative efficiency = Error mean square (RCBD)*100/
                              Error mean square (analysis 2,3,..or 9).
* Trials with regression coefficient significantly greater than zero.
N= Number of plots in a trial.

Table 33. Relative efficiency based on the error mean squares of
eight analyses when compared to the randomized complete
block design in nine replicated yield trials when
correlation of adjacent plot residuals are less than
0.4 but significant.

Trial	RCBD 1/	MMCA 2/	PCA 3/	W-NNA 4/	I-NNA 5/	WAITE NNA 6/	MMA 7/	WMMCA 8/	WPM 9/
8	100	103	99	100	92	-10/	88	100	100
12	100	109*	109*	118	129	-	108	107*	110*
17	100	101	102	89	89	73	86	100	100
19	100	110*	104*	109	115	79	92	106*	103
20	100	105	100	109	112	78	95	105	103
24	100	112*	102	91	99	73	104	102	99
26	100	125*	124*	134	167	122	115	102	120*
27	100	102	104*	80	85	-	62	101	100
32	100	131	98	88	52	81	87	147	99
Minimum RE11/		101	98	80	52	59	62	100	99
Maximum RE		131	124	134	167	122	115	147	120
Average		**111**	**105**	**102**	**104**	**84**	**93**	**108**	**104**

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.
7/ Moving mean analysis.
8/ Weighted moving mean covariance analysis.
9/ Weighted Papadakis method.
10/ Unequal plots per range in a replication.
11/ Relative Efficiency = Error mean square (RCBD)*100 /
                          Error mean square (analysis 2,3, .,or 9)
* Trials with regression coefficient significantly greater than zero.
N= Number of plots in a trial.

Table 34. Relative efficiency based on the error mean squares
of eight analyses when compared to randomized complete block
design in 16 replicated yield trials when correlation of
adjacent plot residuals is greater than and equal 0.4.

Trial	RCBD 1/	MMCA 2/	PCA 3/	W-NNA 4/	I-NNA 5/	WAITE NNA 6/	MMA 7/	WMMCA 8/	WPM 9/
1	100	101	105*	107	109	78	81	100	108*
2	100	115*	106*	124	132	100	105	118*	112*
4	100	112*	126*	173	177	- 10/	89	110*	134*
7	100	135*	133*	175	190	-	136	136*	151*
9	100	118*	133*	157	185	154	103	115*	139*
11	100	118*	118*	138	161	-	110	113*	125*
13	100	106*	119*	127	154	-	96	102	115*
14	100	173*	154*	223	243	-	166	171*	164*
16	100	116	127*	119	115	86	113	112*	122*
21	100	109*	112*	116	131	117	69	107*	110
23	100	102	107*	123	136	116	78	101	112*
25	100	125*	128*	167	188	156	111	126*	137*
28	100	127*	174*	220	238	175	105	124*	173*
29	100	105*	99	92	99	70	90	103	99
30	100	101	99	109	121	105	90	101	105
31	100	139*	111*	134	142	134	95	125*	112*
Minimum RE 11/		101	99	92	99	70	69	100	99
Maximum RE		173	174	223	243	175	166	171	173
Average RE		**119**	**122**	**144**	**158**	**117**	**102**	**117**	**126**

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.
7/ Moving mean analysis.
8/ Weighted moving mean covariance analysis.
9/ Weighted Papadakis method.
10/ Unequal plots per range in a replication.
11/ Relative Efficiency = Error mean square (RCBD)*100 /
                          Error mean square (analysis 2,3,.,or 9).
* Trials with regression coefficient significantly greater than zero.
N= Number of plots in a trial.

Within the high r group, PCA and WPM were superior to MMCA, WMMCD and
MMA.

In 16 trials with r $\geqslant$ 0.4 shown in Table 34, the association of
regression coefficient with r was more obvious in MMCA, PCA, WMMCA and
WPM. In 12 of the 16 trials the regression coefficient (b) was
significantly greater than zero in MMCA with an average efficiency of
123% as compared to 105% in four other trials with non-significant
positive b values. In all of the trials MMCA was more efficient than
RCBD. The number of plots for a moving mean covariable showing greatest
reduction in error varied from two to 12 plots (Appendix Table 22).

The value of b in PCA was significantly greater than zero in 14
of the 16 trials while b was positive in the two remaining trials (29,
30). With the exception of Trials 29 and 30, PCA was invariably
superior to RCBD.

With the exception of of Trial 16 (W=0.37) and 23 (w=0.39), the
value of W was greater than or equal to 0.5 (Appendix Table 21). The
efficiency of W-NNA was greater than RCBD ranging from 107 to 223%. The
exception was Trial 29 (92%). Recently proposed I-NNA was the most
efficient (158%) and superior to all other analyses. Less than 100%
efficiency was recorded only in Trial 29 (99%) for I-NNA.

The efficiency of Waite NNA was higher than RCBD in seven trials
and less in three when compared in trials with r $\geqslant$ 0.4 (Table 34).
However, Waite NNA was more efficient than RCBD in only one of the 16
trials with low (Table 32) and medium r values (Table 33).

Moving mean analysis was slightly more efficient than RCBD in only
one trial when r was nonsignificant (Table 32) and three trials when r

was medium (Table 33). Nevertheless with r $\geqslant$ 0.4, MMA was more than 100% efficient in half of the 16 trials (Table 34). In most of the trials where MMA was more efficient, when the r value was greater than 0.5. The number of plots included in a moving mean showing greatest resuction in error was eight in most of the trials (Appendix Table 22).

In 11 of 16 trials with r $\geqslant$ 0.4, the regression coefficient was significantly greater than zero in WMMCA (Table 34) while b was positive in remaining five trials. The average efficiency was 123% in trials with significant b value as compared to 101% in the remaining five trials.

Less than 100% efficiency was recorded for WPM in one of the 16 trials (Table 34). The b value in WPM was significantly greater than zero in 13 trials with average efficiency of 131% as compared to 105% in the remaining three trials.

c.5 Efficiency of eight analyses at three locations in Oregon.

c.5.1. Hyslop agronomy and Holmes Farms.

Seven of the 32 trials were grown at Hyslop agronomy and Holmes Farms near Corvallis and results are shown in Table 35. The average coefficient of variation in CRD was 11.17% (Table 35). Iterated nearest neighbour analysis (139%) was the most efficient followed by W-NNA (136%). However, both of these analyses were most variable from trial to trial. The efficiencies of MMCA (121%), PCA (122%), WMMCA (117%) and WPM (124%) were consistent. But in terms of maximum efficiency, PCA and WPM were superior to MMCA and WMMCA.

Sherman Station Trials

This was the most variable of the three sites. The average

coefficient of variation in CRD was 16.93% (Table 35). Highest efficiency of 131% was recorded for I-NNA at Sherman Station trials (Table 35). In four of the eleven trials W-NNA and I-NNA were less efficient to RCBD. Moving mean covariance analysis (111%) was better than WMMCA (105%). Analyses I-NNA and W-NNA were far superior than other six analyses. In all trials MMCA was superior to RCBD. Also the regression coefficient was significantly greater than zero in eight trials while significant b values in PCA, WMMCA and WPM were found in seven, five and six of the 11 trials, respectively.

Rugg Farm Trials.

The average coefficient of variation in CRD was 11.48% of 14 trials established at Rugg Farm (Table 35). The differences in average efficiency of four analyses; MMCA (114%), PCA (108%), WMMCA (112%) and WPM (110%) with the I-NNA (119%) and W-NNA (117%) were not as profound as observed at Holmes and Hyslop Agronomy Farms and Sherman Station. Iterated nearest neighbour analysis was less efficient than RCBD in six of the 14 trials, while MMCA was only less efficient in one trial.

Table 35. Average relative efficiency and range based on randomized complete block design being 100% in efficiency in eight analyses at three experimental sites in Oregon.

Analyses	Hyslop and Holmes Farms		Sherman Station		Rugg Farm	
	Mean	Range	Mean	Range	Mean	Range
MMCA	121 1/	103-139	111 2/	101-125	114 3/	98-173
PCA	122	99-174	112	99-133	108	98-154
W-NNA	136	91-220	120	89-173	117	88-223
I-NNA	139	62-238	131	89-185	119	52-243
Waite NNA	118	76-175	89	70-154	97	69-156
MMA	98	69-136	97	81-115	95	62-166
WMMCA	117	100-136	105	100-115	112	97-171
WPM	124	100-173	113	99-139	110	98-164
Average Base CV	11.17		16.93		11.48	

1/ Mean of seven trials.
2/ Mean of 11 trials.
3/ Mean of 14 trials.

DISCUSSION

The field is a plant breeders laboratory. From the point of view of its physical environment, an ideal field would be one that is completely uniform. However, in reality a soil is never homogeneous. Heterogeneity of the soil and other abiotic factors frequently confuse the breeder in identifying genetically superior progeny. Methods of estimating the magnitude of experimental error which result from systematic gradients in the field are receiving renewed interest in field crop research. Studies employing uniformity trials have clearly shown that neighboring plots are often positively correlated with common tendencies or trends in their productivity. If such associations can be recognized and accounted for by an appropriate analysis, then breeders could attach a greater degree of confidence in their estimates of the nature of gene action in the F1 generation and selection in segregating populations, F5 genetically relatively uniform lines grown in unreplicated yield trials, and advanced selections planted in replicated yield trials.

Since a breeder of self pollinated species is restricted to using the additive portion of the total genetic variation, estimates of the nature of gene action for specific traits will provide some information of whether early generation selection will be effective. Such estimates are frequently based on evaluating the performance of the F1 generation using a biometrical model like combining ability. When employing the commonly used pedigree system of handling segregating populations, the breeder selects plants based on their phenotypic expression when grown under space planted conditions starting in the F2 through F4

generation. Effective selection for qualitatively inherited traits such as disease resistance, height, maturity and grain color can be achieved in these early generations as few genes are involved with little environmental influence. However, a quantitative trait, such as grain yield, is controlled by many genes with small, cumulative effects with the genotypic expression being masked by a large environmental influence. Thus, to increase the probability of finding a desirable gene combination for grain yield it is necessary to carry a considerable number of progeny rows until a reasonable level of homozygosity is reached in the F5 generation.

Since the number of lines by the F5 is large and seed supply per line limited, it is not generally possible to use replications to estimate experimental error. Frequently check plots are used to discriminate among large numbers of F5 lines, but this system does not provide an estimate of the experimental error. When sufficient quantities of seed are available, advanced selections are tested in replicated yield trials, frequently using a randomized complete block design. The application of randomized complete block design is useful provided the blocks match soil gradients in the field. However, often information for grouping of plots into blocks is not available which makes it difficult to insure that the experimental area within blocks will be uniform. Where there is considerable variation within blocks, such experiments returned little useful information because of the difficulties in obtaining a valid statistical estimate of the environmental variability. As pointed out by Fowler and Heyne (1955), present techniques employed to determine yield in cereals are not

refined enough to detect yield differences if they are of the magnitue of 10% or less. Since future wheat cultivars may reflect only small incremental increases in grain yield due to present yield levels, breeders will have to employ improved analyses to isolate the more productive progeny.

In the past few years there has been a resurgence in developing analyses to remove systematic variation in unreplicated and replicated yield trials. Hopefully these analyses can provide more flexibility in controlling the continuous abiotic gradients in the field and thereby increasing the chances of identifying genetically superior progeny. In this study several of these analyses were also used to estimate the nature of the genetic variation associated with two traits in the F1 and F2 generations.

Results of this investigation will be discussed as they relate to: a) evaluation of early spaced planted F1 and solid seeded F2 populations, b) evaluation of F5 lines in unreplicated yield trials, and c) evaluation of advanced selections in replicated yield trials. Analyses in these three phases of a breeding program were assessed primarily on the basis of estimates of the error mean square. Error mean square represents the variability that remains among the experimental units after other sources of variation have been removed.

a) Evaluation of space planted F1 and soild seeded F2 populations.

Parents were selected based on differences in their pedigree and other morphological components of yield. In order to study the amount of variability in F1 and F2 populations, plant height a qualitative inherited trait and the quantitatively inherited trait grain yield were

measured.

The following basic analyses were compared with randomized complete block design to account for the impact of plot to plot variation in the field on genotypic expressions of F1 and F2 populations: 1) moving mean covariance analysis, 2) productivity covariance analysis, 3) weighted nearest neighbour analysis, 4) iterated nearest neighbour analysis, and 5) Waite nearest neighbour analysis.

Results in this section showed that none of the five analyses provided a better estimate of environmental variation for F1 and F2 populations when compared to randomized complete block design for plant height. Lower coefficients of variation for plant height were obtained compared to grain yield in all three trials at both sites. This might be expected as plant height is highly heritable trait controlled by few genes, while heritability of grain yield is low because grain yield is controlled by many genes with small effects.

There was no variability at Hyslop Agronomy Farm (correlation of adjacent plot residual =-0.19). Consequently, Waite nearest neighbour analysis, iterated nearest neighbour analysis and weighted nearest neighbour analysis were less precise than randomized complete block design in the evaluation of F2 populations.

Control in error was more effective for grain yield in F1 (1984-85) and F2 populations (1985-86) grown at Rugg Farm since some variability was present indicated by the correlation of adjacent plot residual (r=0.21 for F1 and r=0.26 for F2 populations). In these two trials the weighted nearest neighbour analysis, iterated nearest

neighbour analysis and moving mean covariance analysis appeared more efficient than randomized complete block design.

The results do not indicate the general utility of the five analyses compared to randomized complete block design for early generation material grown under the environments observed at the Hyslop Agronomy Farm and at the Rugg site. A possible explanation for low to marginal efficiency for five analyses is that substantial gradients were not present in the trials sites. Recently, Wynn-Williams et al. (1984) could not find advantage of Waite nearest neighbour over randomized complete block design in the evaluation of a 19 cultivar barley trial planted at two locations. The coefficient of variation for Waite NNA was 5.5% compared to 5.0% for randomized complete block design at Swannanoa site. The only possible explanation of such results according to them was the uniformity of the experimental sites.

There is a statistical explanation of low efficiency observed for Waite nearest neighbour analysis, iterated nearest neighbour analysis and weighted nearest neighbour analysis. In this study two plots along the longer edge of the experimental area were used as neighbours in iterated nearest neighbour analysis, weighted nearest neighbour analysis and Waite nearest neighbour analysis, so a cultivar with n replicates, has $2n$ neighbors. The variance of a treatment mean in these analyses is therefore $S^2/n + S^2/2n$ (S^2 = variance) as indicated by Schwarzbach (1985). Whereas, in case of randomized complete block design the variance of a treatment mean is S^2/n. Consequently, if there are no gradients in the experimental site, the above noted three analyses would be less precise than randomized complete block design

which was observed for plant height in all three trials and grain yield
for F2 populations at Rugg Farm.

The lower efficiency of productivity covariance analysis when
compared to randomized complete block design in the evaluation of F1
populations at Rugg Farm (1984-85) for both plant height and grain
yield was due to loss of one degree of freedom from error which was
used in the estimation of regression coefficient. In analyses using
covariance analysis such as productivity covariance analysis and moving
mean covariance analysis, a chance of lower precision than randomized
complete block design is only due to loss of one degree of freedom. In
large cultivar trial this will not be a problem and where no soil
variation exists, the efficiency of moving mean covariance analysis and
productivity covariance analysis will be equal to randomized complete
block design.

The results suggested that the analyses evaluated in this section
are not a universal substitute for a randomized complete block design.
This issue will be further examined in section c where a comparison of
same analyses is made using 32 replicated yield trials and situations
for the applications of the analyses are discussed.

Combining Ability Analysis.

Knowledge of the nature of inheritance and the manner in which
parents can transmit favorable alleles for desired traits to their
progeny enhances the breeders ability to choose genetically superior
parents and select within segregating populations. Since the phenotype
of the individual for plant height is highly correlated with their
genetic constitution, reliable selection can be performed on the

phenotypic expression of individuals in segregating populations. However, in this study significant specific combining ability effects were indicated both in F1 and F2 generation that might complicate selection in early generations. The effect of analyses on the magnitude of general and specific combining ability was marginal since there were little difference in the efficiency of deigns for controlling environmental variation for plant height when compared to randomized complete block design.

The improvement of grain yield is complicated due to large masking effect of abiotic environmental factors on the expression of cumulative action of minor genes controlling inheritance of grain yield. Thus if a breeder had better means of identifying those parents with the greatest genetic potential, the results of plant improvement efforts will be more productive. Estimate of genetic effects using combining ability analysis are usually obtained in F1 space planted conditions. In this study both general and specific combining ability effects were significant for grain yield in randomized complete block design and other analyses for F1 populations grown at Rugg Farm, however, general combining ability effects were of higher magnitude in all analyses. This indicates that of the total genetic variation, a higher percentage of the genes responded in an additive manner.

Selected genotypes under space planted conditions may not perform well under high competitive conditions of commercial production. In F2 large quantity of seed is available which permit solid seeding and can provide additional information on the predominant type of gene action involved. The absence of significant specific combining ability effects

for F2 populations grown at two sites indicated that non-additive genetic effects were less important. The results were same for the six analyses used. Since large effect of soil gradients was not present in three trials, results do not provide a clear pattern as to the effect of five analyses on portioning the component of genetic variation.

b. Evaluation of F5 lines in unreplicated yield trials.

To investigate the possibility of abiotic gradients in the evaluation of F5 lines, five analyses were evaluated. These included: 1) augmented design, 2) moving mean analysis, 3) moving mean covariance analysis, 4) weighted moving mean covariance analysis, and 5) weighted nearest neighbour analysis.

It was pointed out in section 'a' that the differences in the analyses were not evident due to the absence of gradients in the trial sites. However, at three sites used in this section the patterns of variation were different from one site to the other which affected the efficiency of the five analyses.

Results obtained for five analyses applied to materials grown at three sites are provided and the advantages and problems of their application discussed.

Hyslop Agronomy Farm.

Improved efficiency of five analyses when compared to completely randomized design was modest ranging from 111% in augmented design to 122% in moving mean covariance analysis. Efficiency of weighted nearest neighbour analysis (72%) was less than completely randomized design. Unadjusted F5 lines yielding higher than the trial mean came randomly from the experimental area. In a recent study Besag and Kempton (1986)

found that the 10% higher yielding lines were from one part of the field which was highly fertile. Comparison of their results and those obtained in this study suggest that a plausible explanation of low to modest results is the limited variation at the trial site. This conclusion is also supported by the absence of significant block effects in augmented design and the weighting factor being zero in weighted nearest neighbour analysis. The magnitude of weighting factor indicates the magnitude of soil gradients in the experimental area (Schwarzbach and Betzwar, 1985). Results from this study indicate that weighted nearest neighbour analysis had no value at sites of low variability, while moving mean covariance analysis appeared more useful.

Sherman Station.

High yielding F5 lines at Sherman site were more concentrated in a strip stretching diagonally in the experimental area. This pattern affected the efficiency of five analyses. Gradient in the experimental site resulted heterogeneous blocks, thus augmented design was least efficient (82%).

The other significant outcome of the trial at Sherman Station was that the moving mean analysis, moving mean covariance analysis, and weighted moving mean covariance analysis were effective, but not to the same degree as the recently proposed weighted nearest neighbour analysis (536%). Schwarzbach and Betzwar (1985) explained that higher efficiency of W-NNA in their study could be due to additional information coming from the non-adjusted yields, especially in case of nonlinear trends within the space between two standard cultivars.

Rugg Farm.

At the time of planting no obvious gradients were present at Rugg Farm. The high yielding unadjusted F5 lines were from various positions in the experimental area. However, there was a tendency of more high yielding lines being concentrated in some blocks. Therefore, the application of the augmented design indicated significant block effects and demonstrated an efficiency of 212%. Also the correlation of F5 lines with average of checks was significant, but low (r=0.24). Such correlation in trials at Hyslop Agronomy Farm and Sherman Station was almost zero which indicate that F5 lines performance matched check performance at Rugg Farm. These results at the Rugg Farm provided evidence that the usefulness of augmented designs increases when field variation matches the blocks. Moving mean covariance analysis also showed similar efficiency as augmented design. This was expected since the neighboring plots constituting moving means were in the same direction as the blocks. The efficiency of weighted nearest neighbour analysis was equal to completely randomized design because it failed to recognize the kind of soil gradients present at Rugg Farm.

Relative merits of five analyses.

The results from the unreplicated F5 yield trial identified the practical use of the five analyses when employed under different environmental conditions. The utility of augmented designs is indicated only when field variation can be removed effectively by blocks. There is an abundant evidence in the literature that the soil is a very complex manifestation of nature. It is difficult to form homogenous blocks in the field. Also the random allocation of checks in a block

may not provide a good productivity index. For example if all checks lie on one side of the block then there is a danger that the average of checks may not represent the variability of a block.

The main advantage of the augmented design is that randomization of F5 lines is not required thus permitting a visual comparison of agronomic characteristics of F5 lines within a family. Since all the F5 lines need not be harvested, augmented design would be useful for error control in situations where undesirable entries are discarded before harvest.

The most important outcome of this study was that the moving mean analysis, moving mean covariance analysis and weighted moving mean covariance analysis were effective in reducing the errors at all sites and the efficiency varied depending upon the variability of the trial site. At two of the three sites, moving mean covariance analysis was superior to moving mean analysis and weighted moving mean covariance analysis. The main problem in the application of the moving mean analysis is that it is assumed that there is a high association of adjacent plot yields which might not be true in all experimental conditions. Moving mean covariance analysis is more flexible in which moving means are used as the independent covariate. The regression of the dependent variable on the independent variable is linear so changes in yield are represented by the linear regression coefficient. Where there is no association between the yield of moving mean with the plot yields, the covariance method will give a regression coefficient of zero and over adjustment will be avoided. However, in this study, an increase in error using the moving mean analysis was not observed.

The application of a moving mean covariance analysis was not cost effective since several analysis were necessary to find an appropriate moving mean covariable. A weighted moving mean was constructed involving eight adjacent plots, with more weight put on nearest plots. The weighted moving mean covariance analysis was less efficient when compared to the moving mean covariance analysis at Hyslop Agronomy and Rugg Farms. However, at all three sites, the ranking of the top yielding F5 lines were almost the same in both the moving mean covariance analysis and the weighted moving mean covariance analysis. In projects with limited computing facilities, the weighted moving mean covarinace analysis could be satisfactory alternative to the moving mean covariance analysis.

The disadvantages of moving mean analysis, moving mean covariance analysis and weighted moving mean covariance analysis are that a complete randomization of F5 lines within replicates are required thus making it difficult to visually compare agronomic characteristics of lines from the same family. It requires that all the plots be harvested. Missing plots could also be a major problem.

The main disadvantages of weighted nearest neighbour analysis appeared that it was only useful on highly variable trial site which the breeder should avoid in the first place. Also it required randomization of F5 lines.

The results indicate that either the moving mean covariance analysis or weighted moving mean covariance analysis can be more useful at Hyslop Agronomy and Rugg Farms compared to other analyses. At high variability sites such as Sherman Station, the weighted nearest

neighbour analysis appeared most appropriate.

Genotype x Location Interaction (G x L).

The genotype x location mean square represents the failure of the differences between genotypes to remain constant in terms of their ranking from location to location. In this study such evidence was observed from performance of check cultivars and F5 lines over locations. At Hyslop Agronomy Farm, Stephens was better than Malcolm while reverse was true at the Rugg Farm. There were several F5 lines (for example 212 and 191) which were high yielding at three locations, however, there were also lines such as 4, 13 and 228 which were among top yielding at one of three locations.

Mareck (1981) found that the reduction in genotype x location mean square due to adjustment of grain yield by moving means represented a reduction in the error component. In the present study the reduction in error and reduction in genotype x location mean square with the application of moving mean analysis, moving mean covariance analysis and weighted moving mean covariance analysis were observed. However, the pattern in reduction in G x E interaction did not match the reduction in error observed for each analysis at a location. Also the results for augmented design and weighted nearest neighbour analysis did not provide a clear pattern as to the effect of analyses on genotype x environment interactions partly because the reduction in error was not consistent from trial to trial. It is not necessary that by removing the effect of soil gradients from F5 line performance, that a corresponding decrease in G x E would result.

c) Evaluation of advanced selections in replicated yield trials.

Thirty two yield trials were grown over three locations representing a wide range of agro-climatic conditions covering a four year period. The results were analyzed with analyses used in previous sections with the exception of augmented design. A weighted version of moving residual mean (noted as weighted Papadakis Method) was also included in this phase of study.

The results obtained indicated that the recently proposed nearest neighbour analyses such as iterated nearest neighbour analysis and weighted nearest neighbour analysis are more efficient than other six analyses in reducing error when compared to randomized complete block design. However, iterated nearest neighbour analysis (52 - 243%) and the weighted nearest neighbour analysis (80 - 223%) were the most variable from trial to trial when compared to the moving mean covariance analysis (98 -176%), productivity covariance analysis (98 - 174%), weighted moving mean covariance analysis (97 - 171%) and weighted Papadakis method (98 173%) in reducing error.

To provide some information as to which one of the eight analyses might be more useful, the following factors were considered: a) base coefficient of variation, b) number of entries per trial, c) effectiveness of blocking, and d) correlation of adjacent plot residuals.

Base Coefficient of variation.

The coefficient of variation indicates the degree of precision with which the cultivars can be compared and is a good index of the reliability of the experimental results. In completely randomized

design, only the cultivar effects are removed and the remaining variation constitutes a maximum estimate of the environmental variability in a given trial.

In this study iterated nearest neighbour analysis was better than other analyses at low (CV< 10), medium (CV>10 to <15) and high (CV>15) levels of coefficients of variation. However, the results for iterated nearest neighbour analysis and other seven analyses were variable from trial to trial at all three levels of variation. These results indicated that the high coefficient of variation may be due to unknown causes other than the variation due to soil gradients.

Number of entries per trial.

In 11 trials comprising of 48 to 90 entries, efficiency of iterated nearest neighbour analysis was 153% as compared to 111% when compared to the remaining 21 trials with 18 to 33 entries. Similar pattern in relative increase in efficiency was found for the seven other analyses. These results provide evidence that randomized complete block design would become less satisfactory as the number of entries in the experiment increased. In the large cultivar trials there is a greater chance for more variability within blocks than between blocks.

Effectiveness of Blocking.

In a randomized complete block design soil variation is removed by grouping the treatments into blocks. Therefore, the variation among plots within each group is minimal in comparison to that among blocks. Variability between blocks is arithmetically eliminated from the estimate of the experimental error in the analysis of randomized complete block design. However, if blocks are not formed without some

knowledge of the experimental site, the soil variability may be greater within the blocks instead of between them. This was the situation in two of the eight trials (Trial 25 and 26) where block effects were not significant. In these two trials, efficiency of all eight analyses was much higher than in the other six trials. For example, the efficiency of iterated nearest neighbour analysis was 177% in these two trials while being only 86% in the other six trials.

It is a requirement for the correct application of randomized complete block design that any components of variation which are not eliminated by the design shall be normally and independently distributed to justify a test of significance. Neighbouring plots tend to be positively correlated as indicated in earlier studies of Riddle and Baker (1944), Barker and Briggs (1950), and Hoyle and Baker (1961). This disturbs the theoretical basis of randomized complete block design and in particular effects the estimate of error and test of significance. Through randomizing the plots the disturbance due to the correlation of neighbouring plots can be reduced, so that yields can be treated as if their errors were uncorrelated. Randomization, however, will ordinarily remove the bias, but not the unequal impact of soil gradients on cultivar performance. Even if blocks were formed effectively intra-block variation may be larger than the inter-block variation. Such evidence was obtained in the present study. The blocking was effective in 24 trials with the average efficiency of iterated nearest neighbour analysis being 134% which indicated that plot to plot variation was present. However, there were two distinct patterns in the results of 24 trials. With the exception of moving mean

analysis and Waite nearest neighbour analysis, all the analyses were consistently better than randomized complete block design in 14 trials. For example the efficiency of iterated nearest neighbour analysis was 160% in 14 trials and only 96% in the remaining 10 trials. The major part of the field variation was taken into account by the blocks in 10 trials while the reverse was true for the remaining 14 trials.

The results of 10 trials where randomized complete block design was effective also indicated that if blocks are used carefully, there is no need of a sophisticated design. But the question remains as to how to be sure that the blocks will be effective in anticipating soil variation which is unpredictable.

Correlation of adjacent plot residual (r).

In all the eight analyses it is assumed that neighbouring plot yields are correlated due to common impact of gradients. Coefficient of variation, size of the trials and effectiveness of blocking did not provide direct evidence for this assumption. In a previous report (Riddle and Baker, 1944) established correlation between fertility levels and residuals. The correlation of adjacent plot residuals was tested in this study as a diagnostic measure of correlated errors in the field and efficiency of eight analyses sharply differed at different levels of correlations.

Where low correlation values of adjacent plot residuals (correlation non significant) existed, iterated nearest neighbour analysis, weighted nearest neighbour analysis, Waite nearest neighbour analysis and moving mean analysis were less efficient than randomized complete block design. At intermediate correlation values (r <0.4),

slightly higher level of efficiency of eight analyses was obtained, but increase in average efficiency for iterated nearest neighbour analysis and weighted nearest neighbour analysis over randomized complete block design were marginal. When individual trials were considered the results were similar as observed where low correlation of adjacent plot residuals were found. The results for nearest neighbour analyses such as iterated nearest neighbour analysis, weighted nearest neighbour analysis and Waite nearest neighbour analysis in particular indicate that before using these three analyses one should have a strong reason to believe that there are trends present within the site. Otherwise as happened in this study, the precision may be less than of a randomized complete block design.

The results at high level of adjacent plot correlations $(r \geqslant 0.4)$ followed a opposite pattern to those revealed at low and medium correlations. Based on average of 16 trials, all eight analyses were more efficient than randomized complete block design. With the exception of Waite nearest neighbour analysis and moving mean analysis, the efficiency of six analyses were consistently higher than randomized complete block design for most of the trials. The efficiencies of iterated nearest neighbour analysis and weighted nearest neighbour analysis were much higher than other six analyses. These results strongly suggest that iterated nearest neighbour analysis and weighted nearest neighbour analysis are certainly a improvement over moving mean covariance analysis and productivity covariance analysis.

The other important outcome at high correlation of adjacent plot residuals was that the regression coefficient was positive in all

trials and significantly greater than zero in most cases for moving mean covariance analysis, productivity covariance analysis, weighted moving mean covariance analysis and weighted Papadakis method. Such a pattern was not found at low and medium levels of adjacent plot correlation. Where the regression coefficient was significant in the above mentioned four analyses, the efficiency was invariably greater than randomized complete block design. This strongly suggests that if the regression coefficient is significantly greater than zero, randomized complete block design fails to control all the variation in the field. The application of these four analyses to remove the impact of plot to plot variation in cultivar performance is more justified when the regression coefficient is significantly greater than zero. This criteria will also avoid the chance of less precision compared to randomized complete block design as happened in trials when adjacent plot yields were independent (r=0).

Also it was possible in this study to differentiate the situations in which covariance of adjacent plot yields or covariance of adjacent plot residuals is more useful. At low and intermediate level of correlation of adjacent plot residuals, weighted moving mean covariance analysis was more efficient than weighted Papadakis method while opposite was true at high level of correlation of adjacent plot residuals.

Schwarzbach (1985) using simulations involving ten trials compared weighted nearest neighbour analysis and iterated nearest neighbour analysis with randomized complete block design. In simulations arbitrary yield trends across the trials were constructed

assuming a particular true yield for a cultivar and adding a normally

distributed random value with known variance to the sum of the trend

and true yields on each plot. He reported that iterated nearest

neighbour analysis and weighted nearest neighbour analysis were always

superior to randomized complete block design. However, in real trials

in the experimental conditions of Oregon such consistency was not

observed in 32 advanced selection yield trials. The present study

indicate that iterated nearest neighbour analysis and weighted nearest

neighbour analysis were less efficient than randomized complete block

design in 12 and nine trials respectively. The results in this study

suggest that if iterated nearest neighbour analysis and weighted

nearest neighbour analysis are used only when at $r \geq 0.4$, there is a high

probability that these analyses will be more efficient than the

randomized complete block design.

Application of analyses in replicated yield trials in Oregon.

Except for the moving mean analysis and Waite nearest neighbor

analysis, all design were useful in reducing experimental error. Moving

mean analysis was better than randomized complete block design in 12 of

the 32 trials. These results are in contrast to earlier studies of

Townley-Smith and Hurd (1973) and Lawrence and Townley-Smith (1975).

Moving mean analysis was found superior to randomized complete block

design in all 13 trials by Townley-Smith and Hurd (1973). Lawrence and

Townley-Smith (1975) found moving mean analysis superior to completely

randomized design in 55 of the 59 forage trials. The reason might be

that the trials they used were grown at highly variable sites since in

the present study moving mean analysis was mostly efficient when

correlation of adjacent plot residuals was greater than 0.5.

Moving mean covariance analysis was superior to moving mean analysis in all trials. The optimum number of plots to include in the moving mean covariable varied from two to twelve. This was due to the level and nature of variability being at various sites.

A nearest neighbour analysis named as Waite nearest neighbour analysis was recently suggested to replace randomized complete block design by Wilkinson et al., (1983). They said " we are envisaging the new nearest neighbour methodology as a replacement for classical methods in many areas of application particularly for plant breeding experiments such as varietal trials". The results in this study suggest that Waite nearest neighbour analysis has limited value in the experimental conditions of Oregon. It was less efficient than randomized complete block design in 13 of the 22 trials. It require extra plots as borders which make it less efficient in terms of resources. It requires equal plots in all ranges so it could be only applied to 22 of the 32 trials in the present study. This also makes it less applicable than other analyses which were more flexible.

Advanced selection yield trials were established at four sites in Oregon. Sherman site at Moro appeared the most variable compared to Hyslop Agronomy and Holmes Farms in the Willamette valley and Rugg Farm near Pendleton. The main reason of soil gradients at Sherman Station was the uneven moisture distribution, which affects crop growth and forms gradients in the field due to variation in soil depth.

Iterated nearest neighbour analysis proved more efficient at all sites, however, results were variable from trial to trial. It could be

useful at all sites if only used when correlation of adjacent plot residuals is greater than 0.4. A more consistent alternate choice at Hyslop Agronomy Farm and Sherman Station would be weighted Papadakis method and moving mean covariance analysis, while at Rugg Farm moving mean covariance analysis appeared more useful.

None of the eight analyses used could be singled out as a universal substitute for randomized complete block design. Every effort should be made to block the field carefully using randomized complete block design. The use of some of the analyses such as iterated nearest neighbour analysis, weighted Papadakis method and moving mean covariance analysis would be applicable if: a) prior or during the course of the experiment, systematic trends are indicated due to pests, diseases and other environmental conditions b) fertility or moisture gradients are irregular and cannot be eliminated with the application of randomized complete block design, and c) the correlation of adjacent plot residuals is higher than 0.4 and substantial block effects in randomized complete block design are not indicated. These analyses could be new tools of breeders if appropriately used and would provide a greater degree of confidence in identifying and evaluation of progeny in various phases of the breeding program.

SUMMARY AND CONCLUSIONS

The objective of this investigation was to evaluate the utility of several different analyses in estimating environmental variation in three phases of a plant breeding program in Oregon. These phases involved: a) evaluation of F1 space planted and solid seeded F2 populations, b) F5 lines grown in unreplicated yield trials, and c) advanced selections grown in replicated yield trials. Nine different analyses were evaluated using data from 38 wheat trials grown over three environmentally diverse locations involving four sites in Oregon during four testing years. The experimental material comprised of five selected winter wheat cultivars and the resulting F1 and F2 generations. For the unreplicated and replicated yield trials selected F5 lines and advanced selections developed at Oregon State University cereal breeding program were used.

The analyses were: a) moving mean covariance analysis (MMCA), b) productivity covariance analysis (PCA), c) weighted nearest neighbour analysis (W-NNA), d) iterated nearest neighbour analysis (I-NNA), e) Waite nearest neighbour analysis (Waite NNA), f) moving mean analysis (MMA), g) weighted moving mean covariance analysis (WMMCA), h) weighted Papadakis method (WPM), and i) augmented design (AD).

The first five analyses were compared with a randomized complete block design (RCBD) in controlling environmental variation in F1 space planted populations grown at Rugg Farm and F2 bulked populations solid seeded at Hyslop Agronomy and Rugg Farms.

In the evaluation of 200 F5 lines grown at Hyslop Agronomy Farm,

Sherman Station and Rugg Farm, AD, MMA, MMCA, WMMCA, W-NNA were compared with completely randomized design (CRD).

Thirty two replicated yield trials were grown at Hyslop Agronomy and Holmes Farms near Corvallis, Sherman Station at Moro and Rugg Farm near Pendleton were used to evaluate the efficiency of first eight analyses noted above when compared to RCBD.

Based on the results, the following conclusions were drawn.

a) Evaluation of F1 and F2 populations.

1. The coefficient of variation in randomized complete block design ranged from 2.9 (F1 population at Rugg Farm) to 4.1% (F2 population at Hyslop Agronomy Farm) for plant height, while 8.9 (F2 population at Hyslop Agronomy Farm) to 13.1% (F2 population at Rugg Farm) for grain yield.

2. None of the five analyses appeared more efficient than the randomized complete block design in estimating environmental variation for plant height. Results were inconsistent for grain yield depending upon the variability of the trial. Hyslop Agronomy Farm, with a negative correlation of adjacent plot residuals, was less variable and consequently none of the five analyses showed an increase in efficiency over randomized complete block design for grain yield evaluation in F2 populations.

3. Field variability at Rugg Farm was indicated from correlation of adjacent plot residuals for grain yield evaluation in F1 and F2

populations. This resulted an increase in efficiency of all analyses, except Waite nearest neighbour analysis.

4. General combining ability estimates were more important than specific combining ability effects for both plant height and grain yield in three trials.

5. Since large effect of soil gradients were not present in the three trials, results did not provide a clear pattern as to the effect of five analyses on portioning the component of genetic variation. However, some increase in general combining ability effects was observed following weighted nearest neighbour analysis when compared to randomized complete block design for grain yield in F1 and F2 generations at Rugg Farm.

b) Evaluation of F5 lines in unreplicated yield trials.

1. Patterns of field variation were different at Hyslop Agronomy Farm, Sherman station and Rugg Farm which affected the efficiency of five analyses.

2. Based on consistency of results and efficiency, the moving mean covariance analysis appeared to be the most useful for the evaluation of F5 lines in unreplicated yield trials at the three experimental sites.

3. The soil heterogeneity at the Hyslop Agronomy Farm was low resulting in the efficiency of analyses being low in weighted nearest neighbour analysis (72%) to a modest 122% in moving mean covariance analysis when compared to completely randomized

design.

4. Efficiency of analyses ranged from 82% in augmented design to 536% for weighted nearest neighbour analysis at Sherman Station. High soil gradients at Sherman site were due to uneven distribution of moisture.

5. Significant block effects were identified at Rugg Farm and the efficiency of analyses ranged from 100% in weighted nearest neighbour analysis to 212% for augmented design and moving mean covariance analysis.

6. Weighted moving mean covariance analysis was less expensive in computing cost compared to moving mean covariance analysis and could be a useful alternative to moving mean covariance analysis in projects where computing costs is a concern.

7. Reduction in genotype x location interaction using the moving mean analysis, moving mean covariance analysis and weighted moving mean covariance analysis were observed.

8. Evaluation of F5 lines at different locations is important due to the diverse climatic conditions of Oregon. Ranking of the check cultivars Stephens and Malcolm at Hyslop Agronomy Farm and Rugg Farm were different which indicated the effect of location on performance of cultivars.

c) Evaluation of advanced selections in replicated yield trials.

1. Since the variability from trial to trial was different, the efficiency of eight analyses also showed considerable variation in efficiency. The most variable were iterated nearest neighbour

analysis, weighted nearest neighbour analysis, Waite nearest

neighbour analysis and moving mean analysis.

2. On the basis of average efficiency, iterated nearest neighbour

    analysis and the weighted nearest neighbour analysis were the

    most efficient followed by moving mean covariance analysis,

    weighted Papadakis method and weighted moving mean covariance

    analysis. The least efficient were the Waite nearest neighbour

    analysis and the moving mean analysis.

3. The results at three levels of coefficient of variation were not

    consistent. However, moving mean covariance analysis,

    productivity covariance analysis, weighted moving mean

    covariance analysis and weighted Papadakis method were

    relatively less efficient to iterated nearest neighbour analysis

    and weighted nearest neighbour analysis at high coefficient of

    variation compared to low and intermediate coefficient of

    variation.

4. The eight analyses were particularly more useful in reducing

    error in trials with more than 40 entries.

5. In eight of the 32 trials block effects were non-significant. In

    two of the eight trials with non-significant block effects most

    of the environmental variation was trapped within blocks.

6. When blocks effects were significant, the plot to plot variation

    was not accounted for by the blocks in 14 of the 32 trials.

7. Correlation of adjacent plot residual appears to be a useful

    diagnostic measure of correlated error between plots.

8. With no soil gradients in the field (correlation of adjacent

plot residual non significant), iterated nearest neighbour analysis, weighted nearest neighbour analysis, Waite nearest neighbour analysis and moving mean analysis were less precise than randomized complete block design.

9. At low and medium level of correlation of adjacent plot residuals, the moving mean covariance analysis was the best alternative to randomized complete block design.

10. At high correlations of adjacent plot residuals ($r \geqslant 0.4$), iterated nearest neighbour analysis and weighted nearest neighbour analysis were most efficient and consistent in controlling environmental variation. These two analyses should be used only when high variability in the experimental area is known.

11. Moving mean covariance analysis, productivity covariance analysis, weighted moving mean covariance analysis and weighted Papadakis method were consistently superior to randomized complete block design when regression coefficient was significantly greater than zero.

12. Moving mean analysis appears to have little value under the experimental conditions observed in Oregon. It was superior to the than randomized complete block design in only 11 of the 32 trials. Also, it was less efficient to moving mean covariance analysis in all trials.

13. Waite nearest neighbour analysis has limited value for cultivar evaluation in the experiment sites of Oregon, since it was more efficient in only eight of the 22 trials when compared to

randomized complete block design.

14.   Moving mean analysis and Waite nearest neighbour analysis were more efficient than randomized complete block design mostly in trials with correlation of adjacent plot residuals greater than 0.5.

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APPENDIX

Appendix Table 1. Details of the field management at four
                  experimental sites over four years.

1981-82

Hyslop Agronomy Farm:
      Fields were plowed in August, disced and harrowed to break down
the clods. Just prior to planting, 40 kg of nitrogen per hectare was
applied as urea and worked into the soil with a danish harrow. Planting
was done on 20th October. Diuron was applied in the first week of
December at a rate of 2.03 kg/ha active ingredient on wheat trials to
control annual blue grass. Alley ways were sprayed out in April using
1.41 litre of Glyphosate and 1.41 litre of surfactant per hectare.
Nitrogen levels were increased by applying 203 Kg/ha of nitrogen as
urea in the 2nd week of March.

Sherman Branch Experimental Station:
      Propham was used to keep the field clean of volunteer wheat.
Field was disced and chisel plowed during the spring. A rod-weeder was
used to control weeds and set the moisture level. In late June,
anhydrous ammonia was applied at a rate of 81 Kg/ha. A density of 80
kg/ha of seed was used. Planting was done on 29th September. Cheat
grass Bromus tectorum and volunteer wheat was extremely bad this year.
Rain right after planting helped germinate cheat grass seeds close to
the surface. Metribuzin at a rate of 0.34 kg/ha.

Rugg Farm:
      Previous crop was Phaseolus vulgaris. Anhydrous ammonia was
applied at a rate of 134 kg/ha plus 20 kg/ha of sulphur. Seeding rate
was 120 Kg/ha. Stand establishment was good. Planting date was
September 19, 1981. Harvesting was done the third week of July.

1982-83

Hyslop Agronomy Farm:
      Fields were plowed in the spring and disced to break down the
clods. A danish harrow was used to prepare the seed bed. All trials
received 40 kg/ha of nitrogen (16-20-0). Planting was completed between
19 to 20th October. Diuron 1.34 kg/ha and Chlorsulfuron 35 gm/ha were
applied to control grasses and broad leaves. Fertilizer was applied in
March at a rate of 200 kg/ha, (80 kgs as NH(4)Cl and 120 kgs as urea).

Sherman Branch Experiment Station:
      Fallow fields were kept clean with an application of Glyphosate.
The field was disced and then chisel plowed in the spring prior to
planting. Weeds were controlled with two rod weeding operations.
Anhydrous ammonia was applied during late June at a rate of 80 kg/ha of
nitrogen per hectare. Planting was done on October five and seven. Soil
moisture was good so there was no problem with germination.
Chlorsulfuron 35 gm/ha was used to control broad leaf weeds in spring.

Appendix Table 1 continued.

Rugg Farm:
      Previous crop was Pisum sativum. Anhydrous ammonia was applied at
the rate of 120 kg/ha. Planting was accomplished on 6th October.
Seeding rate was 120 Kg/ha.

1984-85

Hyslop Agronomy Farm:
      Sixty seven Kg/ha of nitrogen and 8 kg/ha of sulfur were applied
prior to planting in fall as 40-0-0-6. Planting was done on 15th
November. In the spring 160 kg/ha of nitrogen and 24 kg/ha of sulfur
were applied as 40-0-0-6. Alachlor at a rate of 1.75 litre/ha and
Chlorsulfuron 35 gm/ha were applied to control the weeds.

Sherman Branch Experiment Station:
      In fall 81 kg/ha of nitrogen in the form of anhydrous ammonia was
applied. Planting was done on October 17. Herbicide Dicamba 140 gm/ha ,
23 gm/ha of Chlorsulfuron and Metribuzin 0.34 kg/ha were applied to
control the weeds.

Rugg Farm:
      One hundred kg/ha of nitrogen in the form of anhydrous ammonia was
applied to bring total available nitrogen to 120 kg/ha. Previous crop
was Pisum sativum. Planting was done on 5th October. An additional 80
kg/ha of nitrogen was applied in the spring in the form of urea.
Herbicide 2,4, D at the rate of 1 kg/ha was applied to control the
weeds.

1985-86
Hyslop Agronomy Farm:
      In the fall prior to planting 67 kg/ha of nitrogen and 8 kg/ha of
sulfur were applied as 40-0-0-6, which was boosted by applying 195
kg/ha of nitrogen and 30 kg/ha of sulfur in spring. Alachlor and
Chlorsulfuron were applied at a rate of 1.76 litre/ha and 23.35 gm/ha,
respectively. F5 line unreplicated trial was planted on October 15th.
Trial B and Trial 42 was planted on October 12.

Sherman Branch Experiment Station:
      Anhydrous ammonia was applied at a rate of 67 kg/ha in fall.
Diclofop was applied at a rate of 2.46 litre/ha and incorporated in the
soil. Bromoxynil was applied in April at a rate of 2.1 litre/ha. F5
line unreplicated trial was planted on September 24.

Rugg Farm:
      Nitrogen in the form of anhydrous ammonia and sulphur in the form
of nitrosol at a rate of 100 kg and 20 kg/ha, respectively was applied
at the time of planting. Two herbicide Bromoxynil and Dicamba were
applied in spring at a rate of 1.4 litre and 140 gm/ha. F5 unreplicated
trial and Trial C were planted on October two.

Appendix Table 2. Summary of climatic data at Corvallis, Moro and Pendleton for four crop years.

	LOCATION								
MONTH	CORVALLIS TEPM (C)		PREC	MORO TEMP (C)		PREC	PENDLETON TEMP(C)		PREC
	MAX	MIN	(cm)	MAX	MIN	(cm)	MAX	MIN	(cm)
(1981-82)									
SEPTEMBER	25.1	8.5	7.85	23.2	7.4	2.34	26.1	5.9	3.84
OCTOBER	16.5	4.9	14.02	15.0	8.6	2.08	16.4	1.9	4.11
NOVEMBER	12.4	4.3	17.09	10.0	0.6	5.05	12.6	1.2	6.12
DECEMBER	9.3	2.8	35.51	4.6	-1.8	12.01	7.0	-1.3	8.31
JANUARY	6.1	0.4	18.31	3.7	-3.8	2.79	7.0	-3.8	6.63
FEBRUARY	9.6	1.6	18.08	5.6	-3.3	1.83	7.9	-1.6	4.72
MARCH	12.4	2.0	8.99	10.3	-1.1	1.40	11.4	0.4	5.05
APRIL	14.3	2.4	11.61	12.4	-0.4	3.68	15.2	0.5	3.91
MAY	20.0	5.9	1.24	18.1	3.1	0.94	20.4	4.8	1.22
JUNE	23.5	10.6	3.84	24.4	9.4	2.92	26.9	10.8	2.84
JULY	25.4	10.8	1.09	26.1	11.9	0.53	30.2	11.6	2.59
AUGUST	27.2	10.8	0.71	26.9	11.8	11.02	30.7	11.4	1.27
(1982-83)									
SEPTEMBER	23.3	9.6	4.80	21.0	7.7	3.61	24.0	6.5	4.27
OCTOBER	17.9	5.8	9.25	12.6	8.0	4.98	17.0	2.1	6.81
NOVEMBER	9.7	1.4	14.00	5.6	-2.2	2.74	6.8	-1.8	3.71
DECEMBER	8.2	1.8	26.82	3.3	-2.9	4.80	5.2	-1.4	6.83
JANUARY	9.0	2.4	17.55	6.4	-0.8	3.56	8.9	0.1	4.14
FEBRUARY	11.2	4.1	26.19	6.9	-0.2	6.17	11.1	1.4	7.54
MARCH	13.5	5.7	22.30	11.1	1.7	9.96	13.6	3.0	9.91
APRIL	16.1	4.1	7.65	13.8	1.9	1.55	16.4	1.9	3.12
MAY	20.8	7.0	3.84	19.9	6.0	4.98	22.4	5.6	5.28
JUNE	21.1	9.3	3.53	21.4	7.2	0.99	24.3	8.4	4.88
JULY	23.3	11.2	6.48	24.0	11.5	2.03	27.9	10.8	2.54
AUGUST	26.4	11.9	5.64	27.4	12.7	1.52	31.2	12.4	1.73
(1984-85)									
SEPTEMBER	23.6	8.5	1.88	20.8	6.4	3.88	23.6	6.2	2.49
OCTOBER	15.0	5.4	11.81	13.6	17.8	2.18	16.4	0.9	2.99
NOVEMBER	10.6	3.9	34.41	7.5	-0.3	8.07	9.9	0.6	8.71
DECEMBER	6.4	-0.1	10.18	1.7	-5.7	1.04	2.6	-5.6	4.98
JANUARY	5.8	-2.2	0.64	-1.9	-6.3	0.68	-1.2	-6.1	1.75
FEBRUARY	9.2	-0.1	9.27	4.5	-5.5	2.46	5.9	-6.2	3.78
MARCH	11.7	1.1	12.55	10.2	-1.2	1.12	11.8	-0.7	3.38
APRIL	16.7	5.5	2.67	16.2	3.4	0.36	19.0	3.4	1.65
MAY	19.6	6.0	2.39	19.5	5.6	1.60	22.3	5.7	2.26
JUNE	24.1	8.6	5.64	23.8	9.2	2.34	26.9	8.1	3.61
JULY	30.6	11.3	1.37	31.7	14.5	0.13	35.1	12.1	0.13
AUGUST	27.2	10.0	1.22	25.7	10.0	0.36	28.3	9.6	2.49

Appendix Table 2. Continued

(1985-86)

MONTH	CORVALLIS TEMP (C) MAX	CORVALLIS TEMP (C) MIN	CORVALLIS PREC (cm)	MORO TEMP (C) MAX	MORO TEMP (C) MIN	MORO PREC (cm)	PENDLETON TEMP (C) MAX	PENDLETON TEMP (C) MIN	PENDLETON PREC (cm)
SEPTEMBER	22.0	7.6	1.98	19.0	5.2	2.82	20.8	4.3	3.91
OCTOBER	17.6	4.7	9.88	14.7	2.3	2.90	16.8	1.5	3.40
NOVEMBER	7.1	-0.2	11.91	0.8	-7.3	3.02	1.8	-8.6	6.76
DECEMBER	4.5	-3.6	9.45	-4.3	-10.7	2.84	-3.6	-10.7	3.23
JANUARY	9.7	2.1	16.59	3.7	3.0	4.67	6.0	-2.4	6.05
FEBRUARY	10.0	3.0	25.15	5.8	-1.4	6.07	7.7	-0.5	7.72
MARCH	15.6	5.3	7.72	12.7	2.6	2.49	14.7	3.2	4.93
APRIL	15.1	4.1	4.67	13.2	1.7	0.86	15.9	1.7	2.11
MAY	18.7	6.9	6.35	19.3	7.1	0.89	20.8	6.0	4.75
JUNE	25.2	10.6	0.79	26.4	10.9	0.15	29.7	9.9	0.23
JULY	24.6	10.0	2.92	24.1	10.5	1.37	28.2	9.6	1.55
AUGUST	30.6	11.3	0.00	30.7	13.9	0.18	33.9	11.4	0.48

Appendix Table 3. Pedigree and description of parental cultivars
used in developing F1 and F2 populations.

STEPHENS: (Nord Desprez/Pullman Selection 101).

An awned, semi dwarf, soft white winter wheat released by Oregon
State University. Stephen is mid to late in maturity, moderate to high
tillering, and moderate in head fertility. Stephens kernel are large in
size. Stephens is widely adaptable to the Pacific northwest.

YAMHILL: (Heines VII/Redmon (Alba).

A soft white common winter wheat cultivar released by Oregon
State University in 1969. Yamhill is late maturing, medium in height
and awnless. Milling and baking qualities of Yamhill are good.
Spikelets of Yamhill are large fertile with medium to large kernels.

AURORA: (Lutescens 314-h-147/Bezostaya 1).

A hard red common wheat cultivar released in Russia for
commercial cultivation in 1971. Spikes of Aurora are large,
cylindrical, white and awnless. Aurora is early in maturity, tall, low
tillering, large in seed size with good milling and baking qualities.

MALCOLM: (Stephen//63-189-7/Bezostaya).

Malcolm was released in 1985 by Oregon State University. Malcolm
is semi dwarf soft white winter wheat with stiff white straw. Spikes of
Malcolm are awned, oblong, mid-dense and nodding. Glumes are of medium
size with a shallow crease. Malcolm is better in leaf rust resistance
than available commercial cultivars and possesses higher resistance to
powdery mildew as compare to Stephens.

JACKMAR:

Spikes of Jackmar are apically awnletted and glume is of red
color. Average height of Jackmar is about 86 centimeters. Jackmar is a
soft white club wheat. Jackmar is susceptible to stripe and leaf rust.

Appendix Table 4. Trial numbers, title of trials, locations, number of entries, number
of replications and trial year of 32 advanced selection yield trials.

No	Title of the trials	LOC 1/	ENT 2/	REP 3/	YEAR
1	Hard red winter wheat elite yield trial (HRELTM)	MOR@	18*	4	81-82
2	Hard red winter wheat elite yield trial (HRELTP)	PEN#	18*	4	81-82
3	Hard white winter wheat replicated yield trial (HWAYPC)	COR$	20*	4	81-82
4	Hard red replicated winter wheat yield trial (HRAYPM)	MOR	21*	3	81-82
5	Hard red replicated winter wheat yield trial (HRAYPP)	PEN	21*	3	81-82
6	Hard red winter wheat replicated advanced yield trial (HRAYAP)	PEN	26	3	81-82
7	Western regional soft white winter wheat performance nursery (WRWWN)	COR	31*	4	81-82
8	Soft white winter wheat elite line trial (SWELTC)	COR	32*	4	81-82
9	Soft white winter wheat elite line trial (SWELTM)	MOR	32	4	81-82
10	Soft white winter wheat elite line trial (SWELTP)	PEN	32	4	81-82
11	Soft white winter wheat advanced yield trial (SWAYAM)	MOR	69	3	81-82
12	Soft white winter wheat advanced yield trial (SWAYPP)	PEN	69	3	81-82
13	Soft white winter wheat preliminary yield trial (SWAYPM)	MOR	76	3	81-82
14	Soft white winter wheat preliminary yield trial (SWAYPP)	PEN	76	3	81-82
15	Hard red replicated advanced nursery (HRRANP)	PEN	18*	3	82-83
16	Hard red winter wheat elite trial (HRELTC)	COR	28	4	82-83
17	Hard red winter wheat elite trial (HRELTM)	MOR	28*	4	82-83
18	Hard red winter wheat elite trial (HRELTP)	PEN	28*	4	82-83
19	Hard red replicated preliminary nursery (HRRPNM)	MOR	30*	3	82-83
20	Hard red replicated preliminary nursery (HRRPNP)	PEN	30*	3	82-83
21	International winter wheat performance nursery (IWPPN)	COR	30*	4	82-83
22	Soft white winter wheat elite nursery (SWELTM)	MOR	33	3	82-83
23	Soft white winter wheat elite nursery (SWELTP)	PEN	33	4	82-83
24	Soft white winter wheat advanced nursery (SWRANM)	MOR	56	3	82-83
25	Soft white winter wheat advanced nursery (SWRANP)	PEN	56	3	82-83
26	Soft white winter wheat replicated advanced nursery (SWRANM)	MOR	90	3	82-83
27	Soft White winter wheat replicated advanced nursery (SWRANP)	PEN	90	3	82-83
28	Hard red replicated preliminary yield nursery (HRPYNC)	COR	48	3	84-85
29	Hard red replicated preliminary yield nursery (HRPYNM)	MOR	48	3	84-85
30	Hard red replicated preliminary yield nursery (HRPYNP)	PEN	48	3	84-85
31	21 elite line single row trial (21ELTC)	COR	21	3	85-86
32	21 elite line single row trial (21ELTP)	PEN	21	3	85-86

1/ Location. 2/ Entries. 3/ Replications.
@. Moro #. Pendleton $. Corvallis
* Number of plots included in moving means of MMD and MMCD were only two to 8,
while two to 12 in remaining trials.

Appendix Table 5. Regression coefficients (b) used to adjust plot values in moving mean covariance analysis (MMCA) and productivity covariance analysis (PCA), correlation (r), F ratio (F) for blocks in randomized complete block design and weighting factor (W) in weighted nearest neighbour analysis for plant height and grain yield in Trails A to C.

Trait	MMCA (b)	PCA (b)	r	F	W
		Trail A			
Plant Height	-0.57 (10)	0.04	0.7	24.79*	0.75
Grain Yield	-0.99*1/ (10)2/	-0.22	0.21 1/	0.68	0.15
		Trial B			
Plant Height	-0.68 (10)	-0.45	-0.20	0.30	0.06
Grain Yield	-0.53 (8)	-0.91*	-0.19	1.05	0.18
		Trial C			
Plant Height	-0.55 (10)	-0.58	0.28	4.52*	0.48
Grain Yield	0.59 (6)	0.46	0.26*	1.48	0.14

* Significant at the .05 level of probability.
1/ N= 60.
2/ Number of plots are presented for the moving mean covariable with greatest reduction in error mean square amongst six moving means.

Appendix Table 6. Mean values of five parents and 10 F1 crosses for Plant height (cm) obtained via six analyses in Trial A grown at Rugg Farm during 1984-85.

Parents/F1s	RCBD1/	MMCA2/	PCA3/	W-NNA4/	I-NNA5/	Waite6/ NNA
Parents						
Stephen (SPN)	68.00	68.03	68.01	68.20	68.30	68.19
Malcolm (MCM)	70.25	70.15	70.27	70.10	70.00	70.01
Yamhill (YMH)	70.00	70.21	69.98	70.10	70.20	70.62
Aurora (AU)	69.75	69.92	69.74	69.90	69.90	69.68
Jackmar (JM)	55.50	56.11	55.50	56.00	56.20	56.19
F1s						
SPN X MCM	68.50	68.47	68.49	68.10	67.90	67.85
SPN X YMH	78.25	77.91	78.21	77.40	77.10	77.21
SPN X AU	76.00	76.02	75.99	76.10	76.10	76.24
SPN X JM	70.75	70.44	70.72	70.20	70.00	69.92
MCM X YMH	76.00	75.93	75.99	75.20	75.00	75.56
MCM X AU	76.50	76.35	76.52	76.90	77.00	77.00
MCM X JM	68.25	68.07	68.26	68.00	67.90	67.02
YMH X AU	77.50	77.35	77.50	77.50	77.50	77.30
YMH X JM	67.75	68.01	67.78	68.70	69.00	68.99
AU X JM	65.00	65.03	65.04	65.60	65.80	66.17
L.S.D. (.05).	2.9	2.8	2.9	3.1	3.1	3.0

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.

Appendix Table 7. Mean values of five parents and 10 F1 crosses for
grain yield (gms) obtained via six analyses in
Trial A grown at Rugg Farm during 1984-85.

Parent/cross	RCBD1/	MMCA2/	PCA3/	W-NNA4/	I-NNA5/	Waite6/ NNA
Parents						
Stephen (SPN)	47.75	47.17	47.65	47.80	47.90	47.93
Malcolm (MCM)	45.75	46.07	45.77	45.90	46.80	46.88
Yamhill (YMH)	40.25	40.42	40.15	40.30	40.40	40.99
Aurora (AU)	21.50	22.73	21.33	21.60	22.40	22.05
Jackmar (JM)	35.00	35.64	35.49	34.60	32.60	32.39
F1s						
SPN X MCM	44.50	44.02	44.88	44.40	43.80	43.69
SPN X YMH	53.25	52.08	53.16	53.30	53.30	53.77
SPN X AU	42.00	42.61	42.10	42.00	41.80	41.90
SPN X JM	44.75	43.53	44.93	44.70	44.10	43.96
MCM X YMH	58.00	57.45	57.96	58.10	58.70	59.87
MCM X AU	42.25	42.81	42.10	42.30	42.70	42.59
MCM X JM	46.00	45.05	45.83	46.10	46.80	45.77
YMH X AU	44.25	45.06	44.13	44.20	44.00	43.71
YMH X JM	43.75	44.07	43.47	44.00	45.10	44.98
AU X JM	41.50	41.79	41.54	41.30	39.90	40.07
L.S.D (.05)	5.6	5.3	5.6	5.2	5.5	6.1

1/ Randomized complete block design.
2/ Moving mean covariance design.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.

Appendix Table 8. Mean values of five parents and 10 F2 crosses for plant height (cm) obtained via six analyses in Trial B grown at Hyslop Agronomy Farm during 1985-86.

Parents/F2s	RCBD 1/	MMCA 2/	PCA 3/	W-NNA 4/	I-NNA 5/	Waite 6/ NNA
Parents						
Stephen (SPN)	112.50	113.80	112.60	112.50	112.80	113.63
Malcolm (MCM)	120.00	119.90	119.60	120.10	121.10	121.00
Yamhill (YMH)	129.75	129.40	129.70	129.80	130.50	130.99
Aurora (AU)	131.75	131.40	131.40	131.80	132.30	132.25
Jackmar (JM)	116.00	116.00	116.10	115.90	114.00	113.62
F1s						
SPN X MCM	117.50	117.60	117.50	117.50	117.00	117.05
SPN X YMH	130.50	130.70	130.60	130.40	129.10	131.00
SPN X AU	133.50	133.40	133.70	133.60	134.80	134.62
SPN X JM	117.50	118.40	117.80	117.50	117.80	117.27
MCM X YMH	133.75	133.60	133.90	133.70	133.20	130.95
MCM X AU	134.75	133.90	134.30	134.90	137.30	137.10
MCM X JM	118.75	119.40	118.60	118.90	121.20	121.23
YMH X AU	133.50	133.20	133.80	133.40	131.60	131.65
YMH X JM	131.50	131.30	131.60	131.40	130.60	130.95
AU X JM	128.25	127.40	128.30	128.10	126.30	126.24
L.S.D. (.05)	7.3	7.4	7.3	7.9	8.8	9.1

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.

Appendix Table 9. Mean values of five parent and 10 F2 crosses for grain
yield (Kg/Ha) obtained via six analyses in Trial B
grown at Hyslop Agronomy Farm during 1985-86.

Parents/F2s	RCBD 1/	MMCA 2/	PCA 3/	W-NNA 4/	I-NNA 5/	Waite 6/ NNA
Parents.						
Stephen (SPN)	6264.76	6243.24	6275.53	6252.92	6199.10	6104.49
Malcolm (MCM)	8410.88	8417.60	8487.57	8392.31	8309.42	8574.33
Yamhill (YMH)	6644.20	6593.07	6657.66	6639.36	6616.22	6598.45
Aurora (AU)	4137.49	4247.02	4111.92	4128.61	4089.32	4110.79
Jackmar (JM)	5793.83	5774.99	5834.20	5759.39	5604.38	5638.45
F1s.						
SPN X MCM	7602.22	7594.14	7728.70	7591.45	7543.01	7574.87
SPN X YMH	6715.52	6716.86	6754.54	6691.03	6579.62	6446.73
SPN X AU	5462.83	5398.25	5379.41	5478.98	5551.10	5554.54
SPN X JM	6044.10	6054.86	5931.07	6083.39	6259.38	6290.49
MCM X YMH	6820.47	6636.13	6754.54	6886.40	7183.49	7174.55
MCM X AU	6033.33	6049.48	5931.07	6081.23	6298.13	6329.51
MCM X JM	6772.03	6630.75	6733.01	6752.38	6662.50	6638.77
YMH X AU	6167.89	6270.15	6130.21	6175.42	6208.25	6198.67
YMH X JM	6348.19	6485.43	6463.90	6313.74	6158.20	6131.45
AU X JM	4826.40	4932.69	4879.95	4818.06	4781.46	4672.79
L.S.D. (.05)	801	793	774	824	922	1030

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.

Appendix Table 10. Mean values of five parents and 10 F2 crosses for
plant height (cm) obtained via six analyses in
Trial C grown at Rugg Farm during 1985-86.

Parents/F2s	RCBD 1/	MMCA 2/	PCA 3/	W-NNA 4/	I-NNA 5/	Waite 6/ NNA
Parents						
Stephen (SPN)	92.00	93.14	92.19	91.90	91.70	91.75
Malcolm (MCM)	96.75	96.83	97.09	96.40	96.10	95.47
Yamhill (YMH)	104.75	104.60	104.90	104.20	103.60	103.48
Aurora (AU)	111.75	111.20	112.10	111.20	110.50	110.62
Jackmar (JM)	98.75	98.72	98.26	99.50	100.30	100.36
Fls						
SPN X MCM	94.50	94.60	94.26	94.80	95.10	95.49
SPN X YMH	106.00	106.20	105.80	106.20	106.50	106.03
SPN X AU	109.25	109.20	108.60	109.30	109.40	109.54
SPN X JM	98.75	99.32	99.02	98.80	98.80	98.84
MCM X YMH	111.00	110.80	111.10	110.90	110.90	110.80
MCM X AU	114.50	114.00	114.80	113.90	113.10	113.20
MCM X JM	100.50	101.00	100.30	100.50	100.60	100.62
YMH X AU	114.50	114.30	114.70	114.90	115.40	115.60
YMH X JM	108.75	108.60	108.90	108.50	108.20	108.32
AU X JM	107.50	106.80	107.30	108.30	109.20	109.20
L.S.D. (.05)	4.2	4.2	4.1	4.3	4.3	4.6

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.

Appendix Table 11. Mean values of five parents and 10 F2 crosses for
grain yield (Kg/Ha) obtained via six analyses in
Trial C grown at Rugg Farm during 1985-86.

Parents/F2s	RCBD 1/	MMCA 2/	PCA 3/	W-NNA 4/	I-NNA 5/	Waite 6/ NNA
Parents						
Stephen (SPN)	4165.82	4103.93	4206.19	4193.00	4358.77	4424.42
Malcolm (MCM)	4879.64	4852.05	4884.35	4885.96	4925.52	5024.02
Yamhill (YMH)	4586.98	4599.09	4647.53	4633.27	4915.83	4925.53
Aurora (AU)	4802.94	4744.41	4765.94	4785.31	4678.48	4702.03
Jackmar (JM)	3592.62	3458.06	3530.72	3518.08	3063.01	3070.31
F1s						
SPN X MCM	5326.36	5417.18	5371.44	5315.19	5246.57	5117.19
SPN X YMH	5058.59	5199.21	5164.22	5080.53	5215.62	5123.24
SPN X AU	5450.82	5462.93	5368.74	5437.91	5358.52	5343.03
SPN X JM	4515.67	4556.03	4518.36	4525.62	4586.98	4559.16
MCM X YMH	5087.52	5086.18	5051.19	5088.87	5097.48	5097.70
MCM X AU	5119.82	5045.81	5088.87	5123.85	5149.15	5162.21
MCM X JM	4426.19	4416.09	4373.04	4391.88	4181.97	4138.33
YMH X AU	5312.23	5355.29	5293.39	5313.85	5323.80	5314.10
YMH X JM	4658.29	4760.56	4776.70	4720.73	5102.06	5058.87
AU X JM	4623.98	4547.96	4566.80	4593.17	4403.72	4547.35
L.S.D.	893	884	881	857	860	950

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.

Appendix Table 12. Treatment mean square for plant height and grain yield in three early generation trials determined via six analyses.

Trait	RCBD	MMMCA	PCA	W-NNA	I-NNA	Waite NNA
		Trial A				
Plant height	138**	109**	131**	29 #	28 #	134**
Grain yield	261**	198**	260**	57	10	332**
		Trial B				
Plant height	248**	181**	247**	47	50	315**
Grain yield	4289815**	3853908**	4368152**	885251	902972	5351051**
		Trial C				
Plant height	213**	144**	214**	46	46	273**
Grain yield	967967**	1007364**	986363**	122484	250964	1638037**

Variances.
Note: Analyses W-NNA and I-NNA use component of variance approach as compare to other analyses which use sum of squares to estimate treatment effects.

Appendix Table 13. Error mean squares for grain yield
(gm/plot) obtained via six analyses
in 200 F5 line unreplicated trial
grown at three locations during
1985-86.

No	Analysis	Hyslop Agronomy Farm	Sherman Station	Rugg Farm
1	CRD 1/	181705	157701	211848
2	AD 2/	167789	192243	100078
3	MMA 3/	156262	100788	114785
4	MMCA 4/	148700	105100	100100
5	WMMCA 5/	156500	104300	127200
6	W-NNA 6/	251242	29404	212463

1/ Completely randomized design.
2/ Augmented design.
3/ Moving mean analysis.
4/ Moving mean covariance analysis.
5/ Weighted moving mean covariance analysis.
6/ Weighted nearest neighbour analysis.

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Appendix Table 14. Error mean squares for six configurations of moving means in moving mean analysis for grain yield (gm/plot) of check cultivars in 200 F5 line unreplicated trial grown at three locations during 1985-86.

Moving means	Hyslop Agronomy Farm	Sherman Station	Rugg Farm
Nearest 2 plots	236461	129215	175439
Nearest 4 plots	224094	116849	147151
Nearest 6 plots	156262	128085	124318
Nearest 8 plots	197067	100788	114785
Nearest 10 plots	215834	119317	119236
Nearest 12 plots	221669	140391	117906
CRD	181705	157701	211848

Appendix Table 15. Error mean squares of six configurations of moving
means in moving mean covariance analysis for grain
yield (gm/plot) of check cultivars in 200 F5 line
unreplicated trial grown at three locations
during 1985-86.

Moving mean	Hyslop Agronomy Farm	Sherman Station	Rugg Farm
Nearest 2 plots	148700	113600	171700
Nearest 4 plots	168400	111700	153300
Nearest 6 plots	154900	125300	118900
Nearest 8 plots	181200	105100	100100
Nearest 10 plots	185700	123600	109500
Nearest 12 plots	185700	143200	106500
CRD	181705	157701	211848

Appendix Table 16. Correlation of moving means in MMA, MMCA and WMMCA
with corressponding plot values, correlation
of average of three checks (AD) with the
corressponding F5 lines in a block and W in W-NNA
in 200 F5 line unreplicated grian yield trial
grown over three locations during 1985-86.

Analysis	Hyslop Agronomy Farm	Sherman Station	Rugg Farm
MMA 1/	0.34*	0.26*	0.24*
MMCA 2/	0.32* (N=227) (0.41*) 5/	0.26* (0.57*)	0.24* (0.55*)
WMMCA 3/	0.36* (N=227) (0.67*) 6/	0.23* (0.43*)	0.28* (0.53*)
AD 4/	-0.02 (N=200) (1.3) 7/	0.06 (0.5)	0.24* (4.4*)
W-NNA 8/ (W)	0.0	0.72	0.0

* Significant at .05 level of probability.
1/ Moving mean analysis. 2/ Moving mean covariance deisgn.
3/ Weighted moving mean covariance analysis.
4/ Augmented design.
5/ Regression coefficients are presented in parenthesis for the moving
mean covariable with greatest reduction in error mean square (N=227).
6/ Regression coefficient are presented in parenthesis for the weighted
moving mean covariable (N=227).
7/ F-ratio for blocks in parenthesis for Augmented design.
8/ Weighted nearest neighbour analysis.

Appendix Table 17. Error mean square for 32 advanced selections replicated yield trials
estimated via ten experimental dsigns.

Trial	Experimental analyses (Mean square errors)									
	CRD 1/ (Base)	RCBD2/	MMCA3/	PCA 4/	W-NNA5/	I-NNA6/	WAITE7/ NNA	MMA 8/	WMMCA 9/	WPM 10/
1	163454	127192	126100	120800	118490	117055	162966	157229	127100	118300
2	146167	104591	91280	98450	84255	79053	104451	99597	88760	93450
3	111647	104512	89210	103800	115072	167471	138174	130096	92280	104600
4	256056	66963	60000	53350	38685	37784	- 11/	75488	60710	49920
5	96474	99632	85970	102100	100942	112887	-	123549	98570	102100
6	143851	101508	100600	102900	101492	100849	127823	108401	102400	101600
7	321024	247434	183300	186200	141118	130122	-	181876	182000	164100
8	357512	298404	291000	301600	299781	322929	-	338523	297200	299800
9	79825	71479	60590	53710	45653	38594	46505	69680	62360	51270
10	270863	270411	270200	267600	245042	276886	314620	305286	272100	267500
11	222106	198484	168216	168327	143878	123015	-	180739	175480	158486
12	315665	284735	261033	260373	242001	220342	-	263857	265859	259818
13	208849	125610	118525	105460	99003	81496	-	131337	122725	109338
14	185268	148200	85647	96213	66477	61053	-	89265	86442	90484
15	411315	405663	413300	405000	438442	464715	591230	469364	417500	401900
16	92124	78891	68040	62010	66384	68331	91459	69593	70140	64610
17	126725	95587	94920	93360	106848	107027	131336	111251	95140	96060
18	238912	236625	213200	227600	263337	248400	-	303787	238200	236600
19	124441	111239	101300	107200	102189	96952	141523	121094	105300	108500
20	676337	599457	570600	599500	551552	535230	769209	634275	572700	579200
21	133030	117751	107800	105600	101135	90150	100517	171432	109600	107400
22	207493	211898	194700	204800	206507	238469	325758	210669	205800	209600
23	238604	208342	204800	194400	168889	153187	178956	266541	206700	186700
24	145087	112768	100737	110616	124087	113663	154473	107927	110878	113760
25	245010	236649	188602	185366	141892	125843	151675	213040	187700	172183
26	121406	119846	96132	96823	89280	71599	98456	104045	117658	99976
27	161280	120772	118000	115796	150282	141827	-	194191	120057	121276
28	222262	156808	123366	90310	71269	65993	89418	148927	126018	90429
29	111637	48888	46547	49405	53273	49363	69653	54246	47580	49365
30	100938	74299	73272	74686	67951	61186	70602	82359	73372	70858
31	28948	16551	11950	14860	12313	11623	12374	17415	13240	14780
32	16928	13273	10120	13480	15126	25393	16429	15189	9032	13460

1/ Randomized complete analyses. 2/ Randomized complete block design.
3/ Moving mean covariance analysis. 4/ Productivity covariance analysis.
5/ Weighted nearest neighbour analysis. 6/ Iterated nearest neighbour analysis.
7/ Waite nearest neighbour analysis. 8/ Moving mean analysis.
9/ Weighted moving mean covariance analysis. 10/ Weighted Papadakis Method.
11/ Unequal plots per range in a replication.

Appendix Table 18. Relative efficiency based on the error mean square of eight analyses when compared to the randomized complete block design in 32 replicated yield trials.

Trial	RCBD 1/	MMCA 2/	PCA 3/	W-NNA 4/	I-NNA 5/	WAITE 6/	MMA 7/	WMMCA 8/	WPM 9/
1	100	101	105	107	109	78	81	100	108
2	100	115	106	124	132	100	105	118	112
3	100	117	101	91	62	76	80	113	100
4	100	112	126	173	177	-10/	89	110	134
5	100	116	98	99	88	-	81	101	98
6	100	101	99	100	101	79	94	99	100
7	100	135	133	175	190	-	136	136	151
8	100	103	99	100	92	-	88	100	100
9	100	118	133	157	185	154	103	115	139
10	100	100	101	110	98	86	89	99	101
11	100	118	118	138	161	-	110	113	125
12	100	109	109	118	129	-	108	107	110
13	100	106	119	127	154	-	96	102	115
14	100	173	154	223	243	-	166	171	164
15	100	98	100	93	87	69	86	97	101
16	100	116	127	119	115	86	113	112	122
17	100	101	102	89	89	73	86	100	100
18	100	111	104	90	95	-	78	99	100
19	100	110	104	109	115	79	92	106	103
20	100	105	100	109	112	78	95	105	103
21	100	109	112	116	131	117	69	107	110
22	100	109	103	103	89	65	101	103	101
23	100	102	107	123	136	116	78	101	112
24	100	112	102	91	99	73	104	102	99
25	100	125	128	167	188	156	111	126	137
26	100	125	124	134	167	122	115	102	120
27	100	102	104	80	85	-	62	101	100
28	100	127	174	220	238	175	105	124	173
29	100	105	99	92	99	70	90	103	99
30	100	101	99	109	121	105	90	101	105
31	100	139	111	134	142	134	95	125	112
32	100	131	98	88	52	81	87	147	99

1/ Randomized complete block design.
2/ Moving mean covariance analysis.
3/ Productivity covariance analysis.
4/ Weighted nearest neighbour analysis.
5/ Iterated nearest neighbour analysis.
6/ Waite nearest neighbour analysis.
7/ Moving mean analysis.
8/ Weighted moving mean covariance analysis.
9/ Weighted Papadakis Method.
10/ Unequal plots per range in a replication.

Appendix Table 19. Coefficient of variation (%) for 32 advanced selection
replicated yield trials determined via 10 xperimental
analyses.

Trial	Experimental analyses(coefficient of variation)									
	CRD (Base) 1/	RCBD 2/	MMCA 3/	PCA 4/	W-NNA 5/	I-NNA 6/	WAITE NNA 7/	MMA 8/	WMMCA 9/	WPM 10/
1	22.4	19.8	19.7	19.3	19.1	19.0	22.4	22.0	19.8	19.1
2	9.5	8.0	7.5	7.8	7.2	7.0	8.0	7.9	7.4	7.6
3	7.6	7.4	6.8	7.4	7.7	9.3	8.5	8.2	6.9	7.4
4	23.3	11.9	11.3	10.6	9.1	8.9	-11/	12.6	11.3	10.3
5	7.8	7.9	7.4	8.0	8.0	8.4	-	8.8	7.9	8.0
6	9.4	7.9	7.8	7.9	7.9	7.8	8.8	8.1	7.9	7.9
7	14.3	12.5	10.8	10.9	9.5	9.1	-	10.7	10.7	10.2
8	14.1	12.9	12.7	12.9	12.9	13.4	-	13.7	12.8	12.9
9	13.8	13.1	12.0	11.3	10.5	9.6	10.6	12.9	12.2	11.1
10	12.5	12.4	12.4	12.4	11.8	12.6	13.4	13.2	12.5	12.4
11	19.4	18.3	16.9	16.9	15.6	14.4	-	17.5	17.2	16.4
12	12.3	11.7	11.2	11.2	10.8	10.3	-	11.3	11.3	11.2
13	21.2	16.4	15.9	15.0	14.6	13.2	-	16.8	16.2	15.3
14	10.1	9.0	6.8	7.2	6.0	5.8	-	7.0	6.9	7.0
15	16.3	16.2	16.3	16.2	16.8	17.3	19.5	17.4	16.4	16.1
16	7.5	7.0	6.5	6.2	6.4	6.5	7.5	6.5	6.6	6.3
17	10.2	8.8	8.8	8.7	9.4	9.4	10.4	9.5	8.8	8.9
18	12.0	11.9	11.3	11.7	12.6	12.2	-	13.5	12.0	11.9
19	10.7	10.2	9.7	10.0	9.7	9.5	11.5	10.6	9.9	10.0
20	19.7	18.6	18.1	18.6	17.8	17.5	21.0	19.1	18.1	18.2
21	10.2	9.6	9.2	9.1	8.9	8.4	8.9	11.6	9.3	9.2
22	14.1	14.3	13.7	14.0	14.1	15.1	17.7	14.2	14.0	14.2
23	7.0	6.6	6.5	6.3	5.9	5.6	6.1	7.4	6.5	6.2
24	12.7	11.2	10.6	11.1	11.7	11.2	13.1	11.0	11.1	11.2
25	11.7	11.5	10.2	10.2	8.9	8.4	9.2	10.9	10.2	9.8
26	8.9	8.8	7.9	7.9	7.6	6.8	8.0	8.2	8.7	8.0
27	12.8	11.1	11.0	10.9	12.4	12.0	-	14.1	11.1	11.1
28	11.0	9.2	8.2	7.0	6.2	6.0	7.0	9.0	8.3	7.0
29	29.5	19.5	19.0	19.6	20.4	19.6	23.3	20.5	19.2	19.6
30	8.8	7.6	7.5	7.6	7.2	6.9	7.4	8.0	7.5	7.4
31	13.5	10.2	8.7	9.7	8.8	8.5	8.8	10.5	9.1	9.6
32	10.9	9.6	8.4	9.7	10.3	13.3	10.7	10.3	7.9	9.7

1/ Completely randomized design. 2/ Randomized complete block design.
3/ Moving mean covariance analysis. 4/ Productivity covariance analysis.
5/ Weighted nearest neighbour analyis. 6/ Iterated nearest neighbour
analysis. 7/ Waite nearest neighbour analysis.
8/ Moving mean analysis. 9/ Weighted moving mean covariance analysis.
10/ Weighted Papadakis Method. 11/ Unequal plots per range in a replication.

Appendix Table 20. Correlation of adjacent plot residual and
F-ratio in randomized complete block design
in 32 advanced selection replicated yield
trials.

Trial	r 1/	F-ratio
1	0.5*	6.13*
2	0.6*	8.16*
3	0.0	2.37
4	0.9*	60.23*
5	0.0	0.33
6	0.1	11.85*
7	0.7*	10.22*
8	0.3*	7.34*
9	0.5*	4.74*
10	0.2	0.94
11	0.5*	9.21*
12	0.3*	8.50*
13	0.6*	51.36*
14	0.6*	20.01*
15	0.0	1.25
16	0.5*	5.70*
17	0.3*	10.12*
18	0.1	1.27
19	0.3*	4.56*
20	0.3*	4.85*
21	0.4*	4.89*
22	0.1	0.31
23	0.4*	5.79*
24	0.3	17.05*
25	0.5*	2.98
26	0.3*	2.17
27	0.2	31.19*
28	0.7*	21.04*
29	0.7*	62.61*
30	0.5*	4.00*
31	0.7*	6.95*
32	0.3	4.94*

* Significant at .05 level of probability.
1/ Correaltion coefficient.

Appendix Table 21. Regression coefficient in MMCCD, PCA, WMMCA, WPM and weighting factor (W) in W-NNA in 32 advanced selection replicated yield trials.

Trial	Regression coefficient (b)				W (W-NNA) 5/
	MMCA 1/	PCA 2/	WMMCA 3/	WPM 4/	
1	0.17	0.56*	0.23	0.56*	0.47
2	0.51*	0.53*	0.60*	0.65*	0.64
3	-1.77*	-0.27	-0.94*	-0.39	0.00
4	0.27	0.94*	0.41*	0.95*	0.86
5	-0.92*	0.07	-0.47	-0.06	0.17
6	-0.51	0.12	0.20	0.19	0.42
7	0.91*	0.91*	0.85*	1.02*	0.63
8	0.25	-0.03	0.22	0.17	0.42
9	0.42*	0.94*	0.59*	0.91*	0.55
10	0.19	0.25	0.14	0.31	0.24
11	0.57*	0.75*	0.43*	0.84*	0.53
12	0.69*	0.51*	0.47*	0.58*	0.40
13	0.43*	0.85*	0.20	0.70*	0.57
14	0.79*	1.06*	0.84	1.04*	0.75
15	0.20	-0.56	-0.06	-0.47	0.14
16	0.49	0.76*	0.51*	0.68*	0.37
17	0.17	0.49	0.19	0.16	0.48
18	0.23*	0.43*	0.07	0.21	0.57
19	0.42*	0.58*	0.36*	0.42	0.41
20	0.23	0.48	0.40	0.44	0.36
21	0.28*	0.65*	0.28	0.59*	0.61
22	0.50*	0.50	0.38	0.29	0.24
23	0.14	0.57*	0.18	0.66*	0.39
24	0.59*	0.39	0.22	0.04	0.31
25	0.48*	0.94*	0.71*	0.96*	0.63
26	0.63*	0.82*	0.10	0.75*	0.45
27	0.17	0.51*	0.11	-0.07	0.25
28	0.50*	1.13*	0.56*	1.06*	0.76
29	0.29*	0.03	0.36	0.07	0.66
30	0.14	0.17	0.20	0.52	0.49
31	0.41*	0.57*	0.53*	0.71*	0.77
32	-0.99	-0.07	-1.51*	-0.12	0.00

* Significant at .05 level of probability.
1/ Moving mean covariance analysis.
2/ Productivity covariance analysis.
3/ Weighted moving mean covariance analysis.
4/ Weighted Papadakis method.
5/ Weighted nearest neighbour analysis.

Appendix Table 22. Number of plots included in a
moving mean showing largest
reduction in error in MMCA and
MMA in the analysis of 32
advanced selection replicated
yield trials.

Trial No	MMCA 1/	MMA 2/
1	2	8
2	4	8
3	8	8
4	2	8
5	4	8
6	12	10
7	8	8
8	2	8
9	2	6
10	4	12
11	10	12
12	12	12
13	10	10
14	4	4
15	8	8
16	4	8
17	4	12
18	2	6
19	4	4
20	2	8
21	4	8
22	4	6
23	2	8
24	10	8
25	2	4
26	12	8
27	8	8
28	4	8
29	2	6
30	2	10
31	2	10
32	4	12

1/ Moving mean covariance analysis.
2/ Moving mean analysis.

Appedix Figure1. Yield trend map of Hyslop
                Agronomy Farm Trial obtained
                via weighted nearest neighbour
                analysis.

```
Trend in std. dev. units (x10) *

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   B l o c k s
   9  8  7  6  5  4  3  2  1
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Variation less than .5 std. dev. is ignored.

Appendix Figure 2. Yield trend map of Sherman Station Trial obtained via weighted nearest neighbour analysis.

Trend in std. dev. units (x10)[*]

==============================

Blocks								
9	8	7	6	5	4	3	2	1
-14	-11	-9	-22	10	13	.	-9	14
-14	-11	-14	-22	10	8	.	-9	14
-14	-14	-8	-22	11	7	-6	-9	20
-15	-10	-6	-22	13	7	-6	-10	14
-21	-9	.	-33	15	7	-8	-11	15
-13	-9	.	-14	18	7	-9	-16	14
-12	-8	.	-6	22	8	-11	-11	22
-11	-11	.	.	27	9	-13	-11	13
-10	-6	.	11	31	11	-21	-10	11
-9	.	.	20	50	13	-15	-10	9
-9	.	7	28	31	15	-15	-10	8
-9	.	9	52	26	18	-15	-10	7
-9	.	12	31	21	20	-15	-15	.
-12	.	14	27	15	33	-16	-9	.
-14	6	17	22	10	18	-21	-7	.
-19	9	27	18	7	13	-12	.	.
-34	13	13	13	.	8	-8	.	.
-23	17	.	10	.	.	.	.	.
-23	21	.	7	.	.	.	.	.
-23	26	-10	.	-8	-7	.	.	.
-23	30	-18	.	-11	-17	7	.	.
	49	-26	.	-15	-11	11	.	.
	35	-45	.	-19	-10	15	.	.
	34	-33	.	-31	-10	25	.	.
	34	-33	-7	-21	-9	18	.	.
	34	-33	-13		-9	18		.

Variation less than .5 standard deviation is ignored.

Appendix Figure 3. Yield trend map of Rugg
                   Farm Trial obtained via
                   weighted nearest neighbour
                   analysis.

Trend in std. dev. units (x10)*

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        13   .   .

        .   .   .   .

        .   . -15   .   .   .

Variation less than .5 std. dev. is ignored.