

Statistical and Biometrical Techniques in Plant Breeding

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The study of genetic variation in quantitative traits is essential for successful exploitation of genetic variability. The quantitative traits can be analysed following statistical and biometrical tools to help breeder in designing a suitable breeding methodology. Such analyses include estimation of parameters of genetic variability, nature of gene action and gene interactions, genotypes \times environment interactions, estimation of parameters useful in selection etc.

Most plant breeders generally lack the mathematical training needed for utilization of such available statistical tools. Therefore, they depend on computer software packages and help books available on the subject. Quite a few handbooks on such biometrical tools have been written in the last decade in India. The present book is another addition in the list, where such analyses have been explained with the help of solved examples along with inference to be drawn from them.

The book has been divided into five parts namely, 1. General Statistical/Biomtrical Parameters and Field Designs, 2. Mathematical Analysis of Genetic Divergence, 3. Analysis of $G \times E$ Interaction and Stability Parameters, 4. Analysis of Gene Action and Variance Components and 5. Statistical/Genetical Parameters in Selection and Mutation Experiments.

Critically seen, each part has its plus and minus points e.g., in part I measures of dispersion have been presented from an example of date of 7 F_3 families on numbers of tillers/plant in wheat grown in RCBD. An example of raw data and from which frequency distribution is prepared and estimates of measures of central tendency and dispersion worked out would have been more appropriate.

In section 3 of this part, only two field designs namely Randomised Complete Block Design and Augmented Designs have been presented but more often than not plant breeders use split plot/compact family block designs and some incomplete block designs such as simple lattice.

Again the concepts of standard deviation and standard error have to be qualified by referring to a

given statistic. Likewise concept of degree of freedom has to be related to concept of unbiasedness of the estimator.

In Chapter 6 (Part II) on D^2 -statistic, choice of characters for this analysis has been discussed only passingly. D^2 analysis has been rather indiscriminately used by many plant breeders with the results that outcome of such analysis has not been consistent with practical utilization part. Many a times, characters which do not follow normal probability/frequency distribution and the groups of character which do not follow multivariate normal distribution are included in D^2 analysis. Therefore, while giving the example on D^2 , these points need to be explained much more explicitly.

In Chapter 8 (Part III) on $G \times E$ interaction, expectation of mean squares have been based on "Random effect model" but in actual multi location trials, more often than not, mixed or fixed effect models are needed. A basic assumption on analysis of such trials, which has been and generally ignored, is homogeneity of error variances in such trials. Attention towards this should have been drawn in the worked example.

While dealing with "Regression analysis of Stability" in Chapter 9, the mistake committed in original papers by the authors on allotment of degrees of freedom has again been repeated in the example e.g., regression S.S. should carry 7 d.f. (Table 9-2) instead of 6, since there are seven genotypes, performance of each of which has been regressed on location means with 1 d.f., while the degrees of freedom for S.S. due to deviation from regression should be 28. In example on Eberhart and Russell Stability model (Chapter 10), the mistake committed by authors on allotment of one degree of freedom for Environment (linear), which should actually should carry $(l-1)$ d.f. where l is number of locations, (c.f. Daljeet Singh, Ind. J. Genet.,) needed to be pointed out and attention of readers should have been drawn to this inconsistency.

Part IV on "Analysis of gene action and variance components" gives analysis of (i) Top cross and polycross, (ii) Line \times Tester, (iii) Partial diallel, (iv) Tests of epistasis, (v) Hayman model of diallel analysis, (vi)

Griffings model of diallel analysis, (vii) Variety-diallel cross model of Eberhart and Gardner, (viii) Emara's model of analysis of population (ix) Kearsley's model of biparental progeny analysis (x) NCD I, II and III designs, (xi) Analysis of generation means and (xii) Detection of epistasis and variance components. Where the aim of plant breeder is to estimate the genetical components of variation, most plant breeders and students alike are prone to confuse between "Reference" and "Inference" populations. Some of the mating designs like NCD I, II and III, Biparental matings, Triple test cross, Diallel (Eberhart and Gardner model, Griffings model) and Partial Diallel Cross matings are based on generating different types of families and working out variances and covariances from relatives, the "Reference" population is the random mating population from which through appropriate sampling procedures, selection of parents is done and mating carried out. Therefore such points/explanations are to be brought out very clearly along side with solved examples as also to what appropriate inference can be drawn in each case. Also the assumptions required for drawing valid inferences e.g. (i) Parents randomly drawn (ii) The population is in random mating equilibrium (iii) Normal diploid behaviour at meiosis (iv) No environmental correlation among progenies (v) Progenies are not inbred (vi) Linkage equilibrium exists (vii) Experimental errors are normally and independently distributed, should have been emphasized upon in the example.

Similarly when dealing with fixed effect models (Hayman, 1954, Griffings, 1956) of diallel analysis, We wish author should have devoted some space to drawing of valid inference and uses (and misuses) of statistical

models in plant breeding with appropriate examples from literature.

Part V of the book which deals with statistical/genetical parameters in "Selection and Mutation Experiments" gives solved examples on estimation of parameters of expected and realised heritability, expected and realised response to selection, intra-class correlation and correlated response etc. In addition, part V also includes analysis of data of an experiment on Disruptive selection. However, an example on "Discriminant Function for Plant Selection" should have also been included.

Chapter 25, (Part V) of the book deals with analysis of data of variation in polygenic traits induced through mutations. An important consideration in any mutation experiments is the nature of frequency distribution in M_2 and M_3 populations. Measure of skewness and kurtosis should have been elaborated with an example to reveal the behaviour of such populations.

It is hoped, the author would take care of some of the points discussed above as well as of the points not discussed. The arrangement of the book also needs some attention.

The book will be useful to the graduate/post graduate students as well as researchers in plant breeding in Agricultural Universities in India in undertaking biometrical analysis of their research data.

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Introduction to Plant Biotechnology

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The subject of Biotechnology has recently attained a great significance as this branch of science is being visualized as the science of twenty first century that will play a very significant role in shaping human life. Consequently, the study of biotechnology has occupied a prominent place in the syllabi of almost all the Indian universities. To cater the needs of students and teachers, many books by foreign authors are available,

which are basically reference books dealing with specialized topics in biotechnology. A few Indian authors have tried to fill the vacuum by writing textbooks according to syllabi prescribed in Indian Universities. However, facing the constraint of size and price, these books try to include all aspects of biotechnology and fail to give a fairly detailed treatment to the different topics covered. In this context, the book under review