

Contents

Preface

vii

1. Genes, Chromosomes and Characters

1.1

1.1 The Gene

1.1

1.2 Biochemistry of the Gene

1.2

1.3 Chromosomes

1.5

1.4 Characters

1.6

1.5 Protein Synthesis

1.6

References

1.8

2. Analysis of Qualitative Traits

2.1

2.1 Gene Action and Interaction

2.1

2.1.1 Dominance

2.1

2.1.2 Overdominance

2.2

2.1.3 Co-dominance

2.3

2.1.4 Multiple alleles

2.3

2.1.5 Epistasis or non-allelic interaction

2.3

2.2 Application of Laws of Probability

2.5

2.2.1 Application to cases of two or more genes

2.6

2.2.2 Types of probability

2.6

2.2.3 Binomial probability

2.7

2.2.4 Multinomial probability

2.7

2.3 Test of Goodness of Fit

2.8

2.3.1 Two factor segregation

2.8

2.3.2 Test of heterogeneity of families

2.9

2.3.3 Testing of independence

2.9

2.4 Experimental Size

2.10

2.4.1 Distinction between two hypotheses

2.10

2.5 Linkage and Pleiotropy

2.12

2.5.1 Detection of linkage

2.12

2.5.2 Estimation of recombination frequency

2.13

2.5.3	Efficiency of different types of families	2.14
2.5.4	Factors affecting the recombination frequency	2.15
2.5.5	Pleiotropy	2.15
2.6	Extra Chromosomal Inheritance	2.16
2.6.1	Criterion for extra-chromosomal inheritance	2.16
2.6.2	Cell organelles	2.17
2.7	Sex-Determination	2.19
2.8	Expression of Qualitative Gene(s)	2.20
2.8.1	Penetrance and expressivity	2.21
2.9	Estimation of Gene Frequency	2.21
2.9.1	Incomplete dominance	2.21
2.9.2	Multiple alleles	2.21
2.10	Estimation of Genetic Diversity	2.22
	<i>References</i>	2.22
3.	Analysis of Quantitative Traits	3.1
3.1	Theories of Quantitative Variability	3.3
3.2	Description of Normal Distribution Curve	3.4
3.2.1	Mean	3.5
3.2.2	Mode and median	3.6
3.2.3	Variance and covariance	3.6
3.2.4	Range	3.6
3.2.5	Skewness and kurtosis	3.6
3.3	Threshold Variability	3.8
3.4	Meristic Variability	3.9
3.5	Poisson Distribution	3.9
3.6	Modifications of Binomial and Poisson Distributions	3.10
3.6.1	Gamma distribution	3.10
3.6.2	Hypergeometric distribution	3.10
3.7	Bi-modal and Multimodal Distributions	3.11
	<i>References</i>	3.11
4.	Statistical Estimations, Tests, Models and Designs	4.1
4.1	Estimation and Inference	4.1
4.1.1	Methods of estimation	4.1
4.2	Test of Significance	4.2
4.2.1	Chi-square test	4.3
4.2.2	F-test	4.3

4.2.3	The t -test	4.4
4.2.4	Z-distribution	4.5
4.2.5	Relationship between different distributions	4.5
4.2.6	Non-central chi-square	4.5
4.2.7	Non-central F	4.5
4.3	Statistical Models and Expectation of Mean Squares	4.6
4.3.1	Fixed model	4.6
4.3.2	Random model	4.6
4.3.3	Mixed model	4.7
4.4	Experimental Designs and Calculation of Mean Squares	4.7
4.4.1	Randomized Complete Block Design (RBD)	4.7
4.4.2	Nested design	4.8
4.4.3	Cross-classified design	4.9
4.4.4	Factorial experiment	4.10
4.4.5	Analysis of co-variance	4.11
4.5	Correlation and Regression Analysis	4.12
4.5.1	Correlation coefficient	4.12
4.5.2	Regression analysis	4.13
4.5.3	Joint regression analysis	4.14
4.5.4	Multiple regression	4.15
4.5.5	Partial correlation and regression	4.15
4.5.6	Multiple correlation	4.15
4.6	Orthogonal Polynomial	4.15
4.7	Non-Parametric Statistics	4.16
4.8	Multivariate Analysis	4.17
4.8.1	Principal component analysis	4.17
4.8.2	Factor analysis	4.18
4.8.3	Canonical analysis	4.18
4.8.4	Discrimination and classification	4.19
4.8.5	Principal co-ordinate analysis	4.19
4.9	Growth Curves	4.20
4.9.1	Competition	4.22
	<i>References</i>	4.23
5.	Analysis of Means	5.1
5.1	Scaling Tests	5.2
5.2	Estimation of Parameters	5.3
5.3	Epistasis or Non-allelic Interaction	5.4
5.4	Estimation of Coefficient of Dispersion	5.6

5.5	Concept of Average Effect of Gene	5.7
5.6	Other Models of Estimation of Genetic Effects	5.9
5.7	Detection of Epistasis by other Methods	5.10
	<i>References</i>	5.12
6.	Analysis of Variance and Covariance	6.1
6.1	Partitioning of Variance	6.1
6.2	Estimation of Variances in Generations Derived from Cross of two Pure Breeding Lines	6.1
6.3	Covariance/Correlation	6.3
6.4	Estimation of Variances in Random Mating Population	6.4
6.5	Development of Progenies	6.4
6.6	Estimation of Components of Variation	6.5
6.7	Expectations of σ_w^2 , σ_b^2 , σ_m^2 (or σ_f^2),	6.7
6.7.1	Covariance between relatives in random mating population	6.9
6.6	NCM III and TTC	6.10
6.6.1	NCM III	6.10
6.8.2	TTC (Triple Test Cross)	6.10
6.8.3	Consequences of inadequacy of testers in triple test cross	6.12
6.9	Variants of TTC	6.13
6.9.1	TTC with population of inbred lines	6.13
6.9.2	Triple test cross (selfed families)	6.13
6.10	Model Fitting to Mean Squares	6.14
6.11	Comparison of Efficiency of the Mating Designs	6.14
6.11.1	Selection of a particular mating design	6.20
6.12	Uses of Estimates of Components of Variation	6.20
6.13	Negative Estimates of Variance Components	6.20
6.14	Comparison of Variability	6.20
6.15	Partitioning of Covariance/Correlation	6.21
6.15.1	Partitioning of correlation coefficient	6.21
6.15.2	Calculation of additive genetic correlation	6.22
6.15.3	Standard error of correlation coefficient	6.22
6.16	Intra-Class Correlation	6.23
6.17	Repeatability	6.23
	<i>References</i>	6.24
7.	Diallel Analyses	7.1
7.1	Full Diallel Analysis	7.1

7.2	Half Diallel Analysis	7.3
7.3	Genetical Structure of Quantitative Traits	7.3
7.3.1	$W_r - V_r$ analysis	7.4
7.4	Estimation of Genetical Components of Variation	7.6
7.4.1	F_2 Diallel	7.8
7.5	Diallel Analysis with Heterozygous Parents	7.9
7.5.1	Identification of heterozygous parent(s)	7.10
7.6	Combining Ability Analysis	7.10
7.6.1	Estimation of GCA and SCA effects	7.11
7.6.2	Estimation of GCA and SCA variances	7.12
7.7	Partial Diallel	7.14
7.7.1	Number of crosses per parent in partial diallel	7.15
7.8	Number of Parents, Family Size and Number of Replications in Diallel	7.16
7.9	Reference Population in Diallel	7.17
7.10	Comparison with other Mating Designs	7.18
7.11	Assumptions under Diallel Analysis	7.18
7.12	Varietal Diallel	7.19
7.13	Triallel Analysis	7.20
7.13.1	Order of lines in three-way hybrids	7.22
	<i>References</i>	7.22
8.	Genotype $\times$ Environment Interaction	8.1
8.1	Definition	8.1
8.2	ANOVA for Genotype $\times$ Environment Interaction	8.2
8.3	Types of Environment	8.4
8.4	Approaches to Analysis of $g \times e$ Interaction	8.5
8.4.1	Regression analysis	8.5
8.4.2	Analysis of non-linear genotype $\times$ environment interaction	8.15
8.4.3	Limitations with regression models	8.17
8.5	Multivariate Analysis of Genotype $\times$ Environment Interaction	8.18
8.5.1	Principal component analysis	8.18
8.5.2	Biplot method	8.18
8.5.3	GGE biplot	8.20
8.6	Non-Parametric Approach	8.22
8.6.1	Cluster analysis	8.22
8.6.2	Ranks of genotypes	8.24
8.6.3	Study of environmental factors	8.25

8.7	Genetical Analysis of Genotype $\times$ Environment Interactions	8.26
8.7.1	Generations derived from cross of two pure breeding lines	8.27
8.7.2	Multiple mating design	8.30
8.7.3	Interaction between epistatic gene action and environment	8.32
8.8	Genetic Control of Environmental Sensitivity	8.33
8.8.1	Theories of environmental sensitivity	8.33
8.8.2	General or specific nature of genotypes involvement in environmental sensitivity	8.35
8.8.3	Choice of selection environment and the effect of the chosen environment on the properties of the selected lines	8.35
	<i>References</i>	8.36
9.	Analysis of Reciprocal Differences	9.1
9.1	Maternal Effects	9.1
9.2	Estimation of Maternal Effects	9.2
9.2.1	Generations derived from the cross of two pure breeding lines	9.2
9.2.2	Multiple mating designs	9.4
9.3	Detection of Epistasis and Linkage of Epistatic Genes in the Presence of Reciprocal Differences	9.5
9.4	Reciprocal Effects Model	9.6
9.5	Covariances between Relatives	9.11
9.6	Sex Linkage	9.11
9.7	Sex Limitation	9.13
	<i>References</i>	9.16
10.	Linkage and Epistasis	10.1
10.1	Linkage	10.1
10.2	Effect of Random Mating on Linkage Disequilibrium	10.2
10.3	Effect of Linkage on Variances of Advancing Generations Derived by Selfing Cross between Pairs of Purebreeding Lines	10.2
10.4	Detection of Linkage Disequilibrium	10.4
10.5	Generation that Yields an Approximate Estimate of DVF_{∞}	10.5
10.6	Effect of Linkage on Covariances	10.6
10.7	Linkage vs. Pleiotropy	10.7
10.8	Epistasis	10.7
10.9	Effect of Non-allelic Interaction on Estimation of Variance Components	10.9
10.9.1	Biases in D and H components obtained from T.T.C.	10.9
10.10	Comparison of Tests of Epistasis	10.10

10.11	Epistasis in Random Mating Population	10.10
10.12	Detection of Linked Epistasis	10.13
	<i>References</i>	10.14

11.	Heterosis and Inbreeding Depression	11.1
11.1	Heterosis	11.1
11.2	Theories of Heterosis	11.1
11.3	Expressing Heterosis in Terms of Biometrical Parameters	11.3
11.3.1	Generation means	11.3
11.3.2	Variances	11.4
11.4	Effect of Linkage Disequilibrium on Dominance Ratio	11.4
11.5	Effect of Interaction on Dominance Ratio	11.5
11.6	Environmental Heterosis	11.6
11.7	Dominance Ratio	11.7
11.8	Maternal Effects in Heterosis	11.7
11.9	Heterosis in Population Cross	11.9
11.10	Misinterpretation of Heterosis	11.10
11.11	Genetic Distance/Divergence	11.10
11.11.1	Estimation of genetic distance	11.11
11.11.2	Cluster formation	11.12
11.11.3	Intra- and inter-cluster distances	11.12
11.11.4	Use of genetic parameters in the estimation of genetic distance	11.13
11.12	Inbreeding Depression	11.13
11.13	Inbreeding in Random Mating Population	11.14
11.14	Estimation of Inbreeding Coefficient	11.16
11.15	Other System of Inbreeding	11.19
	<i>References</i>	11.21

12.	Polyploids and Haploids	12.1
12.1	Definition and Classification	12.1
12.2	Biometrical Genetics of Autotetraploids	12.2
12.3	Scaling Tests	12.4
12.4	Variances and Covariances	12.4
12.5	Random Mating Population	12.5
12.6	Triploids	12.6
12.7	Haploids	12.8
12.7.1	Production of haploids	12.8
12.7.2	Identification of haploids	12.9

12.7.3	Advantages and disadvantages	
12.7.4	<i>Biometrical genetics of haploids</i>	12.9
12.8	Doubled Haploids	12.11
12.8.1	Analysis of means	12.12
12.8.2	Analysis of variances	12.12
12.8.3	Estimation of additive and additive $\times$ additive interaction variances	12.13
12.8.4	Estimation of dominance variance and the degree of dominance	12.14
12.8.5	Linkage disequilibrium	12.15
12.8.6	Estimation of recombination value	12.16
12.8.7	Skewness and kurtosis	12.16
12.8.8	Estimation of number of effective factors	12.17
12.8.9	Covariances/correlation	12.17
12.8.10	Generation of deriving <i>DH</i> lines	12.19
12.8.11	Efficiency of <i>DH</i> method	12.19
	<i>References</i>	12.20
13.	Competition	13.1
13.1	Definition and Types	13.1
13.2	Yield-Density Relationship	13.2
13.3	Mixture Diallels	13.3
13.4	Intergenotypic Competition	13.4
13.4.1	Estimation of a , b_m and b_d	13.4
13.4.2	Partitioning of C -values	13.6
13.5	Nature of the Underlying Genetical Control of Competition and Competitive Ability	13.7
13.6	Competition in Natural Population	13.8
13.7	Estimation of Outcrossing Rate	13.8
13.8	Detection of Competition	13.11
	<i>References</i>	13.11
14.	Environmental Variation	14.1
14.1	Definition and Types	14.1
14.2	Estimation of Environmental Variation	14.1
14.3	Individual Plant Randomization	14.2
14.4	Sampling Variation	14.3
14.5	Other Experimental Designs	14.3
14.6	Estimation of Experimental Error	14.4
14.7	Augmented Design	14.4

14.8	Environmental Covariance	14.5
	<i>References</i>	14.5
15.	Heritability	15.1
15.1	Definition and Types	15.1
15.2	Heritability a Characteristic of Population	15.2
15.3	Estimates of Heritability	15.2
15.4	Effect of $G \times E$ Interaction	15.3
15.5	Uses of Estimates of Heritability	15.3
15.6	Changing Estimates of Heritability	15.4
15.7	Problems in use of Estimate of Heritability	15.4
	<i>References</i>	15.4
16.	Estimation of the Number of Effective Factors	16.1
16.1	Approaches to Estimation of Number of Genes	16.1
16.2	Chromosome Assay	16.2
16.3	Statistical Properties of Distribution	16.2
16.4	Estimate of k using Dominance Genetic Effect and Dominance Genetic Variance	16.3
16.5	Use of F_2 Derived Generation Variances	16.3
16.6	Estimation of Number of Effective Factors in Random Mating Population	16.3
16.7	Genotype Assay	16.5
16.7.1	Theory	16.5
16.8	Use of Dihaploids in the Estimation of Number of genes	16.7
16.8.1	Use of range and genetical variance of an F_1 , F_2 derived DH populations	16.8
16.8.2	Use of variances of F_2 -derived population	16.8
16.8.3	Genotype assay	16.9
16.9	Estimation of the Number of Effective Factors in Haploids	16.9
16.10	Method for Locating Genes	16.9
	<i>References</i>	16.9
17.	Analysis of Skewness and Kurtosis	17.1
17.1	Genetical Causes of Skewness and Kurtosis	17.1
17.2	Information on Gene Action and Interaction	17.1
17.3	Estimation of Coefficients of Skewness and Kurtosis in Population of Pure Breeding Lines	17.2

17.4	Effects of Random Environmental Variation and Genotype $\times$ Environment Interaction	17.3
17.5	Estimation of Skewness and Kurtosis in Dihaploid Population	17.4
17.6	Effect of Skewness on Selection	17.4
	<i>References</i>	17.5
18.	Transformation of Scale	18.1
18.1	Tests of Non-normality	18.1
18.2	Relation of Variability to Mean	18.2
18.3	Scale Effect	18.3
18.4	Variance Stabilizing Transformation	18.3
18.5	Poisson Distribution	18.3
18.6	Binomial Distribution	18.3
	<i>References</i>	18.4
19.	Genetic Structure of Population	19.1
19.1	The Hardy-Weinberg Equilibrium	19.1
19.1.1	Testing goodness of fit	19.1
19.1.2	Extension of H. W. equilibrium to cases of multiple alleles, sex-linked genes and polygenic inheritance	19.2
19.1.3	Sex-linked loci	19.3
19.1.4	Polygenic traits	19.3
19.2	Changes in Gene Frequency	19.4
19.2.1	Effects of non-random mating	19.4
19.2.2	Self-fertilization	19.4
19.2.3	Sib mating	19.4
19.2.4	Assortative mating	19.4
19.2.5	Negative assortative mating	19.5
19.3	Mutation	19.5
19.3.1	Balance between mutation and selection	19.6
19.4	Selection	19.8
19.4.1	Complete elimination of recessive homozygotes	19.9
19.4.2	Balance between selection and inbreeding	19.10
19.5	Competitive Selection	19.10
19.6	Migration	19.11
19.6.1	Balance between selection and migration	19.11
19.6.2	Models for studying the population structure	19.11

19.7	Drift	19.12
19.7.1	Effective population size	19.14
19.7.2	Random genetic drift in natural populations	19.15
19.8	The Founder Principle	19.16
19.9	Gametic Selection	19.16
19.10	Meiotic Drive	19.17
19.11	Genetic Load	19.17
19.11.1	Segregational load	19.17
19.11.2	Mutational load	19.19
	<i>References</i>	19.19
20.	Selection Theory	20.1
20.1	Response to Selection	20.1
20.1.1	Selection differential	20.2
20.1.2	Response due to selection in tetraploid	20.3
20.2	Correlated Response	20.3
20.3	Path Analysis	20.5
20.3.1	Determination of residual variability	20.6
20.3.2	Path coefficient vs correlation coefficient	20.6
20.3.3	Application of path analysis	20.7
20.4	Yield and Yield Components	20.7
20.5	Types of Selection	20.8
20.5.1	Efficiency of different methods	20.8
20.5.2	Combined selection	20.10
20.6	Selection Criterion	20.10
20.6.1	Single trait selection	20.10
20.6.2	Multitrait selection	20.10
20.7	Comparison of Efficiency of Different Methods	20.13
20.8	Selection Limit	20.13
20.9	Natural Selection	20.14
20.9.1	Stabilizing selection	20.15
20.9.2	Directional selection	20.16
20.9.3	Disruptive selection	20.16
	<i>References</i>	20.18
21.	QTL Analysis	21.1
21.1	QTL Analysis	21.1
21.1.1	Linkage between QTL and molecular marker	21.2
21.1.2	Mapping methods	21.2

21.2	Models for Estimating Genetic Effects of QTL	21.10
21.3	Mapping Populations	21.19
21.4	Population Size	21.20
21.5	Experimental Design	21.20
21.6	Mapping in Polyploids	21.22
21.6.1	Methods of linkage analysis	21.24
21.7	Genetic Mapping	21.25
21.8	Information from QTL Mapping	21.28
21.9	Comparative Mapping and Orthologous Poly Genes	21.32
21.10	Identification of Links between Genotype and Phenotype	21.33
	<i>References</i>	21.35

22. Matrix

22.1	Definition and Types	22.1
22.2	Matrix Operations	22.1
22.3	Dispersion Matrix	22.5
22.4	Orthogonal Matrix	22.6
22.5	Diagonalization of Matrix	22.6
	<i>References</i>	22.6

23. Problems in Biometrical Genetics**23.1***Index**I.1-I.5*