ADAPTABILITY OF SAFFLOWER (*Carthamus tinctorius* L.) GENOTYPES TO SOME NEW ZEALAND ENVIRONMENTS

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ABSTRACT

Seven safflower (Carthamus tinctorius L.) genotypes were grown at three sites (Massey, Aorangi and Flockhouse) in the Manawatu area in years 1978 and 1979. Three additional genotypes from the world germplasm collection were included in the study in 1979. The experimental design was a randomized complete block with three replications.

The safflower genotypes were evaluated with respect to several morphological traits, and some important agronomic traits, such as yield, % oil content, % hull content and susceptibility to head rot disease. Data collected on seven safflower genotypes were analysed as a combined experiment with 3 sites and 2 years (Expt. I). The data available on 10 genotypes in 1979 were analysed separately with respect to ten important characters (Expt. II).

Of the 23 characters studied in Expt. I, the genotypic variance component (σ^2_G) was significant only for the following 6 characters: mid stem leaf length, primary head diameter, involucral bract length and length/width, bract spine index and susceptibility to head rot disease. The addition of 3 genotypes in Expt. II had a marked effect on the magnitude of σ^2_G component. Of the environmental components, site x year interaction effect was the most significant for the majority of traits.

Most of the characters studied in Expt. I showed significant genotype x environment interactions, and in most instances the second order interaction of genotype x site x year being highly significant. Adaptation analyses were performed following procedures of Finlay and Wilkinson (1963). The genotypes Leed and Dart with adaptation coefficients 1.52 and 1.75 respectively were specifically adapted to favourable environments with respect to yield. Cultivar 0-22 and Rio showed general adaptability to the same trait. For % oil content all genotypes except Rio showed general adaptability. Cultivar Rio was slightly specifically

adapted to favourable environments.

Two forms of broad sense heritabilities (full and restricted) were estimated. In Expt. I, relatively high restricted heritability estimates were obtained for the following traits: leaf length, primary head diameter, bract length and length/width, spine index and susceptibility to head rot disease. The heritability estimates obtained in Expt. II were higher than Expt. I, due to the additional genetic variability in the population. Of the additional traits studied in Expt. II, lodging and susceptibility to leaf spot disease, showed high heritability estimates.

Resistances to two fungal diseases - head rot (Botrytis cinerea Pers.) and leaf spot (Stemphylium/Alternaria species) - were assessed in field conditions. The leaf spot disease was detected only in the second year of this study. The cultivars VFSTP-1 and Partial-hull were highly susceptible to head rot disease. The two genotypes from safflower germplasm collection, PI 262437 and PI 306684 had considerable tolerance to leaf spot disease.

The optimum plot allocation study indicated that, disregarding costs, an allocation of 2 years, 4 sites and 2 replications would be more efficient than the present allocation.

There was no significant correlation between spininess and bird damage. The % oil content and % hull content were negatively correlated at both phenotypic and genotypic levels. Susceptibility to the two diseases were negatively correlated with yield. The susceptibility to head rot disease also showed a significant negative correlation with the % oil content.

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INTRODUCTION

Safflower, Carthamus tinctorius L. is one of the world's oldest crops. However till about 1950's safflower was grown mainly for it's colourful florets. The orange dye from the florets was used for colouring fabrics and food materials. In India safflower was also used as a medicinal plant, and the young leaves were eaten as a vegetable dish. Through intensive breeding, mainly in the United States, it was possible to increase the oil percentage of safflower seed from 27-28% to about 40% (Kneeland, 1966). Thin hull commercial cultivars with very high oil contents are now grown extensively in parts of United States, Mexico, India and Australia (Weiss, 1971).

An interesting feature of safflower oil is the different oil compositions found in different cultivars. In addition to the common cultivars with about 80% linoleic acid, cultivars with about 75% Oleic acid have been developed (Knowles and Hill, 1965; Urie et al., 1979). The industrial uses of safflower oil are due to it's high linoleic acid content, which makes it an ideal non-yellowing drying oil (Kneeland, 1966). Apart from it's various other industrial uses (Weiss, 1971), safflower oil is widely used as a cooking oil and in the production of margarines. With the increasing demand for polyunsaturated oils in food, safflower oil would become a very good source of edible oils.

An increase in returns from safflower meal should enable stabilization of the safflower industry (Kohler et al., 1966). The safflower meal from undecorticated (with hull) seed, with about 20-22% protein and 60% hull, is useful feed for ruminant animals. The high proportion of undigestable hull content makes it unsuitable for poultry and pigs. The partial decortication of seed, mechanically, should improve the value of safflower meal as an animal feed (Kohler et al., 1966). Safflower meal is deficient in amino acids lysine and

methionine (Kohler et al., 1966). If supplemented with the above ingredients, safflower meal could be successfully used as an animal feed.

Basically safflower is a dry-land crop. However highest yields are obtained by careful irrigation. In areas of high atmospheric humidity safflower is susceptible to fungal diseases (Weiss, 1971).

Safflower is a relatively new crop in New Zealand. Earlier safflower trials in the Manawatu area have revealed that head rot disease, caused by Botrytis cinerea Pers. is the main problem limiting safflower production (Anonymous, 1975).

The main purpose of the present study was to evaluate the potential usefulness of seven safflower genotypes for New Zealand conditions. For a range of agronomic and morphological traits, the total phenotypic variance was partitioned into it's components and estimates of heritabilities, adaptabilities, optimum plot allocations and correlations between traits were computed. Also a comparison of genotypic performances with respect to different characters were made. Considerable attention was given to identifying any sources of resistance to major diseases, which limit safflower production in the area.

CHAPTER 1

LITERATURE REVIEW

1.1 PHENOTYPIC ANALYSIS AND ASSUMPTIONS

Phenotypic analysis refers to partitioning of the total phenotypic variance into genetic, and various environmental components. In plant breeding experiments, usually a set of genotypes are grown in a series of environments, the environments being a representative sample of the area to which the results will apply. In such experiments it may be possible to conduct a combined analysis across all environments (Le Clerg et al., 1962; Comstock and Robinson, 1952; Comstock and Moll, 1963). The pooled analysis in addition to genotype performances provides information about the genotype x environment interactions. A split-plot in time model (Steel and Torie, 1960) may be used to analyse perennial crop data. Environments and site-year models used for phenotypic partitioning of annual species will be discussed in section 2.6.1.

For a valid analysis of variance, the data must satisfy certain basic assumptions. These assumptions have been discussed in detail by Cochran (1947) and Eisenhart (1947). The effects described in the model must be additive, independent, and normally distributed. Independence of effects implies that the covariance between any two effects must be zero. In addition to these assumptions, for a valid pooled analysis across all experiments, the individual experimental errors must have a common variance (be homogeneous).

Cochran (1947) outlined the possible consequences when each of the above assumptions is not satisfied. Several assumptions may be invalid in a given situation.

Non normality may not seriously affect the significance levels in the F-test or the two tailed t-test. If the deviation from normality is not great, the tabular probability

level may only be a slight underestimate of the true value. Obviously such a small difference in the probability level would only affect the marginal significances. The one-tailed t-test is more vulnerable. With a distinct skewness in the errors, where one tail is much longer than the other, taking significance probability as one half of the tabular value for a one-tailed t-test may give rise to a serious over or under-estimate.

When error variances of individual experiments are heterogeneous there will be a loss in sensitivity of significance testing. However as Cochran (1947) pointed out the validity of F-test for overall treatments will be least affected. If the phenotypic value of the i-th genotype in the j-th block in k-th environment is expressed as X_{ijk}, the t-test using pooled error for comparing genotypic performances between different environments ($\bar{X}_{i.k}$), may give erroneous results. However the pooled error is the best estimate for comparing genotypic performances based on all environments ($\bar{X}_{i..}$).

Homogeneity of error variances is commonly examined by a χ^2 test (Bartlett, 1937). When individual error variances are heterogeneous there are three possibilities for performing a valid analysis of variance. Each observation can be standardised by dividing by the corresponding standard error (σ), and the analysis performed on the standardised data. Alternatively individual experiments with error variances of similar magnitudes may be combined to form subsets, the error variances being homogeneous within each subset. The third possibility can be applied to a special form of regular heterogeneity, usually arising from non-normality in the data. Data can be transformed to a new scale, such that the transformed data are approximately normally distributed. The more common transformations are the square root, logarithm and angular or arcsin transformation.

Independence of error variances is usually taken care of by proper randomization.

Non-additivity in effects could inflate the error variance and may lead to loss of information. However as Cochran (1947) pointed out the loss may be negligible unless the error variance is low and non-additivity is considerable. Non-additivity may frequently be checked by Tukey's one degree of freedom test (Tukey, 1949). The basis of Tukey's test is to isolate a sum of squares with one degree of freedom from error, which is due to non-additivity and test it's significance by a F-test, with the balance error mean square. For a randomized complete block design, the sum of squares attributable to non-additivity is computed as the ratio of Q^2/K, where Q and K are defined as follows:

$$Q = \sum_{ij} (\bar{x}_i - \bar{x}_{..})(\bar{x}_{.j} - \bar{x}_{..})(x_{ij} - \bar{x}_{i.} - \bar{x}_{.j} + \bar{x}_{..})$$

where x_{ij} = the i-th treatment value in j-th block.

$$K = \sum_{ij} \left[(\bar{x}_{i.} - \bar{x}_{..})(\bar{x}_{.j} - \bar{x}_{..}) \right]^2$$

The non-additivity in effects may be removed by transformation to a different scale (Bartlett, 1947). A common form of non-additivity occurs when effects are multiplicative, and in such instances a logarithmic transformation is appropriate. Other transformations such as square root and angular, may be used in other types of non-additivity. When a transformation is made, all comparisons and significant differences are performed on the transformed scale (Steel and Torie, 1960).

1.2 HERITABILITY

Heritability was first defined by Lush (1940) as the fraction of observed phenotypic variance caused by differences in heredity. Lush's heritability estimates were based on parent-offspring regression technique, which will be discussed shortly. Such heritability estimates are predictive statistics, and determine the proportion of phenotypic variance of the parents which is transmitted to the offspring.

Fisher (1918) partitioned total genetic variance (σ^2_G) into three components: additive (σ^2_A), dominance (σ^2_D) and epistatic (σ^2_I) variances. Two forms of heritability

estimates are mentioned in the literature. Heritability in the broad sense is the ratio of total genetic variance (σ^2_G) to phenotypic variance (σ^2_P). The additive genetic variance (σ^2_A) divided by the phenotypic variance (σ^2_P) is commonly called the narrow sense heritability. Lush's heritability estimates, based on parent-offspring regression, were, in fact, narrow sense heritability.

As Hanson (1963) pointed out, to define heritability explicitly one must delineate a model characterizing the variability for a set of observations. Gordon et al. (1972) proposed two forms of broad sense heritability estimates applicable to phenotypic partitioning models, commonly employed in plant breeding experiments (Le Clerg et al., 1962; Comstock and Robinson, 1952). When all components of phenotypic variance are included in the denominator it was called "full" heritability. In the case of "restricted" heritability only part of the total phenotypic variance was included in the denominator. These heritability estimates, based on phenotypic partitioning methods, are descriptive statistics, and estimate the proportion of phenotypic variance in a population, which is due to genetic differences. Methods for estimating the two forms of broad sense heritabilities, for the environments and site-year models will be discussed in section 2.6.4. The broad sense heritability estimates applicable to perennial crop data have also been reported (Gordon, 1979). The standard errors corresponding to these broad sense heritability estimates have been described by Gordon et al. (1972) and Gordon (1979).

Hanson (1963) stated the importance of defining heritability in terms of selection concepts. If the selection unit is the genotypic mean, obtained from replicated plots grown in a number of environments, the appropriate broad sense restricted heritability estimate ($\bar{h}^2_B$) would be:

$$\bar{h}^2_B = \frac{\hat{\sigma}^2_G}{\hat{\sigma}^2_G + \hat{\sigma}^2_{GE}/e + \hat{\sigma}^2/be}$$

where $\hat{\sigma}^2_G$, $\hat{\sigma}^2_{GE}$ and $\hat{\sigma}^2$ are genotypic, genotype x environment interaction and error variance component estimates respectively; b = number of replications per experiment; e = number of environments.

Parent-offspring regression technique for estimating narrow sense heritability was first developed by animal geneticists (Lush, 1940) and has subsequently been used by plant breeders (Robinson et al., 1949; Vogel et al., 1980). If the values are expressed as deviations from the population mean, in a random mating population, the mean value of the offspring is, by definition, half the breeding value (A) of the parent (Falconer, 1975):

$$G = A + D$$

where G = genotypic value of the parent; A = breeding value (= additive effect); D = dominance deviation.
Taking the sum of cross products between G and ½A, we have:

$$\text{Sum of cross products} = \Sigma \tfrac{1}{2}A(A+D)$$
$$= \tfrac{1}{2}\Sigma A^2 + \tfrac{1}{2}\Sigma AD$$

Since A and D are uncorrelated, ½ΣAD is zero. Dividing by the number of paired observations we have:

$$COV_{OP} = \tfrac{1}{2}V_A$$

where COV_{OP} and V_A are covariance of offspring on parent, and additive genetic variance respectively.

Provided both sexes have equal variances, the covariance of offspring on mid parent value is also equal to $\frac{1}{2}V_A$. Narrow sense heritability (h^2_B) is, additive genetic variance (V_A) divided by the total phenotypic variance (V_P). Hence, regression of offspring on parent would give a regression coefficient, b, ($b = COV_{OP}/V_P$), which is $\frac{1}{2}h^2_B$. The phenotypic variance of mid parent values, $V_{\overline{P}}$, is $\frac{1}{2}V_P$, and hence the regression coefficient, b', for offspring-mid parent regression is equal to h^2_B.

In practice offspring-parent regressions in plant crops often involve regressing the progeny values in one year upon the parental values in the previous year. Environmental correlations may have an inflationary effect on heritability

estimates obtained by such regression methods. Frey and Horner (1957) proposed heritability estimates based on standard units to circumvent this.

Resemblance between relatives, such as full sibs and half sibs, have been used to estimate heritability ratios. The general formula for the covariance among relatives may be described as follows (Cockerham, 1954; Kempthorne, 1955).

$$C = \alpha\sigma^2_A + \delta\sigma^2_D + \alpha^2\sigma^2_{AA} + \alpha\delta\sigma^2_{AD} + \delta^2\sigma^2_{DD} + \alpha^3\sigma^2_{AAA} + \ldots$$

where C = covariance among relatives; σ^2_A, σ^2_D, σ^2_{AA} and σ^2_{AD} so on are additive, dominance and the various interaction components of genetic variance.

Assuming that inbreeding coefficients of male and female parents are equal, the α and δ values for full sibs (FS) and half sibs (HS) may be described as follows (Cockerham, 1963):

for FS $\quad \alpha = (1 + F)/2 \qquad \delta = (1 + F)^2/4$

for HS $\quad \alpha = (1 + F)/4 \qquad \delta = 0$

where F = inbreeding coefficient.

Robinson et al. demonstrated the use of offspring-parent regression and covariances among relatives, in estimating heritabilities in corn. The F_2 population of each corn hybrid were planted in 7 row blocks. The plants of the center row of each block were used as pollen parents and sib pollinations made with plants occurring in the three adjacent rows on each side. The seeds from female plants were grown as F_3 progeny test. The progeny arising from each male parent forms a set of half sibs. In the subsequent analysis of variance of F_3 data, the male variance component, M, is equal to covariance among half sibs.

Assuming no epistatis and an inbreeding coefficient of 1, the covariance among half sibs may be obtained by substituting α and δ to the equation described earlier.

$$M = \text{COV (HS)} = \frac{1}{4}\sigma^2_A$$

hence $\sigma^2_A = 4M$.

Robinson et al. divided σ^2_A by the total phenotypic variance to estimate narrow sense heritability. Heritability estimates, by regression method, were determined using F_2 female parent values as x variable and F_3 plot means as the y variable.

Warner (1952) estimated narrow sense heritability estimates for a number of characters of corn using variances of F_2 and the back crosses of F_1 to each inbred parent. Formulas for computing heritability estimates from variance components of segregating generations are given by Mather and Jinks (1977).

Methods for estimating broad sense and narrow sense heritability ratios from diallel crossing systems have been presented (Griffing, 1956a; Griffing 1956b). Estimates of general combining ability (g.c.a.) and specific combining ability (s.c.a.) variances can be related to covariances among relatives as follows:

$$\sigma^2_{gca} = COV(HS)$$

$$\sigma^2_{sca} = COV(FS) - 2\,COV(HS)$$

where σ^2_{gca} and σ^2_{sca} are general and specific combining ability variances respectively; COV(HS) is half sib covariance; COV(FS) is full sib covariance.

Using Kempthorne (1955) formulae for covariance among relatives and assuming no epistatis:

$$\sigma^2_{gca} = \left[(1+F)/4\right] \sigma^2_A$$

$$\sigma^2_{sca} = \left[(1+F)^2/4\right] \sigma^2_D$$

If the inbreeding coefficient of the parent in the diallel is 1, $\sigma^2_{gca} = \frac{1}{2}\sigma^2_A$ and $\sigma^2_{sca} = \sigma^2_D$. Hence, $\sigma^2_A = 2\sigma^2_{gca}$ and $\sigma^2_G = 2\sigma^2_{gca} + \sigma^2_{sca}$.

The type of heritability estimate applicable depends on the kind of selection to be practised and the cultivar itself. Hanson (1963) presented two situations when broad sense heritability may be appropriate: selection among clones for a superior clone and selection among F_1 hybrids. When the

objective in a selection experiment is to improve performance of a random mating population or to select among homozygous lines for a pure line, the narrow sense heritability may be utilized.

1.3 EXPECTED GENETIC ADVANCE

The general formula for the expected genetic advance (ΔG) is as follows:

$$\Delta G = i\sigma_p h^2$$

where i = standard selection differential; σ_p = phenotypic standard deviation; h^2 = the appropriate heritability estimate for the system.

The standard selection differential, i (intensity of selection), depends only on the proportion of the population selected, and provided the distribution of phenotypic values is normal it can be expressed as i = z/p, where z = height of the ordinate at the point of truncation; p = proportion selected. The i values have been tabulated by Fisher and Yates (1953), Falconer (1960), and Shelbourne (1969).

The genetic gain under different selection procedures has been discussed by several workers (Shelbourne, 1969; Sprague, 1966; Falconer, 1960). Falconer (1960) outlined four basic selection methods commonly applied: individual, line, within line and combined selections. The appropriate heritabilities for each method may be derived from heritabilities of individual values, phenotypic correlation between members of lines and number of individuals in the lines (Falconer, 1960).

The appropriate phenotypic variance for line means (σ^2_l), and within line deviations (σ^2_{wl}), to be used in the genetic advance formula may be derived from the total phenotypic variance (σ^2_p) as:

$$\sigma^2_l = \frac{1 + (n-1)t}{n} \sigma^2_p$$

$$\sigma^2_{wl} = \frac{(n-1)(1-t)}{n} \sigma^2_p$$

where n = number of individuals in a line; t = phenotypic correlation between members of lines.

Relative merits of the four methods have also been reviewed (Falconer, 1960).

The response of a correlated character may be predicted if the genetic correlation and the heritabilities of the two characters are known. The genetic gain in character y (ΔG_y), by selecting for the correlated character x may be described as follows (Falconer, 1960):

$$\Delta G_y = i h_x h_y r_A \sigma_{py}$$

where i = standard selection differential; h^2_x and h^2_y are heritabilities of characters x and y respectively; σ_{py} = phenotypic standard deviation for character y.

1.4 GENOTYPE x ENVIRONMENT INTERACTION AND ADAPTATION

Genotype x environment interactions (GxE) exist, when a set of genotypes is grown over a range of environments, and the genotypes do not perform in the same relative way in all the environments. In statistical models, GxE interaction is a deviation from the expectations of genotypic and environmental main effects. Much work has been done on the subject of GxE interaction, both by statisticians interested in non-additivity and by plant breeders and agronomists interested in it's presence and meaning in field experimentation.

The use of variance component estimates to identify the presence of GxE interaction was first proposed by Sprague and Federer (1951). Further development in the use of analysis of variance to investigate GxE interactions were carried out by other workers (Comstock and Robinson, 1952; Comstock and Moll, 1963).

1.4.1 Linear Regression Models

A method for partitioning the total GxE interaction sums of square into several parts, belonging to individual genotypes does not provide adequate information about the response types of individual genotypes. The linear regression method, developed by Finlay and Wilkinson (1963) provides a basis for identifying genotypes according to their

response types to the environment. They employed this technique to study the adaptation of 277 barley genotypes, across several environments. In an experiment of this nature, no single physical factor can effectively discriminate between the range of environments. Finlay and Wilkinson (1963) overcame this problem by using a biological assessment of the environment, namely the mean of all genotypes in a particular environment as the environment index. This method employing linear regression was subsequently developed further by Eberhart and Russell (1966), Bucio Alanis (1966) and Bucio Alanis and Hill (1966).

The basic model for the analysis of data from g - genotypes in e - environments (Le Clerg et al., 1962) is as follows:

$$Y_{ijk} = \mu+\gamma_i+\lambda_k+\rho_{j(k)}+\gamma\lambda_{ik}+e_{ijk}$$

where Y_{ijk} = the phenotypic value of i-th genotype in j-th block in k-th environment, (i = 1, ...g; j = 1,...b; k = 1,...3); μ = grand mean; γ_i = additive effect of i-th genotype; λ_k = additive effect of k-th environment; $\rho_{j(k)}$ = j-th block effect in k-th environment; $\gamma\lambda_{ik}$ = the ik-th GxE interaction effect; e_{ijk} = ijk-th residual error.

In linear regression techniques this model is expanded, basically in two ways to provide more information about the interaction component, ($\gamma\lambda_{ik}$).

One approach is to regress the genotypic mean in a particular environment ($\bar{Y}_{i.k}$) onto the environmental mean ($\bar{Y}_{..k}$). Since $\bar{Y}_{i.k} = \mu+\gamma_i+\lambda_k+\gamma\lambda_{ik}$, and $\bar{Y}_{..k} = \mu+\lambda_k$, and also since μ and γ_i are constants for a particular genotype, the regression is in effect between ($\lambda_k+\gamma\lambda_{ik}$) as y-variate against λ_k as x-variate (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966). The appropriate effects model for the regression of ($\lambda_k+\gamma\lambda_{ik}$) against λ_k has been developed (Perkins and Jinks 1968) from the basic model described earlier.

$$\text{i.e.} \quad \gamma\lambda_{ik} = \beta_i\lambda_k+\delta_{ik},$$

where β_i = regression coefficient of the i-th genotype;
δ_{ik} = deviation from the fitted regression line.

Substituting this to the basic model:

$$Y_{ijk} = \mu+\gamma_i+\rho_{j(k)}+(1+\beta_i)\lambda_k+\delta_{ik}+e_{ijk}$$

Working with means, the model can be written as:

$$\bar{Y}_{i.k} = \mu+\gamma_i+(1+\beta_i)\lambda_k+\delta_{ik}+\bar{e}_{i.k}$$

where $\bar{e}_{i.k}$ is the error effect of i-th genotype in k-th environment. Putting $\alpha_{ik} = \delta_{ik}+\bar{e}_{i.k}$ we obtain

$$\bar{Y}_{i.k} = \mu+\gamma_i+(1+\beta_i)\lambda_k+\alpha_{ik}$$

The regression of $\bar{Y}_{i.k}$ against $\bar{Y}_{..k}$ would provide an estimate of the slope, $(1+\beta_i)$, which is termed the adaptation coefficient by Finlay and Wilkinson (1963).

A direct estimate of β_i can be obtained by regressing $(\bar{Y}_{i.k}-\bar{Y}_{..k})$ against $(\bar{Y}_{..k}-\mu)$. This is in effect regressing $(\gamma_i+\gamma\lambda_{ik})$ against λ_k, γ_i being a constant (Bucio Alanis, 1966; Bucio Alanis and Hill, 1966; Perkins and Jinks, 1968).

It may be desirable to know how much GxE interaction is accounted for by linear regression. Perkins and Jinks (1968) proposed the following partitioning model, applicable to Finlay and Wilkinson (1963) type of regression.

$$\sum_i (\text{regression s.s.})_i = \sum_i (1+\beta_i)^2 \sum_k (\lambda_k)^2$$

where β_i = regression coefficient of i-th genotype, i = 1,...,g;
λ_k = additive effect of k-th environment, k = 1,...,e.

Since $\Sigma\beta_i = 0$ this becomes:

$$g\sum_k(\lambda_k)^2+\sum_i\beta_i^2\sum_k(\lambda_k)^2$$

$g\sum_k(\lambda_k)^2$ is the joint regression s.s. which is equal to environments s.s., and $\sum_i\beta_i^2\sum_k(\lambda_k)^2$ is the heterogeneity between regressions. It should be noted that s.s. for heterogeneity between regressions is also the total regression s.s. in the analysis based on Bucio Alanis (1966).

In this context GxE interaction s.s. with (g-1)(e-1) degrees of freedom (df) has two orthogonal components: s.s. for heterogeneity of regressions $(\sum_i \beta_i \sum_k (\lambda_k)^2$ with (g-1) df; and the remainder (deviation from regression s.s), $\sum_{ik} \alpha_{ik}^2$, with (g-1)(e-2) df.

Perkins and Jinks (1968) proposed the method of testing the significances of mean squares for heterogeneity between regressions and the remainder against an error mean square derived from e_{ijk}. According to Perkins and Jinks (1968), the practical usefulness of regression technique depends on the relative magnitudes of the two mean squares. However even when the heterogeneity mean square is not significant, regression s.s. of individual genotypes may be significant, when tested against remainder mean square. Eberhart and Russell (1966) have also discussed the relevance of heterogeneity among regression lines. Based on the facts presented here it seems that a better approach would be to test the significances of regression coefficients of individual genotypes, against 1 and 0 for Finlay and Wilkinson (1963) and Bucio Alanis (1966) regression models respectively.

There is a basic statistical objection to the regression methods described above, namely intrinsic non-independence of effects in x and y variates used in the regression (Freeman and Perkins, 1971). The genotype means, $\bar{Y}_{i.k}$ (y variate) contribute to, and hence are not independent of, the environmental mean, $\bar{Y}_{..k}$ (x variate). Alternative methods developed, as solutions to this objection, will be discussed shortly. Linear regression techniques, in general, have been criticised on various other grounds as well. Easton and Clements (1973); Mungomery, Shorter and Byth (1974) pointed out that there was no a priori reason to believe that GxE interaction was a linear function of the environmental effect. However such criticism may not be valid, when in fact a linear trend does exist in the data. Furthermore curvilinearity may be removed by transformation. Knight (1970, 1973), Witcombe and Whittington (1971)

stated that linear regression may oversimplify the response pattern of genotypes to changing environments.

In spite of these criticisms linear regression is simple and effective and has been widely applied to study GxE interactions of several crop plants: barley (Finlay and Wilkinson, 1963); wheat (Kaltsikes and Larter, 1970); maize (Eberhart and Russell, 1966); grasses (Breese, 1969) and Nicotiana rustica (Bucio Alanis, 1966). The method provides estimates (β_i) for the characterization of genotypes based on their GxE interactions.

Bucio Alanis (1966) initiated the concept of partitioning GxE interaction into components representing biometrical genetical parameters. The literature on the subject now contains many reports (Bucio Alanis and Hill, 1966; Bucio Alanis et al., 1969; Perkins and Jinks, 1968; Perkins and Jinks, 1973). Bucio Alanis (1966) described the application of regression technique, to explain GxE interaction for plant height in two inbred homozygous lines (P_1 and P_5) of Nicotiana rustica. The regression coefficient, β, was computed by regressing $[d] + \gamma$ against λ_k: $\lambda_k = \frac{1}{2}(\bar{P}_1+\bar{P}_5)$ and $[d] + \gamma = \frac{1}{2}(\bar{P}_5-\bar{P}_1)$, where $\bar{P}_1$ and $\bar{P}_5$ were phenotypic performance of P_1 and P_5 lines; $[d]$ = additive genetic effect and γ = the interaction. A similar analysis for F_1 generation has been suggested by Bucio Alanis and Hill (1966). Perkin and Jinks (1968) constructed models to extend the above analysis to a number of inbred lines and F_1 hybrids. The genetic implications of results from these analysis were interesting. Perkins and Jinks (1968) found significant positive correlation between β_i and d_i (additive genetic effect) for 20 inbred lines of Nicotiana rustica, for plant height. The taller genotypes were more sensitive (higher β_i) to the invironment. In most instances the F_1's had higher mean performances and regression coefficients than the mean of their respective parental lines. Hence heterosis exhibited by many F_1's was generally associated with greater sensitivity to the environment (Perkins and Jinks, 1968). Another implication of these analyses is the possibility to predict the mean phenotypic performance in any generation, within the range of environments sampled.

In recent years linear regression techniques have been utilized to study GxE interactions in diallels. Hinkelmann (1974) partitioned the sum of squares for heterogeneity of regression into general and specific combining-ability components, in order to interpret GxE interaction, in terms of additive and non-additive gene action. Models which specifically relate regression parameters to the appropriate genetical parameters have been developed by Perkins (1970). Another model, based on Griffings (1956) combining ability approach, suggested by Lin et al. (1977) may be described as follows:

$$Y_{ijk} = \mu+\alpha_{ij}+\lambda_k+\beta_{ij}\lambda_k+\delta_{ijk}$$

where Y_{ijk} = the phenotypic performance, in k-th environment, of the progeny from a cross between i-th and j-th parental lines; α_{ij} = genetic effect of ij-th progeny; λ_k = k-th environmental effect; β_{ij} = regression coefficient of ij-th progeny (equivalent to β_i mentioned earlier); δ_{ijk} = ijk-th residual effect.

Also, $\alpha_{ij} = g_i+g_j+s_{ij}$

where g_i and g_j represent g.c.a. effects and s_{ij} is the s.c.a. effect.

If the interactions of these three effects with the environment is expressed as a linear function of λ_k:

$$Y_{ijk} = \mu+g_i+g_j+s_{ij}+\lambda_k+\left[\beta_{(g)i}+\beta_{(g)j}+\beta_{(s)ij}\right]\lambda_k+\delta_{ijk}$$

where $\beta_{(g)i}$, $\beta_{(g)j}$ and $\beta_{(s)ij}$ are regression coefficients for g_i, g_j and S_{ij} respectively.

1.4.2 Stability

The term "stability", with respect to GxE interaction, has been interpreted in a rather loose sense in the literature. Several parameters have been proposed to measure stability. Allard and Bradshaw (1964) used the term "well-buffered" for a stable variety, with low GxE interaction. They also identified the occurrence of two general forms of buffering, the individual and population buffering. Obviously individual

buffering is more important in homogeneous populations, the property being associated with specific genotypes in the population. Population buffering, which arises from interactions among different coexisting genotypes, is commonly associated with heterogeneous populations (Allard and Bradshaw, 1964).

Plaisted and Peterson (1959) considered ecovalance, the contribution of a genotype to the GxE interaction sum of squares, as a stability parameter. Shukla (1972) pointed out that characterisation of genotypes, based on regression coefficients, may not be effective when only a small fraction of GxE interaction was accounted for by regression. Shukla (1972) proposed an unbiased estimator of stability variance, σ^2_i, for the i-th genotype, which is estimated as follows:

$$\hat{\sigma}^2_i = \frac{1}{(e-1)(g-1)(g-2)}\left[g(g-1)\sum_k(\bar{Y}_{i.k}-\bar{Y}_{i..}-\bar{Y}_{..k}+\bar{Y}_{...})^2 - \sum\sum_{ik}(\bar{Y}_{i.k}-\bar{Y}_{i..}-\bar{Y}_{..k}+\bar{Y}_{...})^2\right]$$

The notations are similar to those in Le Clerg et al. (1962) model described earlier. The term $(\bar{Y}_{i.k}-\bar{Y}_{i..}-\bar{Y}_{..k}+\bar{Y}_{...})$ is in fact the interaction effect $\gamma\lambda_{ik}$. Hence the square of this term represents the sum of squares for GxE interaction contributed by i-th genotype. The significance of σ^2_i is tested by an approximate F-test, $F' = \hat{\sigma}^2_i/\hat{\sigma}^2$, $\hat{\sigma}^2$ being the pooled error variance. A genotype whose σ^2_i is not significant is defined as stable (Shukla, 1972).

The stability parameters obtained from regression techniques have been used more widely. Finlay and Wilkinson (1963) proposed the concept of adaptability, in relation to genotypic means and their corresponding regression coefficients. Genotypes with above average yields, and regression coefficients of the order of 1.0 were considered as showing general adaptability. Cultivars which had regression coefficients greater than 1.0 were specifically adapted to favourable environments, whereas those which had coefficients less than 1.0 were specifically adapted to poor environments. In the context of stability, a genotype with a very low regression coefficient ($\beta \simeq 0$) was classified as highly stable (Finlay

and Wilkinson, 1963).

In addition to the regression coefficient, Eberhart and Russell (1966) proposed another stability parameter ($\sigma^2_{d_i}$) for the i-th genotype as

$$\hat{\sigma}^2_{d_i} = \left[\sum_k \hat{\delta}^2_{ik}/(e-2)\right] - \hat{\sigma}^2/b_i$$

where $b_i = (1+\beta_i)$, is the regression coefficient of the i-th genotype; δ_{ik} = the deviation from regression line for the i-th genotype in k-th environment; σ^2 = pooled error variance and e = number of environments. According to Eberhart and Russell (1966) an ideal cultivar is one with high genotypic mean, unit regression coefficient, and least amount of lack of fit from regression ($\hat{\sigma}^2_{d_i} = 0$).

Tai (1971) suggested two stability parameters, α_i and λ_i based on partitioning of GxE interaction effect of i-th genotype into two components. The statistic $\hat{\alpha}_i$ measured the linear response to the environment, whereas $\hat{\lambda}_i$ represented the deviation from the linear response.

$$\alpha_i = \frac{\sum_k I_k \cdot (\gamma I)_{ik}/e-1}{(MSL-MSB)/gb}$$

where I_k = the k-th environment effect; $(\gamma I)_{ik}$ = interaction effect of i-th genotype with k-th environment; MSL and MSB are mean square estimates for environments and blocks respectively; g, b, and e are numbers of genotypes, blocks and environments respectively. The term in the numerator is a form of mean cross product estimate, between I_k and $(\gamma I)_{ik}$ effects. The denominator is an estimate of environment variance component. The stability parameter, λ_i is estimated as $(\sigma^2_{\delta_i}+\sigma^2_e)/\sigma^2_e$, where $\sigma^2_{\delta_i}$ and σ^2_e are variance component for deviations from regression of i-th genotype and error variance respectively (Tai, 1971).

The two statistics α_i and λ_i have equivalent meaning to β_i (b_i-1, of Eberhart and Russell, 1966), and stability statistic, $\hat{\sigma}^2_{d_i}$, of Eberhart and Russell (1966). Two statistics, $\hat{\alpha}_i$ and $\hat{b}_i$ are related as follows:

$$\hat{\alpha}_i = \frac{MSL}{MSL-MSB} \quad (b_i-1)$$

According to Tai (1971) a variety with average stability has $(\alpha, \lambda) = (0, 1)$.

Hanson (1970) proposed a stability parameter (D_i) similar to ecovalance, but also taking into account the regression.

$$D_i^2 = \sum_k \left\{\gamma\lambda_{ik} + (1-\alpha)\lambda_k\right\}^2$$

The term α here is the minimum observed value of $(1+\beta_i)$. $\sum_k \gamma\lambda_{ik}^2$ is the ecovalance of i-th genotype.

1.4.3 Independent Assessment of Environment

Following the criticism of Freeman and Perkins (1971), several workers have attempted to find an independent assessment of the environment, both biological and physical. Bucio Alanis and Hill (1966) used the mid parental mean as an independent assessment of the environment, in testing F_1 hybrids.

In more recent years, principal component analysis has been used to construct environment indices, based on linear functions of a set of environmental variables (Hardwick and Wood, 1972; Wood, 1976; Perkins, 1972). The objective of principal component analysis is to represent the total variability and covariability present in a set of variables, by fewer orthogonal linear functions (principal components) of the variables. The eigenvalue associated with each component estimates the variance of that component (Seale, 1966). Because climatic variables are measured on different scales, it is convenient to standardise all variables converting them to unit variance over environments.

Perkins (1972) measured six climatic factors to represent the environment: percentage relative humidity at 6a.m. (RH6), percentage relative humidity at 12 p.m. (RH12), daily rainfall in inches (RAIN), daily sunshine in hours (SUN), maximum air temperature in ^{o}F (MXT), and minimum air temperature in ^{o}F (MNT). He found that the first 3 principal

components, P_1, P_2 and P_3 accounted for 95 percent of total variability in the climatic data. Correlations between standardised scores of each climatic factor and scores of each of the 3 components (the "factor structure") revealed that in P_1, RH6, RH12 and RAIN were in opposite directions to SUN, MXT and MNT. The scores for RH6, RH12 and MNT were highly correlated with P_2, whereas RAIN contributed mainly to the P_3 component. The percentage GxE interaction explained by regression, on an environment index derived from these principal components, ranged from 24-100 percent.

Freeman and Crisp (1979) followed a procedure in which one character was regressed on another unrelated character, and attempted to explain the GxE interaction of the character of primary interest in terms of the other. In conclusion they pointed out that this technique may also be useful to explain large GxE interactions for a variable in terms of a relatively small variation in a related variable. Where both variables showed large GxE interactions, Freeman and Crisp (1979) suggested the approach of Boughey and Jinks (1978), of measuring the same variable at different times. Another approach to obtain an independent assessment of the environment is to estimate $\overline{Y}_{..k}$ (refer to the linear model in section 1.4.1) on a wider (or different) range of genotypes than those used to get $\overline{Y}_{i.k}$.

1.4.4 Reducing GxE Interaction

The GxE interaction, in certain instances can be removed by transformation of the scale (Mather, 1971). However, as Breese and Hill (1973) pointed out, this could completely alter the interpretation of the results. An altogether different method for reducing GxE interaction was first proposed by Horner and Frey (1957): the dilineation of testing zones based on results of earlier analysis. Using estimates of GxE interactions from nine locations, over 5 years, for oats, they found that the GxE component could be reduced by 11, 21, 30 and 40 percent by dividing the test area into two, three, four and five sub-areas respectively. Following these procedures Abou-El-Fittouh

et al. (1969) suggested the application of clustering analysis, for classifying environments, to minimize the within cluster GxE interaction. They employed two similarity coefficients, distance coefficient ($d_{kk'}$) and correlation coefficient ($r_{kk'}$), for clustering environments.

$$d_{kk'} = \left\{\sum_i \left[(\hat{\gamma\lambda})_{ik} - (\hat{\gamma\lambda})_{ik'}\right]^2 / g\right\}^{1/2}$$

$$r_{kk'} = \sum_i (\hat{\gamma\lambda})_{ik} (\hat{\gamma\lambda})_{ik'} / \left[\sum_i (\hat{\gamma\lambda})^2_{ik} \sum_i (\hat{\gamma\lambda})^2_{ik'}\right]^{1/2}$$

where $d_{kk'}$ and $r_{kk'}$ are distance coefficient and correlation coefficient of environments k and k'; $(\gamma\lambda)_{ik}$ and $(\gamma\lambda)_{ik'}$ are GxE interaction effects of i-th genotype in k and k' environments respectively.

The above estimates were computed for lint yield data in cotton. The method could be extended to include all traits of importance as follows (Abou-El-Fittouh et al., 1969).

$$d_{kk'} = \left[\sum_{j=1}^{m} W_j d_{kk'j}\right]^{1/2}$$

where $d_{kk'j}$ and W_j are the distance coefficient and the relative weight for trait j and m is the number of traits included. When a number of traits are considered, principal components may also be used.

1.4.5 Multivariate Techniques

Several multivariate techniques have been applied in the analysis of GxE interactions. The use of multivariate techniques to construct independent environment indices, based on a set of environmental variables, has already been discussed in section 1.4.3. Perkins (1972) used principal component analysis to study GxE interactions for plant height in inbred lines of Nicotiana rustica. He identified 4 groups of lines for plant height: mop head M_1 and M_2, non-mop head m_1 and m_2. The first principal component was related to the general response of all lines to the environmental component, while the second component was specifically related to differences in response of mop head and non-mop head lines (Perkins, 1972). Freeman and Dowker

(1973) applied principal component analysis to analyse carrot cultivar performances, and concluded that it provided no additional information to that obtained by the analysis of variance.

Clustering analysis has been used to study GxE interactions (Mungomery et al., 1974; Byth et al., 1976). Byth et al. employed this technique to study yield data from 49 wheat cultivars grown in 63 international environments. They found that linear regression accounted for only 8.9 percent of GxE interaction. The basis of Byth et al. (1976) method was to reduce the original data matrix, by a two-way classification of environments and cultivars, using clustering techniques. Subsequent analysis was done using cultivar group means and environment group means. Obviously some information is lost in this procedure. However it has the advantage of reducing the original data matrix, thereby facilitating further analysis.

Tai (1975), using the concept of sequential development of yield components, proposed a method based on path analysis. The two basic assumptions of the method were: (a) the yield, W, was the final product of sequential development process from x, y, z, to W. (b) the environmental resources can be separated into three independent groups, R_1, R_2 and R_3, each group supporting the development of x, y, and z respectively. The stability parameters based on the above analysis have been compared with those of two other methods (Tai, 1979).

Multivariate techniques will undoubtedly play an important role in studying GxE interactions, especially where functional linearity fails. However as Hill (1975) pointed out despite it's imperfection, linear regression technique has the advantages of simplicity and biological relevance, which are lacking from most multivariate methods.

1.5 OPTIMUM PLOT ALLOCATION

In cultivar evaluation studies it is necessary to collect data at several locations over a number of years.

As Jones et al. (1960) pointed out, under these circumstances it may be desirable to conduct experiments in such a way to provide required precision at a specified or minimum expense. However the optimum allocation of replicates, locations and years needed to obtain an estimate of cultivar potential has not received much attention in the literature.

Miller et al. (1959) estimated the variety x location, variety x year and variety x location x year interaction components in cotton variety tests. Based on the magnitude of these estimates, they pointed out the implications of such interactions on variety evaluating procedures. Taking the cost factor into consideration Sprague and Federer (1951) constructed formulae to determine the optimum number of locations and replications needed to make the maximum genetic advance in hybrid corn yield trials. To illustrate the principles involved, the solution for optimum allocation of numbers of replicates and locations in a single year is described below.

The formula for average genetic advance, ΔG, in positive standard units due to selection of the highest yielding hybrid (Cochran, 1948 quoted by Sprague and Federer, 1951)

$$\Delta G = \bar{d}_p \bar{x}_m \{ \bar{d}_p + \frac{\bar{b}_p}{p} + \frac{1}{rp} \}^{\frac{1}{2}}$$

where $\hat{b}_p$ and $\hat{d}_p$ were unbiased estimates of ratios of variety x location to error variance, and variety to error variance component respectively; $\bar{b}_p$ and $\bar{d}_p$ are arithmetic averages of $\hat{b}_p$ and $\hat{d}_p$ from different experiments; $\bar{X}_m$ = average value of the largest normal deviate from a sample of size m; r and p are numbers of replications and locations respectively.

The equation for cost is: $X = \frac{(P+1)}{2} A + rpB$, where X = total amount of money spent on the experiment; A = cost of one round trip including payment for meals and labour (an experiment cost); B = cost of planting and harvesting including meals and lodging (a plot cost).

The procedure for calculating optimum r and p is to maximise, θ, in the following function:

$$\theta = G - \chi \left\{ \frac{(p+1)A}{2} + rpB - X \right\}$$

where χ is a Lagrange multiplier. Upon partial differentiation with respect to r, p and χ, the solutions for r and p are found to be:

$$r = \sqrt{A/2B\bar{b}_p} \qquad p = \frac{2X-A}{A+\sqrt{2AB/\bar{b}_p}}$$

The computed r and p values are rounded off to the nearest whole numbers.

From the studies of Sprague and Federer (1951), it was apparent that cost per plot decreased rapidly as the number of plots per location was increased. Hence B values were based on a constant number of plots. The cost estimates calculated under a particular situation may not be applicable to others.

Jones et al. (1960) employed the equation for the variance of a genotypic mean to compute expected variances of genotypic mean for various plot allocations. The variance of a genotypic mean ($V_{\bar{x}}$) may be expressed as follows:

$$V_{\bar{x}} = \frac{\sigma^2}{bsy} + \frac{\sigma^2_{GSY}}{sy} + \frac{\sigma^2_{GS}}{s} + \frac{\sigma^2_{GY}}{y}$$

where b, s and y are numbers of blocks, sites and years respectively. Variance component estimates used were those obtained from experiments. The principle involved here is to find out whether a different allocation, of approximately the same number of plots, could give a lower $V_{\bar{x}}$. A lower $V_{\bar{x}}$ means an increased efficiency in detecting differences among genotypes. To facilitate comparison of $V_{\bar{x}}$ from different allocations Jones et al. computed an index called relative efficiency for each allocation as:

$$\text{Relative efficiency} = \frac{\text{actual } V_{\bar{x}} \text{ from the estimating expt.}}{\text{expected } V_{\bar{x}} \text{ from the allocation}} \times 100$$

A relative efficiency greater than 100 percent indicated a better allocation compared to the present experiment. However several other factors should be considered when comparing different allocations. For many characters an

increase in number of plots means a higher cost in obtaining information. The addition of a location involves establishing new facilities and the cost may be considerable, as indicated by the cost equation of Sprague and Federer (1951) described earlier. Furthermore an increase in number of years would delay the release of the new cultivar.

Jones et al. also used three dimensional drawings to visualize the joint effect of changing number of years, locations and replications on $V_{\bar{x}}$.

1.6 SAFFLOWER

1.6.1 Origin and Related Species of Cultivated Safflower

The genus Carthamus can be divided into four basic sections based on the chromosome number: n = 10, 12, 22 and 32 (Ashri and Knowles, 1960). In a taxonomic sense the section with n = 12 includes Carthamus tinctorius L. (cultivated safflower), and other related wild species such as Carthamus palaestinus Eig., Carthamus oxycantha M.B. and Carthamus flavescens Spreng. However Carthamus tinctorius L., Carthamus oxycantha M.B. and Carthamus palaestinus can be intercrossed to yield fertile F_1 and F_2 hybrids (Ashri and Rudich, 1965; Ashri and Efron, 1964). In the context of biological species concept, these three taxonomic species may be regarded as representing different ecotypes of the same species. Ashri and Knowles (1960) provides a detailed description of the species belonging to the four sections of the genus Carthamus, previously mentioned.

The induction of tetraploidy in cultivated safflower by using colchicine solutions has also been described (Schank and Knowles, 1961). A 0.1 percent aqueous solution of colchicine applied to the young seedlings was found to be most successful. The tetraploids had larger stomata, pollen grains and seeds, compared to diploids. However the increase in seed size was largely due to the very thick hull. Triploids often found in populations of autotetraploids of cultivated safflower are considered to be products of outcrosses to diploid plants during the previous generation.

Estilai and Knowles (1980) identified several aneuploids (2n = 25, 26) of cultivated safflower in the progenies of open pollinated triploid populations.

Carthamus tinctorius L. probably originated in an area bounded by eastern mediterranean and Persian Gulf. It would appear that Carthamus oxycantha M.B. and Carthamus palaestinus Eig. are the most likely ancestors. However Carthamus tinctorius L. has dominant seed shape and pappus, while these are recessive in Carthamus oxycantha M.B. (Ashri and Efron, 1964; Ashri and Rudich, 1965). Probably Carthamus palaestinus Eig. or a closely related species has been the progenitor of cultivated safflower.

1.6.2 Evaluation of Safflower Germplasm

The pioneering work of P.F. Knowles of the United States Department of Agriculture (USDA) has led to the establishment of an extensive germplasm collection of both cultivated and wild species of the genus Carthamus. The collection has already been valuable in breeding for disease resistance and quality and quantity of oil (Leininger, 1963; Zimmer and Leininger, 1965; Knowles et al., 1968; Knowles, 1969a; Knowles, 1969b; Knowles, 1971). At least 2000 lines from the safflower germplasm collection were evaluated by Ashri, in several locations both in Israel and the United States. In a series of papers he presented the immense variability found in the collection (Ashri, 1971a; Ashri, 1971b; Ashri et al., 1974; Ashri et al., 1975; Ashri, 1975; Ashri et al., 1976; Ashri et al., 1977).

Considerable variability for morphological characters was observed in the germplasm. Shape of the upper stem leaves, primary head shape, appressed or spreading outer involucral bracts, spininess (both spine length and number), corolla colour, level of branching and number of branches per plant showed much variation (Ashri, 1975). There was divergence for plant height and length of the period from planting to flowering. Tallest plants tend to come from Turkey-Afghanistan area and shortest from India (Ashri et al., 1975). Both natural and human selection has

contributed to the divergence of safflower germplasm (Ashri, 1975).

Plants with long rosette period (winter-types) were identified in local populations of Carthamus tinctorius L. from north-western Iran. Lines developed from these plants showed considerable variation for desirable traits such as winter hardiness, seed yield, oil content, number of heads per plant and 1000 seed weight, indicating scope for breeding (Ghanavati and Knowles, 1977). Bahman and Zali (1979) reported a comparison study of winter and spring type cultivars.

Correlations were calculated between plant height, length of growing period and yield components by Ashri et al., 1974. The length of growing period was not correlated with yield components in Iranian and Egyptian lines, but correlated with some components in Indian lines. It was concluded that some selection pressure can be applied to shorter growing period and higher yield simultaneously. Studies on germplasm collection also revealed that plant height was not highly correlated with yield components indicating the possibility of breeding for high yielding shorter cultivars (Ashri et al., 1975).

Considerable attention has been given to sources of disease resistance in safflower germplasm evaluation studies. Accessions from Carthamus flavescens Willd. and Carthamus palaestinus Eig. were free from safflower fly Acanthophilus helianthi R. and may prove to be promising in breeding for resistant cultivars (Ashri, 1971b). It was also concluded that fly damage can be reduced by breeding for earliness in Mediterranean conditions. In India late maturing cultivars may be desirable.

Lines resistant to the following diseases have been found in the germplasm collection: Rust - Puccinia carthami Cda.; Powdery mildew - Erisiphe cichoracearum D.C.; Ramularia leafspot - Ramularia carthami Zaprom; Cercospora leafspot - Cercospora carthami Sund and Ramak; Phyllody - a mycoplasma disease. Association of resistance with other

traits have also been reported (Ashri, 1971a). Some lines resistant to Phytopthora root rot have been identified. A high level of resistance to root rot may be valuable when safflower is grown under irrigation. Germplasm from several countries was found to have resistance to Fusarium oxysporium f carthami Klis & Hous (Knowles et al., 1968) and has been successfully incorporated into commercial cultivars. Resistance has been found to Verticillium wilt - Verticillium albo-atrum Reinke & Berth (Urie and Knowles, 1972), which when incorporated into commercial cultivars should make safflower safer to grow in cotton areas. Several introductions resistant to rust have been extensively tested in United States for breeding purposes (Zimmer and Leininger, 1965; Zimmer and Urie, 1969).

Leaf-spot disease caused by Alternaria carthami Chowd, can be particularly severe on irrigated plantings, and in warmer areas where periods of heavy dew or frequent showers occur (Weiss, 1971). The disease can be seed borne and causes seed-rot and damping off of seedlings. In mature plants it causes leaf spots. Ashri (1961) identified resistance to leaf spot disease in, low iodine value, Indian line U.C. 57-146. Carthamus lanatus is resistant to leaf spot, caused by Alternaria carthami Chowd, but when crossed with cultivated safflower yields sterile hybrids.

Head rot disease caused by Botrytis cinerea Pers. can hamper safflower growth in high humid areas (Weiss, 1971). Spores of the fungus are wind-borne and infection of flower heads may occur at any stage from budding to post-flowering. The disease affects the entire head and invades the receptacle, so that the head lifts off easily. Barash et al. (1964) found that leachates from safflower florets contain nutrients that stimulate germination of the conidia of Botrytis cinerea Pers. It has been reported that introductions from Rumania are more resistant to head rot disease (Scheibe, 1938, after Knowles, 1958). Knowles (1958) identified high resistance to Botrytis cinerea Pers. in an introduction from Egypt, PI 209290. Lines originating from India were highly susceptible.

Studies on yield components have revealed considerable differences in potential lines from different origins. Ashri et al. (1974) studied a collection of 903 genotypes of safflower for mean yield per plant and 3 yield components, number of heads per plant, number of seeds per head and seed weight. A stepwise regression analysis of the data revealed that number of heads per plant was the most important component affecting plant yield. They concluded that there was abundance of genetic variability for breeding high yielding cultivars.

The oil content and iodine value also showed extensive variability. Higher oil content lines originated from Iran and India. Most correlations of oil content with yield components and other traits were low. The iodine value is a measure of unsaturation in the oil, a higher value indicating the presence of more unsaturated fatty acids. Lines originating from Afhanistan, Iran and Turkey had higher iodine values than those from India, Pakistan and Syria (Ashri et al., 1977). Safflower oil, with high iodine value, is commonly used as a non-yellowing drying oil. The low iodine value safflower oil is similar to olive oil and is more suitable as a cooking oil.

An allozyme investigation, using alcohol dehydragenase (ADH), has added more information to the divergence pattern of safflower. Two genes involved in the production of this enzyme, Adh_1 and Adh_2, have been identified. These findings were in agreement with the cytogenetic interpretation of interspecific relationships in the genus Carthamus (Efron et al., 1973).

1.6.3 Inheritance Studies

Information on inheritance of various characters is useful for a successful breeding programme. Furthermore inheritance studies with wild relatives contribute to the elucidation of ancestry.

1.6.3.1 Inheritance of plant characteristics

Ashri and Efron (1964), using interspecific crosses between Carthamus palaestinus Eig., Carthamus oxycantha M.B. and two Carthamus tinctorius L. cultivars concluded monogenic control for the following characters:

1. Shape of cotyledon - elongated, narrow dominant to short rounded.
2. Pigmentation of cotyledon midvein - green dominant to purple.
3. Margin of rosette leaves - lobed partially or not dominant to entire.
4. Spininess - presence dominant to absence.
5. Spine colour - yellow dominant to white.
6. Corolla colour - yellow dominant to white.
7. Pappus - presence dominant to absence.
8. Seed shattering - presence dominant to absence. Plants whose outer involucral bracts open are considered as shattering.
9. Seed shape - obpyramidal ribbed dominant to oval smooth.

Kotecha (1979), using crosses of Carthamus tinctorius L. and Carthamus palaestinus Eig., studied the inheritance of plant height, time of flowering (TF), time to maturity (TM), time from flowering to maturity (TFM), leaf length and stem diameter. He reported that gene action for plant height and leaf length was additive but non-additive for TF, TM and TFM. Narrow sense heritability estimates for TM and plant height were 11% and 79% respectively.

Rosette habit in safflower results from nonelongation of internodes. Imrie and Knowles (1970) reported that short rosette period of Carthamus tinctorius L. was dominant over long rosette period of Carthamus flavescens Spreng. and was monogenic controlled. Zimmerman (1976) studied the inheritance of rosette habit, in F_1, F_2 and F_3 generations following a cross between Carthamus tinctorius L. and Carthamus flavescens Spreng. His results indicated that a multiallelic major locus and modifier genes were involved in the inheritance of rosette habit in safflower.

Inheritance studies, based only on the cultivated species, are also available in the literature. Abel (1976b) studied the inheritance of plant height components and reported that lower stem node number, upper stem internode length and total upper stem length could be explained by a simple additive-dominance model. Investigations, with a completely branched mutant, revealed that incomplete branching habit was due to a single dominant gene. Variability within incomplete branched types may be a result of additional gene effects (Abel, 1975). Temple and Knowles (1975) found that a single recessive allele, br, determines the brittle stem character in safflower.

Reproductive sterility has been reported in segregating generations of crosses involving cultivar US 10 and an Indian introduction 57-147. Carapetian and Knowles (1976) suggested that 3 unlinked genes (A, B and C) are involved in the inheritance of sterility. Sterility occurs when homozygous recessive at A locus interacts with a homozygous recessive at either B or C locus. The lines US10 and 57-147 appeared to have genotypes AAbbcc and aaBBCC. The F_2 families segregating at the 3 loci gave a good fit to 57:7 (fertile:sterile) ratio (Carapetian and Knowles, 1976), in which the sterile genotypes are aabbC_, aaB_cc, and aabbcc. Meiotic irregularities caused by interacting sterility genes are reported by Carapetian and Rupert (1977).

Several reports are also available on inheritance of resistance to various diseases of safflower (Thomas, 1976; Bockelman, 1974). Thomas (1976) studied the inheritance of resistance to Phytopthora root rot, incited by Phytopthora drechsleri, using resistant cultivars VFR1 and USB. It was evident that there are two separate and distinct types of resistance in safflower to Phytopthora drechsleri, root resistant shown by cultivar VFR1 inherited through a single dominant gene, and hypocotyl resistance in cultivar USB inherited by a recessive gene.

1.6.3.2 Inheritance of seed characteristics

Much of the success in breeding high oil safflower cultivars is a result of inheritance studies on oil composition and hull mutants. Most of the safflower cultivars grown are high linoleic types (linoleic 75-80%, oleic 10-15%), with iodine values ranging from 137-145. The high percentage of unsaturated linoleic acid makes it an ideal non-yellowing drying oil for paint industry (Kneeland, 1966). Knowles and Mutwakil (1963) found a low iodine value (85-100) safflower line with a high oleic acid level (linoleic 12-30%, oleic 64-83%), in selections from India. The high oleic acid safflower oil is very similar to olive oil and may be used as a cooking oil. Knowles and Hill (1964) reported another introduction from Iran (PI 254717) which had an iodine value intermediate to the above two types. Inheritance studies, conducted by Knowles and Hill (1964), on these different lines revealed that three alleles Ol, ol' and ol, showing graded dominance, mainly determine the proportion of linoleic and oleic acids in safflower oil. The alleles Ol, ol' and ol give rise to high, intermediate and low linoleic acid levels respectively. The effects of alleles on composition of safflower oil can be described as follows (Knowles and Hill, 1964):

Genotype	Linoleic acid	Oleic acid
	%	%
OlOl	75-80	10-15
Olol'	70-75	15-20
Olol	60-75	18-35
ol'ol'	42-54	35-50
ol'ol	30-40	55-63
olol	12-30	64-83

It has been reported also that the oil composition is determined by the genotype of the embryo and not by the parent (Yermanos et al., 1967). Inheritance studies with flax and rapeseed have also indicated that oil composition is governed by the genotype of the embryo (Harvey and Downey, 1964; Yermanos and Knowles, 1962). Maternal

effects were not involved in the inheritance of oil composition of safflower (Yermanos et al., 1967).

Based on data from 372 F_2 plants, from a cross between lines N-1 and N-8, Claassen et al., (1950) concluded that there was a high negative correlation between oil content and hull content in safflower seed. Thick hull lines are low in oil content. Plant breeders have attempted to reduce the pericarp tissue of the seed, by breeding and selection, in order to produce cultivars with higher oil contents. Two types of hull mutants have been isolated in safflower. Rubis (1957), (quoted by Urie and Zimmer, 1970a) identified these as thin hull and striped hull mutants. Thin hull condition is controlled by a recessive gene, th, and striped hull is conditioned by a multiple allelic series at stp locus, independent of th gene. Thin hull character is due to a reduction of the formation of secondary walls in the outer sclerenchyma layers of the pericarp (Ebert and Knowles, 1968). The striped hull mutants are characterized by regular alternating thick and thin areas in both outer and inner sclerenchyma tissues. Experimental lines with any of the 3 striped hull alleles, stp, stp^g and stp^p (purple-striped), yield more oil than normal hull types (Rubis, 1967; quoted by Urie and Zimmer, 1970a). However the two experimental lines (A101 and A12417) with Stp allele contain a colourless compound which darkens during oil processing to give an undesirable colour (Burkhardt, 1970).

The thin hull types have weak stems and are structurally male sterile. These undesirable characters associated with thin hull mutants are considered to be due to pleiotropic effects of the th allele (Rubis, 1967; quoted by Urie and Zimmer, 1970a).

Urie and Zimmer (1970a) reported another hull type, reduced hull, from a cross between normal hull cultivar Ute and a purple striped hull line 13049. The reduced hull lines show an overall reduction of outer sclerenchyma tissue of the achene, allowing underlying phytomelanin area to show through as blotches. According to Urie and

Zimmer (1970a), reduced hull types do not possess the undesirable characteristics of thin and striped hull types and contain 41-44 percent oil. The inheritance of reduced hull character is not well understood.

1.6.4 Breeding

Safflower is basically a self-pollinated crop, but the degree of outcrossing varies with the cultivar and presence of insect pollinators (Claassen, 1950). In India a range of 11.5-25% for natural crossing, with an average of 16.5%, has been recorded (quoted by Weiss, 1971).

Several techniques have been suggested for controlled crossing of safflower. According to the method described by Claassen and Kiesselbach (1945), (quoted by Weiss, 1971) the anthers are removed about 12-24 hours prior to dehiscence. The emasculated florets are rinsed first in 57% ethyl alcohol and then in water. These florets are pollinated the following morning. Claassen and Kiesselbach (1945) found seed set in 71% of their attempts. However the average number of seeds per capitulum was 6.2. Knowles (1958) suggested a much quicker method which does not involve rinsing. First the floret is squeezed with a sharp tweezers just below the attachment of anthers. The corolla is detached by slightly bending, and corolla and anther tube are gently slipped off the style. The possibility of style breakage is more in this method, but it minimizes the amount of pollen escaping from anthers. The type of bag used to cover pollinated heads affects the amount of seed set (Patil and Chavan, 1958). It was noted that cloth bags frequently touched the inflorescence and lowered the seed set.

The majority of commercial cultivars of safflower are selections in early selfed generations following a cross. Several authors have reported heterosis and inbreeding depression in safflower (Yazdi-Samadi et al., 1975; Deokar and Patil, 1979). Yazdi-Samadi et al. (1975) estimated heterosis for plant height, yield, seed weight, oil content and flowering time. The hybrids may outyield the best pure line by as much as 10-20% (Claassen, 1963,

quoted by Urie and Zimmer, 1970b). The discovery of thin hull mutants offered a method for commercial production of hybrids. However the development of hybrid cultivars has been slow compared to pure lines. This is mainly due to the pleiotropic effect of th allele, which makes the thin hull female line less vigorous. Also as Urie and Zimmer (1970b) pointed out, the limited self-fertility in thin hull lines, results in some selfing and sibbing among females in the hybrid seed field. This can lead to hybrid seed lots containing as much as 30% female selfs.

Resistance to several diseases has been incorporated into commercial safflower cultivars. Identification of hull mutants has made it possible to produce cultivars with oil contents as high as 45%. Two oil types of safflower are grown commercially. The original, high linoleic acid types are grown on a larger scale. A high oleic acid cultivar, UC-1, has been released (Knowles and Hill, 1965). The importance of the two oil types have been discussed in section 1.6.3.2. In recent years a cultivar, Oleic-Leed has been produced from a cross between UC-1 and Leed (Urie et al., 1979).

As Knowles (1977) points out further studies of safflower may involve identifying resistance to diseases favoured by high humidities, development of male sterile lines and exploiting the potential of polyploids.

CHAPTER 2

MATERIALS AND METHODS

2.1 NATURE OF THE EXPERIMENT

The study was conducted at three sites in the Manawatu area: Massey University crop research unit; DSIR research station, Aorangi, and Flockhouse research station. These sites were considered as a representative sample of the varying environmental conditions prevalent in the area. Data were collected on seven safflower genotypes in 1978 and ten genotypes in 1979. The three additional genotypes included in the study in 1979, were chosen from the safflower germplasm collection. Preliminary studies had indicated the potential usefulness of these three genotypes.

The main purpose of the experiment was to partition the phenotypic variance into it's components, and to estimate heritabilities, adaptabilities and optimum plot allocations. A comparison of performances of the genotypes indicated their relative usefulness for Manawatu conditions. Considerable attention was also given to the aspect of disease resistance. Earlier safflower trials conducted in the area had revealed that head-rot caused by Botrytis cinerea Pers. was the most important disease affecting safflower cultivation (Anonymous, 1975).

2.2 EXPERIMENTAL DESIGN

A randomized complete block design with three replicates was used for each individual experiment. An experimental plot consisted of two adjacent rows, 0.9 m. apart and 5 m. in length. There was a 1 m. lane between plots end to end. Plant spacing within a row was approximately 10 cm. Guard rows, of cultivar 0-22, were included on either side of each block to eliminate border effects.

2.3 DESCRIPTION OF GENOTYPES

A description of the genotypes used in this study is presented in Table 2.1.

2.4 FIELD CONDITIONS

The sowing dates for the three sites are presented in Table 2.2.

During seed bed preparation all sites were given a uniform application of fertilizer (Amophos at 100 kg/ha). Preplanting, soil incorporated weedicide, treflan (1 kg a.i./ha) was used at all sites to control weeds. However occasional hand weeding and rotary hoeing were needed when weed growth was noticeable.

Seeds were hand sown, except at Aorangi, where a corn seeder was employed in both years. About two weeks after germination plots were thinned out to approximately 10 cm. spacing between plants. Irrigation was necessary at Flockhouse, when continuous dry weather was experienced. Other sites were not irrigated.

Half of each experimental block was sprayed twice with benomyl (250 gm. a.i./ha), prior to and following flowering, to control head-rot disease. This was a precautionary measure taken to prevent complete destruction of the experiment by a severe disease condition.

Except at Massey in 1978, where a combine harvester was used, experimental plots were hand cut and threshed with a stationary thresher.

2.5 CHARACTERS STUDIED

Several morphological and agronomic traits of safflower were evaluated. Resistance to head-rot (Botrytis cinerea Pers.) and leaf spot (Alternaria/Stemphylium species) diseases were assessed under field conditions. Leaf spot disease appeared only in the second year of this study. Although time did not permit for complete identification of the pathogen, both Stemphylium and Alternaria species were associated with diseased stems and leaves of infected plants

Table 2.1 Description of genotypes

GENOTYPE	DESCRIPTION
VFSTP-1	High oil line, recessive marker gene for seed stripe, U.S.A.
Partial-hull	High oil line, U.S.A.
Leed	Commercial Cultivar, U.S.A., Zimmer and Urie (1968).
Dart	Commercial Cultivar, U.S.A., Abel and Lorance (1975).
PI 195895	World germplasm collection, U.S.D.A.
0-22	New Zealand Cultivar, U.S.A. originally (Slack, pers comm.)
Rio	Commercial Cultivar, U.S.A.
PI 253515†	World germplasm collection, U.S.D.A.*, origin Portugal.
PI 262437†	World germplasm collection, U.S.D.A., origin Africa.
PI 306684†	World germplasm collection, U.S.D.A., origin Italy.

† Additional genotypes included in the study in 1979.

* United States Department of Agriculture.

Table 2.2 Sowing dates for the three sites

SITE / YEAR	Massey	Aorangi	Flockhouse
1978	10-th November	30-th October	31-st October
1979	30-th October	25-th October	19-th September

(Long, pers.comm.). Ashri (1961) also identified both Stemphylium and Alternaria species from safflower plants infected with leaf spot disease.

In each experimental plot, ten plants were randomly selected and tagged. For some characters the average of measurements taken on these ten plants was used as the plot value in later analyses. However for traits studied on a whole plot basis, a graded scoring system was used. This procedure is typical of early generation plant breeding programmes, where a large number of genotypes are evaluated. A given score reflects the integrated value of a plot.

2.5.1 Scales of Measurement

Based on the number of distinct values the variable may assume, variables may be classified as follows (Anderberg, 1973): continuous, discrete and binary. Variables have also been categorised according to their scales of measurement (Anderberg, 1973) as: nominal, ordinal, interval and ratio scales. A ratio scale is an interval scale with a meaningful zero point. In the present study, measurements taken on characters such as plant height, leaf length and length/width are continuous variables on ratio scales. Where a scoring system was used in the present study, frequently on a scale of 0-5, ½'s were included to represent values lying between two main categories. The original scores were multiplied by 2 giving a meristic (Clifford and Stephenson, 1975) or quasi-continuous scale, prior to statistical analyses. When legitimate zero's were present in the data a ½ was added to the original score prior to multiplication by 2. The ranges of converted scores are listed in Table 3.1. Original ranges are given in the following.

2.5.2 Character Measurements

2.5.2.1 Stem diameter (mm.)

Plant stem diameter was measured about 2 cm. above the ground level using a vernier caliper. Measurements were taken on the ten tagged plants in each experimental plot.

2.5.2.2 Plant height (cm.)

Heights of tagged plants were measured from ground level to top of the canopy.

2.5.2.3 Branching level (score 1-5)

When fully developed individual plants were scored on a graded scale of 1-5. A higher score represented branches arising from a lower level on the main stem.

Score 1 = Lowest branch arising from the uppermost 1/5 of main stem.

5 = Lowest branch arising from the lowermost 1/5 of main stem.

Scores 2, 3 and 4 represented intermediate levels. A value between two main categories was given a score of ½. Original scores were multiplied by 2 prior to analysis.

2.5.2.4 Mid-stem leaf length and width

Leaf characters were assessed on tagged plants. A leaf half way along the main stem was considered as representative. Mid stem leaf length and width was measured in mm. The ratio of mid-stem leaf length to width was computed.

2.5.2.5 Primary head diameter (mm.)

Primary heads are those which form at the ends of branches arising directly from the main stem. Diameters of primary heads of tagged plants were measured at the flowering stage using a vernier caliper.

2.5.2.6 Bract characters

An outermost involucral bract of a primary head was sampled from each of the ten tagged plants. Bract length and width were measured in mm. Ratio of length to width was computed.

Number of spines in a bract was scored on a scale of 0-3: 0 = no spines; 1 = apical spine and few (1-4) marginal spines; 2 = more spines along the margin, but not extending to base of the bract; 3 = spines along the entire margin. Length of longest spine was measured in mm.

Spine index was computed as a product of spine length and spine number (after Claassen et al., 1950). Plants were grouped firstly into four categories according to spine length: 0 = < 1 mm.; 1 = 1-2.5 mm.; 2 = 2.5-4.5 mm.; 3 = 4.5-6.5 mm. Next, spine index was calculated as follows:

Spine index = number of spines x group score for spine length.

Spine index had a scale of 0-9. Legitimate zero's were absent in the data, hence rescaling was not necessary.

2.5.2.7 Establishment density (score 0-5)

About a week after germination, seedling establishments were scored on a graded scale of 0-5: 0 = none or few plants (< 6); 1 = < 1 plant/4 dm.; 2 = 1 plant/4 dm.; 3 = 1 plant/ 2 dm.; 4 = 1 plant/10 cm.; 5 = > 1 plant/10 cm.

A ½ was given to a value lying between two main categories. The scores were multiplied by 2 prior to analysis.

2.5.2.8 Flowering time (50%)

A scoring system was adopted. In each site the first plot, which showed 50% of flower heads at flowering stage was assigned a score of 1. Measurements were taken twice a week, and a unit increment in the score was equivalent to a 3½ days interval. Prior to pooled analysis scores of different experiments were transformed to a common scale. A score of 1 in this new scale was equivalent to 105 days after sowing. An increment of 1 still represented a 3½ days interval.

2.5.2.9 Bird damage (score 0-5)

Prior to harvesting bird damage in experimental plots were assessed on a graded scale of 0-5: 0 = no damaged heads; 1 = < 10% damaged heads; 2 = 10-25%; 3 = 25-50%; 4 = 50-75%; 5 = >75%. A ½ was added to the original score and multiplied by 2 before statistical analysis.

2.5.2.10 Susceptibility to head rot disease (score 0-5)

Infection by Botrytis cinerea Pers. may occur at any stage from flowering to harvesting, depending on weather

conditions and presence of inoculum. Due to sporulation of the fungus, the tissues surrounding flower heads turn into a black colour (Plate 2.3).

A visual graded score of 0-5 was adopted. A higher score represented an increased amount of infected tissue in an experimental plot. The assessment was made prior to harvesting.

Score 0 = no infected tissue; 1 = < 10% infected tissue;
2 = 10-25%; 3 = 25-50%; 4 = 50-75%; 5 = > 75%.

A value between two main categories was represented by a ½. The original scores were multiplied by 2 prior to statistical analysis.

2.5.2.11 Sprouting damage of harvested grain (score 0-5)

A graded score of 0-5 was used. The scores reflected sprouting damage according to grain appearance, a higher score indicating worse damage: 0 = embryo hole not visible; 1 = embryo hole with slight opening, no radical; 2 = embryo with slit >½ mm., radical about 3 mm.; 3 = well marked embryo, radical about 5 mm.; 4 = embryo hole extended considerably, shoot visible; 5 = shoot separated from seed coat. Original scores were transformed to 2x(original score + ½) prior to statistical analysis.

2.5.2.12 Lodging (score 0-5)

Lodging was scored on plot basis using a graded scale of 0-5. A higher score represented an increased tendency to lodge.

Score 0 = plants erect; 1 = plants slightly bent from upright position $<30^{o}$; 2 = approximately 30^{o} from upright; 3 = about 45^{o}; 4 = about 60^{o}; 5 = $>60^{o}$.

Original scores were multiplied by 2 prior to analysis.

2.5.2.13 Susceptibility to leaf spot disease

The disease spreads from the base of the plant upwards. Early symptoms are leaf spots and apical necrosis of lower leaves (Plate 2.4). Chlorotic streaks may appear on the lower part of main stem (Plate 2.5). As the disease progresses,

Plate 2.1 A safflower head at an early stage of infection, by Botrytis cinerea Pers., causative organism of head rot disease.

Plate 2.2 A cross section of a safflower head, infected with Botrytis cinerea Pers., showing disintegrating receptacle tissue at the base of seeds.

Plate 2.3 A safflower head, at a later stage of infection by Botrytis cinerea Pers., showing extensive sporulation on the head and surrounding involucral bracts.

Plate 2.4 Safflower leaves infected with Stemphylium and Alternaria species, causing leaf spot disease.

Plate 2.5 A stem portion of a safflower plant infected with Stemphylium and Alternaria species.

Plate 2.6 A safflower plant severely infected with leaf spot disease.

necrosis of leaves begins to spread upwards. Extensive sporulation may be seen on stems and leaves of infected plants (Plate 2.6).

The experimental plots were assessed for resistance to leaf spot disease, on a graded scale of 0-5, about 2 weeks after first symptoms were noticed. A higher score indicated increased susceptibility.

Score 0 = no symptoms; 1 = only the lowermost leaves showing necrosis; 2 = necrosis of leaves in lowermost ¼ of main stem; 3 = necrosis extended up to ½ of main stem, lower leaves curled and showing extensive sporulation; 4 = necrosis in upper half of main stem, also spreading into branches; 5 = completely dead plants.

Original scores were multiplied by 2 before analysis.

2.5.2.14 Yield and yield components

Numbers of primary and total heads, bearing seeds, were counted on tagged plants. A random sample of 20 heads were taken from the unsprayed half of each experimental plot, threshed and average number of seeds/head determined. Seed weight (gm./1000 seeds) was calculated by weighing a 250 seed sample.

Prior to harvesting numbers of plants in unsprayed and sprayed halves of each plot were counted. Yield was expressed in kg/ha.

2.5.2.15 Percentage oil content of seed

Several methods are available to determine the oil content of seeds. Rapid methods for determining oil content of seeds, for plant breeding work, are described in literature (Kennedy and Unrau, 1949; Comstock and Culbertson, 1958). The standard method of determining the oil content of seeds, the extraction method, is a time consuming process. In recent years the nuclear magnetic resonance (NMR) spectrometry has been utilized successfully to determine oil contents of dried seeds (Conway, 1963; Madsen, 1976). The advantages of NMR spectrometry method are the very short time needed for

the examination (about 5 min per sample), and the fact that it does not require inflammable solvents. However use of NMR technique was beyond the scope of this study.

The traditional extraction method was used in this study (Slack, pers comm.). A sample of 4-8 grams (200 seeds) of sound seeds was ground in a laboratory mill. The crushed material was transferred to a cellulose extraction thimble and weight recorded. The material was extracted continuously for 4 hours, with petroleum ether, in a soxhlet apparatus. The contents of the flask were evaporated, using a rotary evaporator, for about 15 min. to remove solvent, and the oil residue was dried off by adding 20 ml. of a mixture of ethanol and benzene (90:10, by volume). Weight of dried oil was measured and oil content was expressed as a percentage of fresh seed weight.

Another sample of about 10 gms was weighed, oven dried at 105^{o}C for 24 hours, and moisture content of seed determined.

2.5.2.16 Percentage hull content of seed

A sample of 40 seeds was weighed and germinated at 21^{o}C for 48 hours. Next, the hulls were separated from the kernels (after Leininger and Urie, 1964). The ungerminated seeds were split by a scalpel to facilitate separation. Hulls were dried at 105^{o}C overnight and weight recorded. Hull content was expressed as a percentage of fresh seed weight.

2.5.2.17 Iodine value of oil

The iodine value of an oil is the amount of halagen absorbed under specified conditions, and is expressed as the number of grams of iodine per 100 grams of oil. It is a measure of the proportion of unsaturated constituents present. Wijs' solution was used to determine iodine values in this study.

Wijs' solution was prepared from iodine trichloride (Icl_3) and pure resublimed iodine in glacial acetic acid and carbon tetrachloride. Procedure for preparation of Wijs' solution (after Devine and Williams, 1961) is given in Appendix I.

About 0.15 gms of oil was weighed into a small glass tube. The tube was placed in a 300 ml. conical flask, with ground glass stopper. The oil was dissolved by adding 15 ml. carbon tetrachloride. Next, 25 ml. of Wijs' solution was added, mixed, and allowed to stand for 30 minutes in the dark. Then 100 ml. water and 20 ml. of potassium iodide solution (10% aqueous, w/v) were added. The contents were titrated with 0.1N sodium thiosulphate solution, using starch solution as indicator. Methods for preparations of sodium thiosulphate solution and starch solution are described in Appendix I. A blank was run in the same way. Iodine value of oil was computed as follows (Devine and Williams, 1961):

If w = weight of oil sample in grams; v = volume of thiosulphate solution used in ml.; x = volume of thiosulphate solution used in blank; and N = normality of thiosulphate solution, then,

The number of equivalent weights of iodine absorbed by w grams of oil = $\frac{N\ (x-v)}{1000}$

Taking the equivalent weight of iodine as 126.9, the number of grams of iodine absorbed by 100 grams of oil (iodine value) is = 12.69 N (x-v)/w.

Larger iodine values indicate greater degree of unsaturation in the oil.

2.6 STATISTICAL ANALYSIS

Complete data sets were available on seven genotypes for 1978 and ten genotypes, including the original seven for 1979. Data based on seven genotypes were analysed as a site-year (3 sites and 2 years) model (experiment I). Results from 1979 on ten genotypes were analysed as an environments (3 environments) model (experiment II).

Prior to any statistical analysis, missing values were computed by regression (Steel and Torie, 1960). This procedure gives unbiased estimates of both genotypic and error variance components. However for each missing value estimated, one degree of freedom had to be subtracted from the error, when mean squares were computed.

2.6.1 Phenotypic Models Used

Two models appropriate to randomised complete block designs were considered for the two experiments.

Model I:

$$X_{ijkl} = \mu+\gamma_i+\beta_{j(kl)}+\lambda_k+\tau_l+\lambda\tau_{kl}+\gamma\tau_{il}+\gamma\lambda_{ik}+\gamma\tau\lambda_{ikl}+\varepsilon_{ijkl}$$

where X_{ijkl} = ijkl-th phenotypic observation; i = 1,..., g; j = 1,...,b; k = 1,...,s; l = 1,...,y.

g, b, s and y are numbers of genotypes, blocks per experiment, sites and years respectively.
μ = grand mean; γ_i = the i-th genotype effect; $\beta_{j(kl)}$ = the j-th block effect in k-th site in l-th year; λ_k = the k-th site effect; τ_l = l-th year effect; $\lambda\tau_{kl}$, $\gamma\tau_{il}$, $\gamma\lambda_{ik}$ and $\gamma\tau\lambda_{ikl}$ are interactions among the indicated main effects; and ε_{ijkl} = ijkl-th residual error effect.

Model II:

$$X_{ijm} = \mu+\gamma_i+\beta_{j(m)}+\eta_m+\gamma\eta_{im}+\varepsilon_{ijm}$$

where X_{ijm} = ijm-th phenotypic observation; i = 1,...,g; j = 1,...,b; m = 1,...,e.
g, b and e are numbers of genotypes, blocks per experiment and environments respectively.
μ = the grand mean; γ_i = the i-th genotype effect; $\beta_{j(m)}$ = the j-th block effect in m-th environment; $\gamma\eta_{im}$ = the im-th genotype x environment interaction; ε_{ijm} = ijm-th residual error effect.

In both models all effects were considered to be random, normal, independent deviates with expectations equal to zero. Random models may be considered appropriate if sites, years and genotypes are not deliberately chosen for particular properties inherent to them and the population of inference is properly defined. The environmental population referred to in this study is the different climatic and adaphic conditions prevalent in the Manawatu area. The genotypic populations for Expt. I and Expt. II consisted of 7 and 10 safflower genotypes respectively (refer to Table 2.1), which are potentially useful to New Zealand.

2.6.2 Pooled Analysis of Variance

. Two computer programmes were employed to analyse the experimental data: PANSY for the site-year model and PHANIE (Gordon, pers. comm.) for the environments model.

Prior to pooled analysis each character was tested for homogeneity of error variances using a χ^2 (chi-square) test (Steel and Torie, 1960; after Bartlett, 1937). The χ^2 value was computed as follows:

$$\chi^2 \text{ (uncorrected)} = (\text{PDFE}.\ln\text{PMS}) - \sum_n (\text{DFE}_n.\ln\text{MS}_n)$$

$$\text{correction factor} = 1 + \frac{1}{3(k-1)}\left[\frac{k}{\text{DFE}} - \frac{1}{\text{PDFE}}\right]$$

$$\text{corrected } \chi^2 = \frac{\text{uncorrected } \chi^2}{\text{correction factor}}$$

where DFE_n = degrees of freedom for error in the n-th individual experiment; PDFE = pooled degrees of freedom for error, $\sum_n \text{DFE}_n$; MS_n = mean square for error in the n-th individual experiment; PMS = pooled mean square for error; and k = total number of individual experiments involved in pooling.

Next, for k-1 degrees of freedom, the probability of obtaining a χ^2 value greater than the computed value was determined using a χ^2 table (Steel and Torie, 1960). If the probability was more than 5%, individual mean squares (MS_n) were considered as estimates of the same population mean square (PMS). In contrast a probability less than 5% indicated heterogeneity of individual mean squares (MS_n).

The pooled analysis of variance including mean squares, degrees of freedom, expectations of mean squares and appropriate F ratios for testing significances of variance components are presented in Tables 2.3 (Model I) and 2.4 (Model II). The expectations of mean squares were estimated following the procedures of Crump (1946).

Estimates of variance components were obtained for each character from linear functions of mean squares (after Comstock and Moll, 1963). The general formula for the

Table 2.3 Degrees of freedom, expectations of mean squares and F-ratios for Model I.

Source of variation	DF	MS	E(MS)	F-ratio
Years	y-1	MS9	$\sigma^2+g\sigma^2_R+b\sigma^2_{GSY}+bs\sigma^2_{GY}+bg\sigma^2_{SY}+bgs\sigma^2_Y$	(MS9+MS2)/(MS7+MS4)
Sites	s-1	MS8	$\sigma^2+g\sigma^2_R+b\sigma^2_{GSY}+by\sigma^2_{GS}+bg\sigma^2_{SY}+bgy\sigma^2_S$	(MS8+MS2)/(MS7+MS3)
Sites x years	(s-1)(y-1)	MS7	$\sigma^2+g\sigma^2_R+b\sigma^2_{GSY}+bg\sigma^2_{SY}$	(MS7+MS1)/(MS6+MS2)
Blocks within environments	sy(b-1)	MS6	$\sigma^2+g\sigma^2_R$	MS6/MS1
Genotypes	(g-1)	MS5	$\sigma^2+b\sigma^2_{GSY}+by\sigma^2_{GS}+bs\sigma^2_{GY}+bsy\sigma^2_G$	(MS5+MS2)/(MS4+MS3)
Genotype x years	(g-1)(y-1)	MS4	$\sigma^2+b\sigma^2_{GSY}+bs\sigma^2_{GY}$	MS4/MS2
Genotype x sites	(g-1)(s-1)	MS3	$\sigma^2+b\sigma^2_{GSY}+by\sigma^2_{GS}$	MS3/MS2
Genotype x sites x years	(g-1)(s-1)(y-1)	MS2	$\sigma^2+b\sigma^2_{GSY}$	MS2/MS1
Error	sy(g-1)(b-1)	MS1	σ^2	

Table 2.4 Degrees of freedom, expectations of mean squares and F-ratios for Model II

Source of variation	DF	MS	E(MS)	F-ratio
Environments	e-1	MS14	$\sigma^2+g\sigma^2_R+b\sigma^2_{GE}+bg\sigma^2_E$	(MS14+MS10)/(MS13+MS11)
Blocks within environments	e(b-1)	MS13	$\sigma^2+g\sigma^2_R$	MS13/MS10
Genotypes	g-1	MS12	$\sigma^2+b\sigma^2_{GE}+be\sigma^2_G$	MS12/MS11
Genotype x environments	(g-1)(e-1)	MS11	$\sigma^2+b\sigma^2_{GE}$	MS11/MS10
Error	e(g-1)(b-1)	MS10	σ^2	

standard error (S.E.) of a variance component estimate (after Crump, 1946 and 1951) is as follows:

$$S.E.\ \hat{\sigma}^2_t = \sqrt{\frac{1}{n_t^2} \sum_u \frac{2\,[E(MS_u)]^2}{f_u + 2}}$$

where $\hat{\sigma}^2_t$ = variance component estimate; n_t = divisor appropriate to $\hat{\sigma}^2_t$; MS_u = u-th mean square in estimating $\hat{\sigma}^2_t$; and f_u = degrees of freedom of u-th mean square.

The significances of variance components were determined by the F-test. In this context, a F-ratio was formed by choosing two estimates of mean squares, such that the mean square estimate in the numerator differed from that in the denominator only by the variance component under consideration (Le Clerg et al., 1962). Next, for the appropriate degrees of freedom of the numerator and denominator, the probability of obtaining a F-value greater than the computed value was determined using the F-table (Steel and Torie, 1960). Significances of variance components were described using the following notations: NS = $P>0.10$; (NS) = $0.10\geq P>0.05$; * = $0.05\geq P>0.01$; ** = $0.01\geq P>0.005$; *** = $0.005\geq P>0.001$; **** = $0.001\geq P$.

When the appropriate numerator or denominator was a linear function of mean squares (Tables 2.3 and 2.4), the approximate F-test (F') was used. The appropriate degrees of freedom for the F'-test were computed as follows (after Satterthwaite, 1946):

$$f' = \frac{(\sum_n (MS_n)^2}{\sum_n MS_n^4 / f_n}$$

where f' = the degrees of freedom for the linear combination of mean squares, to permit approximation to the F-distribution; MS_n = the n-th mean square; f_n = the degrees of freedom appropriate to n-th mean square.

2.6.3 Comparison of Genotypic Means

A significant F-value for genotypic effects provided evidence for rejecting the null hypothesis, that genotypic

means were the same. When genotypic effects were significant, a comparison of genotypic means was made using the least significant difference (l.s.d.) estimate (after Steel and Torie, 1960). As Balaam (1963) pointed out, l.s.d. procedure is preferable to Duncan's multiple ranges, when the number of means is small.

The l.s.d. values were computed as follows:

$$l.s.d._{(p)} = t_{(p)} \cdot \sqrt{2V_{\bar{x}}}$$

where $l.s.d._{(p)}$ = l.s.d. estimate at p-probability level; $t_{(p)}$ = the tabular value of t - for error degrees of freedom at p - probability level; $V_{\bar{x}}$ = the variance of genotypic mean, $2V_{\bar{x}}$ is in fact the variance of a difference between two genotypic means.

The variances of genotypic means for the two models were determined as follows:

Model I: $$V_{\bar{x}} = \frac{\sigma^2}{bsy} + \frac{\sigma^2_{GSY}}{sy} + \frac{\sigma^2_{GY}}{y} + \frac{\sigma^2_{GS}}{s}$$

Model II: $$V_{\bar{x}} = \frac{\sigma^2}{be} + \frac{\sigma^2_{GE}}{e}$$

Notations presented here are in Tables 2.3 and 2.4.

2.6.4 Heritability Estimates

Two forms of broadsense heritability (h^2) estimates were computed, for each character in the pooled analysis (after Gordon et al., 1972), as follows:

$$h^2 \text{ (full)} = \sigma^2_G / \sigma^2_{P_1}$$

$$h^2 \text{ (restricted)} = \sigma^2_G / \sigma^2_{P_2}$$

where σ^2_G = genotypic variance component. The phenotypic variances, $\sigma^2_{P_1}$ and $\sigma^2_{P_2}$, appropriate to the two models were defined as follows:

Model I: $\sigma^2_{P_1} = \sigma^2_G + \sigma^2_{GSY} + \sigma^2_{GY} + \sigma^2_{GS} + \sigma^2_R + \sigma^2_{SY} + \sigma^2_S + \sigma^2_Y$

$\sigma^2_{P_2} = \sigma^2_G + \sigma^2_{GSY} + \sigma^2_{GY} + \sigma^2_{GS}$

Model II: $\sigma^2_{P_1} = \sigma^2_G + \sigma^2_{GE} + \sigma^2_R + \sigma^2_E$

$\sigma^2_{P_2} = \sigma^2_G + \sigma^2_{GE}$

The full broadsense heritability estimates the fraction of total phenotypic variance among genotypes attributable to genetic differences between them. However the restricted type is the more commonly used (Allard, 1960). Restricted heritability is more appropriate when comparison is made between phenotypic performances of two genotypes within the same block at a particular site.

Following the procedures of Gordon et al. (1972) the standard errors of heritability estimates were determined as follows:

The approximate formula for the variance of a ratio ($z = x/y$) is:

$$\sigma^2_z = \left[\mu_y^2\sigma_x^2 + \mu_x^2\sigma_y^2 - 2\mu_x\mu_y\mathrm{cov}(\hat{x},\hat{y})\right]/\mu_y^4$$

where $\mu_y = E(\hat{y})$; $\mu_x = E(\hat{x})$; σ^2_z, σ^2_x and σ^2_y are variances of z, x and y respectively. When variances of heritability estimates are computed, the parameters may be replaced by the corresponding estimates (Osborne and Paterson, 1952). The factors z, x and y correspond to h^2, σ^2_G and σ^2_P in the heritability equation.

The σ^2_x, σ^2_y and cov(x,y) needed for the above mentioned equation were computed using the estimators of Gordon et al. (1972). The coefficients of variation of heritability estimates were expressed as $\sigma^2_{(h^2)}/h^2$.

2.6.5 Adaptation Analysis

Data were available on seven genotypes evaluated at three sites over a two year period (6 environments). An adaptation analysis was performed for those characters which

showed a significant genotype x environment interaction in the analysis of variance. For each cultivar a linear regression of it's mean in a particular environment ($\bar{X}_{i.k}$) on the environmental mean ($\bar{X}_{..k}$) was computed (after Finlay and Wilkinson, 1963). A computer programme in "Statistical Package for Social Sciences" (SPSS) was used for regression analysis. The model employed was as follows:

$$\bar{X}_{i.k} = \mu_i + b_i (\bar{X}_{..k} - \mu) + \delta_{ik}$$

where $\bar{X}_{i.k}$ = i-th genotype mean in k-th environment; $i = 1,\ldots, g$; $k = 1,\ldots,e$; $\bar{X}_{i.k} = \frac{1}{b} \sum_j X_{ijk}$

μ_i = i-th genotype mean, $\frac{1}{be} \sum_k \sum_j X_{ijk}$

$\bar{X}_{..k}$ = k-th environmental mean, $\frac{1}{gb} \sum_i \sum_j X_{ijk}$

δ_{ik} = deviation from regression of the i-th genotype in the k-th environment.

μ = grand mean, $\frac{1}{gbe} \sum_k \sum_i \sum_j X_{ijk}$

b_i = regression coefficient of the i-th genotype, which is the adaptation coefficient in this context (after Finlay and Wilkinson, 1963).

The notations used in the model have already been discussed in section 2.6.1.

The significances of adaptation coefficients from one were determined by a two-tailed t-test as described by Draper and Smith (1966). Estimate of standard error (S.E.) of regression coefficient (b_i) was found in the usual way (after Draper and Smith, 1966) as:

$$\text{S.E. } (b_i) = \sqrt{\frac{\hat{\sigma}^2}{\sum_k (\bar{X}_{..k} - \mu)^2}}$$

where $\hat{\sigma}^2$ = estimate of residual (about regression) variance for a particular genotype.

The usefulness of a regression line as a predictor of the genotype's performance was assessed by the R^2 value (after Draper and Smith, 1966).

Ecovalances for all genotypes were computed using the pooled environments model, with respect to each character under study. In the present context, ecovalance of the i-th genotype was defined as follows: It is a form of a mean square estimate, rather than a sums of square estimate as described in section 1.4.2.

Ecovalance of the i-th genotype = $\sum_k (\gamma\eta_{ik})^2 / DFECO$

where $\gamma\eta_{ik}$ = genotype x environment effect of the i-th genotype in k-th environment; DFECO = degrees of freedom for ecovalance; DFECO = (e-1)-{(e-1)/g}, where e and g are number of environments and genotypes respectively.

2.6.6 Optimum Plot Allocation

The optimum plot allocation study was conducted with the following four characters in experiment I: yield (unsprayed)/plot, susceptibility to head rot disease, % oil content and % hull content.

Variance of the genotypic mean for the site-year model (refer Section 2.6.1) may be expressed as follows:

$$V_{\bar{x}_{i...}} = \frac{\sigma^2}{bsy} + \frac{\sigma^2_{GSY}}{sy} + \frac{\sigma^2_{GS}}{s} + \frac{\sigma^2_{GY}}{y}$$

For various allocations of blocks (b = 2-5), sites (s = 1-5) and years (y = 1-4), expected variances of the genotypic mean were computed using the variance component estimates from the pooled ANOVA (refer Table 2.3). The relative efficiency of each plot allocation was computed as follows:

$$\text{Relative efficiency} = \frac{\text{Estimated } V_{\bar{x}_{i...}} \text{ for the present expt.}}{\text{Expected } V_{\bar{x}_{i...}} \text{ for the particular allocation}} \times 100$$

Relative efficiency of an allocation, in this context, measures the effectiveness of that allocation in reducing $V_{\bar{x}_{i...}}$, compared to the present allocation. A value greater

than 100 indicates a better allocation compared to the present one.

2.6.7 Correlation Coefficients

For both experiments, phenotypic and genotypic correlation coefficients between characters were estimated using the computer programme PHANIE (Gordon pers. comm.). In computing correlations, the data from Experiment I were also analysed as an environments model (6 environments).

The phenotypic (r_p) and genotypic (r_g) correlation coefficients between characters may be expressed by the following formulae (Falconer, 1975):

$$r_p = COV_{p(ij)} / \left[(\sigma^2_{p_i})(\sigma^2_{p_j}) \right]^{\frac{1}{2}}$$

$$r_g = COV_{g(ij)} / \left[(\sigma^2_{g_i})(\sigma^2_{g_j}) \right]^{\frac{1}{2}}$$

where $COV_{p(ij)}$ and $COV_{g(ij)}$ are phenotypic and genotypic covariance components respectively;

$\sigma^2_{p_i}$ and $\sigma^2_{p_j}$ = phenotypic variance components of traits i and j respectively;

$\sigma^2_{g_i}$ and $\sigma^2_{g_j}$ = genotypic variance components of traits i and j respectively.

CHAPTER 3

RESULTS AND DISCUSSION

The results of the analyses of data from two experiments (Expt. I and II, also see section 2.1) will be presented here. The appropriate models used in the analyses have been discussed in section 2.6.1.

The proceeding discussion will be mainly based on the results of 25 traits studied (Table 3.1) in Expt. I. The discussion of Expt. II will be confined to the ten characters listed in Table 3.2.

In presenting the results certain abbreviations will be used to define the traits, and these are presented in Tables 3.1 and 3.2. Results of traits, Pr. Hd. No and Tot. Hd. No are based on data from two sites only (Flockhouse and Massey). These traits involved counting numbers of heads in each tagged plant and time was insufficient to carry out the assessments at Aorangi. Results of all traits presented here, except for yield, are based on unsprayed half of the plot (refer also section 2.4). The yield/plot in unsprayed and sprayed halves were analysed as two separate variables.

3.1 HETEROGENEITY OF EXPERIMENTAL ERRORS

A pooled ANOVA for each trait in Expt. I and Expt. II was performed using site-year model and environments model respectively (see section 2.6.1). Such a pooling is strictly valid only when the error variances of individual experiments are homogeneous. The results of χ^2 test for homogeneity of error variances (refer to section 2.6.2) in Expt. I and Expt. II are presented in Tables 3.3 and 3.4 respectively. If the probability (p), of obtaining a χ^2 value greater than that computed, was more than 0.05, the individual error variances were considered as homogeneous. In Expt. I, of the 22 characters analysed only the following 5 showed homogeneity of error variances: Pl. Ht, Lf. Lth, Lf. L/W, Es. Den, and I. val. The traits, Lodging and Sus. St/Al were homogeneous in Expt. II.

Table 3.1 Expt. I. Abbreviations used, units of measurement, grand means and coefficients of variation (CV) for all the characters studied.

Character	Abbreviation	Unit (Converted)	Grand Mean ($\bar{X}_{....}$)	C.V. %
(1) Stem diameter	St. Dia	mm.	12.4	8.8
(2) Plant height	Pl. Ht	cm.	75.6	6.4
(3) Branching level	Br. Lev	Score 2-10	7.2	9.2
(4) Mid stem leaf length	Lf. Lth	cm.	129.8	7.0
(5) Mid stem leaf length/ width	Lf. L/W	Ratio	2.7	6.7
(6) Primary head diameter	Hd. Dia	mm.	23.7	3.7
(7) Bract length	Br. Lth	cm.	40.5	8.2
(8) Bract length/width	Br. L/W	Ratio	2.96	8.2
(9) Spine Index	Sp. Inx	Score 0-9	5.0	14.0
(10) Number of primary heads/plant	Pr. Hd. No	Number	8.8	19.1
(11) Total number of heads/plant	Tot. Hd. No	Number	18.3	32.1
(12) Establishment density	Es. Den	Score 0-10	6.5	12.5
(13) Growth period from planting to flowering (50%)	GPPF	Score 1-10	3.2	24.4
(14) Bird damage	Brd. Dam	Score 1-11	3.1	25.5
(15) Susceptibility to head rot disease (*Botrytis cinerea* Pers.)	Sus. Bot	Score 0-10	4.8	19.9
(16) Number of plants/plot (unsprayed)	Pl. No (US)	Number	28.7	22.0
(17) Number of plants/plot (sprayed)	Pl. No (S)	Number	29.9	21.5
(18) Yield (unsprayed)	Yld (US)	Kg/ha	461.3	31.6
(19) Yield (sprayed)	Yld (S)	Kg/ha	614.7	28.4
(20) % Oil content of seed	Oil %	% fresh seed weight	19.6	12.1
(21) % Hull content of seed	Hull %	% fresh seed weight	56.5	4.3
(22) % Moisture content of seed	Mos. %	% fresh seed weight	8.9	4.2
(23) Sprouting damage of seed	Spr. Dam	Score 1-11	4.0	28.3
(24) 1000 seed weight	Sd. Wt	gm.	39.0	12.0
(25) Iodine value of oil	I. Val	Number	125.9	7.4

Table 3.2 Expt. II. Abbreviations used, units of measurement, grand means and coefficients of variation (CV) for the 10 traits.

Character	Abbreviation	Unit (Converted)	Grand Mean ($\bar{X}_{...}$)	C.V. %
(1) Plant height	Pl. Ht	cm.	82.9	6.3
(2) Branching level	Br. Lev	Score 2-10	6.8	12.1
(3) Lodging	Lodging	Score 0-10	4.9	21.1
(4) Susceptibility to leaf spot disease (*Stemphylium*/*Alternaria* species)	Sus. St/Al	Score 0-10	4.2	25.0
(5) Susceptibility to head rot disease (*Botrytis cinerea* Pers.)	Sus. Bot	Score 0-10	5.7	14.7
(6) Number of seeds/head	Sd. No	Number	186.3	35.6
(7) Total number of heads/plant	Tot. Hd. No	Number	21.7	32.7
(8) % oil content of seed	Oil %	% fresh seed weight	14.8	13.0
(9) Yield/plot (unsprayed)	Yld (US)	kg/ha	361	44.7
(10) Yield/plot (sprayed)	Yld (S)	kg/ha	505	30.7

Table 3.3 Expt. I. The error variances of individual experiments, pooled error variance, and the significance of heterogeneity.

CHARACTER	Y1† MS	Y1 AR	Y1 FH	Y2 MS	Y2 AR	Y2 FH	Pooled error	χ^2	P††
St. Dia	0.32	1.29	0.16	1.53	1.33	2.60	1.20	25.9	0.00
Pl. Ht*	22.0	6.9	22.1	34.3	16.7	38.8	23.4	9.7	0.08
Br. Lev	0.51	0.47	0.09	0.58	0.16	0.79	0.43	17.0	0.01
Lf. Lth*	71.1	47.4	81.6	88.0	45.8	157	81.7	6.5	0.26
Lf. L/W*	0.02	0.02	0.06	0.05	0.02	0.03	0.03	8.6	0.13
Hd. Dia	0.74	0.38	0.90	0.52	0.31	1.86	0.79	13.5	0.02
OIB. Lth	2.9	5.5	14.7	8.6	15.5	19.4	11.1	13.7	0.02
OIB. L/W	0.01	0.01	0.01	0.10	0.10	0.13	0.06	49.1	0.00
Sp. Inx	0.42	0.10	0.16	1.29	0.87	0.12	0.49	33.5	0.00
Pr. Hd. No	0.77	-	0.23	1.54	-	8.92	2.86	39.9	0.00
Tot. Hd. No	16.9	-	4.4	25.8	-	90.2	34.3	24.9	0.00
Es. Den*	0.33	0.39	0.53	1.55	0.49	0.67	0.66	10.3	0.07
GPPF	0.24	1.13	0.30	1.22	0.28	0.48	0.61	16.1	0.01
Brd. Dam	0.75	0.74	0.21	1.24	0.72	0.00	0.61	185	0.00
Sus. Bot	1.40	2.11	0.05	1.15	0.51	0.16	0.90	44.1	0.00
Yld (US)	447	30025	21750	5576	34977	35021	21299	46.2	0.00
Yld (S)	1228	72920	21633	9799	40289	37413	30547	40.2	0.00
Oil %	13.9	3.19	3.90	6.08	0.45	6.26	5.63	28.4	0.00
Hull %	4.80	3.24	12.35	9.56	0.55	5.66	6.02	25.5	0.00
Spr. Dam	2.22	3.21	1.61	0.17	0.56	0.00	1.29	211	0.00
Sd. Wt	10.6	53.4	4.7	25.8	8.1	28.6	21.9	23.1	0.00
I. Val*	97.9	104.6	82.0	28.1	130.6	83.6	87.8	6.9	0.23

* Homogeneous sets

† Y1, Y2 are years 1978 and 1979 respectively.
MS, AR, FH are Massey R & D unit, Aorangi and Flockhouse respectively.

†† Probability of obtaining a χ^2 value greater than that computed.

Table 3.4 Expt. II. The error variances of individual experiments, pooled error variance, and the significance of heterogeneity.

Character	MS†	AR	FH	Pooled error	χ^2	P††
Pl. Ht	68.1	46.3	58.3	57.3	9.6	0.01
Br. Lev	3.57	1.56	2.87	2.65	44.5	0.00
Lodging *	0.64	0.98	1.55	1.06	3.5	0.17
Sus. St/Al *	1.55	0.53	1.22	1.10	5.1	0.08
Sus. Bot	1.06	0.77	0.27	0.70	7.9	0.02
Sd. No	1322	9758	2100	4394	20.5	0.00
Tot. Hd. No	98.0	-	145.5	122.4	9.6	0.00
Oil %	4.46	0.34	6.23	3.67	29.8	0.00
Yld (US)	4036	27928	45819	25928	21.9	0.00
Yld (S)	8695	30368	32932	23998	8.3	0.02

* Homogeneous Sets

† MS, AR and FH are Massey, Aorangi and Flockhouse sites respectively.

†† probability of obtaining a χ^2 value greater than that computed.

When error variances are heterogeneous, a valid combined analysis may be performed by any of the following 3 methods (after Cochran, 1947), as described in detail in section 1.1: standardising the data by dividing each observation by it's corresponding standard error; transforming the data into a different scale (after Bartlett, 1947); subdividing the experiment into homogeneous subsets.

The point at issue is whether heterogeneity of error variances observed in this study justify the need for special methods of analysis as described above. As explained in section 1.1, significance testing of genotypic effects, which is the main objective in this study, is least affected by heterogeneity. Furthermore the results obtained here are only to provide guidelines for future research work in this area. Therefore no special techniques were employed to correct for the heterogeneity. However this would lead to some bias on the variance component estimates presented in Tables 3.5, 3.6 and 3.8.

3.2 GRAND MEANS AND COEFFICIENTS OF VARIATION (CV)

The grand means and coefficients of variations for all traits evaluated in Expt. I are presented in Table 3.1, and those for Expt. II are given in Table 3.2. A coefficient of variation less than 20% is acceptable for most biological experiments (Balaam, 1963). Comparatively high CV's were observed for the following traits in Expt. I: Tot. Hd. No; GPPF; Brd. Dam; Yld (US); Yld (S); and Spr. Dam. In Expt. II, the traits, Sd. No; Tot. Hd. No; Yld (US) and Yld (S) showed high CV values. A high CV means the significances of variance component estimates are tested with less efficiency (see Tables 2.3 and 2.4). Thus, relatively small variance component estimates may be made non-significant, due to the high error variance component. It will also affect the LSD values (see section 3.4) for testing differences between genotypes, and a small difference may not be detected. A further discussion, on the control of error variance, will be made in Chapter 4.

3.3 VARIANCE COMPONENT ESTIMATES AND THEIR SIGNIFICANCES

Estimates of variance components involving environmental effects and genotypic effects for Expt. I are presented in Tables 3.5 and 3.6 respectively. These estimates for Expt. II are given in Table 3.8. The associated standard errors indicate the precision of the estimates. Ratios of all variance components to the error variance and their significances for Expt. I and Expt. II are presented in Tables 3.7 and 3.9 respectively.

3.3.1 Variance Components Involving Environmental Effects

For Expt. I this includes block (σ^2_R) sites (σ^2_S), years (σ^2_Y) and interaction of sites x years (σ^2_{SY}). Block effect was significant for 10 of the 22 characters studied (Table 3.5). Usually block variance arises from heterogeneity of soil within each experimental site (Le Clerg et al., 1962). Presence of significant block effects for many characters indicate the importance of replication in field experimentation.

A significant year variance component was obtained only for two characters (Table 3.7). It may be concluded that environmental factors such as climatic and disease conditions were very similar in the two consecutive years included in this study. It is possible that two consecutive years tended to be more alike than a sample of two years drawn at random from a longer year period. If so the year variance component (σ^2_Y) may have been under-estimated. However it should be pointed out that most field experiments are conducted in consecutive years. Absence of significant σ^2_Y component for most traits may also be due to the large σ^2_{SY} component (Table 3.7). Several negative variance component estimates are also present in Table 3.5. If a particular variance component is in reality very small, experimental estimates which are negative may be expected. Therefore negative estimates may be interpreted as sampling deviations from variance component parameters of small magnitudes. Such estimates are reported to eliminate any bias in the results.

Table 3.5 Expt. I. Estimates of all variance components involving environmental effects only, together with their standard errors (in brackets).

Character	$\hat{\sigma}^2_R$	$\hat{\sigma}^2_{SY}$	$\hat{\sigma}^2_S$	$\hat{\sigma}^2_Y$
St. Dia	0.10 (0.11)	8.01 (5.83)	-0.84 (3.69)	-2.71 (1.95)
Pl. Ht	3.7 (2.7)	959.6 (680.7)	-366.0 (350.1)	-321.0 (226.9)
Br. Lev	0.05 (0.04)	0.14 (0.15)	0.50 (0.43)	-0.12 (0.07)
Lf. Lth	15.8 (10.6)	1917.4 (1366.4)	-919.3 (683.9)	-643.6 (455.5)
Lf. L/W	0.00 (0.00)	0.00 (0.00)	0.02 (0.02)	0.00 (0.00)
Hd. Dia	0.05 (0.07)	2.44 (1.77)	4.25 (3.98)	-0.77 (0.59)
Br. Lth	5.60 (2.73)	-2.41 (1.12)	9.83 (6.99)	24.38 (20.44)
Br. L/W	0.00 (0.00)	0.02 (0.02)	-0.01 (0.01)	0.00 (0.01)
Sp. Inx	0.00 (0.03)	0.02 (0.03)	0.00 (0.02)	0.18 (0.16)
Pr. Hd. No†	0.83 (0.47)	13.36 (9.75)	-6.26 (4.89)	-3.72 (3.35)
Tot. Hd. No†	15.2 (7.6)	45.6 (36.9)	-21.8 (18.7)	-8.1 (15.4)
Es. Den	0.01 (0.04)	0.54 (0.41)	0.00 (0.29)	-0.38 (0.17)
GPPF	0.07 (0.06)	3.08 (2.22)	-1.39 (1.12)	-1.05 (0.74)
Brd. Dam	0.16 (0.10)	0.23 (0.24)	2.51 (1.92)	-0.03 (0.11)
Sus. Bot	0.03 (0.07)	0.65 (0.49)	4.38 (3.39)	0.18 (0.38)
Yld (US)	2058 (1992)	74098 (57971)	105170 (110755)	-27209 (19372)
Yld (S)	3987 (3237)	22185 (19466)	293816 (226560)	8708 (16446)

Table 3.5 (continued)

Character	$\hat{\sigma}^2_R$	$\hat{\sigma}^2_{SY}$	$\hat{\sigma}^2_S$	$\hat{\sigma}^2_Y$
Oil %	1.38 (0.84)	13.18 (10.74)	9.06 (13.11)	36.12 (33.89)
Hull %	0.79 (0.64)	23.74 (17.70)	0.66 (12.98)	23.69 (26.92)
Spr. Dam	-0.06 (0.06)	2.45 (1.85)	-0.81 (1.01)	4.32 (4.28)
Sd. Wt	1.26 (1.74)	15.25 (13.97)	30.58 (28.89)	-5.29 (4.69)
I. Val	17.1 (11.4)	-7.9 (4.0)	1.8 (1.5)	0.5 (1.4)

† Estimates based on 2 sites only, Massey R & D Unit and Flockhouse research station.

Table 3.6 Expt I. Estimates of all variance components involving genotypic effects, together with their standard errors (in brackets).

Character	$\hat{\sigma}^2$	$\hat{\sigma}^2_{GSY}$	$\hat{\sigma}^2_{GY}$	$\hat{\sigma}^2_{GS}$	$\hat{\sigma}^2_{G}$
St. Dia	1.20 (0.20)	0.98 (0.53)	0.57 (0.54)	-0.51 (0.27)	0.24 (0.40)
Pl. Ht	23.4 (3.9)	4.5 (4.8)	6.2 (5.4)	2.8 (4.1)	-3.0 (3.3)
Br. Lev	0.43 (0.07)	0.26 (0.15)	0.48 (0.31)	0.00 (0.11)	-0.09 (0.19)
Lf. Lth	81.7 (13.4)	40.4 (26.0)	-3.8 (12.7)	-14.6 (14.7)	109.3 (57.3)
Lf. L/W	0.03 (0.01)	0.03 (0.02)	-0.01 (0.01)	-0.01 (0.01)	0.01 (0.01)
Hd. Dia	0.79 (0.13)	0.01 (0.11)	0.22 (0.16)	0.00 (0.07)	1.35 (0.76)
Br. Lth	11.09 (1.82)	4.79 (3.27)	2.97 (3.09)	-2.08 (1.80)	42.59 (22.45)
Br. L/W	0.06 (0.01)	-0.01 (0.01)	0.01 (0.01)	0.00 (0.00)	0.11 (0.06)
Sp. Inx	0.49 (0.08)	-0.03 (0.06)	0.05 (0.05)	0.01 (0.04)	3.59 (1.82)
Pr. Hd. No†	2.86 (0.47)	0.05 (0.41)	0.85 (0.61)	-0.27 (0.21)	0.00 (0.39)
Tot. Hd. No†	34.3 (5.6)	-1.5 (4.2)	14.4 (8.9)	1.3 (3.0)	-3.1 (5.5)
Es. Den	0.66 (0.11)	0.06 (0.11)	1.39 (0.74)	-0.05 (0.06)	-0.04 (0.51)
GPPF	0.61 (0.10)	0.05 (0.10)	0.08 (0.09)	0.10 (0.10)	0.02 (0.09)
Brd. Dam	0.61 (0.10)	0.13 (0.13)	0.10 (0.12)	0.26 (0.17)	0.24 (0.23)
Sus. Bot	0.90 (0.15)	-0.11 (0.09)	0.14 (0.10)	0.39 (0.19)	1.41 (0.82)
Yld (US)	21299 (3502)	42640 (18836)	2189 (11284)	34915 (24474)	-1807 (13449)
Yld (S)	30547 (5022)	17078 (10439)	4416 (7575)	87470 (38558)	424 (22508)

Table 3.6 (continued)

Character	$\hat{\sigma}^2$	$\hat{\sigma}^2_{GSY}$	$\hat{\sigma}^2_{GY}$	$\hat{\sigma}^2_{GS}$	$\hat{\sigma}^2_{G}$
Oil %	5.63 (0.93)	8.79 (4.04)	0.70 (2.52)	1.82 (3.37)	1.51 (2.63)
Hull %	6.02 (0.99)	5.12 (2.71)	0.91 (1.87)	1.81 (2.44)	-0.09 (1.58)
Spr. Dam	1.29 (0.21)	0.86 (0.49)	0.04 (0.28)	0.54 (0.51)	-0.14 (0.25)
Sd. Wt	21.87 (3.60)	20.42 (10.54)	-4.64 (4.18)	-5.23 (6.17)	3.58 (3.13)
I. Val	87.8 (14.4)	-8.4 (9.3)	3.9 (6.0)	-2.7 (4.9)	12.1 (8.9)

† Estimates based on two sites only, Massey R & D unit and Flockhouse research station.

Table 3.7 Expt. I. Ratio of all variance component estimates to the relevant error variance, and their significances for the site x year model.

Character	$\hat{\sigma}^2_{GSY}$	$\hat{\sigma}^2_{GY}$	$\hat{\sigma}^2_{GS}$	$\hat{\sigma}^2_{G}$	$\hat{\sigma}^2_{R}$	$\hat{\sigma}^2_{SY}$	$\hat{\sigma}^2_{S}$	$\hat{\sigma}^2_{Y}$
St. Dia	0.82 ****	0.47 NS	-0.42 NS	0.20 NS	0.09 NS	6.67 ****	-0.70 NS	-2.26 NS
Pl. Ht	0.19 NS	0.26 (NS)	0.12 NS	-0.13 NS	0.16 *	40.94 ****	-15.61 NS	-13.69 NS
Br. Lev	0.60 ***	1.12 *	0.00 NS	-0.20 NS	0.12 (NS)	0.32 NS	1.16 NS	-0.28 NS
Lf. Lth	0.49 **	-0.05 NS	-0.18 NS	1.34 ***	0.19 *	23.46 ****	-11.25 NS	-7.87 NS
Lf. L/W	1.00 ****	-0.22 NS	-0.22 NS	0.30 NS	0.00 NS	-0.11 NS	0.75 ***	0.14 (NS)
Hd. Dia	0.01 NS	0.28 *	0.00 NS	1.71 ***	0.07 NS	3.09 ****	5.37 NS	-0.98 NS
Br. Lth	0.43 *	0.27 NS	-0.19 NS	3.84 ****	0.50 ****	-0.22 NS	0.89 ***	2.20 ***
Br. L/W	-0.11 NS	0.15 (NS)	0.00 NS	1.83 ****	0.00 NS	0.39 **	-0.17 NS	-0.04 NS
Sp. Inx	-0.05 NS	0.09 NS	0.01 NS	7.32 ****	-0.01 NS	0.04 NS	-0.01 NS	0.37 *
Pr. Hd. No†	0.02 NS	0.30 (NS)	-0.09 NS	-0.00 NS	0.29 **	4.67 ****	-2.19 NS	-1.30 NS
Tot. Hd. No†	0.04 NS	0.42 *	0.04 NS	-0.09 NS	0.44 ***	1.33 *	-0.63 NS	-0.24 NS
Es. Den	0.09 NS	2.10 ****	-0.07 NS	-0.05 NS	0.02 NS	0.82 ***	0.01 NS	-0.58 NS
GPPF	0.09 NS	0.14 NS	0.16 NS	0.04 NS	0.11 (NS)	5.05 ****	-2.27 NS	-1.71 NS
Brd. Dam	0.22 (NS)	0.17 NS	0.42 (NS)	0.40 NS	0.26 ***	0.37 (NS)	4.11 *	-0.05 NS
Sus. Bot	-0.13 NS	0.15 *	0.43 ***	1.57 ***	0.04 NS	0.72 ***	4.86 *	0.20 NS
Yld (US)	2.00 ****	0.10 NS	1.64 (NS)	-0.08 NS	0.10 (NS)	3.48 ***	4.94 NS	-1.28 NS
Yld (S)	0.56 **	0.14 NS	2.86 ***	0.01 NS	0.13 *	0.73 *	9.62 **	0.29 NS
Oil %	1.56 ****	0.12 NS	0.32 NS	0.27 NS	0.25 ***	2.34 **	1.61 NS	6.42 NS
Hull %	0.85 ****	0.15 NS	0.30 NS	-0.02 NS	0.13 *	3.94 ****	0.11 NS	3.94 NS
Spr. Dam	0.66 ***	0.03 NS	0.42 NS	-0.11 NS	-0.04 NS	1.90 ****	-0.63 NS	3.35 NS
Sd. Wt	0.93 ****	-0.21 NS	-0.24 NS	0.16 NS	0.06 NS	0.70 *	1.40 NS	-0.24 NS
I. Val.	-0.10 NS	0.04 NS	-0.03 NS	0.14 (NS)	0.19 *	-0.09 NS	0.02 NS	0.01 NS

Significance Symbols:

NS	=	$P>0.10$
(NS)	=	$0.10\geq P>0.05$
*	=	$0.05\geq P>0.01$
**	=	$0.01\geq P>0.005$
***	=	$0.005\geq P>0.001$
****	=	$0.001\geq P$

† Estimates based on 2 sites only, Massey R & D unit and Flockhouse research station.

Table 3.8 Expt. II. Estimates of all variance components and their standard errors (in brackets), for the ten traits studied in the pooled environments model.

Character	$\hat{\sigma}^2$	$\hat{\sigma}^2_{GE}$	$\hat{\sigma}^2_{G}$	$\hat{\sigma}^2_{R}$	$\hat{\sigma}^2_{E}$
Pl. Ht	26.9 (5.1)	25.1 (10.9)	114.3 (53.7)	4.3 (3.5)	713.6 (508.0)
Br. Lev	0.68 (0.13)	0.41 (0.21)	0.73 (0.41)	0.11 (0.09)	0.35 (0.32)
Lodging	1.06 (0.20)	0.49 (0.27)	2.32 (1.11)	0.02 (0.07)	0.07 (0.12)
Sus.St/Al	1.10 (0.21)	0.85 (0.39)	2.48 (1.24)	0.26 (0.18)	0.71 (0.65)
Sus. Bot	0.70 (0.13)	0.21 (0.15)	1.60 (0.75)	0.03 (0.05)	5.53 (3.95)
Sd. No	4394 (830)	2352 (1238)	6908 (3511)	-317 (103)	7955 (5821)
Tot.Hd.No	50.3 (11.5)	18.7 (15.6)	24.0 (19.4)	27.4 (18.8)	-12.6 (6.4)
Oil %	3.67 (0.69)	5.23 (2.05)	0.79 (1.43)	0.75 (0.56)	54.77 (39.36)
Yld (US)	25928 (4900)	26348 (11185)	22680 (15102)	1899 (2299)	49285 (37796)
Yld (S)	23998 (4535)	99413 (34000)	54044 (39949)	3567 (3018)	110442 (86603)

Table 3.9 Expt. II. Ratio of all variance component estimates to the relevant error variance, and their significances for the pooled environments model.

Character	$\hat{\sigma}^2_{GE}$	$\hat{\sigma}^2_{G}$	$\hat{\sigma}^2_{R}$	$\hat{\sigma}^2_{E}$
Pl. Ht	0.93 ****	4.25 ****	0.16 *	26.54 ****
Br. Lev	0.60 ***	1.07 ***	0.17 *	0.51 *
Lodging	0.46 **	2.20 ****	0.02 NS	0.07 NS
Sus. St/Al	0.78 ****	2.25 ****	0.23 **	0.64 *
Sus. Bot	0.29 *	2.30 ****	0.04 NS	7.93 ****
Sd. No	0.54 ***	1.57 ****	-0.07 NS	1.81 ****
Tot. Hd. No	0.37 (NS)	0.48 NS	0.54 ****	-0.25 NS
Oil %	1.42 ****	0.22 NS	0.20 *	14.91 ****
Yld (US)	1.02 ****	0.87 *	0.07 NS	1.90 ****
Yld (S)	4.14 ****	2.25 *	0.15 *	4.60 ***

Significance Symbols:

NS	=	$P>0.10$
(NS)	=	$0.10 \geq P > 0.05$
*	=	$0.05 \geq P > 0.01$
**	=	$0.01 \geq P > 0.005$
***	=	$0.005 \geq P > 0.001$
****	=	$0.001 \geq P$

Site effects were significant for the following traits of Expt. I: Lf. L/W, Br. Lth, Brd. Dam, Sus. Bot, and Yld (US). The site mean values ($\bar{X}_{..k.}$) for the trait, Sus. Bot, at Massey, Aorangi and Flockhouse were 5.17, 6.69 and 2.38 respectively, on a scale of 0-10. The lowest disease incidence being observed at Flockhouse, may be due to the relatively drier conditions of that site.

The most significant environmental component was the site x year interaction effect. This variance component (σ^2_{SY}) was of sizable magnitude and highly significant for most of the traits studied (Table 3.7). Presence of significant σ^2_{SY} component for most characters studied indicates that general trend in magnitude and/or ranking of certain site means have been different over the years. This means each site-year combination was an independent environment. It was observed that early planting at Flockhouse in the second year (see Table 2.2) enhanced the plant growth. To investigate this, $\bar{X}_{i.kl}$ values for Flockhouse in the two years (Appendix III) were compared using a t-test, for five traits representing plant growth. The results are presented in Tables 3.10. For the traits St. Dia, Pl. Ht and Lf. Lth, all genotypes performed better in the second year. Furthermore Table 3.7 suggests that for these three traits σ^2_{SY} was very high and σ^2_{Y} component was non-significant. The large σ^2_{SY} interaction component observed in St. Dia, Pl. Ht and Lf. Lth may be mainly due to the enhanced plant growth at Flockhouse in the second year.

3.3.2 Variance Components Involving Genotypic Effects

The genotypic component and all first and second order interactions of genotype with environmental components are included in this category. The interaction components are collectively known as genotype x environment interaction. The variance components involving genotypic effects for Expt. I are presented in Table 3.6.

The genotypic variance component was significant for only six of the 22 characters studied in Expt. I (Lf. Lth; Hd. Dia; Br. Lth; Br. L/W; Sp. Inx and Sus. Bot). Most of

Table 3.10 Expt. I. Comparison of genotypic means for five traits at Flockhouse in years 1978 ($\bar{X}_{i.kl_1}$) and 1979 ($\bar{X}_{i.kl_2}$).

CHARACTER	GENOTYPE	VFSTP-1	Partial-hull	Leed	Dart	PI 195895	0-22	Rio
St. Dia (mm.)	$\bar{X}_{i.kl_1}$	9.3	8.6	8.3	10.4	9.1	9.4	8.6
	$\bar{X}_{i.kl_2}$	16.0	16.8	13.8	13.5	15.4	11.4	12.8
	Sig (5%)	*	*	*	*	*	(NS)	*
Pl. Ht (cm.)	$\bar{X}_{i.kl_1}$	57.7	50.5	50.8	62.0	55.2	60.0	56.2
	$\bar{X}_{i.kl_2}$	109.1	105.8	101.2	101.5	114.3	112.2	110.7
	Sig (5%)	*	*	*	*	*	*	*
Lf. Lth (cm.)	$\bar{X}_{i.kl_1}$	109.1	127.5	102.4	86.7	94.2	81.5	93.2
	$\bar{X}_{i.kl_2}$	161.6	189.4	161.9	164.5	173.1	163.3	181.7
	Sig (5%)	*	*	*	*	*	*	*
Tot.Hd.No	$\bar{X}_{i.kl_1}$	10.0	9.1	7.4	12.2	11.5	13.0	8.4
	$\bar{X}_{i.kl_2}$	24.3	25.0	18.5	20.3	40.4	14.0	20.5
	Sig (5%)	*	*	(NS)	NS	*	NS	(NS)
Yld (US) (kg/ha)	$\bar{X}_{i.kl_1}$	92	87	140	302	258	180	227
	$\bar{X}_{i.kl_2}$	302	250	464	412	841	908	722
	Sig (5%)	NS	NS	*	NS	*	*	*

Significance Symbols:

NS	=	$P>0.10$
(NS)	=	$0.10 \geq P > 0.05$
*	=	$0.05 \geq P$

the genotypes evaluated in this study were commercial cultivars (see Table 2.1) with a relatively narrow genetic base. Hence, absence of average genetic differences for most of the traits may be expected. However, the large GxE interaction component observed for many traits (Table 3.6) also could have made the genetic variance non-significant. The presence of significant σ^2_G component for susceptibility to Botrytis cinerea Pers. may be useful in a future breeding programme. The $\bar{X}_{i...}$ values for Sus. Bot in Table 3.11 indicate that cultivars VFSTP-1 and Partial-hull are the most susceptible, whereas other 5 cultivars may be considered as showing certain degree of tolerance to the disease.

Estimates of variance components for the traits in Expt. II are presented in Table 3.8, for comparison. A noticeable feature is the increase in genotypic variance due to the addition of 3 genotypes (see Table 2.1) from the safflower germplasm collection. This point may be illustrated by examining the ratios to error variance in Tables 3.7 and 3.9. Of the additional characters studied in Expt. II, lodging, Sus. St/Al and Sd. No showed highly significant genotypic differences. The genotypic means, $\bar{X}_{i..}$, for these traits will be examined in section 3.4.

In Expt. I, GxE interactions were significant for all characters except for: Hd. Dia, Br. L/W, Sp. Inx, and Pr. Hd. No (Table 3.7). Considering the first order interactions, it is noted that σ^2_{GY} variance component was significant for the following traits: Br. Lev, Tot. Hd. No, and Es. Den. For Yld (S), σ^2_{GS} was the dominant component. In the case of Sus. Bot both first order interactions were significant. This means that there were some environmental factors in site and year effects which were responsible for the differences in cultivar responses to Sus. Bot.

For majority of characters studied, σ^2_{GSY} was the most significant GxE interaction component (Table 3.7). This implies that the cultivars have responded differently when grown in different environments (site-year combination). The high σ^2_{GSY} values observed in most traits may have

contributed to the poor significance of σ^2_G component.

Presence of significant GxE interactions highlights the importance of growing cultivars in number of sites over a period of years, in evaluation studies. Further analyses of GxE interaction effects will be discussed in section 3.6.

3.4 GENOTYPIC MEANS

The genotypic means of all traits, except for yield, are based on the unsprayed plot values. The yields of unsprayed and sprayed halves are presented as two separate variables. The genotypic means ($\bar{X}_{i...}$), LSD estimates, and significant groupings for the characters studied in Expt. I are presented in Table 3.11. Cultivar Partial-hull had the longest leaves and largest primary heads and was significantly different from other genotypes with respect to these two characters. For the traits Br. Lth and Br. L/W, three clearly defined significant groups were distinguished. Cultivars Partial-hull and VFSTP-1 had long and narrow involucral bracts, whereas those of genotype PI 195895 were short and broad. Highest degree of spininess was recorded in cultivars Partial-hull, whereas genotype PI 195895 was the least spiny. With respect to Sus. Bot, two groups were identified, cultivars VFSTP-1 and Partial-hull being the most susceptible. The other 5 genotypes may be considered as showing some tolerance (Table 3.11) to head rot disease.

The genotypic mean yield (unsprayed)/plot for the seven genotypes ranged from 234-600 Kg/ha with a grand mean of 461 Kg/ha (Table 3.11). However there were no significant genotypic differences for yield (unsprayed) or yield (sprayed) per plot in Expt. I. The yield obtained from the 3 additional genotypes included in Expt. II were comparatively poor (Table 3.12). To investigate the effect of spraying (see section 2.4) on yield, the genotypic means ($\bar{X}_{i...}$) in unsprayed and sprayed halves were compared by a t-test. The variance of the genotypic mean ($V_{\bar{x}_{i...}}$) for each trait was determined by the formula described in section 2.6.6. The appropriate standard error for the t-test was computed in the usual way as, $\sqrt{V_{\bar{u}} + V_{\bar{s}}}$ (Steel and Torie, 1960),

Table 3.11 Expt. I. Genotypic means ($\bar{X}_{i...}$), LSD values and grand means ($\bar{X}_{....}$) for all the characters studied on 7 safflower genotypes, in 3 sites, over 2 years. a, b, c, d etc. represent significant groupings.

Genotype and Statistic	St. Dia	Pl. Ht	Br. Lev	Lf. Lth	Lf. L/W	Hd. Dia	Br. Lth	Br. L/W
VFSTP-1	12.9	77.8	6.9	129.6^{bc}	2.81	24.4^{b}	47.9^{a}	3.40^{a}
Partial-hull	13.2	73.4	8.0	152.1^{a}	2.81	26.1^{a}	49.8^{a}	3.25^{a}
Leed	12.5	74.2	7.4	129.4^{bc}	2.67	23.3^{bc}	40.9^{b}	2.97^{b}
Dart	12.5	74.4	7.4	124.2^{cd}	2.66	23.3^{bc}	40.4^{b}	3.00^{b}
PI 195895	13.0	77.5	7.3	122.3^{d}	2.52	23.1^{c}	30.2^{c}	2.32^{c}
0-22	11.1	74.9	6.5	120.0^{d}	2.70	22.2^{c}	36.7^{b}	2.84^{b}
Rio	11.7	76.8	6.8	131.4^{b}	2.73	23.3^{bc}	37.9^{b}	2.95^{b}
Grand mean	12.4	75.6	7.2	129.8	2.70	23.7	40.5	2.96
L.S.D.† (p=0.05)	-	-	-	6.0	-	1.1	4.2	0.23

Table 3.11 (Continued)

Genotype and Statistic	Sp. Inx	Pr.Hd. No	Tot.Hd. No	Es. Den	GPPF	Brd. Dam	Sus. Bot
VFSTP-1	5.60^{bc}	8.4	19.0	6.6	3.4	2.6	6.8^{a}
Partial-hull	6.65^{a}	10.0	19.4	6.7	3.6	2.3	6.2^{a}
Leed	5.43^{bc}	8.9	16.8	5.6	3.4	2.9	4.1^{b}
Dart	5.89^{b}	9.0	17.8	6.1	3.1	2.7	4.1^{b}
PI 195895	0.84^{d}	10.0	24.1	5.7	3.3	3.6	4.3^{b}
0-22	5.16^{c}	7.8	15.8	8.1	2.9	4.2	3.3^{b}
Rio	5.63^{bc}	8.0	14.9	6.6	2.5	3.2	4.3^{b}
Grand mean	5.03	8.8	18.3	6.5	3.2	3.1	4.8
L.S.D.† (p=0.05)	0.61	-	-	-	-	-	1.3

Table 3.11 (Continued)

Genotype and Statistic	Yld(US)	Yld(S)	Oil %	Hull %	Spr. Dam	Sd. Wt	I. Val
VFSTP-1	307	365	16.9	58.4	3.7	37.0	122.8
Partial-hull	234	325	20.1	54.3	3.3	38.8	128.9
Leed	559	801	19.2	56.5	3.6	39.0	131.7
Dart	600	736	21.9	55.4	4.2	41.6	129.3
PI 195895	460	707	17.0	58.2	4.3	37.7	125.2
0-22	545	641	21.9	55.9	4.8	37.0	122.9
Rio	525	729	20.2	56.6	4.3	41.9	120.8
Grand Mean	461	615	19.6	56.5	4.0	39.0	125.9
L.S.D.† (p=0.05)	-	-	-	-	-	-	-

† LSD values are not presented for non-significant traits.

Table 3.12 Expt II. Genotypic means ($\bar{X}_{i..}$), LSD values and grand means ($\bar{X}_{...}$) for ten traits studied on 10 safflower genotypes in 3 sites. a, b, c, d, e etc. represent significant groupings.

Genotype and Statistic	Pl. Ht	Br. Lev	Lodging	Sus. St/Al	Sus. Bot	Sd. No	Tot.Hd.No	Oil %	Yld(US)	Yld(S)
VFSTP-1	80.0^{b}	6.6^{abc}	3.6^{de}	3.7^{bcd}	6.8^{ab}	203.7^{a}	23.9	13 9	291^{bcd}	335^{abcd}
Partial-hull	75.2^{b}	7.9^{a}	3.1^{e}	4.1^{bcd}	7.1^{ab}	196.2^{ab}	23.0	17.8	255^{bcd}	352^{abcd}
Leed	74.6^{b}	7.6^{a}	4.8^{bcd}	4.1^{bcd}	4.4^{cd}	243.3^{a}	20.3	14.0	500^{ab}	849^{a}
Dart	71.1^{c}	7.5^{a}	4.8^{bcd}	4.8^{bc}	4.7^{cd}	254.2^{a}	18.2	15.8	394^{abc}	664^{abc}
PI 195895	81.1^{b}	7.6^{a}	5.3^{bc}	3.2^{cde}	4.7^{cd}	263.6^{a}	32.1	12.5	538^{ab}	852^{a}
0-22	75.4^{b}	5.3^{abd}	3.8^{cde}	5.3^{b}	3.7^{d}	238.7^{a}	12.2	17.0	616^{a}	780^{ab}
Rio	75.9^{b}	7.2^{c}	4.0^{de}	4.6^{bc}	5.1^{c}	269.3^{a}	18.5	14.3	536^{ab}	724^{ab}
PI 253515	96.2^{a}	5.4^{d}	6.2^{b}	7.9^{a}	7.4^{ab}	5.0^{c}	13.2	15.3	64^{d}	69^{d}
PI 262437	100.2^{a}	7.3^{a}	8.7^{a}	1.6^{e}	6.7^{ab}	93.1^{c}	27.7	13.1	137^{cd}	151^{cd}
PI 306684	99.3^{a}	5.9^{bcd}	4.4^{cde}	2.7^{de}	6.3^{b}	95.8^{bc}	28.0	13.7	274^{bcd}	273^{bcd}
Grand Mean	82.9	6.8	4.9	4.2	5.7	186.3	21.7	14.8	361	505
L.S.D. (p=0.05)	9.5	1.3	1.5	1.8	1.1	101.1	-†	-	306	537

† L.S.D. values are not presented for non-significant traits.

where $V_{\bar{u}}$ and $V_{\bar{s}}$ are variances of the genotypic mean yield for unsprayed and sprayed halves respectively. The results for Expt. I and Expt. II presented in Tables 3.13 and 3.14 respectively, suggest that spraying had no significant effect on the yield.

The genotypic means ($\bar{X}_{i..}$), LSD estimates and significant groupings for characters in Expt. II are presented in Table 3.12. The three additional genotypes were highly susceptible to head-rot disease. An interesting feature is that both PI 262437 and PI 306684 showed considerable tolerance to leaf spot disease caused by Stemphylium/Alternaria species. These two genotypes had disease susceptibility scores of 1.6 and 2.7 in a scale of 0-10. However plants of the genotype PI 262437 tended to lodge quite easily (Table 3.12).

3.5 HERITABILITY ESTIMATES

Both full and restricted heritability estimates their standard errors and coefficients of variation, for Expt. I are presented in Table 3.15. The heritability estimates presented here are in broad sense, taking into consideration the total genetic variability present in the population (see also section 1.2). The broad sense full heritability estimates the fraction of total phenotypic variance attributable to genetic differences between genotypes. The restricted heritability is appropriate, when comparison is made between two genotypes within the same block at a particular site.

Broad sense full heritability estimates for most characters were low value. The negative heritability estimates observed for some traits are due to the negative σ^2_{2G} component estimates obtained (Table 3.6). The negative σ_G estimates may be interpreted as sampling deviations from σ^2_G components of very low value. Broad sense full heritability estimates were relatively high for the following traits: Br. Lth (0.44); Br. L/W (0.60); and bract Sp. Inx (0.84). In case of restricted heritability, in addition to the above three traits, Lf. Lth (0.51), Hd. Dia (0.57) and Sus. Bot (0.52) also showed moderately high estimates

Table 3.13 Expt. I. Comparison between mean genotypic yields of unsprayed and sprayed halves for the seven genotypes.

GENOTYPE	$\bar{X}_{i...}$ (kg/ha) (unsprayed)	$\bar{X}_{i...}$ (kg/ha) (sprayed)	Sig.† (5%)
VFSTP-1	307	365	NS
Partial-hull	234	325	NS
Leed	559	801	NS
Dart	600	736	NS
PI 195895	460	707	NS
0-22	545	641	NS
Rio	525	729	NS

† Significance at 5% probability level; * and NS are significant and non-significant respectively.

Table 3.14 Expt. II. Comparison between mean genotypic yields of unsprayed and sprayed halves for the ten genotypes.

GENOTYPE	$\bar{X}_{i..}$ (kg/ha) (unsprayed)	$\bar{X}_{i..}$ (kg/ha) (sprayed)	Sig.† (5%)
VFSTP-1	291	335	NS
Partial-hull	255	352	NS
Leed	500	849	NS
Dart	394	664	NS
PI 195895	538	852	NS
0-22	616	780	NS
Rio	536	724	NS
PI 253515	64	69	NS
PI 262437	137	151	NS
PI 306684	274	273	NS

† Significance at 5% probability level; * and NS are significant and non-significant respectively.

Table 3.15 Expt. I. Estimates of broad sense heritability, full ($\hat{h}^2$) and restricted ($\hat{h}^{2\prime}$), their standard errors and coefficients of variation, based on variance component estimates from the pooled sites x years model.

Character	Heritability (Full)			Heritability (Restricted)		
	$\hat{h}^2$	S.E.	C.V.%	$\hat{h}^{2\prime}$	S.E.	C.V.%
St. Dia	0.03	0.06	169	0.10	0.16	165
Pl. Ht	-0.01	0.01	†	-0.09	0.09	†
Br. Lev	-0.05	0.12	†	-0.08	0.17	†
Lf. Lth	0.19	0.11	58	0.51	0.14	27
Lf. L/W	0.11	0.07	66	0.16	0.10	61
Hd. Dia	0.16	0.11	66	0.57	0.15	26
Br. Lth	0.44	0.16	37	0.72	0.12	16
Br. L/W	0.60	0.13	22	0.64	0.13	20
Sp. Inx	0.84	0.08	9	0.88	0.06	7
Pr. Hd. No	0.00	0.05	†	0.00	0.11	†
Tot. Hd. No	-0.04	0.07	†	-0.07	0.12	†
Es. Den	-0.02	0.23	†	-0.02	0.25	†
GPPF	0.02	0.06	378	0.03	0.10	376
Brd. Dam	0.06	0.06	102	0.18	0.15	84
Sus. Bot	0.18	0.11	64	0.52	0.16	30
Yld (US)	-0.01	0.05	†	-0.02	0.14	†
Oil %	0.02	0.03	178	0.08	0.14	169
Hull %	0.00	0.03	†	-0.01	0.11	†
Spr. Dam	-0.02	0.03	†	-0.05	0.09	†
Sd. Wt	0.05	0.04	92	0.10	0.08	83
I. Val	0.12	0.08	68	0.13	0.09	67

† Very large coefficient of variation.

(Table 3.15). When the genotype x environment interaction components are small compared to environmental components, a marked increase in the restricted estimate in comparison to full heritability estimate may be expected (refer section 2.6.4). This may be illustrated by examining the relative magnitudes of these estimates (Table 3.7) for Lf. Lth, Hd. Dia and Sus. Bot. For these 3 characters restricted heritability estimates are very much higher than full estimates.

The coefficients of variation (CV) values given in Table 3.15 indicate the precision of the heritability estimates. These CV values are very much higher than those obtained for the primary data (refer to Table 3.1). Furthermore there is no indication that coefficients of variation of heritability estimates follow a trend similar to that of primary data. However, Table 3.15 indicates that higher heritability estimates are usually associated with lower CV values. Also, CV values for full and restricted heritability estimates were of similar magnitudes for most traits.

Heritability estimates for ten traits in Expt. II are presented in Table 3.16 for comparison. A noticeable feature is the increase in value of heritability estimates due to the additional genetic variability in the population. Relatively high heritability estimates were also obtained for the following additional traits assessed in in Expt. I: lodging and Sus. St/Al.

It should be noted here that the heritability estimates presented here are strictly applicable only to the genotypic and environmental populations included in this study. Considering the full heritability estimates obtained here, it may be possible to gain genetic advance for the following traits through selection from this gene base: bract length, length/width and spininess; lodging and resistance to leaf spot disease.

Table 3.16 Expt. II. Estimates of broad sense heritability, full ($\hat{h}^2$) and restricted ($\hat{h}^{2'}$), their standard errors, and coefficients of variation, based on variance component estimates from the pooled environments model.

Character	Heritability (Full)			Heritability (Restricted)		
	$\hat{h}^2$	S.E.	C.V.%	$\hat{h}^{2'}$	S.E.	C.V.%
Pl. Ht	0.13	0.09	71	0.69	0.11	17
Br. Lev	0.32	0.14	43	0.40	0.15	37
Hd. Dia	0.35	0.15	45	0.56	0.14	26
Lodging	0.59	0.13	22	0.60	0.13	21
Sus. St/Al	0.46	0.14	31	0.56	0.14	25
Sus. Bot	0.20	0.12	62	0.64	0.12	18
Sd. No	0.32	0.15	45	0.51	0.14	28
Oil %	0.01	0.02	189	0.08	0.14	177
Hull %	0.00	0.02	514	0.03	0.14	510
Yld (US)	0.18	0.12	64	0.30	0.16	52

3.6 ADAPTATION ANALYSIS

Most of the traits studied showed significant GxE interactions. These characters, together with estimates of parameters utilized to study adaptabilities of individual genotypes, are presented in Table 3.17. The GxE interactions were not significant for the following traits and adaptation analyses were not performed: Hd. Dia; Br. Lth; Br. L/W; Sp. Inx and Pr. Hd. No.

The following statistics were considered to examine the adaptabilities of individual genotypes: the ecovalance; adaptation coefficient, b_i (Finlay and Wilkinson, 1963); and R^2 value for the linear regression. The procedures for computation of these statistics have been described in section 2.6.5. Ecovalance is the contribution of individual genotypes to total GxE interaction sum of squares. Ecovalances in Table 3.17, are presented as ratios to least ecovalance (RLE), and provide information as to which genotypes were most variable with changing environment. The SS_{GE} for each genotype may be partitioned into sum of squares due to linear regression (SS_{Reg}) and sum of squares about regression, by regressing $\bar{X}_{i.k}$ against $\bar{X}_{..k}$ (Finlay and Wilkinson, 1963). The adaptation coefficients (b_i), presented in Table 3.17 are the estimates of regression coefficients obtained by this procedure (refer also section 2.6.5). In this context, the R^2 value for the linear regression estimates the proportion of variance in $\bar{X}_{i.k}$ accounted for by regression against the environment mean ($\bar{X}_{..k}$). An adaptation coefficient (b_i) approximately equal to 1.0 indicates general adaptability. Genotypes with adaptation coefficients greater than 1.0 are specifically adapted to favourable environments. Those with adaptation coefficients less than 1.0 are specifically adapted to poor environments (Finlay and Wilkinson, 1963). In the context of stability, a genotype with a very low regression coefficient ($b_i \simeq 0$) is classified as highly stable (Finlay and Wilkinson, 1963).

It may be noticed in Table 3.17, that, for a few traits (Br. Lev; Tot. Hd. No; and Es. Den), performances of majority

Table 3.17 Expt. I. Adaptation coefficients ($\hat{b}_i$), their standard errors and significances, ratios to least ecovalence (R.L.E.), and R^2 values for characters showing significant GxE interactions.

Genotype	$\hat{b}_i$	S.E.	Sig. (From 1)	Sig. (From 0)	R.L.E.	R^2
St. Dia						
VFSTP-1	1.04	0.19	NS	**	3.27	0.88
Partial-hull	1.25	0.26	NS	**	7.14	0.86
Leed	1.01	0.15	NS	***	2.01	0.92
Dart	0.84	0.14	NS	***	2.39	0.89
PI 195895	1.04	0.25	NS	*	5.66	0.81
0-22	0.84	0.29	NS	*	7.79	0.68
Rio	0.97	0.11	NS	****	1.00	0.95
Pl. Ht						
VFSTP-1	0.91	0.07	NS	****	1.29	0.98
Partial-hull	1.05	0.07	NS	****	1.00	0.98
Leed	0.92	0.08	NS	****	1.42	0.97
Dart	0.92	0.10	NS	****	2.31	0.95
PI 195895	1.01	0.09	NS	****	1.40	0.97
0-22	1.08	0.09	NS	****	1.64	0.98
Rio	1.11	0.08	NS	****	1.70	0.98
Br. Lev						
VFSTP-1	1.11	0.47	NS	(NS)	6.38	0.58
Partial-hull	0.72	0.46	NS	NS	6.85	0.37
Leed	1.38	0.32	NS	*	4.03	0.82
Dart	1.08	0.18	NS	***	1.00	0.90
PI 195895	0.49	0.35	NS	NS	5.55	0.33
0-22	1.16	0.88	NS	NS	22.50	0.31
Rio	1.07	0.44	NS	(NS)	5.68	0.59

Genotype	$\hat{b}_i$	S.E.	Sig. (From 1)	Sig. (From 0)	R.L.E	R^2
Lf. Lth						
VFSTP-1	0.74	0.06	*	****	3.01	0.98
Partial-hull	0.87	0.06	(NS)	****	1.19	0.98
Leed	0.87	0.05	(NS)	****	1.00	0.99
Dart	1.18	0.11	NS	****	2.93	0.97
PI 195895	1.00	0.12	NS	***	2.35	0.94
0-22	1.16	0.07	(NS)	****	1.72	0.99
Rio	1.17	0.11	NS	****	2.81	0.97
Lf. L/W						
VFSTP-1	0.06	0.26	*	NS	16.00	0.00
Partial-hull	-0.20	0.50	(NS)	NS	13.00	0.04
Leed	1.18	0.25	NS	**	1.50	0.85
Dart	1.46	0.07	***	****	1.00	0.99
PI 195895	1.16	0.49	NS	(NS)	5.00	0.58
0-22	1.87	0.21	*	****	5.00	0.95
Rio	1.56	0.40	NS	*	5.00	0.79
Br. Lth						
VFSTP-1	0.98	0.33	NS	*	18.51	0.68
Partial-hull	1.41	0.24	NS	***	16.47	0.90
Leed	1.05	0.23	NS	*	8.87	0.84
Dart	0.99	0.16	NS	***	4.17	0.91
PI 195895	0.36	0.26	(NS)	NS	28.50	0.32
0-22	1.12	0.29	NS	*	14.33	0.79
Rio	1.09	0.06	NS	****	1.00	0.99
Tot. Hd. No[†]						
VFSTP-1	1.06	0.35	NS	(NS)	3.37	0.82
Partial-hull	1.25	0.07	(NS)	***	1.00	0.99
Leed	0.97	0.42	NS	NS	4.83	0.73
Dart	0.70	0.31	NS	NS	3.80	0.72
PI 195895	1.85	0.77	NS	NS	25.42	0.74
0-22	0.32	0.81	NS	NS	23.89	0.07
Rio	0.84	0.21	NS	(NS)	1.56	0.89

Genotype	$\hat{b}_i$	S.E.	Sig. (From 1)	Sig. (From 0)	R.L.E	R^2
Es. Den						
VFSTP-1	0.69	0.23	NS	*	1.00	0.69
Partial-hull	1.95	0.91	NS	(NS)	13.48	0.53
Leed	0.87	0.86	NS	NS	9.41	0.20
Dart	0.16	0.42	NS	NS	4.41	0.04
PI 195895	0.89	0.49	NS	NS	3.03	0.45
0-22	1.39	0.89	NS	NS	10.52	0.38
Rio	1.05	0.30	NS	*	1.15	0.76
GPPF						
VFSTP-1	1.11	0.14	NS	***	8.83	0.94
Partial-hull	1.21	0.16	NS	***	12.56	0.93
Leed	0.98	0.15	NS	***	5.44	0.92
Dart	1.10	0.14	NS	***	4.22	0.94
PI 195895	0.68	0.16	NS	*	11.17	0.82
0-22	0.77	0.26	NS	*	21.00	0.69
Rio	1.14	0.03	**	****	1.00	1.00
Brd. Dam						
VFSTP-1	0.84	0.17	NS	**	2.06	0.86
Partial-hull	0.50	0.08	***	***	4.23	0.90
Leed	0.98	0.19	NS	**	2.10	0.87
Dart	0.81	0.12	NS	***	1.44	0.92
PI 195895	1.39	0.21	NS	***	4.97	0.92
0-22	1.30	0.31	NS	*	7.33	0.81
Rio	1.18	0.09	NS	****	1.00	0.98
Sus. Bot						
VFSTP-1	0.78	0.16	NS	**	6.42	0.86
Partial-hull	1.47	0.17	(NS)	****	8.12	0.95
Leed	0.90	0.10	NS	****	1.00	0.95
Dart	1.03	0.12	NS	***	1.58	0.95
PI 195895	1.02	0.11	NS	****	1.37	0.95
0-22	0.63	0.14	(NS)	*	6.73	0.83
Rio	1.16	0.17	NS	***	3.75	0.92

Genotype	$\hat{b}_i$	S.E.	Sig. (From 1)	Sig. (From 0)	R.L.E	R^2
Yld (US)						
VFSTP-1	0.32	0.15	*	(NS)	8.41	0.54
Partial-hull	0.21	0.09	****	(NS)	10.10	0.59
Leed	1.52	0.15	*	****	5.64	0.96
Dart	1.75	0.35	(NS)	**	16.35	0.86
PI 195895	0.79	0.21	NS	*	3.43	0.78
0-22	1.20	0.17	NS	***	2.40	0.93
Rio	1.21	0.07	*	****	1.00	0.99
Yld (S)						
VFSTP-1	0.26	0.07	****	*	7.37	0.79
Partial-hull	0.38	0.06	****	***	5.12	0.92
Leed	1.64	0.23	*	***	7.94	0.93
Dart	1.49	0.17	*	****	4.62	0.95
PI 195895	1.13	0.14	NS	***	1.31	0.94
0-22	0.91	0.18	NS	**	1.78	0.87
Rio	1.19	0.10	NS	****	1.00	0.97
Oil %						
VFSTP-1	0.99	0.23	NS	*	2.43	0.82
Partial-hull	0.58	0.29	NS	NS	5.71	0.51
Leed	1.03	0.15	NS	***	1.00	0.92
Dart	1.10	0.23	NS	**	2.57	0.85
PI 195895	1.09	0.22	NS	**	2.19	0.86
0-22	0.94	0.30	NS	*	4.20	0.71
Rio	1.27	0.09	*	****	1.19	0.98
Hull %						
VFSTP-1	0.97	0.16	NS	***	1.57	0.90
Partial-hull	0.49	0.26	NS	NS	8.14	0.46
Leed	1.07	0.16	NS	***	1.55	0.92
Dart	1.05	0.13	NS	***	1.00	0.94
PI 195895	1.19	0.21	NS	***	3.25	0.89
0-22	0.90	0.19	NS	**	2.45	0.84
Rio	1.34	0.13	(NS)	****	2.80	0.96

Genotype	$\hat{b}_i$	S.E.	Sig. (From 1)	Sig. (From 0)	R.L.E	R^2
Spr. Dam						
VFSTP-1	0.77	0.20	NS	*	5.67	0.79
Partial-hull	0.93	0.23	NS	*	5.64	0.81
Leed	0.91	0.09	NS	****	1.00	0.97
Dart	1.23	0.19	NS	***	5.43	0.91
PI 195895	1.16	0.18	NS	***	4.22	0.91
0-22	0.82	0.57	NS	NS	36.29	0.34
Rio	1.18	0.12	NS	****	2.43	0.96
Sd. Wt						
VFSTP-1	0.49	0.32	NS	NS	4.54	0.37
Partial-hull	0.49	0.20	(NS)	(NS)	2.86	0.60
Leed	1.16	0.48	NS	(NS)	6.40	0.60
Dart	0.85	0.21	NS	*	1.35	0.80
PI 195895	1.36	0.32	NS	*	3.64	0.82
0-22	1.32	0.11	*	****	1.00	0.97
Rio	1.34	0.15	(NS)	****	1.39	0.95

Significance Symbols:

NS	=	$P>0.10$
(NS)	=	$0.10 \geq P > 0.05$
*	=	$0.05 \geq P > 0.01$
**	=	$0.01 \geq P > 0.005$
***	=	$0.005 \geq P > 0.001$
****	=	$0.001 \geq P$

† based on data from two sites only (Massey and Flockhouse), over a two year period.

of genotypes could not be predicted by a linear relationship with the environment. These observations are not in accord with the hypothesis that a linear relationship exists between genotype performances and environmental mean. Relatively low R^2 values were recorded in such instances (Table 3.17). Ecovalances (expressed as ratios to least ecovalance in Table 3.17) do not provide the same information as b_i, with respect to adaptabilities of genotypes. However, where regression fails, ecovalances could provide information as to which genotypes were most variable. In the case of trait Br. Lev, cultivar 0-22 showed the highest variable performance. Both PI 195895 and 0-22 contributed largely to GxE interaction observed in Tot. Hd. No.

For some characters studied, adaptation coefficient (b_i) of none of the seven genotypes were significantly different from unity. This may be seen in traits, St. Dia and Pl. Ht, where all seven genotypes could be regarded as showing general adaptability to the environments sampled. Genotypic differences were also non-significant for the two characters (Table 3.11). Another noticeable feature is that, for Pl. Ht, the total GxE interaction component is more or less equally divided among the seven genotypes as indicated by RLE values. Furthermore none of the adaptation coefficients (b_i) of individual genotypes for Pl. Ht were significantly different from unity. To investigate further, adaptation coefficients (b_i) of individual genotypes for Pl. Ht were tested in pair-wise combinations using a t-test. The appropriate standard errors for the comparisons were computed as $\sqrt{SE_1^2 + SE_2^2}$, where SE_1 and SE_2 are standard errors for the two b_i values (Table 3.17). Results indicated that none of the b_i values were significantly different from the others.

To illustrate the use of Table 3.15, to study the GxE interactions of the seven genotypes, the results for the trait Yld (US) will be discussed here. As indicated by RLE values (Table 3.17), cultivars VFSTP-1, Partial-hull and Dart contributed mostly to the total GxE interaction observed for Yld (US). A linear relationship with the environment was not evident for two genotypes (VFSTP-1 and Partial-hull).

The cultivars Leed and Dart with adaptation coefficients 1.52 and 1.75 respectively were specifically adapted to favourable environments. Cultivars 0-22 and Rio could be considered as showing general adaptability. The results of t-tests of b_i values for Yld (US) are presented in Table 3.18.

The adaptability patterns of the seven genotypes for the traits, Yld (US) and Sus. Bot are graphically represented in Fig 3.1 and 3.2 respectively.

3.7 OPTIMUM PLOT ALLOCATION

The optimum plot allocation study was based on data from seven genotypes evaluated at 3 sites over a two year period (see section 2.6). The following four traits were considered more appropriate for this study, due to their obvious importance in any future safflower cultivar evaluation study: Sus. Bot; Yld (US); Oil %; and Hull %. All four characters showed significant GxE interactions in the pooled ANOVA (Table 3.7).

The important issue is to find out whether a precision comparable to the present experiment could be obtained by a lesser number of plots, by reallocating them with respect to years, sites and replications. It may be also desirable to know if a different allocation could provide a higher precision, keeping the total number of plots approximately constant, or increasing only marginally.

The procedure followed here has been described in section 2.6.6. The relative efficiencies (RE) with respect to various plot allocations, for the four traits are presented in Tables 3.19-3.22. Relative efficiency in this context (refer to section 2.6.6) measures the suitability of a particular allocation, a value greater than 100 indicating a better allocation compared to the present one.

According to results presented in Tables 3.16-3.19, it appears that testing for only one year would be inadequate. If only one year was used for the traits Sus. Bot and Yld (US), at least 5 sites would be necessary to obtain the level of precision of the present allocation (RE = 100). In the case

Table 3.18 Expt. I. The significances between adaptation coefficients ($\hat{b}_i$) of individual genotypes for the trait Yld (US)

GENOTYPE	$\hat{b}_i$	GENOTYPE VFSTP-1	Partial-hull	Leed	Dart	PI 195895	0-22	Rio
VFSTP-1	0.32		†NS(0.49)	*(0.59)	*(1.06)	NS(0.72)	*(0.63)	*(0.46)
Partial-hull	0.21			*(0.49)	*(1.00)	NS(0.63)	*(0.53)	*(0.32)
Leed	1.52				NS(1.06)	*(0.72)	NS(0.63)	NS(0.46)
Dart	1.75					NS(1.13)	NS(1.08)	NS(0.99)
PI 195895	0.79						NS(0.75)	NS(0.61)
0-22	1.20							NS(0.51)
Rio	1.21							

† NS and * are non-significant and significant respectively at 5% probability level. The values within brackets are l.s.d. estimates applicable to pairwise comparisons.

Fig. 3.1 Linear regression lines showing relationship between genotypic yields ($\bar{X}_{i..k}$) and environmental mean yields ($\bar{X}_{..k}$) for seven safflower genotypes grown at 3 sites in years 1978 and 1979: M = Massey; A = Aorangi; F = Flockhouse; 78 and 79 are years 1978 and 1979. (also refer to Table 3.17)

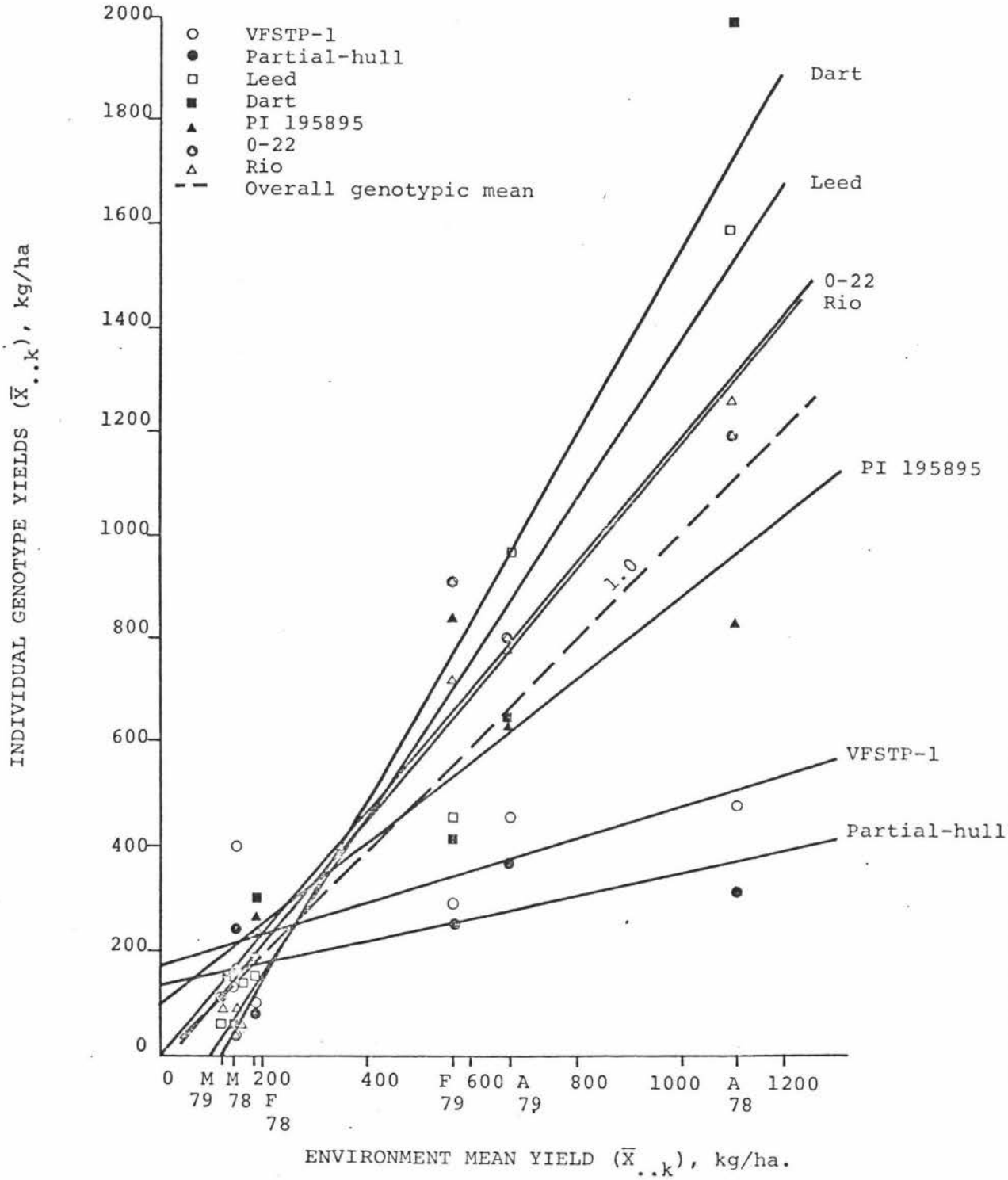

Fig. 3.2 Linear regression lines showing relationship between genotypic values for Sus. Bot. ($\bar{X}_{i.k}$) and environmental means ($\bar{X}_{..k}$) for seven safflower genotypes grown at 3 sites in years 1978 and 1979: M = Massey; A = Aorangi; F = Flockhouse; 78 and 79 represent years 1978 and 1979. (also refer to Table 3.17).

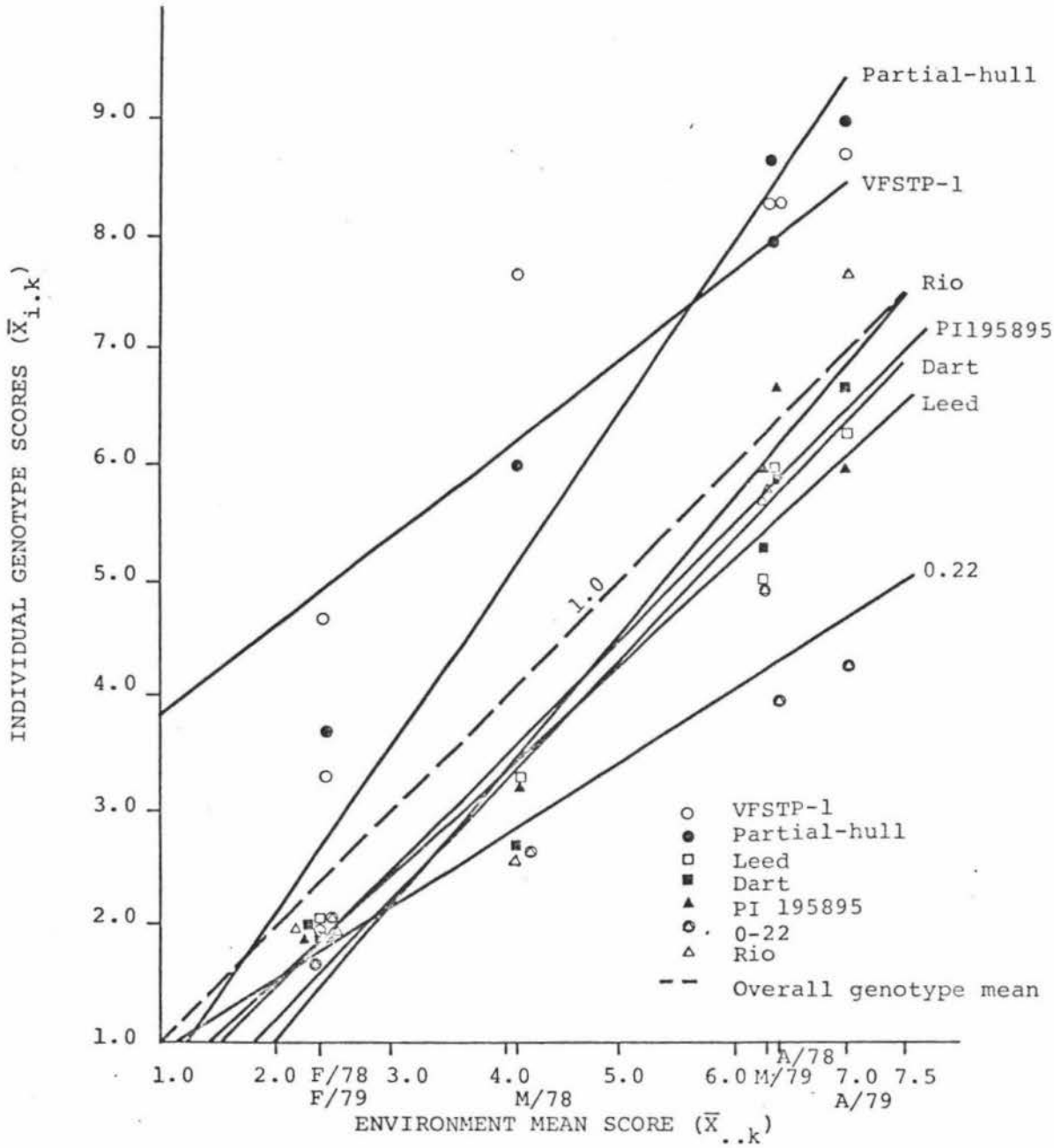

Table 3.19 Expt. I. Optimum plot allocation as indicated by relative efficiencies† for various combinations of blocks, sites and years for the character Sus. Bot.

Years	Blocks	Sites				
		1	2	3	4	5
	2	27	46	61	72	81
	3	32	54	69	81	91
1	4	36	59	75	88	96
	5	39	63	79	91	100
	2	37	66	90	110	127
	3	42	74	100	122	139
2	4	45	79	105	128	145
	5	47	82	110	132	149
	2	42	78	108	133	156
	3	46	85	116	145	169
3	4	49	88	122	152	175
	5	50	91	125	154	179
	2	45	85	119	149	179
	3	49	91	128	161	189
4	4	51	94	132	167	196
	5	52	97	135	169	200

† Relative efficiency =

$$\frac{\text{Actual variance of the genotypic mean estimated}}{\text{Expected variance of the genotypic mean computed for the allocation}} \times 100$$

Variance of the genotypic mean estimated = 0.2283 in the present expt.

Table 3.20 Expt. I. Optimum plot allocation as indicated by relative efficiencies for various combinations of blocks, sites and years for the character Yld (US).

Years	Blocks	Sites				
		1	2	3	4	5
	2	23	45	67	87	106
	3	24	47	69	90	110
1	4	25	48	70	92	112
	5	25	49	71	93	114
	2	34	66	97	128	156
	3	34	68	100	132	161
2	4	35	69	101	133	164
	5	35	69	102	133	164
	2	39	78	115	152	185
	3	40	79	118	154	192
3	4	41	80	119	156	192
	5	41	81	119	156	192
	2	43	85	127	167	208
	3	44	87	128	169	208
4	4	44	88	130	172	213
	5	45	88	130	172	213

Variance of the genotypic mean estimated in the present expt. = 21023

Table 3.21 Expt. I. Optimum plot allocation as indicated by relative efficiencies for various combinations of blocks, sites and years for the character % hull content.

Years	Blocks	Sites				
		1	2	3	4	5
	2	21	38	53	66	78
	3	23	42	58	71	83
1	4	24	44	60	75	86
	5	25	45	62	76	88
	2	35	66	93	116	137
	3	39	71	100	125	147
2	4	40	75	104	130	152
	5	41	76	106	132	154
	2	47	88	123	156	185
	3	50	93	132	167	196
3	4	52	97	137	172	204
	5	53	99	139	175	208
	2	55	104	149	189	227
	3	59	111	159	200	238
4	4	61	115	161	204	244
	5	62	116	167	208	250

Variance of the genotypic mean estimated in the present expt. = 2.2472

Table 3.22 Expt. I. Optimum plot allocation as indivated by relative efficiencies for various combinations of blocks, sites and years for the character % oil content.

Years	Blocks	Sites				
		1	2	3	4	5
	2	19	37	53	68	81
	3	21	39	56	71	85
1	4	22	41	58	74	88
	5	22	42	59	75	90
	2	34	66	94	122	145
	3	36	69	100	128	154
2	4	38	72	103	132	159
	5	38	73	105	133	161
	2	46	88	128	164	200
	3	49	93	135	172	208
3	4	50	96	139	179	213
	5	51	98	141	182	217
	2	56	108	156	200	244
	3	58	114	164	213	256
4	4	60	116	167	217	263
	5	61	118	169	217	263

Variance of the genotypic mean estimated in the present expt. = 2.7322

of other two traits (Tables 3.19 and 3.22), with a single year of testing, even 5 sites and 5 blocks will not give a RE value of 100. Furthermore the presence of significant σ^2_{GY} and σ^2_{GSY} variance components (Table 3.7) for the four traits highlights the importance of testing for more than one year.

Addition of a single year would result in a substantial reduction in variance of a genotypic mean ($V_{\bar{X}_{i\cdot\cdot}}$), as indicated by higher RE values. In general, for all four traits, increase in number of years and sites would be more efficient than increasing replications. Maintaining the present number of years and sites, and increasing replications from 3 to 5 (an extra 84 plots), would result in RE values of 110%, 102%, 106% and 105% respectively for the traits, Sus. Bot, Yld (US), Hull % and Oil %. Conversely for 2 years and 3 blocks, an increase in number of sites from 3 to 4 (an extra 42 plots) would result in RE values of 122%, 132%, 125% and 128% respectively. These results suggest that, optimum allocation of a given number of plots, disregarding costs, should be in the direction of fewer blocks, with an increase in number of sites and years.

An allocation of 2 years, 4 sites and 2 blocks has a consistent decrease in $V_{\bar{X}}$ (high RE values) for all four characters studied. Relative efficiencies expected for Sus. Bot, Yld (US), Hull % and Oil % are 110%, 128%, 116% and 122% respectively, with a reduction in plots from 126 (for present experiment) to 112. Hence, based on results of this study, an allocation of 2 years, 4 sites and 2 replications would be more efficient than the present allocation of 2 years, 3 sites and 3 blocks.

The relative costs of different allocations have not been considered in the preceding discussion. An increase in number of years would delay the release of new cultivars. Addition of sites would involve establishing new facilities and travel, and cost may be quite considerable (see also section 1.5). It is apparent from similar studies with other crops (Sprague and Federer, 1951), that cost per plot

decreases rapidly as number of plots per experiment is increased. Hence as far as cost is concerned, a decrease in replicates per experiment may not have a pronounced effect for traits such as Sus. Bot, for which evaluation is made entirely in the field. However for traits like %Oil content, for which time consuming laboratory analyses are involved, decrease in number of plots would be desirable.

3.8 PHENOTYPIC AND GENOTYPIC CORRELATIONS

Phenotypic and genotypic correlations for different character pairs in Expt. I are presented in Table 3.23. These were estimated by methods described in section 2.6.7. Most of the phenotypic correlations between morphological characters were significant. However a significant phenotypic correlation was not always accompanied by a significant genotypic correlation.

Stem diameter had significant, positive high phenotypic correlations with the following traits: Pl. Ht, Br. Lev, Hd. Dia, Pr. Hd. No and Tot. Hd. No. The corresponding genotypic correlations were not significant except for Br. Lev.

Plant height showed significant positive phenotypic correlations with Pr. Hd. No and Tot. Hd. No, but there was no evidence for any genetic association. Significant positive phenotypic correlations were observed between Br. Lev and the following traits: Hd. Dia, Pr. Hd. No and Tot. Hd. No. High positive genotypic correlations were obtained for Br. Lev with Hd. Dia (0.79) and Pr. Hd. No (0.91). Significant positive genotypic and phenotypic correlations also existed between the following characters: Lf. L/W and Br. L/W; Hd. Dia and Br. Lth; Br. L/W and bract Sp. Inx.

A noticeable feature was the absence of any correlation between bract Sp. Inx and Brd. Dam. Hence the results from this study do not justify the common belief that spiny cultivars are more resistant to bird attack. As expected there was significant negative correlation between Sus. Bot and oil percentage of seed. The high negative correlation,

Table 3.23 Expt. I. Phenotypic (r_p), and genotypic (r_g) correlation coefficients between some traits, studied on seven genotypes in six environments.

Characters pair			r_p	r_g
St. Dia	x	Pl. Ht	0.71****	0.04 NS
St. Dia	x	Br. Lev	0.65****	0.83 *
St. Dia	x	Hd. Dia	0.61****	0.72(NS)
St. Dia	x	Pr. Hd. No †	0.84****	0.74(NS)
St. Dia	x	Tot. Hd. No†	0.71****	0.66 NS
Pl. Ht	x	Br. Lev	0.19 *	-0.50 NS
Pl. Ht	x	Lf. L/W	0.04 NS	-0.18 NS
Pl. Ht	x	Pr. Hd. No†	0.71****	-0.22 NS
Pl. Ht	x	Tot. Hd. No†	0.43****	0.34 NS
Br. Lev	x	Hd. Dia	0.63****	0.79 *
Br. Lev	x	Pr, Hd. No†	0.55****	0.91 **
Br. Lev	x	Tot. Hd. No†	0.59****	0.52 NS
Lf. Lth	x	Br. Lth	0.19 *	0.73(NS)
Lf. L/W	x	Br. L/W	0.34****	0.94 ***
Lf. L/W	x	Pr. Hd. No†	0.07 NS	-0.69(NS)
Lf. L/W	x	Tot. Hd. No†	-0.03 NS	-0.77 *
Hd. Dia	x	Br. Lth	0.44****	0.80 *
Hd. Dia	x	Br. L/W	0.26 ***	0.59 NS
Hd. Dia	x	Pr. Hd. No†	0.42****	0.55 NS
Hd. Dia	x	Tot. Hd. No†	0.45****	0.25 NS
Br. L/W	x	Sp. Inx	0.63****	0.87 *
Br. L/W	x	Pr. Hd. No†	0.20(NS)	-0.24 NS
Br. L/W	x	Tot. Hd. No†	0.08 NS	-0.44 NS
Br. L/W	x	Brd. Dam	-0.17(NS)	-0.71(NS)
Sp. Inx	x	Pr. Hd. No†	-0.14 NS	-0.40 NS
Sp. Inx	x	Tot. Hd. No†	-0.22 *	-0.70(NS)
Sp. Inx	x	Brd. Dam	-0.13 NS	-0.53 NS
Es. Den	x	Pr. Hd. No†	0.11 NS	-0.60 NS
Es. Den	x	Tot. Hd. No†	-0.02 NS	-0.50 NS
Brd. Dam	x	Tot. Hd. No†	0.06 NS	0.03 NS
Brd. Dam	x	Yld (US)	-0.06 NS	0.52 NS

Table 3.23 (continued)

Characters pair			r_p	r_g
Sus. Bot	x	Pr. Hd. No†	-0.12 NS	0.24 NS
Sus. Bot	x	Tot. Hd. No†	0.18 NS	0.27 NS
Sus. Bot	x	Yld (US)	0.15(NS)	-0.90 **
Sus. Bot	x	Oil %	-0.53****	-0.56 NS
Sus. Bot	x	Sd. Wt (US)	-0.19 *	-0.24 NS
Pl. No (US)	x	Yld (US)	0.31 ***	0.04 NS
Pl. No (S)	x	Yld (S)	0.16(NS)	-0.39 NS
Yld (US)	x	Pr. Hd. No†	0.46****	-0.26 NS
Yld (US)	x	Tot. Hd. No†	0.28 *	0.18 NS
Oil %	x	Hull %	-0.93****	-0.79 *
Sd. Wt	x	Tot. Hd. No†	0.00 NS	-0.37 NS

Significance Symbols:

NS	=	$P>0.10$
(NS)	=	$0.10\geq P>0.05$
*	=	$0.05\geq P>0.01$
**	=	$0.01\geq P>0.005$
***	=	$0.005\geq P>0.001$
****	=	$0.001\geq P$

† based on data from two sites only (Massey and Flockhouse), over a two year period.

observed between oil and hull percentages of seed, both at phenotypic and genotypic levels, is in agreement with previous findings (Claassen et al., 1950). Correlation between yield/plot and plant number was relatively low.

Data from Expt. II provided information about the effects of the two diseases (head rot and leaf spot) on yield and yield components. Correlations between other traits estimated in Expt. II are presented in Appendix V.

Correlation coefficients between susceptibility to the two diseases and some agronomic characters are presented in Table 3.24. Susceptibility to head rot and leaf spot diseases were negatively correlated with the yield. In addition significant negative phenotypic correlations existed between susceptibility to leaf spot disease and the following traits: Br. Lev, Pr. Hd. No and Tot. Hd. No. Stemphylium/ Alternaria species, the causal agents of leaf spot disease, infect the leaves and stems resulting in premature death of lower leaves. Under these circumstances, lower branches may fail to develop, resulting in a reduction of primary and total number of heads. Furthermore branching will be restricted to the top half of the plant. Significant negative genotypic correlations were observed between Sus. St/Al and two yield components (Pr. Hd. No and Tot. Hd. No). Selection for resistance to leaf spot disease may result in a favourable increase in the two yield components.

It is noted in Table 3.24 that significant negative phenotypic correlations existed between Sus. Bot and the following traits: Yld (US), Pr. Hd. No, Sd. Wt and Oil %. Infection of flower heads by Botrytis cinerea Pers could adversely affect the seed filling process (refer section 1.6.2). This could result in a reduction of the total oil concentration of seed. However Botrytis cinerea Pers does not impair the plant growth up to flowering stage. The reason for negative correlation between Sus. Bot and Pr. Hd. No is not clear. Susceptibility to head rot and leaf spot diseases were not significantly correlated (Table 3.24).

Table 3.24 Expt. II. Phenotypic (r_p), genotypic (r_g) correlation coefficients between susceptibility to diseases (head rot and leaf spot) and other traits, based on data from ten genotypes at three environments.

Characters pair	r_p	r_g
Sus. St/Al x Es. Den	0.04 NS	0.26 NS
Sus. St/Al x Lodging	-0.11 NS	-0.23 NS
Sus. St/Al x Pl. Ht	-0.18(NS)	-0.20 NS
Sus. St/Al x Br. Lev	-0.46****	-0.47 NS
Sus. St/Al x Pr. Hd. No†	-0.57****	-0.85 ***
Sus. St/Al x Tot. Hd. No†	-0.67****	-0.89****
Sus. St/Al x Oil %	0.01 NS	0.52 NS
Sus. St/Al x Sd. No	-0.36****	-0.18 NS
Sus. St/Al x Sd. Wt	-0.03 NS	0.41 NS
Sus. St/Al x Yld (US)	-0.29 **	-0.05 NS
Sus. St/Al x Sus. Bot	-0.07 NS	0.01 NS
Sus. Bot x Pr. Hd. No†	-0.41 ***	0.08 NS
Sus. Bot x Tot. Hd. No†	0.08 NS	0.18 NS
Sus. Bot x Oil %	-0.63****	0.00 NS
Sus. Bot x Sd. No	-0.18(NS)	-0.75 *
Sus. Bot x Sd. Wt	-0.36****	-0.21 NS
Sus. Bot x Yld (US)	-0.35 ***	-0.92****

Significance Symbols:

NS	=	$P \geq 0.10$
(NS)	=	$0.10 \geq P > 0.05$
*	=	$0.05 \geq P > 0.01$
**	=	$0.01 \geq P > 0.005$
***	=	$0.005 \geq P > 0.001$
****	=	$0.001 \geq P$

† based on data from two sites only (Massey and Flockhouse)

CHAPTER 4

GENERAL DISCUSSION

In the discussion following, techniques employed in present study are assessed, recommendations for future work are made, and prospects for growing safflower in the area are considered in light of the present findings.

4.1 CONTROL OF EXPERIMENTAL ERROR

Proper interpretation of field experiments depends on unbiased estimation of experimental error. Soil heterogeneity and plant variability are two important sources contributing to experimental error. Different methods have been suggested to indicate soil heterogeneity in experimental sites. These include constructing fertility contour maps, and determining correlations between yields of contiguous plots (Le Clerg et al., 1962). In the present study, effects due to soil heterogeneity were minimized by replications. The block effects were significant for 11 of the 22 traits analysed in Expt. I. However, it was observed that at certain experimental sites the soil fertility was more irregular. Such variability within blocks usually leads to a higher estimate of experimental error. In such instances, covariance adjustment by neighbouring plots (Bartlett, 1938; Pearce and Moore, 1975) might have been a more appropriate technique to remove effects due to soil heterogeneity. The covariance adjustment method may also be used as an adjunct to the conventional blocking method. However this was beyond the scope of the present study.

Plant to plant variability may be due to genetic or microenvironment differences, and to plant competition within or between plots. Open-pollinated seeds were used for sowing in the present study, and this may have caused some variability within experimental plots. Safflower is mainly a self pollinated crop, but the degree of outcrossing depends on the cultivar and presence of insect pollinators (Claassen,

1950). The effect of insect pollination in a given line depends on the self fertility of that line. As such some segregation following cross pollination in certain lines may have contributed to the experimental error. Several measures were taken to minimize border effects. Guard rows were employed on either side of each experimental block. The yield assessments were made on the inner 4 metre length of experimental plots, plants at the ends being discarded.

The size and shape of the experimental plot may be quite critical for certain crops (Le Clerg et al., 1962). In the present study an experimental plot consisted of 2 adjacent rows, 5 m. long, and 0.9 m. apart. Wieldemann and Leininger (1963) suggested row plots, 3.67 ft. wide and 20 ft. long, for evaluating safflower cultivars. However, size of the plot largely depends on the magnitude of soil heterogeneity. The coefficients of variation, for most of the traits in Expt. I, were within the usual limits accepted for biological experiments (refer to section 3.2). The plot size used in the present study seems to be adequate in providing the required level of precision.

4.2 HETEROGENEITY OF EXPERIMENTAL ERRORS

The pooled analysis of data from individual experiments, performed in this study is strictly valid only when the error variances of individual experiments are homogeneous. The kind of heterogeneity detected in this study (see section 3.1) may arise in several ways. A higher error variance observed in some experiments (refer to Tables 3.3 and 3.4), compared to others may be due to the use of less homogeneous seed material or irregularity in soil fertility in these experimental sites. Furthermore when data for individual experiments are collected at different times, the variability attributed to time interactions and to human error may vary from one experiment to another.

As Yates and Cochran (1938) pointed out, if error variances are homogeneous, pooling provides a more accurate estimate of experimental error, since a larger number of degrees of freedom is available. The pooled error is the

estimate of the mean of error of individual error variances. Hence, even when individual error variances are heterogeneous, the pooled error will still be the correct estimate for comparing means of cultivars over all experiments ($\bar{X}_{i...}$). Also the validity of F-test for genotypic effects is probably the least affected by heterogeneity (Cochran, 1947). Comparison of genotypic performances being the main objective of this study, no special measures were taken to correct for heterogeneity observed in most of the traits (refer to Tables 3.3 and 3.4). However when heterogeneity is present there will be bias involved in the variance component estimates. The methods for performing a valid analysis, when error variances are heterogeneous, have been discussed in section 1.1.

4.3 VARIANCE COMPONENT ESTIMATES

The variance component estimates presented in Chapter 3 are applicable only to the population of inference referred to in this study. These estimates for Expt. I and Expt. II were based on 7 genotypes, in 3 sites, over 2 years and 10 genotypes in 3 sites, respectively. Exrapolation of these results to a wider genetic or environmental base may be misleading. The genotypic variance, σ^2_G, discussed in this study is the total genetic variance between cultivars. The total genetic variance may be further partitioned into additive, dominance and epistatic variance components by a suitable genotypic partitioning method (Mather, 1971; Griffing, 1956a and 1956b; Cockerham, 1963). The relative proportions of these three components is dependent largely on the reproductive structure of the population. Safflower being largely a self-pollinating crop, most of the genotypic variance (σ^2_G) is probably due to additive and additive x additive gene actions. Lack of significant genotypic differences for most traits in Expt. I (refer to Table 3.7) was possibly due to the narrow genetic base included in the study (see Table 2.1). Addition of 3 genotypes from safflower germplasm collection, increased the genotypic variance, as indicated by results of Expt. II (refer to Table 3.9).

The genotype x environment interaction component was significant for most of the traits studied in Expt. I. This is not unexpected because most of the cultivars used in the study have been developed elsewhere (refer to Table 2.1), and perhaps are better adapted to different environmental conditions. Abel (1976a) conducted a similar study, with seven safflower cultivars, at 3 experimental farms of the University of Arizona. All seven cultivars included were those developed at the breeding nursery of the University of Arizona. The genotype x environment interactions were non-significant for most of the characters studied (Abel, 1976a).

In the present study, the most significant environmental component was the site x year interaction (σ^2_{SY}) effect. As discussed in section 3.3.1, this may have been partly due to the enhanced plant growth at Flockhouse in the second year (refer to Table 3.10), perhaps a manifestation of early planting. Abel (1976a) reported significant cultivar x date-of-planting interaction components for the traits heads/section, seeds/head and seed weight. Based on these results, he recommended certain cultivars as more suitable for early planting. Perhaps it may be desirable to include date of planting as well, in future safflower agronomic trials.

4.4 COMPARISON OF GENOTYPIC MEANS

The extensive variability, for both morphological and agronomic traits, in safflower germplasm collection has been reported in the literature (Ashri, 1971a and 1971b; Ashri et al., 1974; Ashri et al., 1975; Ashri, 1975; Ashri et al., 1976; Ashri et al., 1977). In comparison, these genotypic means were significant only for a few characters in the present study (refer to Tables 3.11 and 3.12).

The mean yield/plot and % oil content of seed, for some commercial cultivars included in this study were relatively poor, compared to those obtained from cultivar evaluation trials in the United States. Under optimum conditions, yields up to 4000 kg/ha and % oil contents as much as 40% have been reported for cultivars Dart (Abel and Lorance, 1975) and

Leed (Zimmer and Urie, 1968). In comparison, the grand means ($\bar{X}_{....}$) for yield (unsprayed) and oil percentage, in Expt. I were 461 kg/ha and 19.6% respectively. The poor genotypic mean yields were probably due to the severe disease conditions experienced. Significant negative phenotypic correlations were observed between yield (unsprayed)/plot, and susceptibility to the two diseases (refer to Table 3.24). The high negative phenotypic correlation between % oil content and susceptibility to head rot disease (refer to Table 3.24) indicates that low oil concentrations may be largely due to infection of flower heads by Botrytis cinerea Pers.

4.5 HERITABILITY ESTIMATES

The heritability estimates obtained in this study are broad sense type, taking into consideration the total genetic variance in the population. These are different to narrow sense heritability estimates, which take into account only the additive genetic variance. The broad sense heritability ratios estimated in this study are descriptive, rather than predictive, in nature (refer to section 1.2). However, safflower being largely a self-pollinating crop, the broad sense estimates obtained here are probably very similar to narrow sense estimates in magnitude.

Broad sense heritability estimates for most traits in Expt. I and Expt. II were low, possibly due to the narrow gene base used in this study. The very high broad sense heritability estimate obtained for spininess is expected, due to the monogenic inheritance of this trait as reported by Ashri and Efron (1964). The heritability estimates obtained are applicable only to the genotypic and environmental populations referred to in this study (refer to section 2.6.1). As Hanson (1963) pointed out generalization beyond these limits to other populations may be misleading.

Kotecha (1979) computed broad sense and narrow sense heritability estimates of few traits using four crosses of safflower involving Carthamus tinctorius L. and Carthamus palaestinus Eig. He reported high broad sense heritability

ratios for the following characters: plant height, time of flowering, time to maturity, time from flowering to maturity, leaf length and stem diameter. Narrow sense estimates for time of flowering and plant height were 11% and 79% respectively. According to Abel (1976a), seed weight in safflower was highly heritable.

Heritability estimate is the critical component in the prediction formula for the genetic advance: $\Delta G = i\sigma_p h^2$ (refer to section 1.3). Restricted heritability estimates are more applicable to practical plant breeding (Allard, 1960). Where selection is based on genotypic means, heritability estimates based on means are more appropriate (see section 1.2). The type of heritability estimate used (broad/narrow sense) depends on the crop and the selection procedure employed (Hanson, 1963).

4.6 ADAPTATION ANALYSIS

In the present study, linear regression technique (Finlay and Wilkinson, 1963) was used to evaluate the adaptabilities of the seven safflower genotypes to the Manawatu region. The main advantages of this method are:

(1) it provides a quantitative measure of the complex environment (environmental mean, $\bar{X}_{..k}$), without problems of defining the interacting edaphic and seasonal factors.

(2) regression coefficients of individual genotypes (b_i) referred to as adaptation coefficients by Finlay and Wilkinson (1963), identify the pattern of response to the environment and also could be used as a variable for selecting stable cultivars.

However there are several drawbacks in this technique, the main objection being the implied non-independence of effects in the x ($\bar{X}_{..k}$), and y ($\bar{X}_{i.k}$) variables used in the regression (Freeman and Perkins, 1971). This means the ANOVA assumption that the effects described in the model (see section 2.6.1) are independent may be violated. The following alternative methods would provide an independent estimate of the environment for the linear regression technique:

(1) a physical measure of the environment based on principal components of environmental variables

(Perkins, 1972) (refer to section 1.4.3).

(2) an environmental mean based on a separate set of genotypes or plots grown at the same site. This provides a biological assessment of the environment, and also satisfies the requirement of intrinsic independence of effects in the linear regression. Ehdai et al. (1977) employed this technique to study the adaptability patterns of 18 safflower genotypes.

Linear regression techniques in general have been criticised by others, on the basis that there is no a priori reason to believe that GxE interaction is a linear function of the environmental effects (Easton and Clements, 1973; Mungomery et al., 1974; Knight 1970 and 1973; Witcombe and Whittington, 1971). However transformation (Bartlett, 1947) permits many non-linear relationships to be analysed by a linear regression.

In the present study, GxE interaction effects of individual genotypes were assessed by 3 statistics: adaptation coefficient (b_i), R^2 value and ecovalance. For a particular trait, not all genotypes performed linearly with changing environment. To illustrate this consider the above mentioned statistics for the trait yield (unsprayed)/plot (refer to Table 3.14). A linear relationship between $\overline{X}_{i.k}$ and $\overline{X}_{..k}$ was not evident for cultivars VFSTP-1 and Partial-hull, as indicated by their non-significance from zero and low R^2 values. However there was no consistency with respect to the genotypes exhibiting non-linear response to the environment. In cases where a linear model was not applicable, ecovalances provided some information about stability of the genotypes.

4.7 PHENOTYPIC AND GENOTYPIC CORRELATIONS

Correlations may be phenotypic, genotypic or environmental. Environmental correlation is due to certain environmental factors being in common to both traits, if environmental factors enhance one trait, the other one is also enhanced. Genotypic correlations arise from linkage or/and pleiotropy between the two characters concerned. Phenotypic correlations are a composite of genotypic and environmental correlations.

The most important of these to plant breeders are the phenotypic and genotypic correlations. Phenotypic and genotypic correlations between character pairs estimated in Expt. I and Expt. II have been discussed in section 3.8.

Simmonds (1979) summarized the implications of correlations on selection. A positive correlation between desired characters is favourable to the plant breeder. High negative correlation between favourable characters will hinder simultaneous expression of them at a high level. In the present study significant negative genotypic correlations were observed between susceptibility to leaf spot disease and two yield components (primary and total head numbers). Selection for resistance to leaf spot disease may result in a favourable increase in the two yield components. However these correlation estimates should be compared with such estimates from a wider genetic base. Sometimes it may be possible to get genetic advance of the desired character, by applying selection to another character which is genetically highly correlated. In safflower, the high genotypic negative correlation between hull content and oil content of seed, has been utilized to gain genetic advance in oil content by selecting for lines with low hull content (Rubis, 1957, quoted by Urie and Zimmer, 1970). This is commonly referred to as indirect selection (Falconer, 1960). The formulae relating to indirect selection have been discussed in section 1.3. The importance of correlation coefficient estimates in selection indices will be discussed very shortly.

4.8 DISEASE ASPECTS

Undoubtedly the two fungal diseases (head rot and leaf spot), reported in this study will be of major concern in growing safflower in the Manawatu region. Leaf spot disease in safflower has not been recorded previously in New Zealand. Two causative organisms responsible for leaf spot disease were identified in the present study: *Stemphylium* and *Alternaria* species. These findings are in agreement with previous reports (Ashri, 1961). Ashri (1961) identified resistance to leaf spot disease in Indian line U.C. 57-146,

which also had a low iodine value. The results of this study indicated that genotypes PI 262437 and PI 306684 were highly tolerant to leaf spot disease. On a scale of 0-10, the genotypes PI 262437 and PI 306684 scored 1.6 and 2.7 respectively. There was no indication that these two genotypes had low iodine values (PI 262437 = 118, PI 306684 = 119, also refer to section 1.6.3.2). However plants of PI 262437 tended to lodge quite easily (refer to Table 3.12).

Head rot disease caused by Botrytis cinerea Pers. commonly occurs in areas where there are long periods of high atmospheric moisture prior to and following flowering (Weiss, 1971). Spores of the fungus are wind-borne and infection of flower heads may occur at any period from budding to post-flowering. The disease affects the entire head and invades the receptacle (see plate 2.2), so that the head lifts off easily. Obviously the stage of development at which heads become infected determines the effect on the seeds. Infection at an early stage would result in considerable reduction in seed set. If the infection occurs during seed filling, seeds would be partially filled, resulting in seeds with a lower oil concentration (as shown by these results). The damage caused by the original infection can be subsequently increased by secondary infection (Weiss, 1971). Insect damage to heads may also facilitate the entry of the pathogen (Peterson, 1965, ex Weiss, 1971).

The local cultivar 0-22 seems to be moderately tolerant to the disease (refer to section 3.4). The two low-hull lines (VFSTP-1 and Partial-hull) were highly susceptible to the disease. Further investigation with a wider gene base may be needed to determine whether hull content of seed is negatively correlated with susceptibility to head rot disease. In safflower, hull content of seed shows a high genotypic negative correlation with oil content, low-hull lines being higher in oil content (Claassen et al., 1950). If a high genotypic negative correlation exists between hull content and susceptibility to head rot disease, it may be difficult to select for recombinants favourable in both traits.

Safflower introductions from Rumania have been reported as more resistant to head rot disease (Scheibe, 1938; quoted by Knowles, 1958). Knowles (1958) identified high resistance to Botrytis cinerea Pers. in an introduction from Egypt (PI 209290). However, evaluation studies on safflower germplasm collection in the Manawatu region has revealed that PI 209290 is susceptible to head rot disease (Gordon, pers. comm.).

Further research on the safflower germplasm collection is needed to uncover new sources of resistance to head rot disease. It was apparent in this study that evaluation for disease resistance to a particular disease was made difficult due to simultaneous occurrence of the two diseases. However, the non-significant genotypic and phenotypic correlations between susceptibility scores for the two diseases (refer to Table 3.23), mean that the scoring systems adopted in this study have been successful in assessing the two diseases separately. In future studies, field evaluation should be followed by screening under controlled conditions. Screening methods may need further improvement in such detailed investigations. After identifying the sources of resistance it may be necessary to investigate into the inheritance of disease resistance. The number of genes conditioning resistance has a direct bearing on the effectiveness by which resistance can be incorporated into commercial cultivars.

4.9 BREEDING PROSPECTS

Safflower is mainly a self-pollinating crop, but the degree of outcrossing depends on the cultivar and presence of insect pollinators (Claassen, 1950). The colourful florets, which produce nectar and pollen, more often attract honey bees (Apis mellifera L.). The effect of bee pollination of a given line depends on the self fertility of that line. Rubis et al. (1966) defined self fertility of a given line as:

$$\% \text{ self fertility} = \frac{\text{seeds/head without insect pollinators}}{\text{seeds/head with insect pollinators}}$$

Rubis et al. (1966) distinguished the effects of nectar collecting bees and pollen collecting bees, on cross-pollination in safflower. Obviously the nectar collecting bees would be very important in the cross-pollination of two lines in hybrid seed production where thin hull lines are used as female parents (refer to section 1.6.3.2).

The majority of commercial cultivars of safflower have been produced by pedigree breeding methods, following an initial cross. However heterosis has also been reported in safflower (Yazdi-Samadi et al., 1975; Deokar and Patil, 1979). The following objectives would be of major concern in breeding safflower for the Manawatu region:

(1) high mean yield and general adaptability
(2) higher oil concentration
(3) resistance to the two major diseases (head rot and leaf spot).

A pedigree breeding scheme may be more appropriate. As well as these objectives, attention to hull content of seed would be desirable. Several thin-hull lines with high oil contents have been developed in the past (Rubis, 1967; quoted by Urie and Zimmer, 1970a). Relative importance of these thin-hull lines in breeding has been discussed in section 1.3.6.2. Although not detected in this study, the two genotypes, VFSTP-1 and Partial-hull are thin-hull types. However their mean % oil content in Expt. I were only 16.9% and 20.1% respectively. This may have been due to the high susceptibility of these two genotypes to head rot disease (refer to section 3.4). Several sources of partial tolerance to the two diseases reported in this study may be useful in a future breeding programme. However further investigation into the safflower germplasm collection for new sources of resistance is needed. The results of this study indicated that in future evaluation trials the optimum allocation of plots should be in the direction of fewer replicates, with an increase in sites and years (refer to section 3.7). Based on these results, an allocation of 2 years, 4 sites and 2 blocks may be recommended. Abel (1976a), also

determined the optimum combination of years, sites, days of planting and replications for testing safflower cultivars in Arizona. Disregarding the cost, he suggested the following combinations as more efficient: (years x sites x dates x replications); (2 x 2 x 2 x 4) or (2 x 2 x 2 x 2).

In a breeding programme it may be necessary to apply selection to more than one character simultaneously. The different kinds of selection methods which may be used in such instances have been discussed by Hazel and Lush, 1942). The selection index method is more effective than tandem selection and independent culling level procedures. The selection index, I, is computed as follows:

$$I = b_1x_1 + b_2x_2 + ... + b_nx_n$$

where x_1, x_2, ..., x_n represent phenotypic values of the characters included in the selection index; and b_1, b_2, ..., b_n are optimum weights assigned to these characters.

These optimum weights may be computed in matrix form as:

$$\underline{b} = \underline{P}^{-1}\underline{G}\underline{Z}$$

where $\underline{b}$ is a vector of partial regression coefficients for the phenotypic values (x_n); $\underline{P}^{-1}$ is the inverse matrix of phenotypic variance-covariance estimates of the characters included in the index; $\underline{G}$ is the genotypic variance-covariance matrix of the characters included; and $\underline{Z}$ is the vector of relative importance values.

Back crossing is another possibility for incorporating disease resistance to a locally adapted cultivar. There are two basic types of disease resistance: vertical and horizontal (Van der Plank, 1963 and 1968, quoted by Simmonds, 1979). Vertical resistance (VR) is pathotype-specific and major gene controlled, whereas horizontal resistance is pathotype-nonspecific and polygenic. Vertical resistance is usually less effective against air-borne pathogens when they are pathotype mutable, but may prove successful against less mobile soil-borne pathogens (Simmonds, 1979). Recent trend is towards the use of horizontal resistance for breeding purposes. However when vertical resistance is available several breeding strategies may be proposed to overcome the frequent problem

of break down of disease resistance (after Dalmacio, 1979). These are:

(1) multilines - mixtures of several lines, each with similar phenotypic traits, but with different genes for vertical resistance;

(2) gene deployment - selective growing of cultivars with several individual genes for vertical resistance in different geographical areas where the crop is grown;

(3) pyramiding genes - incorporation of several VR genes into a single cultivar.

The use of multilines seems to be the most promising of the three methods. Multilines produce a simulated horizontal resistance condition in the field, and may be effective against pathotype mutable, air-borne pathogens in annual crops.

CONCLUSIONS

(1) Of the 22 characters analysed in Expt. I, only 6 showed significant genotypic differences. The genotype x environment interaction effects were significant for majority of characters studied, the σ^2_{GSY} component being the most significant. Of the environmental components, σ^2_{SY} was significant for most traits in Expt. I. The addition of 3 genotypes from safflower germplasm collection in Expt. II, had a marked effect on the genotypic variance component, σ^2_G.

(2) The yield performances of all seven genotypes in Expt. I were low (307-600 Kg/ha), probably due to the disease conditions experienced. The oil percentages obtained for the seven genotypes were relatively poor (16.9%-21.9%), mainly due to head rot disease caused by Botrytis cinerea Pers.

(3) Two diseases of major concern in growing safflower in the region are head rot (Botrytis cinerea Pers.) and leaf spot (Stemphylium/Alternaria species) diseases. The local cultivar 0-22 showed some tolerance to head rot disease. Two genotypes, PI 262437 and PI 306684 were moderately tolerant to leaf spot disease. Further investigations into safflower germplasm collection may be necessary to identify other sources of resistance.

(4) Many characters examined had low broad sense heritability estimates. Relatively high broad sense, full heritability estimates were found for bract length, bract length/width and bract spine index, in Expt. I. In addition to these, in Expt. II, lodging and susceptibility to leaf spot also showed moderately high estimates.

(5) Adaptability studies indicate that cultivars 0-22 and Rio show general adaptability for yield. Cultivars Leed and Dart are specifically adapted to favourable environments for the same trait. For percentage oil content, all genotypes except Rio showed general adaptability. Cultivar Rio was slightly specifically

adapted to favourable environments. With respect to susceptibility to head rot disease, cultivar 0-22 showed moderate stability (b_i = 0.63).

(6) Optimum allocation study revealed that, disregarding costs, the optimum allocation of a given number of plots should be in the direction of increasing sites and years. Based on the results of this study a plot allocation of 2 years, 4 sites and 2 blocks may be recommended for future safflower evaluation trials.

(7) There was no significant correlation between spininess and bird damage. Susceptibilities to the two diseases were significantly negatively correlated with yield and most yield components. There was no evidence of any association between the susceptibilities to the two diseases (head rot and leaf spot). Highly significant, negative genotypic correlations were observed between susceptibility to leaf spot disease and two yield components (primary and total number of heads, per plant). Selection for resistance to leaf spot disease should result in a favourable increase in these yield components. Percentages of oil content and hull content in seed were highly negatively correlated at phenotypic and genotypic levels.

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Note: Journal names are abbreviated according to the American Chemical Society (1974).

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APPENDIX I

1. Preparation of Wijs' Solution

Dissolve about 9 gm. of iodine trichloride in a mixture of 700 ml. glacial acetic acid (at least 99%) and 300 ml. carbon tetrachloride. The strength of this solution is determined as follows.

Measure out 10 ml. of the solution, add 10 ml. of potassium iodide solution (10%) and 60 ml. water and titrate with 0.1N sodium thiosulphate solution, using starch as indicator. The amount of sodium thiosulphate solution used should be 13.0-13.5 ml.

Dissolve,with stirring, about 10 g of powdered iodine in the iodine trichloride solution. A slight excess of iodine is added to ensure complete decomposition of iodine trichloride. Filter the solution and store in a stoppered bottle in the dark for a few days before it is used.

2. Preparation of starch solution

Dissolve 1 gm. of soluble starch and a few crystals of mercuric iodide (preservative) in 3 ml. water. Then pour the mixture into 200 ml. of boiling water and keep the solution at boil for about 3 minutes. The starch solution is stored in a stoppered bottle.

APPENDIX II

IIa Expt. I. Genotypic mean data; Site = Massey R & D Unit; Year = 1978

CHARACTER	VFSTP-1	Partial-hull	Leed	Dart	PI 195895	0-22	Rio
St. Dia	11.73	12.70	12.17	12.40	11.10	11.90	11.20
Pl. Ht	75.00	70.83	79.50	77.50	78.33	72.83	83.83
Br. Lev	7.47	8.93	7.73	7.53	6.87	7.53	6.27
Lf. Lth	139.1	164.1	143.9	149.4	126.1	137.7	140.3
Lf. L/W	2.97	2.81	2.58	2.66	2.53	2.69	2.80
Hd. Dia	25.2	27.9	24.1	23.7	22.8	23.1	24.2
Br. Lth	50.5	56.3	42.3	43.8	29.7	41.9	40.7
Br. L/W	3.44	3.40	3.05	3.05	2.37	3.01	3.20
Sp. Inx	6.00	7.50	5.93	6.43	0.80	6.30	6.13
Pr. Hd. No	8.33	10.57	9.34	10.05	9.20	9.37	8.17
Tot. Hd. No	18.18	22.57	18.97	22.79	20.70	25.58	14.32
Es. Den	6.0	5.7	6.7	6.7	6.7	7.0	7.0
GPPF	2.7	3.7	2.3	2.0	2.0	3.0	1.7
Brd. Dam	4.0	3.0	5.7	4.7	7.0	5.3	5.3
Sus. Bot	7.7	6.0	3.3	2.7	3.3	2.7	2.7
Pl. No (US)	23.0	32.3	39.3	38.7	39.0	32.0	43.0
Pl. No (S)	26.7	35.3	35.0	32.3	29.7	28.0	40.7
Yld (US)	391	228	122	64	60	40	56
Yld (S)	298	166	80	69	38	55	103
Oil %	16.40	21.43	21.00	30.50	16.07	30.63	26.63
Hull %	56.63	51.70	54.07	49.17	58.23	50.57	49.90
Mos. %	8.47	8.17	8.37	8.20	8.57	7.97	8.57
Spr. Dam	3.7	3.0	3.7	4.3	5.3	7.0	4.7
Sd. Wt	33.13	32.80	35.33	38.90	33.10	32.03	37.43
I. Val	121	129	135	135	123	125	122

IIb Expt. I. Genotypic mean data; Site = Aorangi; Year = 1978

CHARACTER	VFSTP-1	Partial-hull	Leed	Dart	PI 195895	0-22	Rio
St. Dia	16.20	17.20	15.03	15.27	15.00	15.07	14.63
Pl. Ht	93.83	93.50	90.83	93.83	88.33	90.33	93.17
Br. Lev	8.07	8.67	8.33	8.13	7.47	8.47	7.93
Lf. Lth	142.0	166.6	147.9	148.3	132.4	142.6	150.2
Lf. L/W	2.63	2.68	2.50	2.37	2.40	2.37	2.47
Hd. Dia	26.4	29.0	25.3	24.8	24.7	23.9	25.6
Br. Lth	58.4	60.1	49.6	46.2	31.4	43.9	45.7
Br. L/W	3.17	3.18	2.93	2.92	1.94	2.77	2.97
Sp. Inx	5.43	7.13	6.53	6.23	0.47	5.97	5.90
Pr. Hd. No	-	-	-	-	-	-	-
Tot. Hd. No	-	-	-	-	-	-	-
Es. Den	7.0	6.0	7.0	7.0	6.7	8.0	6.7
GPPF	5.3	6.0	5.0	5.0	4.0	4.0	4.3
Brd. Dam	2.0	2.3	3.0	2.3	4.7	6.0	3.3
Sus. Bot	8.3	8.0	6.0	6.0	6.7	4.0	6.0
Pl. No (US)	47.7	34.3	33.7	47.3	45.7	46.7	42.0
Pl. No (S)	25.3	47.7	40.3	39.0	41.3	33.0	42.3
Yld (US)	486	322	1589	2050	826	1204	1260
Yld (S)	537	541	1969	2051	1338	1198	1674
Oil %	18.17	16.57	25.40	25.47	24.83	28.17	25.07
Hull %	55.40	56.97	50.20	51.27	49.83	49.63	50.93
Mos. %	8.70	8.30	8.20	8.27	8.40	8.27	8.17
Spr. Dam	4.0	4.0	4.7	6.0	7.0	8.0	5.3
Sd. Wt	40.03	41.37	42.40	42.17	32.67	37.70	47.27
I. Val	123	126	130	125	125	124	124

IIc Expt. I. Genotypic mean data; Site = Flockhouse; Year = 1978

CHARACTER	VFSTP-1	Partial-hull	Leed	Dart	PI 195895	0-22	Rio
St. Dia	9.30	8.57	8.27	10.40	9.07	9.40	8.57
Pl. Ht	57.67	50.50	50.83	62.00	55.17	60.00	56.17
Br. Lev	6.13	6.60	5.40	6.20	6.60	7.33	5.33
Lf. Lth	109.1	127.5	102.4	86.7	94.2	81.5	93.2
Lf. L/W	3.04	2.93	2.73	2.76	2.42	2.74	2.68
Hd. Dia	21.5	22.6	19.7	19.8	19.3	19.1	19.4
Br. Lth	42.7	50.6	38.5	41.3	32.5	40.6	38.7
Br. L/W	3.11	3.03	2.81	2.89	2.18	2.61	2.90
Sp. Inx	5.70	6.40	5.60	5.63	1.50	5.03	5.60
Pr. Hd. No	6.10	6.56	5.93	7.72	6.60	7.80	5.97
Tot. Hd. No	9.97	9.10	7.43	12.22	11.45	13.03	8.43
Es. Den	6.3	4.7	6.0	6.0	5.3	5.7	6.3
GPPF	2.0	2.0	2.7	2.0	3.3	3.7	2.0
Brd. Dam	1.0	1.7	1.7	1.7	1.3	1.7	1.0
Sus. Bot	4.7	2.0	2.0	2.0	2.0	2.0	2.0
Pl. No (US)	33.0	31.3	28.0	40.3	29.3	23.7	37.7
Pl. No (S)	46.7	42.3	47.7	34.7	34.3	30.0	50.0
Yld (US)	92	87	140	302	258	180	227
Yld (S)	350	185	208	304	310	252	427
Oil %	24.93	28.80	26.93	28.00	23.77	21.73	26.60
Hull %	55.30	47.53	49.90	52.03	53.47	56.60	52.97
Mos. %	8.00	7.80	7.43	8.00	7.77	7.90	7.80
Spr. Dam	6.0	7.3	6.7	8.7	7.3	3.3	8.3
Sd. Wt	40.93	42.20	41.10	40.43	37.13	37.30	42.27
I. Val	123	125	128	133	137	132	116

IId Expt. I. Genotypic mean data; Site = Massey R & D Unit; Year = 1979

CHARACTER	VFSTP-1	Partial-hull	Leed	Dart	PI 195895	0-22	Rio
St. Dia	11.60	11.53	10.86	9.63	11.39	7.71	9.30
Pl. Ht	58.54	47.33	51.56	46.83	54.46	43.83	43.71
Br. Lev	7.17	7.44	6.88	6.67	6.78	4.43	7.35
Lf. Lth	111.2	130.3	105.1	88.4	96.7	84.1	95.4
Lf. L/W	2.95	2.92	2.73	2.73	2.43	2.76	2.65
Hd. Dia	23.5	24.4	22.2	22.2	22.3	20.5	22.0
Br. Lth	45.3	43.1	37.1	37.9	30.3	32.4	35.0
Br. L/W	3.34	3.37	2.79	2.98	2.48	2.86	2.87
Sp. Inx	5.53	6.10	4.77	5.53	1.30	4.10	5.39
Pr. Hd. No	7.99	8.75	7.56	5.99	8.49	5.55	6.77
Tot. Hd. No	23.51	20.96	22.20	15.96	23.78	10.44	16.54
Es. Den	6.0	6.0	3.3	5.7	4.3	8.3	5.0
GPPF	4.0	3.3	2.7	2.7	3.3	2.0	2.3
Brd. Dam	3.7	2.7	3.0	3.0	4.0	5.7	4.3
Sus. Bot	8.3	8.7	5.0	5.3	6.0	5.0	5.7
Pl. No (US)	19.7	14.7	3.7	12.7	11.7	22.3	12.0
Pl. No (S)	14.7	15.0	10.7	15.3	10.3	27.7	9.0
Yld (US)	109	146	64	123	136	130	95
Yld (S)	142	165	319	128	204	256	158
Oil %	6.10	16.03	9.70	8.53	4.30	9.63	6.80
Hull %	70.23	58.83	67.47	67.97	72.67	66.67	71.07
Mos. %	9.67	9.73	9.83	11.07	10.27	9.70	10.10
Spr. Dam	2.3	2.0	2.0	2.3	2.3	2.0	2.0
Sd. Wt	30.43	34.87	27.90	32.37	25.40	24.40	27.17
I. Val	124	138	134	130	123	119	120

IIe Expt. I. Genotypic mean data; Site = Aorangi; Year = 1979

CHARACTER	VPSTP-1	Partial-hull	Leed	Dart	PI 195895	0-22	Rio
St. Dia	12.63	12.20	14.53	13.97	15.90	10.97	13.52
Pl. Ht	72.50	72.50	71.17	65.00	74.50	70.17	73.31
Br. Lev	7.60	7.67	8.60	8.50	8.27	6.67	7.92
Lf. Lth	114.3	134.3	114.9	107.6	111.4	110.6	127.5
Lf. L/W	2.75	2.92	2.49	2.48	2.39	2.49	2.58
Hd. Dia	27.2	28.8	25.5	27.1	26.0	25.0	25.9
Br. Lth	45.8	45.1	43.5	41.2	32.8	31.1	37.0
Br. L/W	3.69	3.14	3.16	2.97	2.50	2.90	2.61
Sp. Inx	5.50	6.62	5.11	5.85	0.22	4.80	5.21
Pr. Hd. No	-	-	-	-	-	-	-
Tot. Hd. No	-	-	-	-	-	-	-
Es. Den	7.3	9.3	5.3	5.7	6.0	9.7	7.3
GPPF	2.0	2.0	2.7	2.3	2.3	1.0	1.0
Brd. Dam	3.7	3.0	3.0	3.3	3.7	5.3	4.3
Sus. Bot	8.7	9.0	6.3	6.7	6.0	4.3	7.7
Pl. No (US)	22.7	33.0	18.0	17.3	16.3	39.0	26.0
Pl. No (S)	30.3	41.3	19.7	20.7	20.0	42.7	25.3
Yld (US)	463	369	972	646	637	810	790
Yld (S)	537	631	1890	1341	1428	1097	1223
Oil %	11.57	14.47	11.47	18.33	12.50	18.47	12.13
Hull %	60.70	58.50	62.60	57.67	60.10	57.80	60.27
Mos. %	9.47	9.23	9.43	9.37	9.83	9.30	9.20
Spr. Dam	5.3	2.3	3.3	3.0	3.0	7.3	4.3
Sd. Wt	43.20	41.07	32.20	49.73	47.13	41.40	45.87
I. Val	124	122	128	125	123	122	122

IIf Expt. I. Genotypic mean data; Site = Flockhouse; Year = 1979

CHARACTER	VFSTP-1	Partial-hull	Leed	Dart	PI 195895	0-22	Rio
St. Dia	16.03	16.77	13.87	13.53	15.37	11.37	12.83
Pl. Ht	109.06	105.76	101.17	101.50	114.33	112.17	110.67
Br. Lev	5.10	8.53	7.47	7.20	7.80	4.80	6.20
Lf. Lth	161.6	189.4	161.9	164.5	173.1	163.3	181.7
Lf. L/W	2.52	2.58	2.98	2.97	2.96	3.18	3.20
Hd. Dia	22.3	23.7	22.8	22.2	23.3	21.7	22.5
Br. Lth	44.9	43.3	34.1	31.9	24.4	30.4	30.1
Br. L/W	3.67	3.35	3.07	3.20	2.47	2.91	3.15
Sp. Inx	5.46	6.14	4.67	5.67	0.73	4.77	5.53
Pr. Hd. No	11.03	13.93	12.63	12.03	15.50	8.40	11.20
Tot. Hd. No	24.27	25.03	18.47	20.33	40.37	14.03	20.47
Es. Den	7.0	8.7	5.0	5.7	5.3	9.7	7.0
GPPF	4.3	4.7	5.3	4.7	5.0	4.0	3.7
Brd. Dam	1.0	1.0	1.0	1.0	1.0	1.0	1.0
Sus. Bot	3.3	3.7	2.0	2.0	2.0	1.7	2.0
Pl. No (US)	20.0	31.0	18.7	14.7	14.3	41.7	28.0
Pl. No (S)	19.0	33.3	12.3	17.0	16.0	44.7	27.0
Yld (US)	302	250	464	412	841	908	722
Yld (S)	327	261	339	521	924	988	791
Oil %	24.17	23.00	20.93	20.67	20.67	22.93	23.90
Hull %	51.90	51.97	54.87	54.17	54.73	54.17	52.50
Mos. %	9.43	9.03	9.23	9.13	9.70	9.33	9.07
Spr. Dam	1.0	1.0	1.0	1.0	1.0	1.0	1.0
Sd. Wt	34.47	40.67	54.93	45.87	50.53	49.33	51.57
I. Val	122	134	135	127	120	116	122

APPENDIX III

Expt. II. Estimates of heritability, full ($\hat{h}^2$) and restricted ($\hat{h}^{2'}$), their standard errors (S.E.) and coefficients of variation based on variance component estimates from the pooled environments model.

Character	Heritability (Full)			Heritability (Restricted)		
	$\hat{h}^2$	S.E.	C.V.%	$\hat{h}^{2'}$	S.E.	C.V.%
St. Dia	0.36	0.15	41	0.46	0.15	33
Pl. Ht	0.13	0.09	71	0.69	0.11	17
Br. Lev	0.32	0.14	43	0.40	0.15	37
Lf. Lth	0.04	0.03	82	0.36	0.14	38
Lf. L/W	0.10	0.11	111	0.15	0.16	107
Hd. Dia	0.35	0.15	45	0.56	0.14	26
Br. Lth	0.44	0.14	32	0.54	0.14	26
Br. L/W	0.73	0.09	13	0.73	0.09	13
Sp. Inx	0.84	0.06	7	0.85	0.06	7
Pr. Hd. No	0.13	0.10	76	0.28	0.16	59
Tot. Hd. No	0.22	0.16	70	0.26	0.18	68
Es. Den	0.58	0.14	24	0.73	0.09	13
GPPF	0.52	0.15	28	0.69	0.10	15
Brd. Dam	0.75	0.09	12	0.77	0.08	11
Lodging	0.59	0.13	22	0.60	0.13	21
Sus. St/Al	0.46	0.14	31	0.56	0.14	25
Sus. Bot	0.20	0.12	62	0.64	0.12	18
Oil %	0.01	0.02	189	0.08	0.14	177
Hull %	0.00	0.02	514	0.03	0.14	510
Sd. No	0.32	0.15	45	0.51	0.14	28
Sd. Wt	0.01	0.05	456	0.03	0.13	454
Yld (US)	0.18	0.12	64	0.30	0.16	52

APPENDIX IV

Expt. II. Phenotypic (r_p) and genotypic (r_g) correlation coefficients between traits studied on 10 genotypes in 3 environments.

Characters pair	r_p	r_g
St. Dia x Pl. Ht	0.62****	0.75 *
St. Dia x Br. Lev	0.33***	0.24 NS
St. Dia x Hd. Dia	0.32***	0.38 NS
St. Dia x Pr. Hd. No†	0.62****	0.47 NS
St. Dia x Tot. Hd. No†	0.52****	0.59(NS)
Pl. Ht x Br. Lev	-0.18(NS)	-0.41 NS
Pl. Ht x Lf. L/W	0.34***	0.02 NS
Pl. Ht x Pr. Hd. No†	0.58****	0.06 NS
Pl. Ht x Tot. Hd. No†	0.19 NS	0.32 NS
Br. Lev x Hd. Dia	0.29 **	-0.10 NS
Br. Lev x Pr. Hd. No†	0.54****	0.77 **
Br. Lev x Tot. Hd. No†	0.60****	0.56(NS)
Lf. Lth x Br. Lth	-0.26 *	0.43 NS
Lf. Wth x Br. Wth	-0.21 *	0.72 *
Lf. L/W x Br. L/W	0.36****	0.68 *
Lf. L/W x Pr. Hd. No†	0.28 *	0.27 NS
Lf. L/W x Tot. Hd. No†	0.06 NS	0.23 NS
Hd. Dia x Br. Lth	0.31***	0.22 NS
Hd. Dia x Br. Wth	0.45****	0.75 *
Hd. Dia x Br. L/W	-0.12 NS	-0.21 NS
Hd. Dia x Pr. Hd. No†	-0.01 NS	-0.21 NS
Hd. Dia x Tot. Hd. No†	0.12 NS	-0.12 NS
Br. L/W x Sp. Inx	0.55****	0.69 *
Br. L/W x Pr. Hd. No†	0.25(NS)	0.35 NS
Br. L/W x Tot. Hd. No†	0.21 NS	0.37 NS
Sp. Inx x Pr. Hd. No†	-0.15 NS	-0.07 NS
Sp. Inx x Tot. Hd. No†	-0.20 NS	-0.20 NS
Es. Den x Br. Lev	-0.27 *	-0.54 NS
Es. Den x Pr. Hd. No†	0.12 NS	-0.36 NS
Es. Den x Tot. Hd. No†	-0.14 NS	-0.39 NS

APPENDIX IV(Continued)

Characters pair	r_p	r_g
Brd. Dam x Tot. Hd. No †	-0.24(NS)	-0.39 NS
Brd. Dam x Yld (US)	0.06 NS	0.83***
Brd. Dam x Hd. Dia	0.09 NS	-0.33 NS
Brd. Dam x Sp. Inx	-0.16 NS	-0.28 NS
Lodging x Pl. Ht	0.21 *	0.67 *
Lodging x Tot. Hd. No †	0.33 *	0.31 NS
Yld (US) x Sp. Inx	-0.16 NS	-0.33 NS
Sd. Wt x Hd. Dia	0.19(NS)	0.43 NS
Oil % x Hull %	-0.97****	-0.89****

† Based on data from two sites only (Massey and Flockhouse)