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PREVIEW

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**Estimation of genetic parameters from generation means
analysis in eight parent and related populations of corn**

Mejia-Contreras, Jose Apolinar, Ph.D.

The University of Nebraska - Lincoln, 1990

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PREVIEW

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ESTIMATION OF GENETIC PARAMETERS FROM GENERATION
MEANS ANALYSIS IN EIGHT PARENT AND RELATED
POPULATIONS OF CORN.

by
Jose Apolinar Mejia-Contreras

A DISSERTATION
Presented to the Faculty of
The Graduate College in the University of Nebraska
In Partial Fulfillment of Requirements
For the Degree of Doctor of Philosophy

Major Agronomy

Under the Supervision of Professor W. A. Compton

Lincoln, Nebraska

December, 1990

DISSERTATION TITLE

Estimation of Genetic Parameters From Generation Means Analysis in Eight
Parent and Related Populations of Corn

BY

Jose Apolinar Mejia-Contreras

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ESTIMATION OF GENETIC PARAMETERS FROM GENERATION MEANS
ANALYSIS IN EIGHT PARENT AND RELATED POPULATIONS OF CORN

Jose Apolinar Mejia-Contreras, Ph.D.

University of Nebraska, 1990

Advisor: William A. Compton

Objectives of this study were to: 1) assess the genetic differences among Iowa Stiff Stalk Synthetic and seven populations derived from it at the University of Nebraska, and 2) estimate genetic parameters (a_j , d_j , h_{jj} , and aa_{jj}) and their proportional contribution to the total sums of squares due to differences among the eight populations and derived relatives.

Eight Stiff Stalk Synthetic corn populations and derived generations were evaluated and estimates made of genetic effects from : 1) parents per se and their testcrosses; (2) parents, parents selfed and F_1 's; (3) parents, parents selfed, F_1 's, F_1 's random mated and backcrosses. Parents, testcrosses, parents selfed and F_1 crosses were evaluated in four environments, but F_1 's random mated and backcrosses were evaluated in only two .

The analysis proposed by Eberhart and Gardner was used for the estimation of genetic effects in numbers (2) and (3) above. The latter allowed the inclusion of additive by additive epistasis.

NSS(5) and NS(B)RF(5), selected for yield index were

highest yielding as populations per se, as selfed progenies, and on the average in interpopulations crosses. However, NSCT-15 and NSCT-FT-15 selected for cold and freeze tolerance yielded as well in testcrosses to Mo.17. Furthermore, NSCT-FT-15 exhibited higher heterosis in inter-population crosses.

NSCT-FT-15, NS(B)RF(5) and NSS(5) had the least inbreeding depression and highest cumulative additive effects suggesting an increase of favorable alleles. In general, populations with little or no selection for yield showed greatest inbreeding depression, greatest cumulative intra-population dominance effects, and lowest yields.

Selection for cold and freeze tolerance resulted in intermediate yielding populations but seemed to contribute something to heterosis, both in testcrosses and in interpopulation crosses.

Of the total sums of squares among entry means for yield, dominance effects explained 68 and 50% and additive effects 26 and 40%, for the models without and with epistasis, respectively. Interpopulation heterosis and epistasis were small and generally non-significant.

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J.A.M.C.

PREVIEW

Dedicatoria

A mis padres:

Marciano Mejía,

Alejandrina C. de Mejía (en su memoria).

A mi esposa:

Cristina.

A nuestros hijos:

Karla Mayra,

Mario Alejandro,

Cristinita.

TABLE OF CONTENTS

	Page
LIST OF TABLES	X
LIST OF FIGURES	XIII
LIST OF APPENDIX TABLES.	XIV
INTRODUCTION.....	1
LITERATURE REVIEW.....	3
IMPORTANCE OF THE ESTIMATION OF GENETIC PARAMETERS.....	3
GENERATION MEANS ANALYSIS.....	7
THE GARDNER-EBERHART MODEL.....	16
Use of the Gardner-Eberhart Model.....	20
STIFF STALK SYNTHETIC MAIZE.....	34
MATERIALS AND METHODS.....	38
GENETIC MATERIAL USED.....	38
DEVELOPMENT OF GENERATIONS IN THE NURSERY.....	39
FIELD TRIALS.....	41
DATA COLLECTED.....	46
STATISTICAL ANALYSIS	47
Analysis of Generation Means.....	51
RESULTS AND DISCUSSION.....	61
EVALUATION OF PARENT POPULATIONS.....	61
MEANS OF PARENTS AND DERIVED RELATIVES	69
Parents, parents selfed and F_1 's	69
Parents, parents selfed, F_1 's, F_1 's random mated	

and backcrosses	79
ESTIMATION OF GENETIC EFFECTS.....	90
Parents, parents selfed and F_1 's.....	90
Parents, parents selfed, F_1 's, F_1 's random mated and backcrosses	101
SUMMARY AND CONCLUSIONS.....	110
BIBLIOGRAPHY.....	114
APPENDIX.....	122

PREVIEW

LIST OF TABLES

Table	Page
1. Material developed in the 1987 and 1988 nurseries and evaluated in the 1988 and 1989 field trials at Lincoln and Mead sites.....	42
2. Form of the analysis of variance for model 1 (one environment).....	50
3. Form of the analysis of variance for model 2 (Combined).....	52
4. Form of the analysis of variance, F-tests and null hypotheses in the estimation of genetic effects for n parent and derived populations (P , P^S , F_1) for one environment.....	57
5. Form of the analysis of variance, F-tests and null hypotheses in the estimation of genetic effects for n parent and derived populations (P , P^S , F_1) grown in four environments.....	58
6. Form of analysis of variance, F-tests and null hypotheses in the estimation of genetic effects for n parent and derived populations (P , P^S , F_1 , F_1^I , BC) for one environment.....	59
7. Form of the analysis of variance, F-tests and null hypotheses in the estimation of genetic effects for n parent and derived populations (P , P^S , F_1 , F_1^I , BC) grown in two environments.....	60

Table	Page
8. Analysis of variance (mean squares) of eight maize populations evaluated as populations per se and testcrosses grown over four environments.....	62
9. Mean performance of 8 maize populations, evaluated as populations per se (Ps) and testcrosses (Tc) using Mo.17 as a tester, grown over four environments.....	63
10. Analyses of variance (mean squares) of 8 parent and derived population (P, P ^s , F ₁) grown over four environments.....	71
11. Mean performance of 8 parent and derived populations (P, P ^s , F ₁) grown over four environments.....	72
12. Response to selection of five populations derived from NSo, grown as populations per se, selfed and average F ₁ crosses.....	78
13. Analyses of variance (mean squares) of 8 parent and derived populations (P, P ^s , F ₁ , F ₁ ^t , BC) grown over two environments	80
14. Mean performance of 8 parent and derived populations (P, P ^s , F ₁ , F ₁ ^t , BC) grown at two environments	81
15. Analyses of variance (mean squares) of the genetic effects of the Gardner-Eberhart model from 8 parent and derived populations (P, P ^s , F ₁). (Four environments)	91
16. Percent of the totals of sums of squares among	

Table	Page
generation means (P , P^s , F_1) and the genotype by environment interaction and significance of the corresponding mean squares attributed to different sets of parameters of the Gardner-Eberhart model ...	92
17. Percentages of heterosis in testcrosses and inbreeding depression, additive and dominance effects in yield, for eight parent populations (Four environments)	97
18. Heterosis expressed as percentage of F_1 cross over midparent (above diagonal), and in $Mg\ ha^{-1}$ from the Gardner-Eberhart model (below diagonal). (Four environments)	98
19. Analyses of variance (mean squares) of the genetic effects of the Gardner-Eberhart model from 8 parent and derived populations (P , P^s , F_1 , F_1^r , BC). (Two environments)	102
20. Percent of the totals of sums of squares among generation means (P , P^s , F_1 , F_1^r , BC_1 , BC_2) and the genotype by environment interaction and significance of the corresponding mean squares attributed to different sets of parameters of the Gardner-Eberhart model. (Two environments)	103

LIST OF FIGURES

Figure	Page
1. Yield percentage as populations per se and testcrosses over NSo	66
2. Yield percentage as populations per se and testcrosses over BSSSo	70
3. Yield performance of eight populations and their F_1 crosses. (Four environments)	76
4. Yield performance of parent populations and derived relatives. (Two environments)	88

LIST OF APPENDIX TABLES

Table	Page
A1. Analyses of variance (mean squares) of 8 parent and derived populations (P , P^S , F_1) grown at Lincoln 1988.....	123
A2. Analyses of variance (mean squares) of 8 parent and derived populations (P , P^S , F_1) grown at Mead 1988....	123
A3. Analyses of variance (mean squares) of 8 parent and derived populations (P , P^S , F_1) grown at Lincoln 1989.....	124
A4. Analyses of variance (mean squares) of 8 parent and derived populations (P , P^S , F_1) grown at Mead 1989....	124
A5. Mean performance of 8 parent and derived populations (P , P^S , F_1) grown at Lincoln 1988.....	125
A6. Mean performance of 8 parent and derived populations (P , P^S , F_1) grown at Mead 1988.....	127
A7. Mean performance of 8 parent and derived populations (P , P^S , F_1) grown at Lincoln 1989.....	129
A8. Mean performance of 8 parent and derived populations (P , P^S , F_1) grown at Mead 1989.....	131
A9. Analyses of variance (mean squares) of 8 parent and derived populations (P , P^S , F_1 , F_1^I , BC) grown at Lincoln 1989.....	133
A10. Analyses of variance (mean squares) of 8 parent and derived populations (P , P^S , F_1 , F_1^I , BC) grown	

Table	Page
at Mead 1989.....	133
A11. Mean performance of 8 parent and derived populations (P, P ^s , F ₁ , F ₁ ^r , BC) grown at Lincoln 1989	134
A12. Mean performance of 8 parent and derived populations (P, P ^s , F ₁ , F ₁ ^r , BC) grown at Mead 1989.....	139
A13. Analyses of variance (mean squares) of genetic effects of the Gardner-Eberhart model from 8 parent and derived populations (P, P ^s , F ₁). (Lincoln 1988).....	144
A14. Analyses of variance (mean squares) of the genetic effects of the Gardner-Eberhart model from 8 parent and derived populations (P, P ^s , F ₁). (Mead 1988).....	145
A15. Analyses of variance (mean squares) of the genetic effects of the Gardner-Eberhart model from 8 parent and derived populations (P, P ^s , F ₁). (Lincoln 1989)..	146
A16. Analyses of variance (mean squares) of genetic effects of the Gardner-Eberhart model from 8 parent and derived populations (P, P ^s , F ₁). (Mead 1989).....	147
A17. Analyses of variance (mean squares) of the genetic effects of the Gardner-Eberhart model from 8 parent and derived populations (P, P ^s , F ₁ , F ₁ ^r , BC). (Lincoln 1989).....	148
A18. Analyses of variance (mean squares) of the genetic effects of the Gardner-Eberhart model from 8 parent and derived populations (P, P ^s , F ₁ , F ₁ ^r , BC).(Mead 1989)..	149

INTRODUCTION

The estimation of genetic effects is essential in order to formulate strategies for a breeding program, and to select the most adequate breeding procedure for the improvement of desirable characteristics. Several methods have been used to estimate genetic effects from components of variance or from generation means.

Gardner (1990) indicated that "variance components methods must be used to predict response from selection and to compare different selection systems. Generation means methods are used to compare genetic effects and the contributions of different kinds of genetic effects to the total sums of squares among genotypes in original and selected populations and their relatives. Components of variance frequently lack precision, whereas genetic effects estimated from generation means are much more precise".

The Iowa Stiff Stalk Synthetic (SSS) was developed by Sprague (1946) from 16 lodging-resistant inbred lines. This synthetic has proven to be a most valuable germplasm resource for the entire corn breeding industry. Numerous improved populations and inbred lines have been extracted from it by both public and private breeders, and some of the improved versions of SSS have been the source of further improved lines

such as B73, one of the most widely used inbred lines in the history of the hybrid corn industry.

The objectives of this study were: 1) to assess the genetic differences among Iowa Stiff Stalk Synthetic and seven selected populations derived from it at the University of Nebraska, and 2) to estimate genetic parameters (a_j , d_j , h_{jj} , and aa_{jj}) and their proportional contribution to the total sums of squares due to genetic differences among the eight populations and derived relatives. The seven selected populations were derived using different recurrent selection systems and different selection criteria.

LITERATURE REVIEW

IMPORTANCE OF THE ESTIMATION OF GENETIC PARAMETERS

The development of statistical genetic theory has provided the foundation for a new level of corn breeding. Excellent progress has been obtained where breeding programs have been designed to maximize gain from selection with information based on statistical genetic theory (Eberhart, 1977).

After it was shown that genes controlling quantitative characters are inherited according to Mendelian laws, it was possible to deduce the consequences of segregation and recombination of genes influencing such traits, and to provide the theory for predicting the response to selection (Moll, 1959).

The reliability of the prediction of the response to selection is of concern to both geneticist and plant breeder. For the geneticist, the reliability of the predictions reflects the adequacy of the genetic theory on which the predictions are based. For the plant breeder, predicting response to selection offers a basis for choosing between kinds of selection procedures and between kinds of populations within which to select (Moll, 1959).

The purposes of the estimation of genetic parameters are three: 1) to obtain information about the type of gene action