

South Dakota State University

Open PRAIRIE: Open Public Research Access Institutional Repository and Information Exchange

Electronic Theses and Dissertations

1986

Predicted Response to S1 Selection for Agronomic and Disease Resistance Traits in Two Sunflower Populations

Syed Sadaqat Mehdi

Follow this and additional works at: <https://openprairie.sdstate.edu/etd>



Part of the [Agronomy and Crop Sciences Commons](#)

Recommended Citation

Mehdi, Syed Sadaqat, "Predicted Response to S1 Selection for Agronomic and Disease Resistance Traits in Two Sunflower Populations" (1986). *Electronic Theses and Dissertations*. 5677.

<https://openprairie.sdstate.edu/etd/5677>

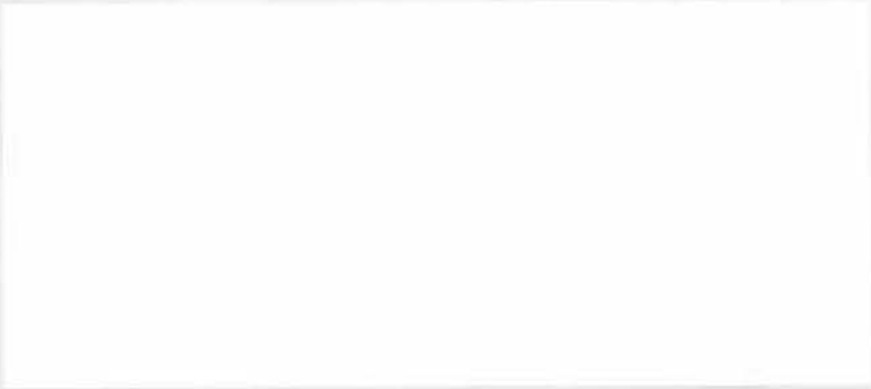
This Dissertation - Open Access is brought to you for free and open access by Open PRAIRIE: Open Public Research Access Institutional Repository and Information Exchange. It has been accepted for inclusion in Electronic Theses and Dissertations by an authorized administrator of Open PRAIRIE: Open Public Research Access Institutional Repository and Information Exchange. For more information, please contact michael.biondo@sdstate.edu.

PREDICTED RESPONSE TO S1 SELECTION FOR AGRONOMIC
AND DISEASE RESISTANCE TRAITS IN TWO
SUNFLOWER POPULATIONS

This thesis is submitted as a candidate for the independent investigation of a candidate for the degree of Philosophy, and it is acceptable for granting the thesis requirements for the degree of Philosophy in the Faculty of Agriculture and Forestry, and the requirements required by the candidate are presented in the following of the thesis department.

BY


SYED SADAQAT MEHDI




A thesis submitted
in partial fulfillment of the requirements for the
degree of Doctor of Philosophy, major in Agronomy
South Dakota State University
1986

PREDICTED RESPONSE TO S1 SELECTION FOR AGRONOMIC
AND DISEASE RESISTANCE TRAITS IN TWO
SUNFLOWER POPULATIONS


This thesis is approved as a creditable and independent investigation by a candidate for the degree, Doctor of Philosophy, and is acceptable for meeting the thesis requirements for this degree. Acceptance of this thesis does not imply that the conclusions reached by the candidate are necessarily the conclusions of the major department.


Dr. Martin L. Carson
Thesis Advisor

Date


Dr. Charles J. Lay
Major Advisor

Date


Dr. Maurice L. Horton
Head, Plant Science
Department

Date

ACKNOWLEDGMENTS

I wish to express my sincere appreciation and gratitude to my thesis advisor, Dr. W. L. Garrison for his generous guidance, encouragement, helpful suggestions, and criticism during the research and writing of this dissertation. A very special thanks to my mother, Dr. C. L. Garrison, for her love, support, and the helpful suggestions during the writing of this dissertation. To my father, I would like to thank for his love and support throughout my college education. I would also like to thank the faculty and staff of the State College for their help and encouragement throughout the duration of my studies.

Special appreciation is also expressed to the State College faculty members and to my fellow graduate students for their encouragement, help, and criticism. Thanks also to my wife, Mrs. L. L. Garrison, for her love and support throughout the writing of this dissertation. The author also wishes to acknowledge the State and City families who have been so kind in providing my stay in State College. David Adams, Librarian, State College, for all the help he provided me in the project. My mother and father for their love and support throughout my college education.

The research was supported financially by the State College Management Office, State College, Texas. I would like to thank the

ACKNOWLEDGEMENTS

I wish to express my sincere appreciation and gratitude to my thesis advisor, Dr. M.L. Carson for his guidance, patience, encouragement, helpful suggestions and criticisms during the research and writing of this dissertation. A very special thanks to major advisor, Dr. C. Lay for his help throughout my study and the helpful suggestions during the preparation of this thesis. To Dr. C.A. Dinkel thanks for being my minor advisor. I would foremost like to thank Dr. Maurice L. Horton, Professor and Head of the Plant Science Department for the warm encouragement he gave me throughout the duration of my studies.

Special appreciation is also expressed to the Plant Science faculty members and to my fellow graduate students for their encouragement, help and friendship. Thanks goes to my unforgettable friends Tanveer, Ashraf, Farid and Dale Lynn for their consistent help and encouragement. The author also wishes to acknowledge the Pierce and Lynn families who made me feel at home during my stay in South Dakota. Sayed Alzaman deserves special thanks for all the help he provided me in the script programming. To my brothers and sisters, thanks for being you.

The research was supported financially by the Plant Science Department (Dr. Maurice Horton, Head). Acknowledgement is also

extended to the U.S. Educational Foundation in Pakistan for permission to pursue this degree after expiration of the Fulbright-Hays (non-degree) program.

SSM

[The following text is extremely faint and illegible.]

[The following text is extremely faint and illegible.]

ABSTRACT

Variances, heritabilities, genetic and phenotypic correlations, and predicted gains were computed for quantitative disease resistance and agronomic traits from pooled S1 family data of Gene Pool II and ND 761 *Helianthus annuus* L. populations. Broad-sense heritability estimates for all traits were significant in both populations. Observed genotypic correlation coefficients were larger than their corresponding estimates of phenotypic correlation coefficients. Significant positive genetic correlations between resistance to *Alternaria* blight and *Septoria* leaf spot; and non-significant genetic correlations between *Sclerotinia* wilt disease reaction and agronomic traits were observed in both populations. Resistance to *Phoma* black stem was not significantly correlated with resistance to other diseases or yield.

Genetic correlations of yield/ha with reaction to *Alternaria* blight and *Septoria* leaf spot diseases in Gene Pool II were negative and significant. There were significant positive genotypic correlations between yield/ha and other agronomic traits except days to flower. The genetic correlation between *Septoria* leaf spot and *Sclerotinia* wilt disease reactions was positive and significant in ND 761. However, resistance to four diseases in ND 761 was inherited independently of yield/ha. Yield/ha was positively significantly genetically correlated with head diameter, head weight, seeds per head and oil yield in ND 761.

The Smith-Hazel index in both populations was efficient in improving predicted gains of resistance to all four diseases (Alternaria leaf blight, Septoria leaf spot, Phoma and Sclerotinia wilt) when selection was focused on Alternaria blight and Sclerotinia wilt resistance simultaneously. This selection index was also effective for both populations in improving gain for agronomic traits (head weight, 200-seed weight, oil content and yield/ha) when selection was for oil percent and yield/ha simultaneously. Smith-Hazel and desired gain indices with simultaneous selection of Alternaria blight and Sclerotinia wilt resistance, oil percent and yield/ha are suggested for the improvement of multiple disease resistance and agronomic traits in Gene Pool II and ND 761, respectively. The restricted selection index and desired gain index were most efficient in controlling gains for restricted traits, plant height and days to flower.

Contents of Chapter I	1
Contents of Chapter II	11
Summary of Chapter III	12
III MATERIALS AND METHODS	16
Experimental materials	16
Statistical analysis	21
IV RESULTS	22
V DISCUSSION	40
VI LITERATURE CITED	48

PART I

TABLE OF CONTENTS

Chapter		Page
	ACKNOWLEDGEMENTS	iii
	ABSTRACT	v
	LIST OF TABLES	x
	INTRODUCTION	1
PART I		
	ABSTRACT: HERITABILITY ESTIMATES, GENETIC AND PHENOTYPIC CORRELATIONS	2
I	INTRODUCTION	4
II	LITERATURE REVIEW	6
	Importance of the Diseases	6
	Genetics of Disease Resistance	8
	Genetics of Agronomic Traits	11
	Correlation Among Characters	14
III	MATERIALS AND METHODS	18
	Experimental Procedures	18
	Statistical Analyses	23
IV	RESULTS	27
V	DISCUSSION	40
VI	LITERATURE CITED	48

PART II

Chapter	Page
ABSTRACT: SELECTION INDICES	54
I INTRODUCTION	56
II REVIEW OF LITERATURE	58
Recurrent Selection	58
Selection Indices	60
III MATERIALS AND METHODS	67
Construction of Selection Indices	68
IV RESULTS	73
Predicted Gains from Index Selection	73
V DISCUSSION	83
VI LITERATURE CITED	89
VII APPENDICES	93
A Estimates of genetic variance, environmental variance and heritability among S1 families of Gene Pool II in 1982 and 1983.	94
B Estimates of genetic variance, environmental variance and heritability among S1 families of ND 761 in 1982 and 1983.	95
C Estimates of genetic and phenotypic correlation coefficients of Gene Pool II in 1982 and 1983	96
D Estimates of genetic and phenotypic correlation coefficients of ND 761 in 1982 and 1983	97
E Estimates of genetic and phenotypic covariances of Gene Pool II during the year 1982 and 1983	98
F Estimates of genetic and phenotypic covariances of ND 761 during the year 1982 and 1983	99
G Index coefficients (b-values) of four diseases from selection ¹ among S1 families by using three selection strategies and two types of selection indices	100

Chapter	LIST OF CHAPTERS	Page
H	Index coefficients (b-values) for six agronomic traits from selection ¹ among S1 families of GP II and ND 761 using three selection strategies and three types of selection indices	101
I	Index coefficients (b-values) for disease and agronomic traits from selection among S1 families of GP II by using nine selection strategies and three selection indices.	102
J	Index coefficients (b-values) for disease and agronomic traits from selection among S1 families of ND 761 by using nine selection strategies and three selection indices.	103
K	Genetic variation and coefficients of variation (CV) of 11 families from ND 761 population under selection 1981 and 1982.	104
L	Genetic variation of agronomic characters of S1, two-way-backcross (B1B1) and F1 population among S1 families of GP II and ND 761 population.	105
M	Genetic variation of growth, disease resistance and phenotypic character (disease resistance) coefficients of GP II (ii) population.	106
N	Genetic variation of growth, disease resistance and phenotypic character (disease resistance) coefficients of ND 761 population.	107
O	Genetic variation of growth, disease resistance and phenotypic character (disease resistance) coefficients of GP II (iii) population.	108
P	Genetic variation of growth, disease resistance and phenotypic character (disease resistance) coefficients of ND 761 population.	109
Q	Genetic variation of growth, disease resistance and phenotypic character (disease resistance) coefficients of GP II (iv) population.	110
R	Genetic variation of growth, disease resistance and phenotypic character (disease resistance) coefficients of ND 761 population.	111

LIST OF TABLES

Table		Page
1	Form of the analysis of variance and covariance of S1 families with r replications and f S1 families.	24
2	Form of the analysis of variance and covariance for S1 families with b blocks, r replications per block, and f _i families in the ith block.	25
3	Means, ranges and coefficients of variation (CV) of S1 families from Gene Pool II population grown during 1982 and 1983.	28
4	Means, ranges and coefficients of variation (CV) of S1 families from ND 761 population grown during 1982 and 1983.	29
5	Pooled estimates of genetic variance ($\hat{\sigma}^2_G$), environmental variance ($\hat{\sigma}^2_E$) and heritability (h^2) among S1 families of Gene Pool II and ND 761 populations.	31
6	Pooled estimates of genetic (above diagonal) and phenotypic (below diagonal) correlation coefficients of Gene Pool II population	33
7	Pooled estimates of genetic (above diagonal) and phenotypic (below diagonal) correlation coefficients of ND 761 population	35
8	Pooled estimate of genetic (above diagonal) and phenotypic (below diagonal) covariances of Gene Pool II population	37
9	Pooled estimate of genetic (above diagonal) and phenotypic (below diagonal) covariances of ND 761 population	38
10	Relative economic values and desired gains used in constructing selection indices for Gene Pool II and ND 761 populations	69

Table	Page
11 List of indices constructed to maximize gain in Gene Pool II and ND 761 populations and traits included in those indices.	71
12 Predicted direct responses and correlated responses to S1 family selection in Gene Pool II population in units of measurements	74
13 Predicted direct responses and correlated responses to S1 family selection in ND 761 population in units of measurements	75
14 Predicted gains and the aggregate genotype for four diseases from selection among S1 families of GP II and ND 761 by using three selection strategies and two selection indices	77
15 Predicted gains and the aggregate genotype for six agronomic traits from selection among S1 families of GP II and ND 761 by using three selection strategies and indices	78
16 Predicted gains and aggregate genotype for diseases and agronomic traits from selection among S1 families of GP II by using nine selection strategies and three types of selection indices	80
17 Predicted gains and aggregate genotype for diseases and agronomic traits from selection among S1 families of ND 761 by using nine selection strategies and three types of selection indices	81

INTRODUCTION

Recurrent selection is a breeding procedure designed to increase the frequency of superior genotypes in a population. This method shifts the mean of a population for one or more traits in a desired direction. Therefore progress in plant breeding primarily depends upon obtaining genetic diversity and the effectiveness of selection.

Reliable estimates of genetic and phenotypic variances, covariances, heritabilities and correlations are necessary to make a recurrent selection program an efficient method for improvement of plant populations. Furthermore, selection indices are considered an aid to the breeder for simultaneous selection for multiple traits in a recurrent selection program. This tool has been applied successfully to a few plant breeding problems. The ability to improve important traits such as disease resistance and yield in sunflower would be valuable in developing improved cultivars. The objective of this study was to evaluate S1 family selection in Gene Pool II and ND 761 populations. This information will be helpful for the initiation of a recurrent selection program for agronomic traits with multiple disease resistance in these two sunflower populations.

I. HERITABILITY ESTIMATES, GENETIC AND PHENOTYPIC CORRELATIONS

ABSTRACT

Pooled estimates of heritability, genotypic and phenotypic variance, covariance and correlation of reactions to four diseases and agronomic traits were obtained among 162 and 104 S1 families of Gene Pool II and ND 761, respectively in 1982; and 150 S1 families from each population in 1983. Genetic variances in Gene Pool II were comparatively higher than in ND 761 for all traits except Sclerotinia wilt resistance and days to flower. Broad-sense heritability estimates for all traits were significant in both populations. Genotypic correlation coefficients were larger than their corresponding estimates of phenotypic correlation coefficients. Both populations had significant positive genetic correlations between resistance to Alternaria leaf blight and Septoria leaf spot. However, non-significant genetic correlations were observed between Sclerotinia wilt resistance and agronomic traits. Genetic correlations of oil content with reactions to four diseases in both populations were negative but non-significant. Resistance to Phoma black stem was not significantly correlated with resistance to other diseases or yield.

Genetic correlations of yield/ha with reactions to Alternaria leaf blight and Septoria leaf spot disease in Gene Pool II were negative

and significant, indicating that low disease score is associated with high yield. There were significant positive genotypic correlations between yield/ha and other agronomic traits except days to flower. Head weight had a positive and significant genetic correlation with all agronomic traits in Gene Pool II.

The genetic correlation between Septoria leaf spot and Sclerotinia wilt disease reaction was positive and significant in ND 761. None of the genetic correlation coefficients of yield/ha with reactions to the four diseases were significantly different from zero. Therefore, resistance to four diseases in ND 761 is inherited independently of yield. However, yield/ha was positively significantly genetically correlated with head diameter, head weight, seeds per head and oil yield.

INTRODUCTION

Sunflower breeders are continually looking for new breeding systems to improve the efficiency of selection for agronomic traits. The prerequisite for any such breeding system is information on the nature and magnitude of genetic variation present in existing germplasm. A plant breeder is concerned with selecting superior genotypes on the basis of phenotypic expressions. The choice of a population to work with and of a breeding system to be practiced in the initiation of crop improvement depends primarily on the mean performance of the population, and the magnitudes of the different kinds of genetic variation in the population. Therefore reliable estimates of the genetic and phenotypic variances for various traits are essential for predicting the success of the breeding system.

Seed yield is a trait of primary importance and of complex inheritance that involves several individual traits. Hence estimates of genotypic and phenotypic correlations among traits are required to maximize gain for all traits. The genetic relationship of disease resistance with agronomic traits is not well documented in sunflower (*Helianthus annuus* L.). Such information would be useful in designing selection procedures to improve both traits, since disease resistance is an insurance against yield losses in years when conditions favor disease development. Genetic correlation between two or more traits originates from pleiotropic effects or linkage of genes affecting each trait.

Therefore, knowledge of genetic correlations among traits is helpful when selection is concerned with changing two or more traits simultaneously.

The objectives of this study were: 1) to obtain estimates of genetic and phenotypic variances and covariances for agronomic and disease resistance traits in the two sunflower populations Gene Pool II and ND 761; 2) to calculate heritabilities and predicted gains from S1 family selection for these traits; and 3) to investigate the degree of genetic and phenotypic correlations between agronomic traits and quantitative resistance to four diseases.

LITERATURE REVIEW

Importance of the Diseases

It is estimated that diseases cause an average annual loss of 12 percent in yield of sunflower in the world (69). The relative importance of sunflower diseases varies annually with variable factors like environment and cultivars grown. Common sunflower diseases in the Minnesota-Dakotas region of the US are downy mildew, rust, Verticillium wilt, Sclerotinia stalk rot, Alternaria leaf blight, Septoria leaf spot, and Phoma black stem. Only the four later diseases will be discussed since they were a subject of this study.

Sclerotinia wilt (caused by *Sclerotinia sclerotiorum* (Lib.) de Bary) is a predominant disease of sunflower. In the United States most damage is caused by root and basal stem attack (26). The wilt symptoms are initiated by root infection which progresses upward into the stem. Infected plants may set seed, but their yield is reduced. Most frequently, infected plants lodge before maturity. Wilting may occur at any stage of plant development and the most prevalent period is from late budding to maturity (49). This disease had the highest severity of any disease in surveyed fields in the Dakotas and Minnesota (20). The disease incidence increased from 32 percent in 1979 to 48 percent in 1984 of surveyed fields (20,21). Fields with the highest wilt severities, ranging up to 60 percent, were reported to be

within the Red River valley (20). The amount of yield reduction due to Sclerotinia wilt is dependent upon the stage of plant development when symptoms develop. When wilting occurred within 4 weeks of flowering, seed yield was reduced more than 70 percent (11). This reduction was due to lower seed weight. However, oil content increased with delayed wilting after the flowering.

Alternaria leaf blight caused by *Alternaria helianthi* (Hansf.) Tubaki and Nishihara is another potentially destructive disease in the major sunflower growing areas. It can cause severe leaf and stem spotting resulting in premature defoliation and stem breakage. This disease causes a significant reductions in yield (4,7,50). The disease has also been recognized as a threat to sunflower production in the United States and sunflower are susceptible to infection at any growth stage (24,54). Alternaria disease is measured as a percent leaf disease severity, and there is a relationship between disease severity and loss. As the percent disease increased, the loss also increased (7,50). The nature of significant yield reduction primarily depends on the plant growth stage when disease epidemics develop. Susceptibility of sunflower plants is greatest during the anthesis and seed filling stages of growth (4). Yield components such as flower size, number of seeds per head, plant seed yield, seed weight and oil content are adversely affected (6).

Septoria leaf spot (caused by *Septoria helianthi* Ell & Kell.) is widely distributed on sunflower and can reduce seed yields by as much as 10 to 15 percent (8). The disease appears to be less damaging

to sunflower compared to *Alternaria* leaf blight. However, 50 to 70 percent affected plants in the field has been reported (25). Infection varied from moderate to severe on 100 percent of plants in 21 percent of the surveyed sunflower fields in Manitoba in 1964.

Phoma black stem (caused by *Phoma macdonaldii*) produces black lesions on the stem and petioles. Under severe conditions, lesions completely girdle the stem and through the union of several patches the whole stem becomes completely blackened (39). Severely infected young plants may be killed by early infection whereas older plants are generally stunted, weakened and produce small heads. The severity of the Phoma black stem was observed in surveyed fields of the Dakotas and Minnesota (20). When compared to other diseases its severity was not considered especially damaging. *P. macdonaldii* is also considered as a contributor to premature ripening of sunflower. The premature ripening complex consists of supplemental stress from drought, nematodes, insects, collateral pathogens, plant maturity and other agents (10). Premature ripening has been observed in field plots and in one field in the Southeastern North Dakota it resulted in 65 percent yield reduction (10).

Genetics of Disease Resistance

Resistance is a genetically controlled plant characteristic which suppresses pathogen and disease development. The magnitude of plant resistance ranges from total resistance to total susceptibility. The use of disease resistant cultivars is the easiest and least expensive method

of controlling plant diseases. It was first indicated by Putt (49) that sunflower cultivars and lines differ in susceptibility to stalk and head rot caused by *Sclerotinia sclerotiorum*. The resistance is expressed as a higher percent of surviving plants in resistant cultivars than susceptible. Resistance has been identified in both adapted inbred lines and in exotic germplasm (19). This resistance has also been shown to be heritable but the level of resistance in current hybrids is not considered adequate for control. Resistance to *Sclerotinia* stalk rot also exists among the perennial *Helianthus* species, and has been utilized in the breeding of cultivated sunflower (47).

Seedlings of inbred lines, F1 hybrids and an open pollinated cultivar varied from moderately resistant to highly susceptible for *Sclerotinia* disease reaction (28). Fifty-one germplasm entries of sunflower under field conditions showed differences in susceptibility and no entry was found to be free from the disease (33). The sunflower inbred line HA 61 has partial resistance which in some crosses is transferred to its F1 progeny (13). Later this resistance was confirmed by Mancl and Shein (37). But two other resistant sunflower lines in the latter study did not convey resistance to F1 crosses with susceptible genotypes, but resistance was expressed in certain advanced generations of the parental lines and crosses made with them, indicating that resistance in these lines was not dominant. However, another study (60) indicated that *Sclerotinia* resistance from inbreds can be transferred to F1 hybrids.

Additive genetic effects are of primary importance in the

inheritance of resistance to Sclerotinia wilt. The largely additive genetic variation and high heritability for Sclerotinia resistance suggest (17) that selection for resistant sunflower genotypes can be effective. The genotypic variance of Sclerotinia resistance is high and the inheritance of resistance complex and determined by several genes (63). Reciprocal recurrent selection followed by inoculation tests should give the best indication of the presence of the desired polygenic resistance for Sclerotinia wilt (23).

Sunflower genotypes exhibit variable amounts of resistance to *A. helianthi*. Some sunflower hybrids and lines were observed to have moderate resistance to Alternaria leaf blight but no immune genotype was found (29). In a field test of 115 sunflower varieties in India under artificial inoculation, only 5 varieties were found resistant to Alternaria disease (2), and no variety was identified as highly resistant. Significant differences were observed between twenty-four inbred lines of sunflower for reaction to *A. helianthi*, as measured by the percentage of leaf area infected (7). This indicates that Alternaria disease resistance in sunflower is expressed quantitatively as a reduction in disease severity. The Alternaria leaf blight resistance also exists in perennial *Helianthus* species. Three out of 37 perennial *Helianthus* species were observed as moderately resistant to *A. helianthi* in the greenhouse (40). This resistance may be transferable to the cultivated sunflower by backcross breeding.

Septoria leaf spot resistance has been reported but its sources are unpublished (69). Resistance has been reported from Zambia (65)

where tropical varieties are less susceptible compared to varieties from temperate regions. Recently Carson (8) detected significant differences between sunflower inbred lines for reaction to *Septoria* leaf spot.

On the basis of field observations various forms resistant to *P. macdonaldii* have been listed (5). The evaluation of wild donors of resistance and their hybrids for resistance *P. macdonaldii* along with other pathogens revealed 12 resistant forms belonging to *Helianthus annuus* subsp. *petiolaris* and *lenticularis*.

Genetics of Agronomic Traits

Knowledge of the heritability, the type of gene action involved, and the number of genes associated in controlling quantitative traits is essential for the choice of the most effective and efficient selection and breeding procedures.

Heritability estimates based on the variance components method in local and introduced sunflower cultivars were relatively high for seed yield, yield components and oil content (44). This indicates that most variability among cultivars was due to genetic causes. Additive gene action may also be responsible for high heritability estimates of seed yield per plant (55). On the basis of high heritability estimates, seed yield per plant was suggested to be most effective trait on which to base selection (45). However, others have reported low heritability for seed yield (30,61). Estimates of heritability in a diallel cross involving six inbred lines of sunflower were low for grain yield and oil percentage compared with traits like plant height, head diameter and

time of flowering (66).

Information about heritabilities of major yield components is also important. This information is needed in selection for increasing seed yield through selection of its components. High heritability estimates for 1000-seed weight have been reported (30,62), and it was also indicated (62) that additive effects are the most important component of genetic variance for this trait. However, others have reported (45,61) low estimates of heritability for seed weight and indicate that selection for this trait will be difficult (45). High heritability estimates for number of seeds per head with very high expected genetic advance suggested that this trait was probably due to additive genetic effects (53).

On the basis of heritability estimates it was indicated that additive gene action may be important for head diameter (55). In a set of diallel crosses involving ten parents and 66 F1's of sunflower grown under seven environments, significant dominance as well as additive genetic variance for head diameter, plant height and seed yield per plant were evident (12). Three to four loci appeared to be the minimum loci governing the inheritance of these traits. In general, dominant genes appeared to have positive effects for all traits in this study but the possibility of having negative effects in some parents was not ruled out. Plant height was moderately heritable. From this study it is clear that plant height, and head diameter were the important attributes of seed yield per plant and these traits appeared to be governed by some common genes having pleiotropic effects.

The additive and nonadditive components are equally important in the inheritance of plant height. Analysis of components of genetic variance and regression analysis (38) indicated the presence of superdominance in the inheritance of plant height. Dominant genes were more frequent than recessive for plant height. The high heritability estimates for plant height (30,43) and high genetic advance suggested that additive gene action may be responsible (55). However, Pathak (45) indicated that selection for plant height will be difficult because of low heritability estimates.

Broad-sense heritabilities estimated in different populations for the number of days to flowering were high (30,43,53) and on the basis of genetic advance estimates, this was considered probably due to non-additive genetic effects (53).

Oil content of sunflower is determined by genes that are partially dominant or complementary in their action (52). The success of the Russian program in increasing oil content by the "Lysenko method" was dependent on a large additive component of genetic variation which exists for this trait (3). Heritability of oil content in the selected plants of the varietal population of "Peredovik" and "Vniimk 8931" were low (42). Low estimates of heritability for oil content have also been reported (30,61). However, high heritability and genetic advance for oil content (62) indicated that additive effects were the most important component of genetic variance for this trait. Fick (14) indicated that genetic effects were largely additive on the basis of the ratio of narrow to broad-sense heritability estimates. The heritability of sunflower

seed-oil content is relatively high and that significant improvements can be made in increasing oil content by selection of individual plants for high oil in early generations (1). The mode of inheritance of oil content in sunflower seed differed among ten sunflower inbreds of S9 generation. The majority of the hybrid combinations showed partial or full dominance; the rest were either intermediate or exhibited heterosis (57).

Correlation Among Characters

In plant breeding, knowledge of genetic correlations among traits in a population can be useful when using selection for secondary traits to improve a primary trait or genetic correlation may be detrimental when selection for one trait results in undesirable correlated responses.

A significant regression between plant height and Sclerotinia disease incidence has been reported (35), with the shortest varieties most often attacked. The relative susceptibility to Sclerotinia is not closely correlated with days to 50 percent flowering nor to plant height (16). Also there is no close correlation between Sclerotinia resistance and earliness (63), between Sclerotinia susceptibility and flowering date, head diameter or oil content (64). Few sunflower forms which showed combined resistance to Phoma, Sclerotinia along with other pathogens have been listed (5).

In another study of inbred lines (8), resistance to Alternaria leaf blight and Septoria leaf spot were significantly positively

correlated. A high correlation between the diseased leaf area of Alternaria leaf blight and Septoria leaf spot and reduction in achene yield have also been documented (65). The S2 testcross reciprocal selection technique used to select for improved yield in sunflower populations in Zambia has not resulted in the improvement of yield to the desired level (22). However, populations selected for Alternaria and Septoria leaf spot disease resistance showed some improvement.

Several studies of the correlation of plant and seed traits with seed yield and oil content have been reported. A positive correlation between plant height and number of days to flowering (43), and 100-seed weight (55) are evident in the literature. Genotypically plant height was positively correlated with head diameter, number of seeds per head but negatively correlated with 100-seed weight and oil content (59).

Days from planting to flowering was positively genotypically and phenotypically correlated with seed yield (30), but earlier maturity has been associated with shorter stems and lower oil content (18). The genetic and phenotypic correlations of seeds per head were negative with 100-seed weight but positive with oil content (59). Phenotypically, 100-seed weight was negatively significantly correlated with oil content but genetically was slightly positively correlated (59).

Mungai (41) examined the possibility of utilizing head diameter and kernel percentage as criteria in breeding for high oil content. He observed a negative correlation between head diameter and kernel

percentage and between head diameter and oil content in the seeds. Head diameter was also significantly correlated with seed yield and oil yield (18), 100-seed weight (55,59), and with seeds per head but negatively and significantly correlated with oil content (59). However, genetic correlations were positive between head diameter and seeds per head, 100-seed weight and negative with oil content (59).

A highly significant positive correlation exists between oil content and plant height and seed yield (51), but no significant relationship exists between oil content and head diameter, and days to full bloom. Russell's data (52) suggested an association between oil content and days to flower, plant height, leaf area, vigor rating, and rust rating among inbred lines and top-cross hybrids. A positive correlation of seed oil content with plant height, maturity, and test weight exists in hybrids and open-pollinated populations (15). Oil content of inbred lines was negatively correlated with seed weight. Seed oil content is also positively correlated with plant height but negatively correlated with head diameter, and seed yield in selected plants from open-pollinated varieties and inbred lines (67). The yield of achenes and of oil were clearly correlated with plant height, less considerably with the head diameter, while a significant correlation with the weight of 1000-achenes and the husk content was noted only sporadically (32). The correlation between oil content and head diameter as well as between oil content and 1000-achenes weight shows that intensive selection for high oil content can sometimes interfere with the trend to increase achene yield. Oil content was negatively

correlated as well having a negative direct effect on yield (46). Correlation coefficients of oil yield and its components seed yield and oil content, were highly significant (18). The simple correlation coefficient between oil yield and plant height was significantly positive in groups of sunflower F1 hybrids (56).

Positive and significant correlations between seed yield and agronomic traits like plant height, head diameter (34,45,46,48,59), 100-seed weight (34,45,59), seeds per head (59), and kernel oil content (34) suggested that selection for seed yield could be based on these "component" characters. Ivanon and Stoyanova (30) noted a relatively higher positive value of the phenotypic correlation between yield and oil content in six late varieties and ten hybrids of sunflower. However, a negative genotypic correlation was observed between these two traits. Genetic and phenotypic correlations between seed yield and plant height were low but positive. The genetic correlation between seed yield and plant height, head diameter, seeds per head, 100-seed weight and oil content were positive. However seed yield and oil percentage were low in association (59).

MATERIALS AND METHODS

Experimental Procedures

Two populations of sunflower viz., Gene Pool II from Agriculture Canada, Morden, Manitoba and ND 761 from the USDA-ARS, Fargo, North Dakota were used in this study. Gene Pool II is a second cycle of selection from an original composite of 50 inbred lines. They were selected from various sources, mostly Russian varieties, for their oil content, agronomic traits and disease resistance. These lines were allowed to interpollinate for three seasons to form Gene Pool 1. In the following season 500 S1 families were selected from Gene Pool 1 and at the S3 generation the best 29 lines selected on the basis of combining ability and agronomic traits were interpollinated for two seasons. The seed harvested from these lines was called Gene Pool II (Personal communication, Walter Dedio, Agriculture Canada, Morden, Canada). ND 761 is a germplasm source for breeding of high oil cultivars and parental lines of hybrids with resistance to the Red river race (race 2) of downy mildew. This germplasm is a composite of seed of individual F2 and F3 plants selected from the cross (P-21 VR1*2/HA 61/2/3* 'Sputnik') involving "Sputnik" as a recurrent parent. ND 761 is variable for flowering and plant height, reaction to rust and Verticillium wilt diseases (68).

One hundred sixty two and 104 S1 families from Gene Pool II

and ND 761, respectively, were evaluated in 1982, whereas 150 different S1 families each from Gene Pool II and ND 761 were tested in 1983. In 1982, two separate experiments, Experiment I and Experiment II, were planted on June 3 on the SDSU Plant Pathology Farm, Brookings. Single row plots of each family were 3.05 m long, spaced 1.02 m apart and were replicated twice in a randomized complete block design. A different randomization of S1 families was used for each experiment. Plots were overplanted and thinned to 10 plants per plot.

In experiment I, each plant in a plot was artificially inoculated with *Alternaria helianthi* when plants were about three weeks old by dropping 10-20 *A. helianthi* infested grains of either sorghum or barley into the leaf whorl. Individual S1 families were rated weekly at mid vegetative stage for percent *Alternaria* leaf blight disease using a 0-11 scale (27). Five of the same plants were inoculated with *Phoma macdonaldii* by injecting with 2 ml of a spore suspension (200,000 spores/ml) below a internode located about 30 cm above the soil level approximately two weeks after flowering using a 50 ml Vaco pistol grip syringe (9). Two weeks later, inoculated plants were cut above the inoculated internode and split to ground level. *Phoma* reaction was recorded by observing stem infection on a 0 to 5 scale (0= no disease spread to 5= premature death). In experiment II, all plants were inoculated with *Septoria helianthi*. The same inoculation and disease rating procedure as with *Alternaria* leaf blight was used. The same plants in experiment II were inoculated with *Sclerotinia sclerotiorum*, 25 days after planting by placing two to three sclerotia 2-3 cm below

the soil 2 cm away from the stalk, using a jab-type hand planter. Sclerotinia disease causes root, basal stem infection and finally wilting of the plant. Therefore, plants were observed weekly for symptoms of Sclerotinia wilt, starting at the mid bud stage until the late seed development stage. The number of wilted plants observed at weekly intervals were converted to percent of plants per plot infected.

In addition to experiments I and II, a third experiment for the study of agronomic traits was planted near White, South Dakota. The 162 S1 families of Gene Pool II were assigned to 6 blocks of 27 families each; whereas 104 S1 families of ND 761 were randomly assigned to 4 blocks of 26 families each. A replicate-within blocks design was used in this experiment. Three replications of S1 families from each population were grown separately in each block on June 5, 1982. A single row 7.2 m long with 76.9 cm between rows was planted for each family. Plots were overplanted and thinned to 25 plants per plot. The following agronomic traits were measured in this experiment:

- (1) Plant height (cm): Distance from soil surface to the base of the sunflower head. Ten plants in each plot were measured after plants had reached full maturity.
- (2) Days to flowering: Data were recorded on the number of days from planting to opening of first row of disc flowers on 50% of the plants in each plot.
- (3) Head diameter (cm): After artificial drying, five randomly picked heads were measured from each plot.
- (4) Seed weight per head (gm): Three artificially dried heads

randomly picked from each plot were individually threshed, and seed cleaned and weighed.

(5) 200-seed weight (gm): Two hundred seed samples were counted from each of the sunflower head (described in trait 4) and weighed.

(6) Seeds per head: $\text{Head weight (gm)} / 200\text{-seed weight (gm)} \times 200$.

(7) Oil content (percent): A seed sample of 40 ml was taken from each of the three random sunflower heads and oil content determined using NMR (nuclear magnetic resonance). Oil content was expressed at less than 10% moisture.

(8) Seed yield (kg/ha): Plots were hand harvested and a plant count was made in each plot. Sunflower heads were artificially dried, threshed, seed cleaned and weighed. Finally plot seed yield were converted into seed yield per hectare.

(9) Oil yield (kg/ha): $\text{Seed yield (kg/ha)} \times \text{Oil content}$.

In 1983, three experiments were planted on the Plant Pathology Farm, Brookings. One hundred fifty S1 families each in Gene Pool II and ND 761 were used. Experiments I and II were planted on May 27, 1983 in same way as in the experiments of 1982. However, plots were not thinned in either experiment. These two experiments were inoculated and evaluated for disease reaction as in 1982, except ten plants in experiment I were inoculated with *P. macdonaldii* instead of five. Also experiment II was inoculated with *S. sclerotiorum*, 6 weeks after planting by using mycelium infested sorghum grains instead of sclerotia.

Whole-plot disease ratings for 7 weeks were made for *Alternaria* leaf blight and *Sclerotinia* wilt in both years. *Alternaria* leaf blight ratings were noted from July 26 to September 6 in 1982, and July 13 to August 24 in 1983. *Sclerotinia* wilt symptoms were recorded from August 17 to September 28, and July 21 to September 1 during 1982 and 1983, respectively. However, only 4 weekly disease ratings were made for *Septoria* leaf spot from August 10 to 31 in 1982, and July 14 to August 4 in 1983. Subsequent weekly ratings in *Septoria* plots were omitted due to the natural infection with *A. helianthi* rather than *S. helianthi* in both years. Plot mean scores of *Phoma* disease reaction were used for analyses. *Alternaria* and *Septoria* leaf blight data were converted to percent disease severity using Elanco Conversion Tables (Eli Lilly and Co., Indianapolis, Indiana). The Area Under Disease Progress Curve (AUDPC) for percent *Alternaria* leaf blight, percent *Septoria* leaf spot and percent *Sclerotinia* wilt was calculated as;

$$\text{AUDPC} = \sum_{i=1}^k 7(0.5(S_i + S_{i-1}))$$

where 7 = number of days in a week; S_i = severity of the disease at the end of the week; and k = number of successive readings of the disease. The third experiment was also planted in a randomized complete block design with two replications. In experiment III twenty plants per plot were planted and later thinned to ten with a distance of 30.8 cm from plant to plant. Agronomic traits, yield and its component data of plant height, days to flowering, head diameter, head weight, 200-seed weight, seeds per head and oil content were recorded in the same way as the 1982 yield trial experiment. Only three sunflower heads were used for head diameter measurements instead of five as in 1982.

In addition to these three experiments in 1983, a fourth experiment for plot seed yield was planted on June 3, 1983 near White, South Dakota. The 150 S1 families of each population were randomly assigned to 5 blocks of 30 families each. A replicates-within-blocks design was used. Each family was replicated three times. An experimental unit was a single row 6.9 m long with 76.9 cm between rows was planted for each family. Plots were overplanted and thinned to 25 plants per plot. The experiment was hand harvested and individual plot seed yield recorded and converted to seed yield (kg/ha) in the same way as in 1982.

Statistical Analyses

A separate analysis of variance and covariance was carried out for each experiment. Analyses of variance and covariance of experiments I and II of 1982, 1983 and of experiment III in 1983 were performed as outlined in Table 1. The 1982 yield trial (Experiment III) suffered considerable damage due to the "head clipping" weevil (*Haplorhynchites aeneus* Boh.) at late bud stage. Also heavy winds and rain prior to harvest caused lodging to some plots. Therefore, in both populations, plots with a minimum number of 13 plants per plot were included for 1982 agronomic data of experiment III. Thereby 2 plots in Gene Pool II and 7 in ND 761 were discarded for all agronomic traits except days to flower, plant height and oil content. Simple regression analysis was performed for each trait on the number of plants per plot in yield trial experiment during 1982. Plot seed yield in Gene Pool II, head diameter and plot seed yield in ND 761 were found to be

significantly affected by plant stand, therefore these traits were adjusted prior to the analyses by using the following equation;

$$Y' = Y - b(X - \bar{x})$$

where Y' = adjusted value of the Y trait; Y = observed value of the Y trait; b = regression coefficient of Y on X and; $(X - \bar{x})$ = deviation of number of plants in the plot from the over-all average number of plants.

Table 1 : Form of the analysis of variance and covariance of S1 families with r replications and f S1 families.

Source of variation	Degrees of freedom	Mean squares	Expected mean squares	Expected mean cross products
Total	$(fr-1)$			
Replication	$(r-1)$			
Families (S_1)	$(f-1)$	MS2	$\sigma^2_e + r \sigma^2_{S_1}$	$\sigma_{e_1 e_2} + r \sigma_{S_1 S_2}$
Error	$(r-1)(f-1)$	MS1	σ^2_e	$\sigma_{e_1 e_2}$

$$\sigma^2_{S_1} = \sigma^2_{\hat{A}}, \text{ if } \sigma^2_{\hat{D}} = 0, \sigma^2_{\hat{I}} = 0$$

$$\sigma^2_{\hat{P}} = MS2/r; \sigma^2_{\hat{G}} = (MS2 - MS1)/r; \text{ and } h^2 = \sigma^2_{\hat{G}} / \sigma^2_{\hat{P}}$$

The fourth experiment of 1983 suffered due to poor stands. Therefore in both populations, plots with a minimum number of ten plants per plot were included for seed yield. Forty-eight plots from GP II and 119 from ND 761 were discarded due to poor stands. The seed yield of each plot for this experiment was also adjusted for plant stand by the regression equation prior to the analysis. Data from missing plots were estimated by General Linear Model Procedure (SAS Institute Inc., Cary, North Carolina). One degree of freedom was subtracted from the degrees of freedom for total and error for each missing plot.

For the 1982 yield trial, the analysis of variance for agronomic traits and also adjusted plot seed yield in the 1983 experiment was carried out as shown in Table 2. The families/block mean squares or mean cross products within experiments were used for the estimation of genotypic and phenotypic variances or covariances respectively. Broad-sense heritabilities for S1 families on a plot mean basis were calculated as the ratio of the genetic variance to phenotypic variance. Standard errors of heritability on a plot mean basis were estimated by using the procedure described by Lothrop et al. (36).

Table 2 : Form of the analysis of variance and covariance for S1 families with b blocks, r replications per block, and f_i families in the ith block.

Source of variation	Degrees of freedom	Mean squares	Expected mean squares or Expected mean cross products
Total	$(r \sum f_i - 1)$		
Blocks	$(b-1)$		
Reps/Blocks	$b(r-1)$		
Families/Block	$\sum (f_i - 1)$	MS2	$\sigma_{e_{ij}}^2 + r\sigma_{g_{ij}}^2$
Error	$(r-1)\sum (f_i - 1)$	MS1	$\sigma_{e_{ij}}^2$

$\sigma_{g_{ij}}^2$ = additive genetic variance ($i=j$) or additive genetic covariance ($i \neq j$) and $\sigma_{e_{ij}}^2$ = environmental variance ($i=j$) or environmental covariance ($i \neq j$).

The genetic component of covariance for two traits measured in different experiments was estimated by the pooled, corrected sums of cross products of observed family means divided by families degrees of freedom. Hence the expected covariance of the observed family means due to common environmental effect is zero as noted by Kempthorne

(31). These same across-experiments covariance estimates were also taken as the phenotypic covariance of two traits measured in different experiments. Genetic correlations (r_g) were calculated for all pairs of traits with data from the 1982 and 1983 experiments. The formula used was:

$$r_g = \hat{\sigma}_{g_{xy}} / \sqrt{\hat{\sigma}^2_{g_x} \cdot \hat{\sigma}^2_{g_y}}$$

where $\hat{\sigma}_{g_{xy}}$ = the genetic covariance between traits x and y, $\hat{\sigma}^2_{g_x}$ = estimate of family genetic variance for trait x, and $\hat{\sigma}^2_{g_y}$ = estimate of family genetic variance for trait y. Phenotypic correlations were calculated in a similar way using phenotypic covariance and variances, respectively.

Estimates of the variance of genetic correlation coefficients within-experiments were calculated by the method of Tallis (58). The variance of across-experiments genetic correlation coefficients were estimated by taking out the environmental covariance from the above method, since there is no environmental covariance between experiments. The genetic variance and covariance estimates from both years of two traits were pooled separately for each population and pooled genetic correlation estimates obtained. Estimates of the variance of genetic correlation coefficients were calculated by the same method (58). However, pooled estimates of mean squares and mean cross-products were obtained by setting the expected mean squares and solving for the desired component. Heritabilities and genetic correlations estimates were considered significant if their absolute value exceeded twice their standard error.

RESULTS

Means, ranges and coefficients of variation (Tables 3 and 4) demonstrated that S1 families of Gene Pool II (GP II) and ND 761 populations contained large amounts of variability for all traits. Mean areas under disease progress curve for percent *Alternaria* leaf blight (AUDALT) and percent *Sclerotinia* wilt (AUDSCL) were greater in 1983 than 1982 in both populations. This was probably due to favorable conditions for development of these two diseases in 1983. However, a reduction in means of area under disease progress curve of percent *Septoria* leaf spot (AUDSEP), plant height, oil content, yield per hectare (yield/ha) and oil yield were evident in 1983. S1 families from ND 761 exhibited an increase in means for days to flower, plant height, head weight and seed weight in 1983.

F-tests of S1 family mean squares were significant at the 0.05 or 0.01 probability level for each trait and in each year in both GP II and ND 761, indicating that genetic variability existed among the S1 families in both sunflower populations for the traits measured. A direct statistical comparison of GP II and ND 761 is impossible since populations were planted in separate experiments.

Estimates of genetic variance for yield/ha were higher in 1982 than 1983 in both populations (Appendix A and B). Estimates of genetic variance for disease reaction to AUDALT and AUDSCL increased

Table 3 : Means, ranges and coefficients of variation (CV) of S1 families from Gene Pool II population grown during 1982 and 1983.

Traits*	Year 1982			Year 1983		
	Mean	Range	CV	Mean	Range	CV
AUDALT	1124.2	601.4-1963.3	14.8	1523.9	1006.2-2373.4	11.3
Phoma	2.6	1.3- 4.2	22.3	2.8	2.1- 3.9	12.5
AUDSEP	611.7	352.7- 918.8	14.9	275.0	127.1- 482.6	27.4
AUDSCL	707.9	181.3-1640.6	55.6	2321.4	1050.0-3345.0	26.2
FLWR	63.8	60.0- 72.0	1.8	64.4	59.0- 71.0	1.9
PLHT	165.6	120.2- 198.6	3.4	156.1	117.6- 185.7	3.6
HDIA	15.4	10.6- 21.4	6.9	16.1	12.5- 21.3	11.2
HDWT	34.6	9.0- 63.5	19.4	44.7	22.4- 78.5	25.0
SDWT	8.1	4.7- 13.1	11.4	10.3	6.2- 16.0	15.9
SDPHD	857.9	274.9-1465.1	16.2	878.4	432.0-1408.7	21.0
OIL	44.0	29.7- 53.4	4.6	36.9	30.7- 41.9	5.7
YLD	1055.4	225.4-2071.9	15.9	884.9	389.7-1297.6	21.8
OYLD	467.1	90.0- 916.2	16.5	326.9	136.1- 495.3	-

*AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, percent Septoria leaf spot and percent Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, OIL= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

Table 4 : Means, ranges and coefficients of variation (CV) of S1 families from ND 761 population grown during 1982 and 1983.

Traits*	Year 1982			Year 1983		
	Mean	Range	CV	Mean	Range	CV
AUDALT	813.0	500.3-1170.3	16.2	1410.3	932.3-2035.7	11.2
Phoma	2.5	0.8- 3.6	19.4	2.5	1.6- 3.4	13.7
AUDSEP	596.8	410.1- 853.1	13.4	244.1	106.5- 410.1	26.0
AUDSCL	368.8	21.9-1303.8	77.8	1455.3	125.0-2975.0	46.3
FLWR	66.2	62.0- 75.0	2.2	69.2	64.0- 77.5	1.5
PLHT	158.0	114.4- 196.1	4.1	161.2	122.3- 193.7	3.5
HDIA	16.5	12.9- 20.5	5.9	16.9	14.0- 20.2	8.0
HDWT	35.8	13.6- 61.5	17.1	44.2	18.0- 64.4	25.6
SDWT	7.7	4.9- 11.3	8.4	9.7	6.1- 15.7	12.6
SDPHD	929.6	399.9-1388.9	13.5	924.0	446.0-1520.8	23.4
OIL	41.3	32.2- 48.2	4.7	36.9	30.4- 43.1	5.9
YLD	1076.3	464.7-1745.1	15.8	1019.3	419.1-1674.4	21.3
OYLD	445.9	173.5- 725.7	16.6	379.1	157.9- 604.8	-

*AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, percent Septoria leaf spot and percent Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, OIL= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

from 1982 to 1983 in both populations, probably due to greater disease development as mentioned earlier. Environmental variance estimates were higher in 1983 than 1982 for all traits except for AUDSEP and Phoma black stem disease reaction.

The high estimates of genetic variance and low estimates of environmental variance in 1982 resulted in larger heritabilities estimates in 1982 than 1983 for both populations for yield/ha. Genetic and environmental variance estimates for AUDALT increased from 1982 to 1983 for both populations resulting in larger heritabilities in 1983. Estimates of broad-sense heritabilities were significant when compared with their respective standard errors. However, in 1983, heritability estimates for AUDSCL in GP II and head weight in ND 761 were non-significant. In general, heritability estimates of most traits in both populations were larger in 1982 than 1983. Highest heritability estimates in both years and in both populations were for plant height and days to flower (Appendix A and B). Among disease reaction traits, AUDALT had the highest heritability estimates (>0.66) in both years and populations.

Pooled genetic variance and heritability estimates were significant for all traits in GP II and ND 761 (Table 5). In GP II genetic variance estimates were larger than environmental variance for all traits except for Phoma and AUDSCL. However in ND 761 three disease ratings namely Phoma, AUDSEP and AUDSCL, and head weight had smaller genetic than environmental variances. Estimates of heritability were high (≥ 0.89) for plant height and days to flower in

Table 5 : Pooled estimates of genetic variance ($\hat{\sigma}^2_G$), environmental variance ($\hat{\sigma}^2_E$) and heritability (h^2) among S1 families of Gene Pool II and ND 761 populations.

Traits#	GENE POOL II			ND 761		
	$\hat{\sigma}^2_G$	$\hat{\sigma}^2_E$	h^2	$\hat{\sigma}^2_G$	$\hat{\sigma}^2_E$	h^2
AUDALT	40102.23**	14323.54	0.74+	26426.30**	10884.00	0.71+
Phoma	0.07**	0.12	0.39+	0.07*	0.08	0.44+
AUDSEP	3858.04**	3532.80	0.52+	2255.76**	2493.10	0.48+
AUDSCL	47979.18*	129315.35	0.27+	113397.73**	150701.49	0.43+
FLWR	4.30**	0.56	0.89+	6.91**	0.68	0.91+
PLHT	134.63**	12.60	0.91+	141.33**	14.83	0.91+
HDIA	0.91**	0.73	0.56+	0.65**	0.53	0.55+
HDWT	49.67**	28.39	0.64+	22.09*	30.77	0.42+
SDWT	1.54**	0.57	0.73+	1.35**	0.35	0.79+
SDPHD	21619.13**	9621.29	0.69+	19078.72**	11712.47	0.62+
OIL	3.34**	1.68	0.67+	3.07**	1.68	0.65+
YLD	39208.27**	10701.02	0.79+	17379.14**	12693.51	0.58+
OYLD	9674.68**	2167.03	0.82+	5051.08**	1993.77	0.72+

*,** Significant at 0.05 and 0.01 probability levels, respectively.

+ Heritability differ significantly from zero as its absolute magnitude exceeded twice its standard error.

#AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, percent Septoria leaf spot and percent Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, OIL= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

both populations compared to other traits in this study. Phoma and AUDSCL ratings showed low (<0.40) but significant heritabilities in GP II. Similarly, head weight, AUDSCL and Phoma also had low (<0.45) but significant heritabilities compared to other traits in ND 761.

Genetic correlations were greater than phenotypic correlations (Appendix C and D). However, genetic and phenotypic correlations were not consistent from year to year in both sunflower populations. These correlations varied in magnitude and as well as in direction for both years. However, in no case were genetic correlation coefficients judged to be significantly negative or positive in one year and the sign significantly reverse in the other year. Pooled estimates of genetic and phenotypic correlation coefficients for all traits studied in GP II and ND 761 are shown in Tables 6 and 7, respectively. Estimated pooled genotypic correlation coefficients tended to be larger than corresponding estimates of pooled phenotypic correlation coefficients for both populations. In GP II, negative and significant genetic correlations were present between yield/ha and AUDALT, yield/ha and AUDSEP; between oil yield and AUDALT, Phoma, and AUDSEP (Table 6). Yield/ha and oil yield were positively and significantly correlated with all agronomic traits except days to flower. However, days to flower was positively and significantly correlated with plant height, head weight, and seed per head. AUDALT was significantly and positively correlated with AUDSEP but negatively with head diameter, head weight, seed weight, yield/ha, and oil yield. Phoma was also negatively and significantly correlated with plant height, head weight,

Table 6 : Pooled estimates of genetic (above diagonal) and phenotypic (below diagonal) correlation coefficients of Gene Pool II population.

Traits#	AUDALT	Phoma	AUDSEP	AUDSCL	FLWR	PLHT	HDIA	HDWT	SDWT	SDPHD	OIL	YLD	OYLD
AUDALT		0.214	0.676*	0.166	-0.161	-0.191	-0.400*	-0.409*	-0.301*	-0.229	-0.109	-0.452*	-0.396*
Phoma	0.154		0.204	0.295	-0.150	-0.326*	-0.204	-0.365*	-0.223	-0.251	-0.271	-0.324	-0.328*
AUDSEP	0.419	0.092		0.166	-0.043	-0.000	-0.316	-0.253	-0.207	-0.160	-0.181	-0.326*	-0.313*
AUDSCL	0.074	0.096	0.142		-0.372	-0.191	0.099	-0.160	-0.040	-0.162	-0.071	-0.236	-0.223
FLWR	-0.130	-0.088	-0.029	-0.182		0.619*	0.220	0.282*	-0.150	0.408*	-0.002	0.173	0.153
PLHT	-0.157	-0.194	-0.000	-0.095	0.558		0.605*	0.666*	0.191	0.579*	0.192	0.518*	0.477*
HDIA	-0.256	-0.095	-0.170	0.038	0.157	0.412		0.889*	0.255	0.853*	0.123	0.866*	0.769*
HDWT	-0.280	-0.181	-0.146	-0.066	0.222	0.516	0.688		0.525*	0.755*	0.303*	0.863*	0.805*
SDWT	-0.221	-0.119	-0.128	-0.018	-0.124	0.147	0.234	0.502		-0.200	0.159	0.538*	0.471*
SDPHD	-0.164	-0.130	-0.096	-0.070	0.328	0.473	0.619	0.759	-0.169		0.250	0.632*	0.611*
OIL	-0.076	-0.138	-0.107	-0.030	-0.010	0.169	0.077	0.262	0.142	0.213		0.399*	0.583*
YLD	-0.344	-0.179	-0.209	-0.109	0.143	0.443	0.564	0.662	0.402	0.510	0.296		1.113*
OYLD	-0.307	-0.185	-0.205	-0.105	0.127	0.420	0.505	0.633	0.360	0.505	0.501	1.046	

*Correlation coefficients differ significantly from zero as its absolute magnitude exceeded twice its standard error.
 #AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, percent Septoria leaf spot and percent Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, OIL= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

and oil yield. Plant height was strongly and positively correlated with head diameter, head weight, seed per head, yield/ha, and oil yield. Similarly head diameter was genetically correlated with head weight, seed per head, yield/ha, and oil yield. There were significant positive genotypic correlations between head weight and seed weight, seed per head, oil content, yield/ha, and oil yield. Seed weight, seed per head, and oil content were positively and significantly correlated with yield/ha and oil yield, respectively. The correlation between yield/ha and oil yield was positive and significant but greater than one. Phenotypically, all four disease ratings were negatively correlated with all agronomic traits except AUDSCL disease reaction which was positively correlated with head diameter. However yield/ha and oil yield were positively phenotypically correlated with all agronomic traits in this study.

The pooled estimate of genetic correlations in ND 761 population (Table 7) were significant and positive between AUPSEP and AUDALT, AUDSCL, and plant height; between Phoma and head diameter; between plant height and days to flower, head weight, and seed per head; and between head diameter and head weight, seed per head, yield/ha, and oil yield. Genetic correlations were also positive and significant between head weight and seed per head, yield/ha, and oil yield; between seed per head and yield/ha, and oil yield and finally between oil yield and oil content, and yield/ha. There were significant and negative genetic correlations between days to flower and AUDALT and seed weight; and between seed weight and seed per head.

Table 7 : Pooled estimates of genetic (above diagonal) and phenotypic (below diagonal) correlation coefficients of ND 761 population.

Traits#	AUDALT	Phoma	AUDSEP	AUDSCL	FLWR	PLHT	HDIA	HDWT	SDWT	SDPHD	OIL	YLD	OYLD
AUDALT		0.087	0.600*	0.172	-0.350*	0.235	0.221	0.071	-0.061	0.117	-0.007	-0.049	-0.044
Phoma	0.089		0.066	0.376	-0.203	-0.006	0.395*	0.219	0.189	0.047	-0.000	0.250	0.193
AUDSEP	0.348	0.030		0.412*	0.117	0.589*	0.156	0.181	0.156	0.028	-0.334	0.018	-0.040
AUDSCL	0.095	0.164	0.295		-0.058	0.018	-0.078	0.124	0.269	-0.159	-0.151	0.074	0.032
FLWR	-0.281	-0.129	0.077	-0.036		0.464*	-0.102	0.060	-0.268*	0.240	-0.271	-0.167	-0.149
PLHT	0.188	-0.004	0.386	0.011	0.410		0.105	0.481*	-0.031	0.386*	0.005	0.229	0.182
HDIA	0.138	0.196	0.080	-0.038	-0.088	0.069		0.748*	0.316	0.619*	-0.152	0.744*	0.462*
HDWT	0.039	0.095	0.081	0.052	0.023	0.300	0.522		0.207	0.761*	0.062	0.886*	0.645*
SDWT	-0.046	0.112	0.096	0.157	-0.225	-0.032	0.195	0.235		-0.569*	0.103	0.312	0.253
SDPHD	0.077	0.025	0.015	-0.082	0.175	0.301	0.417	0.761	-0.438		-0.039	0.620*	0.435*
OIL	-0.005	-0.000	-0.185	-0.079	-0.220	0.032	-0.156	0.029	0.063	-0.018		0.144	0.439*
YLD	-0.031	0.127	0.009	0.037	-0.121	0.200	0.366	0.516	0.167	0.409	0.078		1.363*
OYLD	-0.031	0.109	-0.023	0.018	-0.124	0.189	0.237	0.442	0.157	0.338	0.373	1.095	

*Correlation coefficients differ significantly from zero as its absolute magnitude exceeded twice its standard error.
 #AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, percent Septoria leaf spot and percent Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, OIL= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

In general, there were fewer significant genotypic correlations coefficients in ND 761 than GP II. Phenotypically, AUDALT was negatively correlated with days to flower and to lesser degree with seed weight, oil content, yield/ha, and oil yield. Phoma reaction also was negatively phenotypically correlated with days to flower, and plant height. AUDSCL was negatively phenotypically correlated with days to flower, head diameter, seed per head, and oil content. Oil content and oil yield also were negatively phenotypically correlated with AUDSEP.

Estimates of genetic covariances for all pairs of traits, except Phoma with head diameter in GP II and phoma with seed weight in ND 761 differed from year 1982 to 1983 (Appendix E and F). Genetic covariances in 1982 were greater in value than in 1983 for most of the traits measured in this study. Gene Pool II had greater genetic covariances between yield components and yield/ha, and oil yield in 1982 than 1983. A similar trend was observed in ND 761 except for oil content. In general, phenotypic covariances were greater than the genotypic covariances in both years and in both populations. Also, phenotypic covariances were larger in 1982 than 1983 for both populations with most of the traits. The direction of signs for genotypic and phenotypic covariances are reflected from their respective genotypic and phenotypic correlation coefficients.

Pooled estimates of genetic and phenotypic covariances between disease reactions and agronomic traits in GP II and ND 761 are shown in Table 8 and 9, respectively. Phenotypic covariances were larger than genetic covariances for most traits in both populations.

Table 8: Pooled estimates of genetic (above diagonal) and phenotypic (below diagonal) covariances of Gene Pool II population.

Traits#	AUDALT	PHOMA	AUDSEP	AUDSCL	FLWR	PLHT	HDIA	HDWT	SDWT	SDPHD	OIL	YLD	OYLD
AUDALT		11.63	8410.49	7257.73	-67.04	-443.79	-76.26	-577.71	-74.84	-6751.02	-39.94	-17907.32	-7796.85
Phoma	15.62		3.45	17.52	-0.09	-1.03	-0.05	-0.70	-0.08	-10.00	-0.14	-17.43	-8.76
AUDSEP	8410.49	3.45		2255.65	-5.54	-0.24	-18.69	-110.53	-15.94	-1457.99	-20.51	-4011.91	-1914.05
AUDSCL	7257.73	17.52	5121.58		-168.87	-484.70	20.62	-247.06	-10.78	-5220.21	-28.55	-10227.23	-4808.40
FLWR	-67.04	-0.09	-5.54	-168.87		14.90	0.44	4.12	-0.39	124.58	-0.01	71.18	31.17
PLHT	-443.79	-1.03	-0.24	-484.70	14.92		6.69	54.46	2.75	987.52	4.06	1189.66	544.10
HDIA	-76.26	-0.05	-18.69	20.62	0.44	6.39		5.98	0.30	119.61	0.21	163.45	72.12
HDWT	-577.71	-0.70	-110.53	-247.06	4.32	55.27	7.77		4.60	782.37	3.91	1204.84	558.02
SDWT	-74.84	-0.08	-15.94	-10.78	-0.40	2.58	0.43	6.44		-36.48	0.36	132.32	57.53
SDPHD	-6751.02	-10.00	-1457.99	-5220.21	127.69	1013.69	139.74	1185.48	-43.32		67.18	18385.49	8836.21
OIL	-39.94	-0.14	-20.51	-28.55	-0.05	4.58	0.22	5.18	0.46	84.41		144.49	104.83
YLD	-17907.32	-17.43	-4011.91	-10227.23	70.43	1201.12	160.98	1305.86	130.54	20154.18	148.26		21671.45
OYLD	-7796.85	-8.76	-1914.05	-4808.40	30.45	555.16	70.19	608.13	56.90	9717.99	122.14	25424.99	

#AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, percent Septoria leaf spot and percent Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, OIL= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

Table 9: Pooled estimates of genetic (above diagonal) and phenotypic (below diagonal) covariances of ND 761 population.

Traits#	AUDALT	PHOMA	AUDSEP	AUDSCL	FLWR	PLHT	HDIA	HDWT	SDWT	SDPHD	OIL	YLD	OYLD
AUDALT		3.66	4633.30	9408.02	-149.61	454.71	28.93	54.47	-11.50	2623.27	-1.90	-1049.25	-509.40
Phoma	6.65		0.81	32.55	-0.14	-0.02	0.08	0.27	0.06	1.66	-0.00	8.47	3.53
AUDSEP	4633.30	0.81		6586.08	14.66	332.44	5.96	40.33	8.59	183.84	-27.79	110.04	-133.56
AUDSCL	9408.02	32.55	10434.99		-51.16	73.21	-21.25	195.51	105.27	-7402.64	-88.79	3299.96	757.84
FLWR	-149.61	-0.14	14.66	-51.16		14.51	-0.22	0.74	-0.82	87.24	-1.25	-57.76	-27.90
PLHT	454.71	-0.02	332.44	73.21	14.11		1.00	26.89	-0.42	632.99	0.10	359.29	154.05
HDIA	28.93	0.08	5.96	-21.25	-0.26	0.94		2.83	0.30	68.81	-0.21	78.92	26.43
HDWT	54.47	0.27	40.33	195.51	0.45	27.29	4.11		1.13	494.34	0.51	549.19	215.42
SDWT	-11.50	0.06	8.59	105.27	-0.81	-0.51	0.28	2.23		-91.29	0.21	47.82	20.93
SDPHD	2623.27	1.66	183.84	-7402.64	84.69	660.85	79.29	970.28	-100.34		-9.32	11294.09	4270.49
OIL	-1.90	-0.00	-27.79	-88.79	-1.32	0.87	-0.37	0.46	0.18	-6.70		33.19	54.59
YLD	-1049.25	8.47	110.04	3299.96	-57.93	433.58	68.87	650.81	37.73	12431.74	29.40		12767.82
OYLD	-509.40	3.53	-133.56	757.84	-28.70	198.50	21.60	269.98	17.15	4979.29	68.17	15935.79	

#AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, percent Septoria leaf spot and percent Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, OIL= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

Phenotypic covariances between experiments are the same as genetic covariances, since the expected covariances of the observed S1 family means due to common environmental effect is zero. Therefore, the same across-experiments covariance estimates were taken as the phenotypic covariance of two traits measured in different experiments.

DISCUSSION

Genetic variances are relevant to population improvement projects. For quantitative traits, these are the most sensitive general measures of gene action that are estimable. These estimates pertain to a population from which the experimental material is a sample. Therefore, estimates from one population may not apply to another. In our study pooled genetic variances in GP II were comparatively higher than in ND 761 for all traits except AUDSCL and days to flower. The higher genetic variances in GP II may be due to greater diversity in its germplasm compared to ND 761. However, both populations showed higher genetic variance for AUDSCL and AUDALT diseases, yield/ha, and seed per head compared to other traits measured in this study. The genetic variance of sclerotinia resistance has also been observed to be high by Vranceanu et al. (63). In contrast, Phoma in our study had a smaller but similar genetic variance in both populations. This may be due to the scale used in measuring Phoma disease reaction.

Heritability estimates in the narrow-sense are useful in predicting progress from selection. Narrow-sense heritability is the ratio of the additive genetic variance to the phenotypic variance. Reliable estimates of additive genetic variance cannot be obtained from this study, therefore broad-sense heritabilities on a family mean basis were calculated. These broad-sense heritabilities are the only useful estimates for predicting direct and correlated responses in S1 family

selection schemes. Also, the heritability term must be introduced by a statement of the material and selection unit upon which the heritability is based. Therefore these estimates vary from one experimental material to another. Heritability estimates for all traits in this study were significant in both populations due to significant genotypic variance among S1 families for most traits. Moreover, different sets of S1 families were used in each year of this two year study, therefore genotype-environment interaction variance cannot be estimated. The genotype-environment interaction can bias genetic variance estimates upward, resulting in their over estimation. In GP II, significant but low heritabilities of 0.27 and 0.39 were observed for AUDSCL and Phoma, respectively. This is in disagreement with Fick et al. (17) who observed high heritability for Sclerotinia resistance. The cause for this disagreement may be due to use of different male and female hybrids in their study. High estimates of heritability (≥ 0.89) for plant height and days to flower in both sunflower populations were in agreement with findings of Oka and Campos (43), Shabana (53), and Ivanon and Stoyanova (30). Other high heritabilities (> 0.60) in GP II were for oil yield, yield/ha, AUDALT, seed weight, seed per head, oil content and head weight. Omran et al. (44) also found relatively high heritabilities for yield and its components including oil content. They indicated that most of the variability among cultivars in their study was due to genetic causes. Our results also agree with Vol'f and Dumacheva (62) as they indicated high heritabilities for oil content and seed weight. There were also significant and high heritabilities (> 0.60) for seed weight, oil yield, AUDALT, oil content and seed per head in

ND 761.

Estimates of genetic covariance for most of the traits in GP II and ND 761 differ markedly from year to year, probably indicating an interaction of covariance with different environments. Since the covariances from different years were estimated on different S1 families it is impossible to attribute the differences in the genetic covariance estimates solely to genetic differences or to genotype-environment interaction. Across experiments covariance estimates were taken as estimates of both genetic and phenotypic covariance since the environmental covariance for two traits measured in different experiments is expected to be zero. There was a consistent pattern in the sign of the pooled genetic covariance between reaction to different diseases and yield, and its components in GP II. However, there was no consistent pattern in sign in the pooled genetic covariances for ND 761.

Knowledge about genotypic and phenotypic correlations among and between disease reactions and agronomic traits is important as it permits estimation of the feasibility of indirect selection for yield with disease resistance. Pooled estimated genotypic correlations coefficients in our study tended to be larger than their corresponding pooled estimates of phenotypic correlation coefficients. This tendency was the result of the estimated genotypic variances typically being smaller than corresponding phenotypic estimates. Significant positive genetic correlations of AUDALT with AUDSEP were found in both populations. These were expected from a review of the literature (8,22,65).

However, correlations reported in literature were phenotypic rather than genetic in nature. The strong genetic correlation between these two foliar diseases suggest the use of an either pathogen in disease resistance. In such cases it's desirable to use *A. helianthi* rather than *S. helianthi* since the latter is considered a less important pathogen. Another positive and significant genetic correlation was between AUDSEP and AUDSCL in ND 761. This indicates that selection against one pathogen will indirectly be effective against the other in ND 761, since AUDALT is correlated with AUDSEP and AUDSEP with AUDSCL. These correlations cannot be attributed solely to a genetic association between resistance to the different diseases although a general increase in plant vigor would be expected to result in a reduction in symptoms for these diseases. In both sunflower populations, no significant genetic correlation was observed between AUDSCL and agronomic traits. This lack of association has also been reported by other researchers (16,63,64). The pooled genetic correlations of oil content with reaction to four diseases in both populations were negative and non-significant, indicating that selection for resistance to these diseases should have no marked effect on oil content.

Pooled genetic correlations of yield/ha with reaction to AUDALT and AUDSEP diseases in GP II were negative and significant, indicating that low disease score or high resistance is associated with high yield. The genetic correlations between AUDALT disease and head diameter, head weight, seed weight, oil yield were also negative and significant. This trend was also observed between Phoma and plant

height, head weight, and oil yield; and between AUDSEP and oil yield. These genetic correlations suggest that improvement of these agronomic traits in addition to low disease scores are possible. The significant positive genotypic correlations between yield/ha and agronomic traits except days to flower were expected from a review of the literature (30,45,46,48). These references only reported phenotypic correlations. The genetic correlations of yield with agronomic traits reported by Tyagi (59) and Lakshmanrao et al. (34) are in close agreement with these results. Therefore, we can conclude that most of the variation in yield can be attributed to its agronomic traits except days to flower. Days to flower was positively significantly correlated with plant height, head weight, seeds per head, and oil yield. The positive significant correlations between plant height and head diameter, head weight, seeds per head, and oil yield were similar to the findings of Tyagi (59). Head diameter was genetically strongly correlated with head weight, seeds per head, and oil yield indicating that plants with larger heads contribute more yield and have more seeds (59,67). Head weight had positive and significant genetic correlation with all agronomic traits in GP II. Similarly, seed weight, seeds per head, oil content and yield/ha were significantly and positively correlated with oil yield.

None of the pooled estimates of genetic correlation coefficients of yield/ha with reactions to the four diseases in ND 761 were significantly different from zero. This provides strong evidence that resistance to these four diseases (AUDALT, Phoma, AUDSEP and AUDSCL) in ND 761 is inherited independently of yield. The pooled

genetic correlation of AUDALT with days to flower was negative and significant, indicating that resistance to *Alternaria* blight is associated with late maturity. The only positive significant genetic correlations between disease traits and agronomic traits for ND 761 were between Phoma and head diameter; and between AUDSEP and plant height. Days to flower was negatively and significantly correlated with seed weight but significantly and positively with plant height. This indicates that earliness is associated with increased seed weight and reduced plant height. Plant height was also positively and significantly correlated with head weight, and seed per head. In the literature, positive correlations between plant height and number of days to flowering (43), number of seeds per head (59) are evident. Head weight was positively significantly genetically correlated with seeds per head, yield/ha, and oil yield. Seed weight was negatively and significantly genetically correlated with seeds per head, indicating that a decrease in the number of seeds per head results in increased seed weight. This negative association is in conformity with the results of Tyagi (59). Significant positive genetic correlations were also found between oil yield, oil content, and yield/ha.

In conclusion, pooled estimates of heritabilities for all traits in both populations were significant. These estimates will be useful in determining the best methods of selection to improve these populations for specific traits. Genetic correlations among traits are of primary interest to plant breeders. They indicate the correlated responses that may occur when multiple trait selection is practiced. Knowledge of

genetic correlations is also helpful in identifying traits that have little or no importance in a selection program. However, unfavorable genotypic correlations between traits selected for in a breeding program may result in a reduction in the rate of improvement for some of the traits in comparison to responses that could be attained if the correlations were zero or in a favorable direction. The practical utility of selecting a primary trait as a means of improving secondary trait(s) largely depends on the extent to which improvement of the primary trait is facilitated by selection. Such improvement not only depends on the genotypic correlations but also on the genotypic and phenotypic variances and phenotypic correlations of all the traits included in the selection strategies. In this study resistance to AUDALT is genetically significantly correlated with AUDSEP; and Phoma is positively non-significantly correlated with AUDALT, AUDSEP and AUDSCL in both populations. This positive association among disease reactions indicates that populations with multiple disease resistance can be readily developed.

In GP II, there were favorable and significant genetic correlations of yield/ha with resistance to AUDALT, AUDSEP, and other agronomic traits (except days to flower). This indicates a large correlated response from selection between yield and disease resistance. Therefore, these favorable associations provide the possibility of direct selection of yield and its components with low disease scores against two foliar pathogens. Lack of significant correlations between disease reaction and yield/ha or oil content in ND 761 suggest that improvement

of yield without unfavorable correlated responses in disease reactions is possible.

LITERATURE CITED

- (1) Abd-El-Moneem, S. (1964). Effect of plant density on yield and disease reactions of sunflower in different soils. *Water Inf. Bull.* 7: 4-9. Res. Station for Sunflower No. 4-12-15.
- (2) Agrawal, J.M., U.S., G.P., and C.J. Hanson. (1955). Screening of sunflower genotypes against *Sclerotinia sclerotiorum*. *Indian J. Agric. & Plant Pathol.* 3: 103-16.
- (3) Alexander, O.E. (1951). The "Lyonska Method" of determining the content of the sunflower. *Genet. Sel.* 3: 273-293.
- (4) Allen, S.W., J.K., Finkner, and J.P. Brown. (1955). Losses in sunflower yield caused by *Sclerotinia sclerotiorum* in Spackey Queensland. *Australian Jour. Agric. Res.* 2: 121-131.
- (5) Anandachari, V., and S.M. Karalava. (1955). Identifying forms of sunflower resistant to *Sclerotinia sclerotiorum* and *Ascochyta blight*. *Madras Agricul. Jour.* 17, (1955), 1955. 1955. 1955.
- (6) Balasubramanyam, N., and S.J. Kaul. (1950). Effect of different densities on sunflower yield and on incidence of *Sclerotinia sclerotiorum*. *J. Agric. Sci. Camb.* 1: 34-37.
- (7) Carson, M.C. (1955). Relationship and yield yield associated with *Sclerotinia sclerotiorum* of sunflower. *Phytopathology* 45: 119-121.
- (8) Carson, M.C. (1955). Resistance of sunflower to *Sclerotinia sclerotiorum* in the field. *Phytopathology* 45: 222-223.
- (9) Carson, M.C., and A.L. Brown. (1951). Importance of resistance to *Sclerotinia sclerotiorum* in sunflower. *Phytopathology* 41: 115-118.
- (10) Dey, S.P., J.R. Verma, and T.J. Datta. (1954). Transfers regarding the 10 forms of sunflower. p. 4-7. *Proc. National Res. Institute, Ind. J. Agri. Sci.* 1954. 1954. 1954.
- (11) Dey, S.P., and H.C. Singh. (1955). Influence of maturity on yield and yield components of sunflower raised at different stages of development. *Genet. Sel.* 7: 10-12.
- (12) Dey, S.P., and T.J. Datta. (1954). Correlation of yield and

LITERATURE CITED

- (1) Abd-Elkreem, S., B.A. Elahmar, H. Galal, and M.A. Gazala. 1983. Inheritance of oil content in sunflower seeds. *Helia: Inf. Bull. F.A.O. Res. Network on Sunflower No.6:13-16.*
- (2) Agrawat, J.M., H.P. Chhipa, and S.J. Mathur. 1979. Screening of sunflower germplasm against *Alternaria helianthi*. *Indian J. Mycol. & Plant Pathol.* 9:85-86.
- (3) Alexander, D.E. 1963. The "Lysenko Method" of increasing oil content of the sunflower. *Crop Sci.* 3:279-280.
- (4) Allen, S.J., J.K. Kochman, and J.F. Brown. 1981. Losses in sunflower yield caused by *Alternaria helianthi* in Southern Queensland. *Aust. J. Agric. Anim. Husb.* 21:98-100.
- (5) Anashchenko, A.V., and R.M. Kosheleva. 1984. Identifying forms of sunflower resistant to *Sclerotinia sclerotiorum* and *Botrytis cinerea*. *Maslichnye kul'tury No.1:5-6 (Pl. Breed. Abst. 54:Abstr. 3539:1984).*
- (6) Balasubrahmanyam, N., and S.J. Kolte. 1980. Effect of different intensities of *Alternaria* blight on yield and oil content of sunflower. *J. Agric. Sci. (Camb.)* 94:749-751.
- (7) Carson, M.L. 1985. Epidemiology and yield losses associated with *Alternaria* blight of sunflower. *Phytopathology* 75:1151-1156.
- (8) Carson, M.L. 1985. Reactions of sunflower inbred lines to two foliar diseases. *Plant Disease* 69:986-988.
- (9) Carson, M.L., and A.L. Hooker. 1981. Inheritance of resistance to stalk rot of corn caused by *Colletotrichum graminicola*. *Phytopathology* 71:1190-1196.
- (10) Donald, P.A., J.R. Venette, and T.J. Gulya. 1984. Premature ripening due to *Phoma* girdling. p 6-7. *Proc. Sunflower Res. Workshop, Dec. 10-11, Natl. Sunflower Assoc., Bismarck, North Dakota.*
- (11) Dorrell, D.G., and H.C. Huang. 1978. Influence of sclerotinia wilt on seed yield and quality of sunflower wilted at different stages of development. *Crop Sci.* 18:974-976.
- (12) Dua, R.P., and T.P. Yadava. 1985. Genetics of seed yield and

- its components in sunflower (*Helianthus annuus* L.). P. 627-632. Proc. 11th Inter. Sunflower Conf., MarDel Plata, Argentina.
- (13) Dueck, J., and S.J. Campbell. 1978. Resistance to *Sclerotinia sclerotiorum* (Lib.) de Bary in sunflower. p 305-310. Proc. 8th Inter. Sunflower Conf., Minneapolis, Minnesota.
- (14) Fick, G.N. 1975. Heritability of oil content in sunflowers. *Crop Sci.* 15:77-78.
- (15) Fick, G.N., D.E. Zimmer, and D.C. Zimmerman. 1974. Correlation of seed oil content in sunflowers with other plant and seed characteristics. *Crop Sci.* 14:755-757.
- (16) Fick, G.N., and T.J. Gulya. 1980. Occurrence of sclerotinia wilt of sunflower and preliminary results on breeding for resistance. p.83-87. Proc. 9th Inter. Sunflower Conf., Malaga, Spain.
- (17) Fick, G.N., T.J. Gulya, and G.E. Auwater. 1983. Inheritance of sclerotinia wilt resistance in sunflower. p 21-22. Proc. Sunflower Res. Workshop, January 26. Natl. Sunflower Assoc., Bismarck, North Dakota.
- (18) Ghanavati, N.A., E. Nahavandi, and A. Ghaderi. 1981. Breeding sunflower for semi-arid regions. *Agric. Sci. (Camb.)* 96:447-450.
- (19) Gulya, T., J.S. Baumer, and N.V.R.R. Urs. 1984. Sclerotinia stalk rot resistance in today's commercial sunflower hybrids. p 14. Proc. Sunflower Res. Workshop. Feb.1, National Sunflower Assoc., Bismarck, North Dakota.
- (20) Gulya, T.J., and R.A. MacArthur. 1984. Incidence and severity of sunflower diseases in the Dakotas and Minnesota during the 1984 growing season. Proc. Sunflower Res. Workshop, Dec. 10-11, p.6., National Sunflower Assoc., Bismarck, North Dakota.
- (21) Gulya, T.J., and V.J. Jons. 1981. Incidence of sclerotinia stalk rot of sunflower in the Dakotas and Minnesota. *Phytopathology* 71:221 (Abstr.).
- (22) Habowa, B., W. Roath, P. Lapoint, and G. Ravagnon. 1985. Results of a S2 test cross recurrent selection technique on yield improvement of three sunflower (*Helianthus annuus* L.) populations from the upland tropics of Zambia (Abstr.). p 659. Proc. 11th Inter. Sunflower Conf., MarDel Plata, Argentina.
- (23) Hargitay, L. 1982. The susceptibility of different varieties and hybrids of sunflower to *Sclerotinia sclerotiorum* (Lib) de Bary.

- (23) Novenyvedelem 18:359-361 (Rev. Plant Path.62:Abstr. 1608:1983).
- (24) Herr, L.J. and P.E. Lipps. 1981. Occurrence of *Alternaria helianthi* on sunflower in Ohio. *Phytopathology* 71:880 (Abstr.).
- (25) Hoes, J.A., and E.D. Putt. 1964. Diseases of sunflowers in Western Canada in 1964. *Can. Plant Dis. Surv.* 44:236-237.
- (26) Hoes, J.A., and H.C. Huang. 1980. Effect of population density on development of *Sclerotinia* wilt and yield of sunflower. p 275-280. *Proc. 9th Inter. Sunflower Conf., Malaga, Spain.*
- (27) Horsfall, J.G., and R.W. Barratt. 1945. An improved grading system for measuring plant diseases. *Phytopathology* 35:655 (Abstr.).
- (28) Huang, H.C., and D.G. Dorrell. 1978 Screening sunflower seedlings for resistance to toxic metabolites produced by *Sclerotinia sclerotiorum*. *Can. J. Pl. Sci.* 58:1107-1110.
- (29) Islam, U., A. Maric, L. Cuk, and D. Skoric. 1976. Studies on leaf, stem and head spotting of sunflower caused by *Alternaria helianthi* in Yugoslavia. p.140-141. *Proc. 7th Inter. Sunflower Conf., Krasnodar, USSR.*
- (30) Ivanon, P., and Y. Stoyanova. 1980. Studies on the genotypic and phenotypic variability and some correlations in sunflower (*Helianthus annuus* L.). p. 336-342. *Proc. 9th Inter. Sunflower Conf., Malaga, Spain.*
- (31) Kempthorne, O. 1969. An introduction to genetic statistics. The Iowa State University Press, Ames, Iowa. p. 267.
- (32) Kloczowski, Z. 1974. Correlations of some features in the breeding material of sunflower variety Wielkopolski. p.321-324. *Proc. 6th Inter. Sunflower Conf., Bucharest, Romania.*
- (33) Kolte, S.J., B. Singh, and A.N. Tewari. 1976. Evaluation of sunflower genotypes for resistance to *Sclerotinia sclerotiorum*. *Indian J. Mycol. & Pl. Pathol.* 6:65-67.
- (34) Lakshmanrao, N.G., K.G. Shambulingappa, and P. Kusumakumari. 1985. Studies on path-coefficient analysis in sunflower. p 733-736. *Proc. 11th Inter. Sunflower Conf., MarDel Plata, Argentina.*
- (35) Leclercq, P. 1973. Effect of hereditary factors on the apparent resistance of sunflower to *Sclerotinia sclerotiorum*. *Annales de l'Amelioration des Plantes.* 23:279-286. (Rev. Pl. Path. 55:Abstr. 3246:1976).

- (36) Lothrop, J.E., R.E. Atkins, and O.S. Smith. 1985. Variability for yield and yield components in IAPIR grain sorghum random-mating population. I. Means, variance components, and heritabilities. *Crop Sci.* 25:235-240.
- (37) Mancl, M.K., and S.E. Shein. 1982. Field inoculation of sunflower for *Sclerotinia sclerotiorum* basal stalk rot and virulence of isolates from various hosts. p 167-170. Proc. 10th Inter. Sunflower conf., Surfers Paradise, Australia.
- (38) Marinkovic, R. 1982. Inheritance of plant height and leaf number in diallel crossings of sunflower inbreds. p 232-233. Proc. 10th Inter. Sunflower Conf., Surfers Paradise, Australia.
- (39) McDonald, W.C. 1964. Phoma black stem of sunflowers. *Phytopathology* 54:492-493.
- (40) Morris, J.B., S.M. Yang, and L. Wilson. 1983. Reaction of *Helianthus* species to *Alternaria helianthi*. *Plant Disease* 67:539-540.
- (41) Mungai, P.D. 1976. Correlation between head diameter, kernel percentage and oil content in sunflower (Abstr.). p.76. 7th Inter. Sunflower Conf., June 27-July 3, Krasnodar, USSR.
- (42) Nikolic-Vig, V., D. Skoric, and S. Bedov. 1971. Variability of oil and husk content in the sunflower seed of Peredovik and Vniimk 8931 varietal populations and their heritability. *Contemporary Agric.* 19:23-32.
- (43) Oka, H.I., and F.F. Campos. 1974. Breeding behavior and genetic variations of sunflowers observed in Central Luzon. *SABRAO Jour.* 6:61-67.
- (44) Omran, A.O., A.M. Abol-Zahab, and M.A. Haikal. 1976. Evaluation of sunflower cultivars. I. Heritability and variability of metric traits (Abstr.). p 59-60. Proc. 7th Inter. Sunflower Conf., Krasnodar, USSR.
- (45) Pathak, R.S. 1974. Yield components in sunflower. p.271-281. Proc. 6th Int. Sunflower Conf., July 22-24, Bucharest, Romania.
- (46) Pathak, A.R., M.U. Kukadia, and B.A. Kunadia. 1983. Path-coefficient analysis in sunflower. *Indian J. Agric. Sci.* 53:607-608.
- (47) Pustovojt, G.V. 1968. Breeding sunflowers resistant to *Sclerotinia*. *Sel'skhoz Biol.* 3:91-95 (Pl. Breed. Abst. 38:Abstr.6717:1968).
- (48) Putt, E.D. 1943. Association of seed yield and oil content with

- other characters in the sunflower. *Sci. Agric.* 23:377.
- (49) Putt, E.D. 1958. Note on differences in susceptibility to Sclerotinia wilt in sunflowers. *Can. J. Plant Sci.* 38:380-381.
- (50) Reddy, P.C., and B.M. Gupta. 1977. Disease loss appraisal due to leaf blight of sunflower indicated by *Alternaria helianthi*. *Indian Phytopathology* 30:569-570.
- (51) Ross, A.M. 1939. Some morphological characters of *Helianthus annuus* and their relationship to the yield of seed and oil. *Sci. Agric.* 19:372.
- (52) Russell, W.A. 1953. A study of the inter-relationships of seed yield, oil content, and other agronomic characters with sunflower inbred lines and their top crosses. *Canad. J. Agric. Sci.* 33:291-314.
- (53) Shabana, R. 1974. Genetic variability of sunflower varieties and inbred lines. p.263-269. *Proc. 6th Inter. Sunflower Conf.*, Bucharest, Romania.
- (54) Shane, W.W., J.S. Baumer, and S.G. Sederstrom. 1981. *Alternaria helianthi*: a pathogen of sunflower new to Minnesota. *Plant Disease* 65:269-271.
- (55) Shinde, Y.M., M.J. Wattamwat, and G.D. Patil. 1983. Variability and correlation studies in sunflower. *J. Maharashtra Agric. Univ.* 8:122-123.
- (56) Skoric, D. 1974. Correlation among the most important characters of sunflower in F1 generation. p.283-289. *Proc. 6th Inter. Sunflower Conf.*, July 22-24, Bucharest, Romania.
- (57) Skoric, D. 1976. Mode of inheritance of oil content in sunflower seed of F1 generation and component of genetic variability (Abstr.). p 60-61. *Proc. 7th Inter. Sunflower conf.*, Krasnodar, USSR.
- (58) Tallis, G.M. 1959. Sampling errors of genetic correlation coefficients calculated from analyses of variance and covariance. *Aust. J. Stat.* 1:35-43.
- (59) Tyagi, A.P. 1985. Association and path analysis of field components and oil percentage in sunflower (*Helianthus annuus* L.). p 807-812. *Proc. 11th Inter. Sunflower Conf.*, MarDel Plata, Argentina.
- (60) Urs, N.V.R.R., J. Lofgren, and W. Harada. 1983. Sclerotinia resistance: Problems and progress. p 22. *Proc. Sunflower Res. Workshop*, January 26. *Natl. Sunflower Assoc.*, Bismarck, North

Dakota.

- (61) Vol'f, F.G., and A.N. Kas'Yanenko. 1972. inheritance of character in a sunflower population. Selktsiya i Semenovodstvo. Resp. mezhved. temat. nauch. sb. No. 21:37-42 (Pl. Breed Abstr. 45: Abstr. 5694:1975).
- (62) Vol'f, V.G., and L.P. Dumacheva. 1973. Influence of the parental genotype on variation in economically valuable characters in sunflower hybrids. Selktsiya i Semenovodstvo. Resp. mezhved. temat. nauch. sb. No. 24:36-43 (Pl. Breed. Abstr. 45:Abstr. 7598:1975).
- (63) Vranceanu, A.V., N. Pirvu, F.M. Stoenescu, H. Iliescu, and I. Lascu. 1981. Genetic aspects of the resistance of sunflowers to *Sclerotinia sclerotiorum* (Lib.) de By. Analele Institutului de Cercetari pentru Cereale si Plante Tehnice 48:45-53. (Pl. Breed. Abst. 53:Abstr. 9002:1983).
- (64) Vranceanu, A.V., N. Pirvu, F.M. Stoenescu, and H. Iliescu. 1984. A study in sunflowers of the genetic variability in resistance to *Sclerotinia sclerotiorum* Lib. de By. Analele Institutului de Cercetari pentru Cereale si Plante Tehnice, Fundulea 51:27-35 (Pl. Breed. Abst. 55:Abstr.3821: 1985).
- (65) Wellving, A., and P. Lepoint. 1984. Breeding for resistance to sunflower diseases in Zambia. Sveriges Utsadesforenings Tidskrift 94:197-204. (Pl. Breed. Abst.55: Abstr. 1201:1985).
- (66) Zali, A.A., B.Y. Samadi, and A. Sarafi. 1976. Analysis of diallel crosses among six inbred lines of sunflower (Abstract). p. 62. 7th Inter. Sunflower Conf., June 27-July 3, Krasnodar, USSR.
- (67) Zali, A.A., and B.Y. Samadi. 1978. Association of seed yield and seed oil content with other plant and seed characteristics in *Helianthus annuus* L. p.164-171. Proc. 8th Inter. Sunflower Conf., Minneapolis, Minnesota.
- (68) Zimmer, D.E., and G.N. Fick. 1979. Registration of ND 761 sunflower germplasm. Crop Sci. 19:421.
- (69) Zimmer, D.E., and J.A. Hoes. 1978. Diseases. pp.225-262 In: Sunflower Science & Technology. Agronomy monograph 19. J.F. Carter. ed., Amer. Soc. Agron., Madison, WI. 505pp.

II. SELECTION INDICES

ABSTRACT

Pooled estimates of genetic and phenotypic variances and covariances for multiple disease resistance and agronomic traits were obtained from S1 families of Gene Pool II and ND 761 sunflower populations. Three selection strategies each for disease resistance and agronomic traits; and nine selection strategies combining agronomic and disease resistance traits were used on each population.

Multiple disease resistance was predicted to respond readily to selection. The Smith-Hazel index in both populations was efficient in improving predicted gains for resistance to four diseases (*Alternaria* leaf blight, *Septoria* leaf spot, *Phoma* and *Sclerotinia* wilt) when selection was focused on *Alternaria* blight and *Sclerotinia* wilt resistance simultaneously. This selection index was also effective for both populations in improving predicted gains for agronomic traits (head weight, 200-seed weight, oil content and yield/ha) when selection was for oil percent, and yield/ha simultaneously.

The Smith-Hazel index was most efficient in improving predicted gain in aggregate genotype for Gene Pool II when all four diseases and three agronomic traits (except head weight) were included in the index. The Smith-Hazel and desired gain indices with simultaneous selection of *Alternaria* blight and *Sclerotinia* wilt

resistance, oil percent and yield/ha were suggested for improvement of multiple disease resistance and agronomic traits in Gene Pool II and ND 761 respectively, because of the reduced number of traits included. The restricted selection index and the desired gain index were most efficient in controlling gains for plant height and days to flower, included as secondary traits. After population improvement by index selection they should be a sources of superior inbred lines for hybrid production.

INTRODUCTION

Recurrent selection has been proposed as a method for the improvement of crops by gradually increasing the frequency of favorable alleles in a population while maintaining genetic variability. The effectiveness of this type of selection for single traits in sunflower (*Helianthus annuus* L.) has been well documented in the literature. A population improved for one trait may be deficient in one or more other traits, therefore selection indices have been considered as an effective breeding tool when more than one trait must be considered (35).

The sign and magnitude of genetic correlations between traits and heritabilities of different traits are necessary in deciding the most efficient selection procedures. To calculate a selection index, it is also necessary to know the relative economic value or desired gain of each trait, the genotypic and phenotypic variance of each trait, and the genotypic and phenotypic covariance among each pair of traits.

Seed yield and disease resistance are important traits in any sunflower breeding program. Therefore simultaneous selection for these traits should be an appropriate situation in which to use a selection index. The objective of this study was to evaluate the effectiveness of S1 family index selection based on genetic parameter estimates from Gene Pool II and ND 761 populations in simultaneously improving seed yield, its components and quantitative disease resistance. This

information is a pre-requisite to initiate a recurrent selection program for agronomic and disease resistance traits in both sunflower populations.

Recurrent Selection

Recurrent selection has been shown to be a successful method in increasing the mean yield of mixed seed selected from a population. Population improvement in quality when recurrent in corn breeding has not received much attention in recent years. Yield from the F₂ method (23) for improvement of oil content, which is a modified form of recurrent selection for breeding improvement, probably has received relatively little attention only in oil content improvement has been reported in sunflower (2,3,4,20). The F₂ method of recurrent selection has been successful in improving oil percentage since at the same time maintaining or increasing seed yield.

Genetic improvement based on the method of recurrent selection reported in Natta (23) is an open-pollinated variety of sunflower. Response to selection for seed yield and oil content was reported through five cycles required in a further selection for seed yield. The main effect of selection revealed from 21 to 24 in the first generation to 28 to 31 of the third of selection cycle. The population yield increased large quantity for oil content with improvement of selection. Improving the population of recurrent selection in subsequent cycles. Three cycles of recurrent selection for higher oil content with low oil content population resulted in a total increase of 2.7 and 3.0% in oil

REVIEW OF LITERATURE

Recurrent Selection

Recurrent selection has been shown to be a successful method in improving the mean yield of inbred lines derived from a population. Population improvement in sunflower when compared to corn breeding, has not received much attention in recent years. Aside from the Pustovoit Method (30) for improvement of oil percentage, which is a modified form of recurrent selection not involving self-pollination, relatively few recurrent selection studies involving only oil or yield improvement have been conducted in sunflower (1,8,9,26). The Pustovoit method of reserves has been successful in improving oil percentage while at the same time maintaining or improving seed yield.

Varietal improvement based on the 'method of reserves' was initiated recently in India (11) in an open-pollinated variety of sunflower. Response to selection for seed yield and oil content assessed through five cycles resulted in a negative response for seed yield. The mean seed oil content increased from 41.4% in the base population to 46.9% at the end of the fifth cycle. The population still showed large variability for oil content after five cycles of selection suggesting the possibility of further improvement in subsequent cycles. Three cycles of recurrent selection for high oil percentage within two source populations resulted in a total increase of 3.2 and 3.9 in oil

percentage, respectively (9). Miller et al. (26) observed that heritability values of oil content in sunflower were sufficiently high for selection in early generations to improve oil content. After three cycles of simple phenotypic recurrent selection, oil content increased by 12.4%. A continuous genetic advance (13.18% per cycle) by mass selection was observed in three cycles of selection in an open-pollinated variety of sunflower (2).

Recurrent selection methods utilizing both S1 progeny and test cross evaluation in sunflower indicate that significant improvement in yield and combining ability of populations can be achieved by either S1 or test cross evaluation (8). After one cycle of recurrent selection using S1 progeny evaluation and a selection intensity of 20%, seed yield of a synthetic population was increased 6.9%. The results from reciprocal recurrent selection in two sunflower populations with a wide genetic base (1) suggest the possibility of a 20% advance seed yield in both populations. Three cycles of phenotypic selection in three genetically diverse populations of sunflower improved seed yield in only one population (15). Limited results on the value of recurrent selection for seed yield have been presented by Gundaev (13). One cycle of recurrent selection for high yield, with testcross evaluation of progeny, increased seed yields by 6% over the original cultivar (12). He also indicated that a 13% increase in seed yield by intercrossing the best yielding lines was obtained by Karp in 1946.

Reciprocal recurrent selection using S2 testcrosses has been used to select for improved yield in three sunflower populations in

Zambia (14). The yield performance of composite varieties of these populations were not at the desired level. The probable cause of failure of this selection technique in improving yields was poor random pollination during the dry season because of the lack of pollinators, resulting in inbreeding depression. Populations selected for Alternaria and Septoria leaf spot disease resistance, however, did exhibit a limited improvement in yield. Phenotypic recurrent selection for Sclerotinia wilt resistance within the cultivar Peredovik has resulted in populations with susceptibility reduced to about one-half that of the original population (20).

Selection Indices

Plant breeders have long recognized that the value of a plant is only rarely determined by a single trait. Therefore they work to simultaneously improve several traits within a population. Selection indices can be constructed which describe the value of an individual or family as a function of several traits. For this study three selection indices, estimated selection index, restricted selection index and desired gain index were used. Therefore only these indices will be discussed in this chapter.

The criteria of the choice of an efficient multiple trait selection in plants was first explained by Smith (35). He proposed estimating the relative genetic worth of different individuals through the use of a discriminant function (index) of the form

$$I = b_1X_1 + b_2X_2 + \dots + b_nX_n$$

where X_i is the phenotypic value of the i th trait and b_i 's are calculated so as to maximize the selection index (I). Knowledge of genotypic and phenotypic variances of each trait, genotypic and phenotypic covariances between each pair of traits, and the relative economic value of each trait are necessary to calculate the set of b_i 's. As this index is based on variance-covariance estimates, it is often called an estimated or optimum index. Hazel (17) used path coefficients to obtain results similar to Smith (35), and also explained the genetic theory on which the construction of selection indices is based. He clarified that only additive effects should be included in the genotypic value. Thereby index coefficients are calculated to maximize the correlation between selection index (I) and aggregate genotype (H). Therefore the estimated index is also sometimes referred to as the Smith-Hazel selection index.

A theoretical comparison of the relative efficiency of the optimum index with independent culling levels (rejection of all individuals below a certain level for a given trait regardless of merit for other traits) and tandem selection (selection for a different single trait in subsequent cycles of selection) was compared by Hazel and Lush (18). The comparison of the relative efficiency of these three methods for certain restricted conditions was expanded and given by Young (37) and Finney (10). The general conclusion of these studies is that the optimum index is never less efficient than independent culling level selection which, in turn, is never less efficient than tandem selection in increasing the net economic worth. The superiority

of the optimum index over the other two methods increases with increasing number of traits under selection, decreasing selection intensity and decreasing differences in relative economic value. The relative superiority of the optimum index over independent culling levels or tandem selection, however, may not be sufficient to warrant its use (37). Therefore reliable estimates of heritabilities of the traits, their relative economic values, and the correlations between traits are essential in deciding whether to use an optimum index or a simpler method of multiple trait selection.

In order to realize maximum gain in net economic value, the optimum index may result in a decrease in the genetic value of some traits of low economic value. Kempthorne and Nordskog (23) proposed a restricted index which itself is a modified Smith's index to hold some trait or function of traits constant while selecting for other correlated traits. This index maximizes economic gain in a desired set of traits while having a correlation of 0 with that function of traits which are not to be changed.

It is often difficult or undesirable to assign economic values to traits under selection. Therefore a different approach to the construction of indexes requiring no knowledge of relative economic values was proposed (29). This index, designated as the desired gain index where index coefficients are calculated based on the amount of gain desired for each trait rather than on relative economic values. This type of an index may be superior to the Smith-Hazel index when assigning desired gains is easier than assigning relative economic

values.

Predicted gains from the use of selection indices have been calculated for a number of crops, but limited information on the use of selection indices in sunflower is available. Selection indices in sunflower varieties on the basis of phenotypic traits were constructed by a multiple regression equation (3). Plant height and seed filling percentage were the most important traits, governing 82% of the variability in yield. Selection indices for sunflower were also constructed using dispersion matrices (28). Maximum expected genetic gain was obtained when plant height, basal diameter, number of leaves, capitulum size, percentage of seed filling, seed weight and yield per plant were included in the function. Combinations of these traits showed a relative efficiency of 541% over the function where yield per plant alone was considered.

Several index selection techniques originally constructed for improvement of corn breeding populations appear applicable to sunflower. Based on predicted gains, several authors have compared the relative efficiency of the optimum index with other indexes in specific populations. The expected genetic gains for several estimated indices based on yield components for three F_2 corn populations were calculated by Robinson et al. (31). Predicted gains for all indices were greater than the predicted gain for selection based on yield alone. The index based on plant height, ears per plant, and yield was predicted to give 130% of the gain from selection for yield per se.

Suwantaradon et al. (36) used two sets of arbitrarily assigned relative economic weights to several agronomic traits in 144 S1 lines of maize. Both sets were effective in improving yield, percent emergence, emergence index but undesirable responses were predicted for other traits. Similar problems with a Smith-Hazel Index have been reported (4). The Smith-Hazel index maximizes gain in the aggregate genotype and not necessarily each of the traits within the index. For individual traits, negative responses may occur when they are negatively correlated with traits with higher additive genetic variances and economic weights.

Expected gain for oat grain yield from indices in which plant height and maturity were restricted were examined (33). When changes in plant height and heading date were held to zero, gain in yield was 57% as great as when no restriction was applied. When harvest index was included as a secondary trait, gain was improved to 70% of the gain from unrestricted selection for yield. Population parameters estimated from 1200 oat lines were used to construct indexes including heading date, plant height, grain yield, and straw yield (32). Gains from selection among inbred lines showed reasonable agreement with predicted gains from the restricted selection indexes used.

The use of a desired gain index, a base index where index coefficients were equal to economic weights, and a Smith-Hazel index for improving several agronomic traits in maize were compared (36). Desired gain index was recommended because of the difficulty in estimating economic values which when included in the index would give

predicted responses in the desirable direction for all traits. Expected gains in all traits were found to be a proportion of the desired gains specified when constructing the index. The effectiveness of a desired gain index, direct selection and an estimated index for improvement of corn grain yield and protein percentage in two maize populations was also compared (22). Use of desired gain index was feasible for simultaneous improvement of grain yield and percent protein. The agreement with prediction of gains from an estimated index or a desired gain index was as good as for single trait selection. Others have found the desired gain index to be not as efficient as other types of index selection (4). This was explained in part by the difficulty in specifying meaningful desired gains for the traits studied. The relative efficiency of the index was found to vary substantially depending on the desired gains specified. Assigning desired gains to secondary traits of no economic value would also be difficult.

Results from simultaneous selection for quantitative resistance to more than one disease or simultaneous selection for disease resistance and other traits has not been reported for sunflower. However reports on other crops are in the literature. Mass selection for seven cycles in two alfalfa gene pools for resistance to rust and leaf hopper yellowing was effective in increasing resistance to both the disease and insect simultaneously (5). Two index selection methods were also effective in alfalfa (6) in simultaneously improving resistance to four foliar diseases and recovery after cutting. Suwantaradon et al. (36) estimated phenotypic and genetic variances and covariances and predicted gains

from index selection in the BSSS2 maize population for a number of agronomic traits including yield potential and resistance to two insects. Their data indicated that simultaneous improvement in insect resistance and yield potential in the absence of insect attack should be possible. Jinahyon and Russell (21) observed a small positively correlated response in testcross yield to selection for resistance to Diplodia stalk rot. They attributed the response in yield to indirect selection for late maturity resulting from the method used to select for Diplodia stalk rot resistance. Russell et al. (34) also reported no correlated response in yield potential (after elimination of inbreeding effects) in five maize populations to three cycles of recurrent S1 selection for resistance to first brood European corn borer. Simultaneous improvement in resistance to several diseases of corn was possible because of positive genetic correlations between different disease scores (24). However low estimates of genetic correlations between disease scores and yield in the absence of disease indicated no large correlated response from selection between yield and disease resistance (24). Modified ear-to-row desired gain index selection was effective in increasing northern corn leaf blight resistance in two corn populations, and resistance to Diplodia stalk rot and Anthracnose stalk rot in one population each. No consistent correlated response in grain yield to selection for disease resistance was observed (25). This indicated that selection based on indexes constructed from data on several traits and designed to maximize gain in disease resistance was no more effective than selection for disease score per se.

MATERIALS AND METHODS

Pooled estimates of genotypic and phenotypic variances and heritability for each trait and the genotypic and phenotypic covariances among each pair of traits obtained from S1 families of Gene Pool II and ND 761 (described previously) were used in this study. Predicted gain is a change produced by the selection. This change is of main interest to the plant breeders, since it changes the population mean. Therefore predicted gain (Gs) in this study was calculated as;

$$Gs = i \cdot \hat{\sigma}_P \cdot h^2$$

where $i = 1.755$ (standardized selection differential using a selection intensity of 10%); $\hat{\sigma}_P$ = the phenotypic standard deviation of S1 family means; and h^2 = the broad-sense heritability estimate.

The correlated response (CR) in trait x from selection on trait y was predicted by using the equation (7);

$$CR = i \cdot h_x \cdot h_y \cdot r_{xy} \cdot \hat{\sigma}_{P_y}$$

where $i = 1.755$ (standardized selection differential using selection intensity of 10%); h_x and h_y = the square-roots of heritability for trait x and y respectively; r_{xy} = the genetic correlation between x and y; and $\hat{\sigma}_{P_y}$ = the phenotypic standard deviation of y.

Construction of Selection Indices

Three different types of selection indices for improving Gene Pool II and ND 761 populations by S1 family selection were compared. Measures of resistance to four diseases, namely, Area under disease progress curve of percent *Alternaria* leaf blight (AUDALT), *Phoma* black stem, Area under disease progress curve of percent *Septoria* leaf spot (AUDSEP), and Area under disease progress curve of percent *Sclerotinia* wilt (AUDSCL) were included in separate indices to improve multiple disease resistance. Similarly, four traits of yield and its components, head weight (HDWT), seed weight (SDWT), oil percent (OIL) and yield per hectare (YLD) were included in separate indices. Finally disease resistance, yield and its components were included in indices to improve these populations for all traits. Flowering date (FLWR) and plant height (PLHT) were included as secondary traits with zero economic weight or desired gains attached to their improvement, because no improvement of these traits is needed in these two adapted sunflower populations.

Desired gains of 30% were set for resistance to AUDALT, *Phoma* and AUDSCL; 20% for AUDSEP resistance and YLD; and 10% for HDWT, SDWT and OIL, respectively. The relative economic values and desired gains for these traits are presented in Table 10. Negative signs for disease traits are desired since a low disease score indicates high resistance. A series of indexes were constructed for both sunflower populations to maximize gain. Details of the selection strategies used with three selection indices (Smith-Hazel index, Restricted selection

Table 10 : Relative economic values and desired gains used in constructing selection indices for Gene Pool II and ND 761 populations

Traits*	Gene Pool II		ND 761	
	Rel. econ. value	Desired gain	Rel. econ. value	Desired gain
AUDALT	-2	-397.23	-2	-333.51
Phoma	-2	-0.81	-2	-0.75
AUDSEP	-1	-88.68	-1	-84.10
AUDSCL	-2	-454.41	-2	-273.63
FLWR	0	0	0	0
PLHT	0	0	0	0
HDWT	1	3.97	1	4.00
SDWT	1	0.92	1	0.87
OIL	1	4.05	1	3.91
YLD	2	194.04	2	209.56

*AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, Septoria leaf spot and Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), OIL= Oil content (%) and YLD= Yield/ha (kg).

index and Desired gain index) are outlined in Table 11. The choice of different selection strategies are necessary because inclusion of many traits in the index results in smaller gains for each individual trait. Therefore with different selection strategies we will have the option to pick the index having fewer traits with better gain.

Estimated indices were calculated by the method described by Smith (35). The appropriate weighting factors were obtained by

$$b = V_p^{-1} \cdot V_g \cdot a$$

where b = the vector of b_i 's; V_p^{-1} = the inverse of the phenotypic variance-covariance matrix; V_g = the genotypic variance-covariance matrix; and a = the vector of relative economic values.

Restricted selection indices were calculated as described by Kempthorne and Nordskog (23). The index coefficients were obtained as;

$$b = \{I - P^{-1}GC(C'GP^{-1}GC)^{-1}C'\}P^{-1}Ga$$

where I = the identity matrix; P^{-1} = the inverse of the phenotypic variance-covariance matrix; G = the genotypic variance-covariance matrix; C = the coefficient vector matrix; C' = the transposed coefficient vector; and a = the vector of relative economic values.

Desired gain indices were calculated by the method outlined by Pesek and Baker (29);

$$b = V_g^{-1} \cdot h$$

where V_g^{-1} = the inverse of genotypic variance-covariance matrix; and h = the vector of desired gain.

Table 11 : List of indices constructed to maximize gain in Gene Pool II and ND 761 populations and traits included in those indices.

Index Number	Traits*
Disease Traits	
ID1	AUDALT, Phoma, AUDSEP, AUDSCL
ID2	AUDALT, Phoma, AUDSCL
ID3	AUDALT, AUDSCL
Agronomic Traits#	
IA1	HDWT, SDWT, OIL, YLD
IA2	SDWT, OIL, YLD
IA3	OIL, YLD
Disease and Agronomic Traits#	
IDA1	AUDALT, Phoma, AUDSEP, AUDSCL, HDWT, SDWT, OIL, YLD
IDA2	AUDALT, Phoma, AUDSEP, AUDSCL, SDWT, OIL, YLD
IDA3	AUDALT, Phoma, AUDSEP, AUDSCL, OIL, YLD
IDA4	AUDALT, Phoma, AUDSCL, HDWT, SDWT, OIL, YLD
IDA5	AUDALT, Phoma, AUDSCL, SDWT, OIL, YLD
IDA6	AUDALT, Phoma, AUDSCL, OIL, YLD
IDA7	AUDALT, AUDSCL, HDWT, SDWT, OIL, YLD
IDA8	AUDALT, AUDSCL, SDWT, OIL, YLD
IDA9	AUDALT, AUDSCL, OIL, YLD

*AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, Septoria leaf spot and Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, HDWT= Head weight (gm), SDWT= 200-seed weight(gm), Oil= Oil content (%) and YLD= Yield/ha (kg).

#Flowering days and Plant height (cm) were also included in the indexes as secondary traits.

Expected gain in each trait by index selection was calculated from the formula described by Finney (10);

$$\Delta g_i = k(Gb)_i / \sqrt{b'Pb}$$

where Δg_i = the genetic gain in *i*th trait; $k = 1.755$ (standardized selection differential using selection intensity of 10%); G = the genotypic variance-covariance matrix; b = the vector of index coefficients; $(Gb)_i$ = the *i*th element of the column vector Gb ; b' = the transpose of b ; and P = the phenotypic variance-covariance matrix.

Relative efficiencies of the selection strategies were expressed by their aggregate genotypic values in genetic standard deviations. The aggregate genotype is equal to the sum of the predicted responses in traits. Disease traits with a minus sign (resistance) were considered positive when calculating the aggregate genotype. Predicted gains in secondary traits, irrespective of their positive or negative direction, were deducted from the aggregate genotype.

RESULTS

Predicted primary and correlated responses to single trait selection from a cycle of S1 family selection in Gene Pool II and ND 761 are presented in Tables 12 and 13, respectively. Correlated responses for Phoma and OIL from selection for resistance to AUDALT, AUDSEP and AUDSCL were negligible in Gene Pool II and ND 761. Selection for SDWT is associated with a decrease in SDPHD and an increase in YLD in both populations. Similarly, correlated responses from selection for resistance to four diseases in Gene Pool II were high for YLD and its components except SDWT and FLWR. Favorable correlated responses from selection for YLD in Gene Pool II are predicted in AUDALT, AUDSEP, AUDSCL as well as increases in PLHT, HDWT, SDPHD, OIL and OYLD (Table 12). The expected gain in YLD of ND 761 population will be mainly due to increased HDWT, SDPHD and OYLD (Table 13).

Predicted Gains from Index Selection

Predicted gains from S1 family selection by using three selection strategies for disease resistance and two types of selection indices are given in Table 14. Index coefficients (b-values) for index selection for multiple disease resistance in the two populations are presented in Appendix G. When selection was for all four diseases simultaneously (ID1), predicted gains were greatest using the Smith-Hazel index for both populations. This is evident in the aggregate

TABLE 12: Predicted direct responses (on the diagonal), and correlated responses (off the diagonal) to S1 family selection (10% selection intensity) in Gene Pool II population in units of measurements.

Primary traits*	Secondary Traits												
	AUDALT	Phoma	AUDSEP	AUDSCL	FLWR	PLHT	HDIA	HDWT	SDWT	SDPHD	OIL	YLD	OYLD
AUDALT	301.68	0.09	63.27	54.60	-0.50	-3.34	-0.57	-4.35	-0.56	-50.79	-0.30	-134.71	-58.65
Phoma	46.83	0.30	13.88	70.56	-0.34	-4.13	-0.21	-2.81	-0.30	-40.29	-0.54	-70.18	-35.28
AUDSEP	171.69	0.07	78.76	46.05	-0.11	-0.01	-0.38	-2.26	-0.33	-29.76	-0.42	-81.90	-39.07
AUDSCL	30.25	0.07	9.40	199.98	-0.70	-2.02	0.09	-1.03	-0.05	-21.76	-0.12	-42.63	-20.04
FLWR	-53.35	-0.07	-4.41	-134.38	3.43	11.85	0.35	3.28	-0.31	99.14	-0.01	56.65	24.81
PLHT	-64.19	-0.15	-0.04	-70.11	2.15	19.47	0.97	7.88	0.40	142.83	0.59	172.07	78.70
HDIA	-104.72	-0.07	-25.67	28.31	0.60	9.19	1.25	8.21	0.42	164.24	0.29	224.44	99.03
HDWT	-114.75	-0.14	-21.96	-49.07	0.82	10.82	1.19	9.87	0.91	155.41	0.78	239.32	110.84
SDWT	-90.37	-0.09	-19.25	-13.01	-0.47	3.32	0.37	5.55	1.86	-44.05	0.44	159.77	69.47
SDPHD	-67.03	-0.10	-14.48	-51.83	1.24	9.81	1.19	7.77	-0.36	214.66	0.67	182.56	87.74
OIL	-31.29	-0.11	-16.07	-22.36	-0.01	3.18	0.17	3.06	0.28	52.63	2.62	113.19	82.12
YLD	-140.68	-0.14	-31.52	-80.34	0.56	9.35	1.28	9.47	1.04	144.43	1.14	308.01	170.25
OYLD	-125.75	-0.14	-30.87	-77.55	0.50	8.78	1.16	9.00	0.93	142.51	1.69	349.51	156.03

*AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, percent Septoria leaf spot and percent Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, Oil= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

TABLE 13: Predicted direct responses (on the diagonal), and correlated responses (off the diagonal) to S1 family selection (10% selection intensity) in ND 761 population in units of measurements.

Primary Traits*	Secondary Traits												
	AUDALT	Phoma	AUDSEP	AUDSCL	FLWR	PLHT	HDIA	HDWT	SDWT	SDPHD	OIL	YLD	OYLD
AUDALT	240.10	0.03	42.10	85.48	-1.36	4.13	0.26	0.50	-0.11	23.83	-0.02	-9.53	-4.63
Phoma	16.63	0.30	3.66	148.05	-0.63	-0.08	0.37	1.21	0.26	7.56	-0.00	38.53	16.03
AUDSEP	118.00	0.02	57.45	167.73	0.37	8.47	0.15	1.03	0.22	4.68	-0.71	2.80	-3.40
AUDSCL	32.13	0.11	22.49	387.26	-0.18	0.25	-0.07	0.67	0.36	-25.28	-0.30	11.27	2.59
FLWR	-95.32	-0.09	9.34	-32.60	4.40	9.25	-0.14	0.47	-0.52	55.59	-0.80	-36.80	-17.78
PLHT	63.86	-0.00	46.69	10.28	2.04	19.85	0.14	3.78	-0.06	88.90	0.01	50.46	21.64
HDIA	46.83	0.13	9.64	-34.40	-0.35	1.62	1.05	4.58	0.48	111.40	-0.35	127.78	42.79
HDWT	13.15	0.06	9.73	47.19	0.18	6.49	0.68	5.33	0.27	119.33	0.12	132.56	52.00
SDWT	-15.47	0.08	11.55	141.63	-1.10	-0.57	0.40	1.52	1.82	-122.83	0.28	64.33	28.15
SDPHD	26.24	0.02	1.84	-74.04	0.87	6.33	0.69	4.94	-0.91	190.82	-0.09	112.96	42.71
OIL	-1.53	-0.00	-22.39	-71.51	-1.01	0.08	-0.17	0.41	0.17	-7.50	2.47	26.73	43.97
YLD	-10.62	0.09	1.11	33.40	-0.59	3.64	0.80	5.56	0.48	114.30	0.34	175.88	129.21
OYLD	-10.65	0.07	-2.79	15.85	-0.58	3.22	0.55	4.50	0.44	89.29	1.14	266.97	105.62

*AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, percent Septoria leaf spot and percent Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, Oil= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

genotype (Table 14). However predicted gains for AUDSCL resistance in Gene Pool II were greater with the desired gain index. Desired gain index was also efficient in ND 761 for improving resistance to AUDALT and AUDSEP traits when selection was for ID3 (resistance to AUDALT and AUDSCL simultaneously). Restricted selection indices were not used for disease selection strategies, since all four diseases in this study are economically important.

When selection was for three agronomic traits simultaneously (IA2), aggregate genotype was greatest for agronomic traits using the Smith-Hazel index in Gene Pool II (Table 15). The aggregate genotype was also greatest using the Smith-Hazel index in ND 761 when selection was for four traits (IA1) simultaneously. This index was more efficient in improvement of HDWT, SDWT and YLD traits in both populations. Desired gain index was most efficient in improving the predicted gains for OIL in both populations. However it was less efficient for both populations in improving the aggregate genotype. In ND 761 when selection was for two traits simultaneously (IA3), desired gain index was superior to the restricted selection index in improving the aggregate genotype of agronomic traits. Restricted and desired gain indices were effective in controlling correlated responses for secondary traits in both populations. Index coefficients of indices for the improvement of agronomic traits of both populations are given in Appendix H.

Table 14 : Predicted gains¹ and the aggregate genotype for four diseases from selection² among S1 families of GP II and ND 761 by using three selection strategies and two selection indices

Selection strategy	Index*	AUDALT	Phoma	AUDSEP	AUDSCL	Aggregate genotype
GENE POOL II						
ID1	SHI	-1.362	-0.511	-1.083	-0.652	-3.608
	DGI	-0.666	-0.999	-0.479	-0.696	-2.840
ID2	SHI	-1.318	-0.509	-0.923	-0.682	-3.432
	DGI	-0.670	-1.006	-0.524	-0.701	-2.901
ID3	SHI	-1.327	-0.401	-0.922	-0.663	-3.313
	DGI	-0.850	-0.381	-0.615	-0.889	-2.735
ND 761						
ID1	SHI	-1.019	-0.548	-1.010	-1.052	-3.629
	DGI	-0.698	-0.993	-0.603	-0.277	-2.571
ID2	SHI	-0.974	-0.576	-0.849	-1.056	-3.455
	DGI	-0.739	-1.051	-0.393	-0.293	-2.476
ID3	SHI	-0.991	-0.407	-0.868	-1.031	-3.297
	DGI	-1.432	-0.244	-0.961	-0.567	-3.204

¹ Genetic standard deviation units.

² Ten percent selection intensity.

*SHI=Smith-Hazel index and DGI=Desired gain index.

AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, Septoria leaf spot and Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant.

TABLE 15: Predicted gains (genetic standard deviation) and the aggregate genotype for six agronomic traits from selection (10% selection intensity) among S1 families of Gene Pool II and ND 761 population by using three selection strategies and selection indices.

Selection strategy	Index*	Primary traits				Secondary traits		Aggregate genotype#
		HDWT	SDWT	OIL	YLD	FLWR	PLHT	
GENE POOL II								
IA1	SHI	1.428	0.958	0.693	1.582	0.263	0.855	3.543 (4.661)
	RSI	0.896	0.770	0.571	1.233	0.0	0.0	3.470
	DGI	0.342	0.450	1.344	0.595	0.0	0.0	2.731
IA2	SHI	1.365	0.986	0.709	1.572	0.214	0.794	3.624 (4.632)
	RSI	0.872	0.785	0.581	1.230	0.0	0.0	3.468
	DGI	0.406	0.464	1.387	0.614	0.0	0.0	2.871
IA3	SHI	1.342	0.833	0.721	1.560	0.262	0.806	3.388 (4.456)
	RSI	0.849	0.646	0.595	1.221	0.0	0.0	3.311
	DGI	0.375	0.224	1.378	0.610	0.0	0.0	2.587
ND 761								
IA1	SHI	1.289	0.635	0.294	1.403	-0.244	0.383	2.994 (3.621)
	RSI	1.086	0.506	0.124	1.247	0.0	0.0	2.963
	DGI	0.255	0.224	0.668	0.475	0.0	0.0	1.622
IA2	SHI	1.180	0.716	0.311	1.364	-0.320	0.278	2.973 (3.571)
	RSI	1.012	0.581	0.131	1.212	0.0	0.0	2.936
	DGI	0.607	0.365	1.089	0.775	0.0	0.0	2.836
IA3	SHI	1.178	0.424	0.305	1.338	-0.251	0.304	2.690 (3.298)
	RSI	1.003	0.323	0.131	1.192	0.0	0.0	2.649
	DGI	0.610	0.211	1.083	0.771	0.0	0.0	2.675

*SHI= Smith-Hazel Index, RSI= Restricted selection index and DGI= Desired gain index.
 #Aggregate genotype in parenthesis were summed from predicted gains of primary traits.
 HDWT= Head weight (gm), SDWT= 200-seed weight (gm), OIL= Oil content (%), YLD= Yield/ha (kg), FLWR= Days to flower and PLHT= Plant height (cm).

Predicted responses to index selection for both disease and agronomic traits of Gene Pool II are presented in Table 16. Index coefficients are presented in Appendix I. For all nine selection strategies, the Smith-Hazel index and the restricted selection index were superior to the desired gain index in this population (Table 16). Selection for improvement of resistance to all four diseases and three agronomic traits simultaneously (IDA2) by the Smith-Hazel index was the most efficient for improving the aggregate genotype, followed by the restricted selection index (IDA1). Desired gain index was least efficient compared to the Smith-Hazel and restricted indices but it did give the highest predicted gains for OIL in all selection strategies. Smith-Hazel indices were the most efficient in improving AUDALT, HDWT, SDWT and YLD in all indices. Restricted selection indices were most effective in improving AUDSEP in all indices examined in Gene Pool II.

Responses of individual traits and gain in the aggregate genotype were generally less in ND 761 than those using the same indices in Gene Pool II. The desired gain index was most efficient for improving the aggregate genotype of multiple disease resistance and agronomic traits by using the IDA8 selection strategy (Table 17). Index coefficients for all indices used in ND 761 are presented in Appendix J. Smith-Hazel and restricted selection indices resulted in a negative response for SDWT in most of the indices constructed for ND 761. These two indices were also least efficient in improving aggregate

TABLE 16: Predicted gains (genetic standard deviation) and the aggregate genotype for diseases and agronomic traits from selection (10% selection intensity) among S1 families of Gene Pool II by using nine selection strategies and three types of selection indices.

Selection strategy	Index*	Primary traits								Secondary traits		Aggregate genotype#
		AUDALT	Phoma	AUDSEP	AUDSCL	HDWT	SDWT	OIL	YLD	FLWR	PLHT	
IDA1	SHI	-1.283	-0.630	-0.988	-0.623	1.198	0.784	0.516	1.349	0.387	0.691	6.293 (7.371)
	RSI	-1.261	-0.429	-1.093	-0.539	0.772	0.732	0.429	1.059	0.0	0.0	6.314
	DGI	-0.547	-0.822	-0.394	-0.573	0.156	0.205	0.611	0.270	0.0	0.0	3.578
IDA2	SHI	-1.284	-0.624	-0.994	-0.626	1.163	0.794	0.520	1.339	0.364	0.658	6.322 (7.344)
	RSI	-1.262	-0.429	-1.094	-0.539	0.770	0.731	0.429	1.057	0.0	0.0	6.311
	DGI	-0.546	-0.820	-0.393	-0.572	0.188	0.204	0.610	0.270	0.0	0.0	3.603
IDA3	SHI	-1.283	-0.620	-0.994	-0.630	1.153	0.744	0.523	1.332	0.380	0.661	6.238 (7.279)
	RSI	-1.261	-0.423	-1.095	-0.538	0.756	0.646	0.436	1.050	0.0	0.0	6.205
	DGI	-0.547	-0.821	-0.393	-0.572	0.189	0.209	0.610	0.270	0.0	0.0	3.611
IDA4	SHI	-1.243	-0.631	-0.877	-0.637	1.219	0.792	0.514	1.367	0.403	0.727	6.150 (7.280)
	RSI	-1.221	-0.420	-0.968	-0.556	0.775	0.740	0.422	1.067	0.0	0.0	6.169
	DGI	-0.568	-0.852	-0.540	-0.594	0.161	0.212	0.634	0.280	0.0	0.0	3.841
IDA5	SHI	-1.245	-0.625	-0.844	-0.640	1.183	0.802	0.519	1.356	0.380	0.694	6.180 (7.254)
	RSI	-1.222	-0.420	-0.969	-0.557	0.773	0.739	0.422	1.066	0.0	0.0	6.168
	DGI	-0.567	-0.851	-0.541	-0.593	0.199	0.212	0.633	0.280	0.0	0.0	3.876
IDA6	SHI	-1.244	-0.621	-0.884	-0.644	1.173	0.749	0.521	1.350	0.396	0.697	6.093 (7.186)
	RSI	-1.221	-0.414	-0.969	-0.556	0.757	0.648	0.431	1.058	0.0	0.0	6.054
	DGI	-0.567	-0.850	-0.540	-0.593	0.197	0.213	0.633	0.280	0.0	0.0	3.873
IDA7	SHI	-1.248	-0.575	-0.877	-0.626	1.215	0.790	0.509	1.367	0.398	0.717	6.092 (7.207)
	RSI	-1.225	-0.373	-0.967	-0.547	0.775	0.739	0.419	1.069	0.0	0.0	6.114
	DGI	-0.632	-0.384	-0.558	-0.662	0.179	0.236	0.705	0.312	0.0	0.0	3.668
IDA8	SHI	-1.250	-0.566	-0.884	-0.629	1.177	0.802	0.514	1.357	0.372	0.681	6.126 (7.179)
	RSI	-1.226	-0.373	-0.967	-0.548	0.772	0.739	0.419	1.068	0.0	0.0	6.112
	DGI	-0.630	-0.383	-0.557	-0.659	0.183	0.235	0.703	0.311	0.0	0.0	3.661
IDA9	SHI	-1.249	-0.559	-0.884	-0.633	1.166	0.744	0.517	1.349	0.390	0.684	6.027 (7.101)
	RSI	-1.225	-0.363	-0.967	-0.546	0.756	0.644	0.427	1.060	0.0	0.0	5.988
	DGI	-0.632	-0.376	-0.558	-0.661	0.175	0.173	0.706	0.312	0.0	0.0	3.593

*SHI=Smith-Hazel index, RSI= Restricted selection index and DGI= Desired gain index.

#Aggregate genotype in parenthesis were summed from predicted gains of primary traits.

AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, Septoria leaf spot and Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, HDWT= Head weight (gm), SDWT= 200-seed weight (gm), OIL= Oil content (%), YLD= Yield/ha (kg), FLWR= Days to flower and PLHT= Plant height (cm).

TABLE 17: Predicted gains (genetic standard deviation) and the aggregate genotype for diseases and agronomic traits from selection (10% selection intensity) among S1 families of ND 761 by using nine selection strategies and three types of selection indices.

Selection strategy	Index*	Primary traits								Secondary traits		Aggregate genotype#
		AUDALT	Phoma	AUDSEP	AUDSCL	HDWT	SDWT	OIL	YLD	FLWR	PLHT	
IDA1	SIH	-0.999	-0.393	-0.996	-0.987	0.177	-0.190	0.363	0.359	0.244	-0.181	3.659 (4.084)
	RSI	-0.760	-0.310	-0.833	-0.977	0.358	-0.066	0.501	0.544	0.0	0.0	4.217
	DGI	-0.474	-0.674	-0.409	-0.188	0.197	0.173	0.516	0.367	0.0	0.0	2.998
IDA2	SIH	-1.005	-0.398	-1.005	-0.991	0.132	-0.176	0.364	0.331	0.225	-0.212	3.613 (4.050)
	RSI	-0.763	-0.316	-0.827	-0.982	0.325	-0.053	0.504	0.520	0.0	0.0	4.184
	DGI	-0.537	-0.763	-0.463	-0.213	0.282	0.196	0.584	0.416	0.0	0.0	3.454
IDA3	SIH	-1.010	-0.392	-0.995	-0.979	0.139	-0.078	0.371	0.347	0.198	-0.222	3.735 (4.155)
	RSI	-0.771	-0.314	-0.819	-0.974	0.331	0.007	0.506	0.528	0.0	0.0	4.250
	DGI	-0.535	-0.761	-0.462	-0.212	0.279	0.139	0.582	0.415	0.0	0.0	3.385
IDA4	SIH	-1.135	-0.208	-0.861	-0.727	0.429	0.071	0.302	0.628	0.295	-0.069	3.997 (4.361)
	RSI	-0.740	-0.326	-0.768	-0.977	0.348	-0.053	0.463	0.541	0.0	0.0	4.110
	DGI	-0.505	-0.718	-0.367	-0.200	0.209	0.184	0.549	0.391	0.0	0.0	3.123
IDA5	SIH	-0.962	-0.415	-0.877	-0.993	0.171	-0.162	0.329	0.351	0.272	-0.103	3.561 (3.936)
	RSI	-0.743	-0.333	-0.760	-0.982	0.313	-0.038	0.465	0.515	0.0	0.0	4.073
	DGI	-0.541	-0.769	-0.413	-0.214	0.272	0.197	0.589	0.419	0.0	0.0	3.414
IDA6	SIH	-0.967	-0.408	-0.860	-0.979	0.180	-0.052	0.335	0.370	0.244	-0.109	3.694 (4.047)
	RSI	-0.752	-0.330	-0.748	-0.972	0.319	0.035	0.466	0.525	0.0	0.0	4.147
	DGI	-0.539	-0.767	-0.417	-0.214	0.270	0.172	0.587	0.418	0.0	0.0	3.384
IDA7	SIH	-0.964	-0.296	-0.879	-0.971	0.226	-0.173	0.329	0.392	0.279	-0.078	3.527 (3.884)
	RSI	-0.751	-0.216	-0.777	-0.960	0.359	-0.051	0.463	0.552	0.0	0.0	4.027
	DGI	-0.732	0.003	-0.610	-0.290	0.304	0.267	0.797	0.567	0.0	0.0	3.564
IDA8	SIH	-0.970	-0.301	-0.891	-0.976	0.181	-0.160	0.330	0.363	0.260	-0.111	3.481 (3.852)
	RSI	-0.753	-0.223	-0.770	-0.965	0.325	-0.037	0.465	0.527	0.0	0.0	3.991
	DGI	-0.916	0.013	-0.808	-0.363	0.478	0.334	0.997	0.710	0.0	0.0	4.619
IDA9	SIH	-0.977	-0.285	-0.873	-0.958	0.191	-0.036	0.337	0.386	0.228	-0.118	3.625 (3.971)
	RSI	-0.764	-0.216	-0.756	-0.953	0.332	0.045	0.466	0.538	0.0	0.0	4.070
	DGI	-0.913	0.013	-0.815	-0.362	0.479	0.284	0.993	0.707	0.0	0.0	4.540

*SIH=Smith-Hazel index, RSI= Restricted selection index and DGI= Desired gain index.

#Aggregate genotype in parenthesis were summed from predicted gains of primary traits.

AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, Septoria leaf spot and sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant,

HDWT= Head weight (gm), SDWT= 200-seed weight (gm), OIL= Oil content (%), YLD= Yield/ha (kg), FLWR= Days to flower and PLHT= Plant height (cm).

genotype of resistance and agronomic traits when selection was for four (IDA8) or five (IDA9) traits simultaneously, but were most efficient in improving AUDSCL resistance. Desired gain indices were most efficient in improving OIL and SDWT. Smith-Hazel indices were most effective for improving predicted gains in AUDALT, AUDSEP and AUDSCL but resulted in an undesirable increase in PLHT.

DISCUSSION

A major purpose of this paper is to predict progress from S1 family index selection in Gene Pool II and ND 761 sunflower populations. In a plant breeding program, initial selection and evaluation are typically in the S0 or S1 generation. A review of the literature on recurrent selection in sunflower indicates that either S1 or test cross evaluation are effective in improving sunflower populations (8). The purpose of recurrent selection is to increase the frequency of desirable homozygous lines that can be derived from the improved population.

The selection strategy chosen to improve a population should be one that maximizes the economic value of the derived inbred lines. A review of the trait means of Gene Pool II and ND 761 suggests that a decrease in disease susceptibility and an increase in yield and its components would be desirable. Therefore the economic values and desired gains for the selection indices were set at values that reflect this relationship. Greatest gains in aggregate genotype for multiple disease resistance were produced by the Smith-Hazel index by selection for four diseases simultaneously in both populations. Therefore multiple disease resistance is predicted to respond readily to selection. However, the gain in aggregate genotype for multiple disease resistance is only slightly reduced in both populations when selection was focused on resistance to two diseases (AUDALT and AUDSCL) simultaneously. The significant positive genetic correlations between AUDALT and

AUDSEP in both populations suggest that selection for one will result in gains in the other. Use of the ID3 selection strategy would be easier for multiple disease resistance when compared to selection for resistance to all four diseases in the breeding program, and would certainly reduce cost and time. Moreover, simultaneous selection for reduced AUDALT and AUDSCL (ID3) resulted in desirable predicted gains in Phoma and AUDSEP as well. This strategy can be helpful in situations where first attention might be given to improving disease resistance until an acceptable level is achieved.

Selection for agronomic components, if desired, can be included in a separate selection scheme. In our study, predicted gains in the aggregate genotype of agronomic traits were greatest when selection was based on the Smith-Hazel index for three agronomic traits (IA2) simultaneously in Gene Pool II, and selection for four agronomic traits (IA1) simultaneously in ND 761. However simultaneous selection of three traits (IA2) using the Smith-Hazel index in ND 761 resulted in only a slight decrease (0.021) in aggregate genotype of agronomic traits compared to IA1. The restricted selection index and the desired gain index were effective in controlling the predicted gain for secondary traits (Plant height and days to flower). In both populations, the desired gain index did increase predicted gain for OIL. The desired gain index described by Pesek and Baker (29) restricts responses in individual traits to a fixed proportion of the responses specified by the desired gain vector. Aggregate genotypes of agronomic traits from predicted gains of primary traits alone in both populations indicated

that selection based on the Smith-Hazel index for four agronomic traits (IA1) simultaneously was the most efficient, but inclusion of four traits in the index may not be justified, since there are only slight decreases in aggregate genotypes when selection was focused on three traits (IA2) or only two traits (IA3) simultaneously. In such cases it's appropriate to use the Smith-Hazel index with IA3 strategy in both populations. Use of IA3 strategy in Gene Pool II slightly decreases the gain for YLD and its components but increases gain in OIL compared to IA2. This index also reduces the number of traits to be used in a breeding program. Similarly, use of the Smith-Hazel index with IA3 in ND 761 resulted in a slight decrease in predicted gain compared to IA2, but the decrease in gain for SDWT is comparatively high in this index. However, SDWT is a secondary trait, when selection is focused on improvement of YLD itself.

The development of selection strategies for yield and its components along with multiple disease resistance is another objective of this paper. Selection strategies with different types of indices in Gene Pool II indicated that the Smith-Hazel index was the most efficient in improving gain in aggregate genotype of multiple disease resistance, yield and its components when resistance to all four diseases, and three agronomic traits (IDA2) were included in the index. The restricted selection index was intermediate and the desired gain index the least efficient index for these selections, but were effective in controlling correlated responses of the secondary traits included in the indices. Indices that incorporate more traits will be slower in improvement for

any given trait. This is because inclusion of many traits in the selection index results in smaller predicted gain for each individual trait. Therefore, indices with many traits are of little value compared to those with fewer traits. In this study, the Smith-Hazel index IDA9 which includes two disease as well as two agronomic traits is suitable for Gene Pool II compared to IDA2. This index (IDA9) is free from the problems associated with the inclusion of a large number of traits, and appears applicable in a breeding program for improvement of Gene Pool II. Aggregate genotype of multiple disease resistance and agronomic traits summed from predicted gains of primary traits alone by the Smith-Hazel index in Gene Pool II indicated IDA1 was the most efficient index. Again this index involves many traits and consequences of this type of index have already been discussed.

The desired gain index was most efficient in improving predicted gain in the aggregate genotype of multiple disease resistance and agronomic traits when three agronomic and two disease traits (IDA8) were included in a ND 761 selection scheme. The desired gain index was also the most efficient index for simple selection of resistance to two diseases and two agronomic traits (IDA9) simultaneously in ND 761. However, both selection strategies resulted in undesirable gains (susceptibility) for Phoma but were effective in improving the remaining primary traits. Therefore the choice of IDA9 selection strategy would be warranted since it involves fewer traits.

Based on predicted gains from S1 family selection it appears that use of the Smith-Hazel index with simultaneous selection of

resistance to AUDALT and AUDSCL is effective in improving these populations for disease resistance. This index is also efficient in improving gain for agronomic traits by simultaneous selection for OIL and YLD in Gene Pool II and ND 761. Selection strategies involving disease resistance and agronomic traits suggest simultaneous selection of resistance to AUDALT and AUDSCL, OIL, YLD by the Smith-Hazel and the desired gain index in Gene Pool II and ND 761 respectively. The current practice towards the development and use of single cross sunflower hybrids demands development of productive inbred lines. By use of these indices, these populations may be a source for deriving lines with high yield, its components, and disease resistance.

The superiority of indices over other methods of selection and the correctness of the estimated superiority of one index over another are greatly dependent upon accurate estimates of genotypic and phenotypic variances and covariances, and the relative economic values or desired gains to be used in the index. Their successful application to complex multiple-trait improvement also depends on the judgement of the breeder. The genotypic and phenotypic variances and covariances may be different when considering indexes for populations derived from different sources or for different cycles of selection in the same population. Therefore indices constructed in this paper pertain only to these populations under study. In our study, data used to calculate resistance to AUDALT, AUDSEP and AUDSCL must be collected on weekly basis, and selection is usually based on experiments planted in one location. Therefore estimates of genetic parameters used to

construct selection indices are biased by genotype x environment interactions. Thereby errors in estimating genetic parameters can seriously affect the accuracy of an index and such reports are in the literature (16,19,27).

If further restrictions on days to flower and plant traits in these populations are desired in the later cycles of selection with the assumption that there will be no change in genotypic and phenotypic variances, then expected changes in population parameters will be slow and reconstruction of the index is not required after each cycle of selection. Averaging estimates from different cycles of selection will minimize sampling errors and provide an appropriate index for that cycle of selection as proposed by Suwantaradon et al. (36). However inclusion of new primary traits in later cycles of selection will necessitate the reconstruction of index.

LITERATURE CITED

- (1) Alba, E. 1985. Results of a reciprocal recurrent selection in sunflower populations. p. 789. Proc. 11th Inter. Sunflower Conf., MarDel Plata, Argentina.
- (2) Areco, C.M., P.M. Luduena, and J.M. Bruniard. 1982. Genetic advances by mass selection in the oil percentage of sunflower (*Helianthus annuus* L.). p. 268. Proc. 10th Inter. Sunflower Conf., March 14-18, Surfers Paradise, Australia.
- (3) Asawa, B.M., R.K. Asawa, P.S. Srivastav, and K.P.S. Somavanshi. 1977. Selection indices in sunflower for yield and oil. Indian J. Agric. Sci. 47:505-507.
- (4) Crosbie, T.M., J.J. Mock, and O.S. Smith. 1980. Comparison of gains predicted by several selection methods for cold tolerance traits of two maize populations. Crop Sci. 20:649-655.
- (5) Dudley, J.W., R.R. Hill, Jr., and C.H. Hanson. 1963. Effects of seven cycles of recurrent phenotypic selection on means and genetic variances of several characters in two pools of alfalfa germplasm. Crop Sci. 3:543-546.
- (6) Elgin, J.H., R.R. Hill, Jr., and K.E. Zeiders. 1970. Comparison of four methods of multiple trait selection for five traits in alfalfa. Crop Sci. 10:190-193.
- (7) Falconer, D.S. 1981. Introduction to quantitative genetics. p. 286. 2nd ed. Longman, London.
- (8) Fick, G.N. 1978. Breeding and genetics. p. 296. In: Sunflower Science and Technology. Ed. J.F. Carter. Agron. Ser. No. 19, Amer. Soc. Agron., Madison, Wisconsin.
- (9) Fick, G.N., and D.A. Rehder. 1977. Selection criteria in development of high oil sunflower hybrids. p.26-27. Proc. 2nd Sunflower Forum, Fargo, North Dakota.
- (10) Finney, D.J. 1962. Genetic gains under three methods of selection. Genet. Res. (Camb.) 3:417-423.
- (11) Giriraj, K., U.S. Ujjinaiah, and S.R. Hiremath. 1985. Response to cyclic selection for seed yield and oil content in sunflower population--Armaviriski 3497. p 661-664. Proc. 11th Inter. Sunflower Conf., MarDel Plata, Argentina.

- (12) Gundaev, A.I. 1966. Prospects of selection in sunflower for heterosis. *Sb. Rab. Maslichn. Kult.* 3:15-21 (Transl. Indian Natl. Sci. Documentation Centre, New Delhi, India. 1969). In: *Sunflower Science and Technology*. Ed. J.F. Carter. Agron. Ser. No. 19, Amer. Soc. Agron., Madison, Wisconsin.
- (13) Gundaev, A.I. 1971. Basic principles of sunflower selection. p. 417-465. In *Genetic Principles of Plant Selection*. Nauka, Moscow. (Transl. Dep. of the Secretary of State, Ottawa, Canada. 1972). In *Sunflower Science and Technology*. P 296. ed., J.F. Carter. 1978. Amer. Soc. of Agron., Madison, USA.
- (14) Habowa, B., W. Roath, P. Lapoint, and G. Ravagnon. 1985. Results of a S2 test cross recurrent selection technique on yield improvement of three sunflower (*Helianthus annuus* L.) populations from the Upland tropics of Zambia. p. 659. *Proc. 11th Inter. Sunflower Conf., MarDel Plata, Argentina.*
- (15) Harinarayana, G., P.V. Anantharaman, K.A. Rao, S. Kandlikar, and N.G. Rao. 1980. Breeding Sunflower populations. *Indian J. Genetics Pl. Breed.* 40:212-215.
- (16) Harris, D.L. 1964. Expected and predicted progress from index selection involving estimates of population parameters. *Biometrics* 20:46-72.
- (17) Hazel, L.N. 1943. The genetic basis for constructing selection indexes. *Genetics* 28:476-490.
- (18) Hazel, L.N., and J.L. Lush. 1942. The efficiency of three methods of selection. *J. Hered.* 33:393-399.
- (19) Heidhues, T. 1961. Relative accuracy of selection indices based on estimated genotypic and phenotypic parameters. *Biometrics* 17:502-503.
- (20) Hoes, J.A., and H.C. Huang. 1976. Control of sclerotinia basal stem rot of sunflowers: a Progress report. p 18-20. *Proc. Sunflower Forum, Fargo, North Dakota, USA.*
- (21) Jinahyon, S., and W.A. Russell. 1969. Effects of recurrent selection for stalk-rot resistance on other agronomic characters in an open-pollinated variety of maize. *Iowa State J. Sci.* 43:239-251.
- (22) Kauffmann, K.D., and J.W. Dudley. 1979. Selection indices for grain yield, percent protein, and kernel weight. *Crop Sci.* 19:583-588.
- (23) Kempthorne, O., and A.W. Nordskog. 1959. Restricted selection indices. *Biometrics* 15:10-19.

- (24) Miles, J.W., J.W. Dudley, D.G. White, and R.J. Lambert. 1980. Improving corn population for grain yield and resistance to leaf blight and stalk rot. *Crop Sci.* 20:247-251.
- (25) Miles, J.W., J.W. Dudley, D.G. White, and R.J. Lambert. 1981. Response to selection for resistance to four diseases in two corn populations. *Crop Sci.* 21:980-983.
- (26) Miller, J.F., G.N. Fick, and J.R. Cedeno. 1977. Improvement of oil content and quality in sunflower (*Helianthus annuus* L.). *Amer. Soc. Agron., Madison, USA (abst.)* p 64.
- (27) Mock, J.J. 1979. Investigation of genotype x environment interaction for cold tolerance of maize. *Iowa State J. Res.* 53:291-296.
- (28) Naskar, S.K., M. Ghosh, and P.K. Bhowmik. 1982. Selection index in sunflower. *Indian J. Agric. Sci.* 52:736-737.
- (29) Pesek, J., and R.J. Baker. 1969. Desired improvement in relation to selection indices. *Can. J. Plant Sci.* 49:803-804.
- (30) Pustovoit, V.S. 1964. Conclusions of work on the selection and seed production of sunflowers. *Agrobiologia* 5:672-697 (Transl. R.P. Knowles, Agriculture Canada, Saskatoon, Saskatchewan. 1965). In: *Sunflower Science and Technology*. 1978. Ed. J.F. Carter. *Agron. Ser. No. 19, Amer. Soc. Agron., Madison, Wisconsin.*
- (31) Robinson, H.F., R.E. Comstock, and P.H. Harvey. 1951. Genotypic and phenotypic correlations in corn and their implications in selection. *Agron. J.* 43:283-287.
- (32) Rosielle, A.A., H.A. Eagles, and K.J. Frey. 1977. Application of restricted selection indexes for improvement of economic value in oats. *Crop Sci.* 17:359-361.
- (33) Rosielle, A.A., and K.J. Frey. 1975. Application of restricted selection indices for grain improvement in oats. *Crop Sci.* 15:544-547.
- (34) Russell, W.A., G.D. Lawrance, and W.D. Guthrie. 1979. Effects of recurrent selection for European corn borer resistance on other agronomic characters in synthetic cultivars of maize. *Maydica* 24:33-47.
- (35) Smith, H.F. 1936. A discriminant function for plant selection. *Ann. Eugen.* 7:240-250.
- (36) Suwantaradon, K., S.A. Eberhart, J.J. Mock, J.S. Owens, and W.D. Guthrie. 1975. Index selection for several agronomic traits

in the BSSS2 maize population. *Crop Sci.* 15:827-833.

- (37) Young, S.S.Y. 1961. A further examination of the relative efficiency of three methods of selection for genetic gains under less restricted conditions. *Genet. Res. (Camb.)* 2:106-121.

APPENDICES

APPENDIX A

Factors of genetic variation, environmental variance and heritability among 21 families of Lake Trout in 1962 and 1963.

Family	Genetic Variance		Environmental Variance		Heritability	
	1962	1963	1962	1963	1962	1963
1	18078.4000	12085.9300	17811.80	19495.20	0.214	0.209
2	27300	27300	27300	27300	0.214	0.209
3	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
4	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
5	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
6	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
7	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
8	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
9	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
10	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
11	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
12	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
13	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
14	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
15	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
16	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
17	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
18	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
19	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
20	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209
21	2221.5000	2221.5000	2221.50	2221.50	0.214	0.209

APPENDICES

Genetic and environmental variance components for 21 families of Lake Trout in 1962 and 1963. The data are presented in Appendix A. The heritability estimates are based on the analysis of variance for the two years. The environmental variance is the sum of the within-family variance and the error variance. The heritability is the ratio of the genetic variance to the total variance.

APPENDIX A

Estimates of genetic variance, environmental variance and heritability among S1 families of Gene Pool II in 1982 and 1983.

Traits#	Genetic variance		Environmental variance		Heritability	
	1982	1983	1982	1983	1982	1983
AUDALT	28479.84**	52660.65**	13912.90	14767.26	0.67+	0.78+
Phoma	0.09**	0.06**	0.17	0.06	0.34+	0.50+
AUDSEP	4345.37**	3331.46**	4173.98	2840.00	0.51+	0.54+
AUDSCL	32856.89*	64319.37*	77315.67	185502.91	0.30+	0.26
FLWR	3.39**	5.27**	0.45	0.76	0.88+	0.88+
PLHT	122.72**	147.11**	10.58	15.53	0.92+	0.91+
HDIA	0.99**	0.82**	0.37	1.63	0.73+	0.34+
HDWT	49.78**	49.56**	14.99	62.57	0.77+	0.44+
SDWT	1.20**	1.90**	0.28	1.32	0.81+	0.59+
SDPHD	22543.44**	20651.40**	6417.83	17019.65	0.78+	0.55+
OIL	4.62**	2.01**	1.37	2.19	0.77+	0.48+
YLD	54015.35**	22941.33**	9359.52	12398.43	0.85+	0.65+
OYLD	13253.87**	5850.33**	1986.44	0.0	0.87+	1.00+

*,** Significant at 0.05 and 0.01 probability levels, respectively.

+ Heritability differ significantly from zero as its absolute magnitude exceeded twice its standard error.

#AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, percent Septoria leaf spot and percent Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, OIL= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

APPENDIX B

Estimates of genetic variance, environmental variance and heritability among S1 families of ND 761 in 1982 and 1983.

Traits#	Genetic variance		Environmental variance		Heritability	
	1982	1983	1982	1983	1982	1983
AUDALT	16724.62**	33132.84**	8629.11	12443.21	0.66+	0.73+
Phoma	0.13**	0.03*	0.12	0.06	0.52+	0.30+
AUDSEP	1633.61*	2685.84**	3192.17	2009.86	0.34+	0.57+
AUDSCL	30023.30*	171032.41**	41102.22	226464.74	0.42+	0.43+
FLWR	5.65**	7.76**	0.72	0.54	0.89+	0.94+
PLHT	153.61**	133.09**	13.86	15.49	0.92+	0.90+
HDIA	0.61**	0.67**	0.32	0.90	0.66+	0.43+
HDWT	22.04**	22.13*	12.45	64.23	0.64+	0.26
SDWT	0.62**	1.84**	0.14	0.74	0.82+	0.71+
SDPHD	15596.28**	21392.55**	5262.08	23425.88	0.75+	0.48+
OIL	2.95**	3.14**	1.27	2.36	0.70+	0.57+
YLD	26871.71**	10037.23**	9660.94	15822.85	0.74+	0.39+
OYLD	4872.87**	5184.73**	1827.63	0.0	0.73+	1.00+

*,** Significant at 0.05 and 0.01 probability levels, respectively.

+ Heritability differ significantly from zero as its absolute magnitude exceeded twice its standard error.

#AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, percent Septoria leaf spot and percent Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, OIL= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

APPENDIX C

Estimates of genetic (above diagonal) and phenotypic (below diagonal) correlation coefficients of Gene Pool II population in 1982 (top figure) and 1983 (bottom figure).

Traits//	AUDALT	Phoma	AUDSEP	AUDSCL	FLWR	PLHT	HDIA	HDWT	SDWT	SDPHD	OIL	YLD	OYLD
AUDALT		0.353 0.094	0.881* 0.522*	0.652* -0.111	-0.150 -0.169	-0.244 -0.155	-0.395* -0.418	-0.402* -0.424*	-0.202 -0.365*	-0.326 -0.155	-0.208 -0.005	-0.534* -0.419*	-0.517* -0.303*
Phoma	0.199 0.114		0.162 0.268	0.191 0.411	-0.267 -0.036	-0.401 -0.243	-0.184 -0.232	-0.356 -0.378	-0.158 -0.301	-0.321 -0.157	-0.449 0.078	-0.456 -0.060	-0.476 -0.033
AUDSEP	0.516 0.339	0.067 0.139		0.372 -0.008	-0.026 -0.061	-0.082 0.092	-0.509* -0.053	-0.462* 0.005	-0.210 -0.211	-0.404* 0.155	-0.181 -0.183	-0.383* -0.225	-0.374 -0.204
AUDSCL	0.292 -0.050	0.061 0.147	0.202 0.101		-0.295 -0.421	-0.202 -0.186	-0.125 0.293	-0.334 -0.030	-0.258 0.094	-0.209 -0.129	-0.240 0.116	-0.433 -0.036	-0.430 -0.012
FLWR	-0.116 -0.140	-0.146 -0.023	-0.017 -0.042	-0.151 -0.200		0.595* 0.639*	0.263 0.185	0.128 0.414*	-0.134 -0.160	0.274 0.533*	0.057 -0.077	0.300 0.030	0.278 0.009
PLHT	-0.192 -0.130	-0.225 -0.163	-0.056 0.064	-0.106 -0.090	0.534 0.577		0.643* 0.570*	0.612* 0.719*	0.253 0.144	0.567* 0.594*	0.378* -0.064	0.700* 0.291	0.688* 0.203
HDIA	-0.276 -0.214	-0.092 -0.095	-0.310 -0.022	-0.058 0.086	0.225 0.083	0.503 0.306		0.990* 0.776*	0.605* -0.058	0.965* 0.719*	0.343 -0.258	1.048* 0.573	0.993* 0.396
HDWT	-0.289 -0.249	-0.182 -0.178	-0.289 0.002	-0.160 -0.010	0.111 0.277	0.523 0.460	0.780 0.644		0.685* 0.399	0.847* 0.654*	0.513* -0.014	1.009* 0.680*	0.988* 0.552*
SDWT	-0.149 -0.248	-0.083 -0.163	-0.135 -0.119	-0.127 0.037	-0.121 -0.113	0.208 0.098	0.419 0.227	0.624 0.444		0.064 -0.432*	0.252 0.060	0.541* 0.606*	0.516* 0.470*
SDPHD	-0.236 -0.102	-0.165 -0.082	-0.254 0.084	-0.101 -0.049	0.232 0.383	0.494 0.423	0.751 0.513	0.825 0.726	0.023 -0.269		0.434* -0.045	0.896* 0.213	0.878* 0.188
OIL	-0.150 -0.003	-0.230 0.038	-0.114 -0.093	-0.115 0.041	0.038 -0.056	0.334 -0.017	0.246 -0.066	0.418 0.154	0.208 0.116	0.355 0.083		0.533* 0.068	0.662* 0.385*
YLD	-0.404 -0.298	-0.246 -0.034	-0.252 -0.133	-0.218 -0.015	0.259 0.022	0.624 0.223	0.817 0.267	0.862 0.364	0.445 0.375	0.767 0.127	0.438 0.038		1.047* 1.285*
OYLD	-0.395 -0.268	-0.259 -0.023	-0.249 -0.150	-0.219 -0.006	0.241 0.009	0.622 0.193	0.778 0.230	0.852 0.367	0.429 0.361	0.759 0.139	0.593 0.266	1.018 1.035	

*Correlation coefficients differ significantly from zero as its absolute magnitude exceeded twice its standard error.
 #AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, percent Septoria leaf spot and percent Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, OIL= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

APPENDIX D

Estimates of genetic (above diagonal) and phenotypic (below diagonal) correlation coefficients of ND 761 population in 1982 (top figure) and 1983 (bottom figure).

Traits#	AUDALT	Phoma	AUDSEP	AUDSCL	FLWR	PLHT	HDIA	HDWT	SDWT	SDPHD	OIL	YLD	OYLD
AUDALT		0.197 -0.003	1.060* 0.425*	0.273 0.155	-0.004 -0.497*	0.401* 0.155	0.190 0.239	0.236 -0.007	-0.223 -0.016	0.366 0.014	-0.208 0.089	0.155 -0.241	0.098 -0.121
Phoma	0.111 0.084		0.114 0.028	0.578* 0.471	-0.074 -0.435	0.115 -0.210	0.328 0.588	0.197 0.301	0.212 0.258	0.038 0.072	0.141 -0.216	0.294 0.113	0.329 -0.006
AUDSEP	0.501 0.274	0.048 0.012		-0.003 0.520*	0.097 0.127	0.649* 0.565*	0.427 0.020	0.394* 0.069	-0.070 0.228	0.420 -0.151	-0.318 -0.345	0.332 -0.289	0.257 -0.214
AUDSCL	0.144 0.087	0.270 0.168	0.100 0.379		-0.094 -0.052	0.089 -0.002	0.428 -0.222	0.316 0.079	0.102 0.300	0.191 -0.253	0.109 -0.236	0.434 -0.089	0.442 -0.094
FLWR	-0.003 -0.410	-0.050 -0.229	0.053 0.093	-0.058 -0.033		0.543* 0.421*	-0.087 -0.111	0.061 0.059	-0.275 -0.270*	0.191 0.264	-0.128 -0.352*	-0.066 -0.294	-0.087 -0.190
PLHT	0.312 0.125	0.079 -0.108	0.362 0.404	0.056 -0.001	0.468 0.392		0.208 0.035	0.467 0.492	0.192 -0.125	0.309 0.436*	-0.005 0.011	0.352 0.080	0.339 0.060
HDIA	0.125 0.133	0.192 0.209	0.201 0.010	0.226 -0.095	-0.048 -0.133	0.157 0.018		1.540* 0.250*	1.175* 0.011	1.515* 0.137	0.153 -0.338	1.446* -0.007	1.363* -0.159
HDWT	0.153 -0.003	0.113 0.083	0.183 0.026	0.164 0.026	0.065 -0.022	0.363 0.239	0.897 0.496		0.764* 0.000	1.057* 0.597*	0.096 0.040	1.218* 0.548	1.168* 0.265
SDWT	-0.164 -0.011	0.138 0.118	-0.037 0.145	0.060 0.166	-0.193 -0.253	0.153 -0.099	0.559 0.224	0.568 0.202		0.057 -0.786*	0.379 0.004	0.741* 0.087	0.778* 0.046
SDPHD	0.257 0.008	0.023 0.027	0.211 -0.079	0.107 -0.115	0.168 0.150	0.272 0.294	0.931 0.310	0.914 0.751	-0.059 -0.460		-0.067 -0.023	0.935* 0.369	0.855* 0.179
OIL	-0.141 0.058	0.085 -0.089	-0.155 -0.197	0.059 -0.117	-0.125 -0.250	0.043 -0.001	-0.015 -0.203	0.093 -0.023	0.269 -0.006	-0.029 -0.019		0.070 0.244	0.324 0.520*
YLD	0.108 -0.128	0.181 0.038	0.165 -0.136	0.242 -0.036	-0.053 -0.177	0.317 0.047	0.956 -0.003	0.918 0.173	0.519 0.046	0.731 0.159	0.041 0.115		1.189* 1.682*
OYLD	0.068 -0.103	0.202 -0.003	0.128 -0.162	0.245 -0.061	-0.073 -0.183	0.313 0.057	0.890 -0.104	0.896 0.134	0.554 0.039	0.683 0.124	0.301 0.393	1.064 1.048	

*Correlation coefficients differ significantly from zero as its absolute magnitude exceeded twice its standard error.
 #AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, percent Septoria leaf spot and percent Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant,
 FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm),
 SDPHD= Seeds per head, OIL= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

APPENDIX E

Estimates of genetic (above diagonal) and phenotypic (below diagonal) covariances of Gene Pool II population during the year 1982 (top figure) and 1983 (bottom figure).

Traits#	AUDALT	PHOMA	AUDSEP	AUDSCL	FLWR	PLHT	HDIA	HDWT	SDWT	SDPHD	OIL	YLD	OYLD
AUDALT		17.52 5.27	9799.96 6909.12	19933.70 -6439.12	-46.59 -89.14	-455.52 -431.11	-66.48 -86.83	-478.03 -685.41	-37.21 -115.50	-8264.46 -5115.69	-75.46 -1.56	-20952.30 -14549.50	-10043.40 -5319.48
PHOMA	20.62 10.21		3.14 3.78	10.19 25.45	-0.14 -0.02	-1.31 -0.72	-0.05 -0.05	-0.74 -0.65	-0.05 -0.10	-14.17 -5.50	-0.28 0.03	-31.21 -2.23	-16.15 -0.61
AUDSEP	9799.96 6909.12	3.14 3.78		4448.31 -113.60	-3.15 -8.13	-59.84 64.16	-33.44 -2.76	-214.67 1.99	-15.15 -16.80	-3995.69 1284.10	-25.61 -15.00	-5864.36 -1969.13	-2834.78 -898.73
AUDSCL	19933.70 -6439.12	10.19 25.45	6200.13 3956.18		-98.38 -245.04	-405.31 -570.49	-22.57 67.28	-427.02 -52.59	-51.07 32.77	-5690.47 -4712.07	-93.50 41.63	-18235.90 -1395.74	-8965.12 -224.63
FLWR	-46.59 -89.14	-0.14 -0.02	-3.15 -8.13	-98.38 -245.04		12.14 17.78	0.48 0.38	1.67 6.69	-0.27 -0.51	75.73 175.73	0.23 -0.25	128.16 10.30	58.83 1.61
PLHT	-455.52 -431.11	-1.31 -0.72	-59.84 64.16	-405.31 -570.49	12.08 18.07		7.10 6.26	47.84 61.39	3.07 2.41	942.55 1034.60	9.00 -1.11	1802.62 534.71	877.05 188.36
HDIA	-66.48 -86.83	-0.05 -0.05	-33.44 -2.76	-22.57 67.28	0.52 0.32	6.78 6.09		6.96 4.94	0.66 -0.07	144.51 93.55	0.73 -0.33	242.87 78.59	113.93 27.45
HDWT	-478.03 -685.41	-0.74 -0.65	-214.67 1.99	-427.02 -52.59	1.75 7.21	48.62 62.08	7.33 10.67		5.29 3.88	897.66 661.66	7.77 -0.14	1654.20 724.71	802.30 297.00
SDWT	-37.21 -115.50	-0.05 -0.10	-15.15 -16.80	-51.07 32.77	-0.29 -0.50	2.92 2.24	0.60 0.64	6.10 8.44		10.48 -85.65	0.59 0.12	137.61 126.65	64.98 49.58
SDPHD	-8264.46 -5115.69	-14.17 -5.50	-3995.69 1284.10	-5690.47 -4712.07	77.40 182.48	971.19 1046.03	149.46 155.57	1129.20 1491.34	4.66 -93.83		140.00 -9.06	31252.39 4637.29	15170.77 2067.77
OIL	-75.46 -1.56	-0.28 0.03	-25.61 -15.00	-93.50 41.63	0.18 -0.28	9.42 -0.43	0.70 -0.21	8.22 3.35	0.62 0.43	147.71 33.21		266.12 14.53	163.82 41.79
YLD	-20952.30 -14549.50	-31.21 -2.23	-5864.36 -1969.13	-18235.90 -1395.74	127.47 10.30	1813.13 534.71	240.61 78.59	1746.80 724.71	135.99 126.65	32873.69 4637.29	269.57 14.53		28023.42 14884.40
OYLD	-10043.40 -5319.48	-16.15 -0.61	-2834.78 -898.73	-8965.12 -224.63	58.20 1.61	886.72 188.36	112.24 27.45	846.15 297.00	64.42 49.58	15942.33 2067.77	178.97 41.79	31620.57 14884.40	

#AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, percent Septoria leaf spot and percent Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, OIL= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

APPENDIX F

Estimates of genetic (above diagonal) and phenotypic (below diagonal) covariances of ND 761 population during the year 1982 (top figure) and 1983 (bottom figure).

Traits#	AUDALT	PHOMA	AUDSEP	AUDSCL	FLWR	PLHT	HDIA	HDWT	SDWT	SDPHD	OIL	YLD	OYLD
AUDALT		9.08 -0.09	5540.56 4006.14	6111.81 11686.60	-1.29 -252.13	642.71 324.75	19.11 35.64	143.02 -6.14	-22.70 -3.83	5910.45 372.99	-46.26 28.76	3289.62 -4402.01	884.54 -1586.53
PHOMA	8.81 5.17		1.64 0.23	35.63 30.43	-0.06 -0.19	0.51 -0.38	0.09 0.08	0.33 0.22	0.06 0.06	1.67 1.65	0.09 -0.06	17.15 1.77	8.18 -0.07
AUDSEP	5540.56 4006.14	1.64 0.23		-21.59 11153.80	9.36 18.32	324.94 337.62	13.44 0.83	74.72 16.78	-2.22 15.99	2121.22 -1142.42	-22.12 -31.71	2196.37 -1502.13	725.61 -797.47
AUSCL	6111.81 11686.60	35.63 30.43	1846.18 16372.23		-38.86 -59.67	191.93 -8.86	57.85 -75.40	257.23 153.26	13.90 167.81	4137.65 -15302.70	32.59 -172.69	12325.90 -3674.63	5342.92 -2785.17
FLWR	-1.29 -252.13	-0.06 -0.19	9.36 18.32	-38.86 -59.67		15.99 13.52	-0.16 -0.25	0.68 0.78	-0.52 -1.02	56.64 107.58	-0.52 -1.73	-25.53 -81.94	-14.44 -38.01
PLHT	642.71 324.75	0.51 -0.38	324.94 337.62	191.93 -8.86	15.28 13.75		2.01 0.33	27.18 26.70	1.87 -1.95	478.93 735.35	-0.10 0.23	715.89 91.84	293.01 49.83
HDIA	19.11 35.64	0.09 0.08	13.44 0.83	57.85 -75.40	-0.12 -0.48	1.95 0.27		5.64 0.96	0.72 0.01	147.59 16.46	0.21 -0.49	184.87 -0.54	74.19 -9.39
HDWT	143.02 -6.14	0.33 0.22	74.72 16.78	257.23 153.26	0.96 -0.60	27.58 27.06	5.06 5.78		2.83 0.00	619.93 410.90	0.77 0.34	937.35 258.07	382.80 89.88
SDWT	-22.70 -3.83	0.06 0.06	-2.22 15.99	13.90 167.81	-0.43 -1.17	1.73 -1.93	0.47 0.45	2.91 3.00		5.61 -155.67	0.51 0.01	95.80 11.83	42.86 4.48
SDPHD	5910.45 372.99	1.67 1.65	2121.22 -1142.42	4137.65 -15302.70	61.12 91.48	508.61 757.54	129.21 82.50	774.85 1477.85	-7.44 -156.22		-14.28 -6.02	19134.76 5413.59	7450.76 1885.29
OIL	-46.26 28.76	0.09 -0.06	-22.12 -31.71	32.59 -172.69	-0.65 -1.69	1.14 -0.02	0.03 -0.60	1.13 -0.50	0.48 -0.02	-8.66 -9.48		19.71 43.30	38.85 66.39
YLD	3289.62 -4402.01	17.15 1.77	2196.37 -1502.13	12325.90 -3674.63	-25.68 -81.94	783.98 91.84	175.66 -0.54	1030.50 258.07	86.55 11.83	20177.61 5413.59	16.23 43.30		13609.22 12136.77
OYLD	884.54 -1586.53	8.18 -0.07	725.61 -797.47	5342.92 -2785.17	-15.14 -38.01	331.91 49.83	69.96 -9.39	430.53 89.88	39.56 4.48	8070.96 1885.29	50.73 66.39	16645.19 12136.70	

#AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, percent Septoria leaf spot and percent Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, OIL= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

APPENDIX G

Index coefficients (b-values) of four diseases from selection¹ among S1 families by using three selection strategies and two types of selection indices

Selection strategy	Index*	AUDALT	Phoma	AUDSEP	AUDSCL
GENE POOL II					
ID1	SHI	-1.611	-123.940	-1.154	-0.525
	DGI	-0.007	-9.285	0.004	-0.005
ID2	SHI	-1.633	-123.152	0.0	-0.544
	DGI	-0.006	-9.238	0.0	-0.005
ID3	SHI	-1.666	0.0	0.0	-0.555
	DGI	-0.008	0.0	0.0	-0.008
ND 761					
ID1	SHI	-1.569	-236.736	-1.881	-0.796
	DGI	-0.007	-11.430	-0.027	0.003
ID2	SHI	-1.668	-226.881	0.0	-0.843
	DGI	-0.012	-10.885	0.0	0.002
ID3	SHI	-1.702	0.0	0.0	-0.869
	DGI	-0.012	0.0	0.0	-0.001

¹ Ten percent selection intensity.

*SHI= Smith-Hazel index and DGI= Desired gain index.

AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, Septoria leaf spot and Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant.

APPENDIX H

Index coefficients (b-values) for six agronomic traits from selection¹ among S1 families of GP II and ND 761 using three selection strategies and three types of selection indices

Selection strategy	Index*	Primary traits				Secondary traits	
		HDWT	SDWT	OIL	YLD	FLWR	PLHT
GENE POOL II							
IA1	SHI	6.676	23.297	10.673	1.334	0.0	0.0
	RSI	3.136	21.489	11.630	1.248	38.369	-17.331
	DGI	-0.065	0.529	1.225	0.003	0.362	-0.084
IA2	SHI	0.0	33.826	12.331	1.452	0.0	0.0
	RSI	0.0	26.574	12.317	1.283	38.366	-16.497
	DGI	0.0	0.258	1.182	0.001	-0.144	-0.034
IA3	SHI	0.0	0.0	12.872	1.536	0.0	0.0
	RSI	0.0	0.0	12.436	1.349	32.921	-15.934
	DGI	0.0	0.0	1.204	0.003	0.272	-0.091
ND 761							
IA1	SHI	8.312	24.910	7.090	0.959	0.0	0.0
	RSI	7.657	19.331	4.569	0.926	22.864	-6.105
	DGI	-0.665	0.235	1.282	0.033	0.654	-0.024
IA2	SHI	0.0	31.796	6.577	1.112	0.0	0.0
	RSI	0.0	26.486	4.134	1.055	23.183	-4.987
	DGI	0.0	0.317	1.356	0.012	0.577	-0.091
IA3	SHI	0.0	0.0	7.506	1.150	0.0	0.0
	RSI	0.0	0.0	4.182	1.081	19.843	-4.787
	DGI	0.0	0.0	1.356	0.013	0.545	-0.090

¹ Ten percent selection intensity.

*SHI= Smith-Hazel index, RSI= Restricted selection index and DGI= Desired gain index.

HDWT= Head weight (gm), SDWT= 200-seed weight (gm), OIL= Oil content (%), YLD= Yield/ha (kg), FLWR= Days to flower and PLHT= Plant height (cm).

APPENDIX I

Index coefficients (b-values) for diseases and agronomic traits from selection (10% selection intensity) among S1 families of Gene Pool II by using nine selection strategies and three types of selection indices.

Selection strategy	Index*	Primary traits								Secondary traits	
		AUDALT	Phoma	AUDSEP	AUDSCL	HDWT	SDWT	OIL	YLD	FLWR	PLHT
IDA1	SHI	-1.609	-114.761	-1.161	-0.530	7.155	12.872	6.508	1.750	0.0	0.0
	RSI	-1.546	-86.695	-1.289	-0.474	0.336	42.103	13.415	1.696	19.328	-25.991
	DGI	-0.012	-9.684	0.015	-0.007	-0.104	0.037	1.043	-0.003	-0.222	-0.076
IDA2	SHI	-1.618	-119.545	-1.144	-0.530	0.0	24.039	8.258	1.875	0.0	0.0
	RSI	-1.543	-86.447	-1.286	-0.474	0.0	42.051	13.467	1.687	18.899	-25.721
	DGI	-0.012	-9.515	0.015	-0.007	0.0	-0.026	1.062	-0.006	-0.228	-0.095
IDA3	SHI	-1.630	-123.222	-1.149	-0.527	0.0	0.0	8.596	1.929	0.0	0.0
	RSI	-1.570	-93.488	-1.295	-0.474	0.0	0.0	13.548	1.780	9.893	-24.831
	DGI	-0.012	-9.502	0.015	-0.007	0.0	0.0	1.064	-0.006	-0.223	-0.095
IDA4	SHI	-1.631	-113.720	0.0	-0.550	7.094	13.306	6.912	1.751	0.0	0.0
	RSI	-1.587	-86.491	0.0	-0.498	0.403	42.004	14.108	1.701	20.964	-26.484
	DGI	-0.009	-9.417	0.0	-0.007	-0.108	0.053	0.991	-0.004	-0.243	-0.056
IDA5	SHI	-1.637	-118.437	0.0	-0.549	0.0	24.356	8.607	1.874	0.0	0.0
	RSI	-1.584	-86.243	0.0	-0.498	0.0	42.073	14.168	1.693	20.541	-26.197
	DGI	-0.009	-9.238	0.0	-0.007	0.0	-0.013	1.010	-0.006	-0.250	-0.075
IDA6	SHI	-1.650	-122.171	0.0	-0.547	0.0	0.0	8.964	1.929	0.0	0.0
	RSI	-1.612	-93.324	0.0	-0.498	0.0	0.0	14.270	1.787	11.545	-25.317
	DGI	-0.009	-9.232	0.0	-0.007	0.0	0.0	1.012	-0.006	-0.247	-0.075
IDA7	SHI	-1.651	0.0	0.0	-0.558	7.531	14.405	8.985	1.760	0.0	0.0
	RSI	-1.602	0.0	0.0	-0.504	0.487	43.391	15.637	1.704	20.572	-25.986
	DGI	-0.010	0.0	0.0	-0.010	-0.014	0.258	1.287	-0.007	-0.371	-0.009
IDA8	SHI	-1.659	0.0	0.0	-0.558	0.0	26.266	10.887	1.894	0.0	0.0
	RSI	-1.600	0.0	0.0	-0.504	0.0	43.608	15.712	1.698	20.165	-25.685
	DGI	-0.010	0.0	0.0	-0.010	0.0	0.249	1.289	-0.007	-0.371	-0.012
IDA9	SHI	-1.674	0.0	0.0	-0.556	0.0	0.0	11.351	1.953	0.0	0.0
	RSI	-1.630	0.0	0.0	-0.504	0.0	0.0	15.954	1.795	10.781	-24.727
	DGI	-0.010	0.0	0.0	-0.010	0.0	0.0	1.274	-0.006	-0.422	-0.008

*SHI= Smith-Hazel index, RSI= Restricted selection index and DGI= Desired gain index.
 AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, Septoria leaf spot and Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, OIL= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).

APPENDIX J

Index coefficients (b-values) for diseases and agronomic traits from selection (10% selection intensity) among S1 families of ND 761 by using nine selection strategies and three types of selection indices.

Selection strategy	Index*	Primary traits								Secondary traits	
		AUDALT	Phoma	AUDSEP	AUDSCL	HDWT	SDWT	OIL	YLD	FLWR	PLHT
IDA1	SHI	-1.665	-174.681	-1.632	-0.776	7.216	-40.509	28.919	0.971	0.0	0.0
	RSI	-1.513	-164.354	-1.531	-0.784	7.211	-29.340	33.313	1.035	-48.641	9.731
	DGI	-0.008	-13.970	-0.033	0.004	-0.473	0.328	0.784	0.027	-0.180	0.138
IDA2	SHI	-1.654	-173.638	-1.603	-0.777	0.0	-34.620	28.629	1.102	0.0	0.0
	RSI	-1.498	-162.297	-1.563	-0.783	0.0	-22.281	32.848	1.156	-47.844	10.762
	DGI	-0.011	-13.939	-0.022	0.004	0.0	0.284	0.890	0.012	-0.318	0.083
IDA3	SHI	-1.631	-183.976	-1.673	-0.788	0.0	0.0	26.901	1.064	0.0	0.0
	RSI	-1.469	-167.372	-1.624	-0.790	0.0	0.0	32.460	1.138	-44.422	10.576
	DGI	-0.012	-13.874	-0.017	0.004	0.0	0.0	0.929	0.013	-0.361	0.078
IDA4	SHI	-1.592	-55.264	0.0	-0.420	6.958	-6.376	19.275	0.981	0.0	0.0
	RSI	-1.573	-158.714	0.0	-0.816	7.282	-32.450	36.047	1.045	-45.150	5.933
	DGI	-0.012	-13.514	0.0	0.003	-0.336	0.071	1.059	0.024	-0.211	0.061
IDA5	SHI	-1.722	-165.289	0.0	-0.812	0.0	-36.471	31.564	1.099	0.0	0.0
	RSI	-1.562	-156.422	0.0	-0.817	0.0	-25.493	35.759	1.168	-44.309	6.903
	DGI	-0.014	-13.610	0.0	0.003	0.0	0.105	1.069	0.013	-0.311	0.038
IDA6	SHI	-1.706	-175.582	0.0	-0.826	0.0	0.0	30.132	1.058	0.0	0.0
	RSI	-1.534	-161.824	0.0	-0.827	0.0	0.0	35.717	1.148	-40.261	6.529
	DGI	-0.014	-13.613	0.0	0.003	0.0	0.0	1.069	0.013	-0.330	0.040
IDA7	SHI	-1.763	0.0	0.0	-0.829	6.797	-46.156	32.055	0.936	0.0	0.0
	RSI	-1.591	0.0	0.0	-0.833	7.024	-35.204	36.590	1.014	-42.853	5.906
	DGI	-0.011	0.0	0.0	-0.001	-0.422	0.079	1.115	0.022	0.092	0.050
IDA8	SHI	-1.750	0.0	0.0	-0.829	0.0	-40.481	31.635	1.059	0.0	0.0
	RSI	-1.580	0.0	0.0	-0.833	0.0	-28.461	36.306	1.133	-42.084	6.845
	DGI	-0.012	0.0	0.0	-0.001	0.0	0.122	1.127	0.008	-0.031	0.022
IDA9	SHI	-1.734	0.0	0.0	-0.846	0.0	0.0	30.044	1.010	0.0	0.0
	RSI	-1.550	0.0	0.0	-0.845	0.0	0.0	36.280	1.109	-37.462	6.424
	DGI	-0.013	0.0	0.0	-0.001	0.0	0.0	1.128	0.009	-0.053	0.024

*SHI= Smith-Hazel index, RSI= Restricted selection index and DGI= Desired gain index. AUDALT, AUDSEP and AUDSCL= Area under disease progress curve of percent Alternaria leaf blight, Septoria leaf spot and Sclerotinia wilt respectively. Phoma= Phoma black stem disease measured on a 0 to 5 scale with 0 as most resistant, FLWR= Days to flower, PLHT= Plant height (cm), HDIA= Head diameter (cm), HDWT= Head weight (gm), SDWT= 200-seed weight (gm), SDPHD= Seeds per head, OIL= Oil content (%), YLD= Yield/ha (kg) and OYLD= Oil yield (kg/ha).