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# Analysis Of Diallel Mating Designs Nc State University

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Quantitative Genetics and Crop Breeding  
Analysis of Variance for Random Models, Volume 2: Unbalanced Data  
Research, Management and Development  
Avian Research  
Theory, Methods, Applications, and Data Analysis  
Design and Analysis of Experiments, Special Designs and Applications  
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Applied Quantitative Genetics  
Genetic Evaluation of Rapid Height Growth in Pot- and Nursery-grown Scotch Pine  
Plant Breeding Reviews  
Concepts and Applications in Genetics, Evolution, and Breeding : an Interactive Computer-based Laboratory Manual  
Plant Breeding and Cultivar Development  
Plant Breeding  
Principles of Plant Genetics and Breeding  
Proper Analysis of the Diallel Mating Design  
Scientist and Farmer  
Elements Of Bio Metrical Genetics (revised And Enlarged Edition)  
The Potato Crop  
Genetical Analysis of Quantitative Traits  
Quantitative Genetics and Breeding Methods in Autopolyploid Plants  
Estimation of Genetic Parameters Under Optimal and Suboptimal Environments for Body Weight in Chicken Using a Diallel Mating System  
Genetic Analysis of Diallel Tests of Loblolly Pine (Pinus Taeda L.).  
Quantitative Genetics in Maize Breeding  
An Introduction to Plant Breeding  
SUWAN-1: Maize from Thailand to the world

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## AVA LAILA

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### **Quantitative Genetics and Crop Breeding** Springer

S2Genetic and environmental components of variance for 2-year heights of offspring from inter- and intra-provenance matings in Scotch pine (*Pinus sylvestris* L.) were studied to determine which provenances and selection methods should be used in a program to improve ornamental and Christmas trees. The study represents 11 experiments (parental groups), consisting of families from 7 diallel matings minus selfs in 5 different provenances, 3 factorial matings between provenances, and 1 from open pollination. The seedlings for the 11 experiments were grown in pots and in a nursery for 2 years. Heritability estimates of 2-year height from inter- and intra-provenance matings tended to be larger on a family basis than on an individual basis, with the larger estimates being from nursery evaluations. In general, additive genetic variance was larger than dominance variance, although dominance variance increased in provenance hybrids. Nursery evaluation was preferred to pot evaluation of 2-year height because heritability estimates were larger and error variances were smaller for the experiments evaluated. Individual selection in the nursery within the German provenance seems to be the best method for improvement of 2-year height of the provenances evaluated in this study, although the rate of improvement in the Spanish provenance may be greater. Simple recurrent selection would be a good method for improvement of traits important to the Christmas tree producing industry.S3.

Analysis of Variance for Random Models, Volume 2: Unbalanced Data John Wiley & Sons

Plant Breeding and Cultivar Development features an optimal balance between classical and modern tools and techniques related to plant breeding. Written for a global audience and based on the extensive international experience of the authors, the book features pertinent examples from major and minor world crops. Advanced data analytics (machine learning), phenomics and artificial intelligence are explored in the book's 30 chapters that cover classical and modern plant breeding. By presenting these advancements in specific detail, private and public sector breeding programs will learn about new, effective and efficient implementation. The insights are clear enough that non-plant breeding majoring students will find it useful to learn about the subject, while advanced level students and researchers and practitioners will find practical examples that help them implement their work. Bridges the gap between conventional breeding practices and state-of-the-art technologies Provides real-world case studies of a wide range of plant breeding techniques and practices Combines insights from genetics, genomics, breeding science, statistics, computer science and engineering for crop improvement and cultivar development

**Research, Management and Development** Springer Science & Business Media

The Indian Society of Genetics and Plant Breeding was established in 1941 in recognition of the growing contribution of improved crop varieties to the country's agriculture. Scientific plant breeding had started in India soon after the rediscovery of Mendel's laws of heredity. The Indian Agricultural

Research Institute set up in 1905 and a number of Agricultural Colleges in different parts of the country carried out some of the earliest work mostly in the form of pure-line selections. In subsequent years, hybridization programmes in crops like wheat, rice, oilseeds, grain legumes, sugarcane and cotton yielded a large number of improved cultivars with significantly higher yields. A turning point came in the 1960s with the development of hybrids in several crops including inter-specific hybrids in cotton. And when new germplasm with dwarfing genes became available in wheat and rice from CIMMYT and IRRI, respectively, Indian plant breeders quickly incorporated these genes into the genetic background of the country's widely grown varieties with excellent grain quality and other desirable traits. This was to mark the beginning of modern agriculture in India as more and more varieties were developed, characterized by a high harvest index and response to modern farm inputs like the inorganic fertilizers. India's green revolution which has led to major surpluses of food grains and other commodities like sugar and cotton has been made possible by the work of one of the largest groups of plant breeders working in a coordinated network.

**Avian Research** John Wiley & Sons

Proper Analysis of the Diallel Mating Design Genetic Analysis of Diallel Tests of Loblolly Pine (*Pinus Taeda* L.).

**Theory, Methods, Applications, and Data Analysis** PHI Learning Pvt. Ltd.

The present work is unique in that sense it gives formulae along with actual data analyzed for the easy understanding. This book is mainly meant for post graduate and research scholars in Quantitative Genetics. A careful perusal of the book will give clear cut idea about the interpretation of the data and formulation of breeding strategies.

**Design and Analysis of Experiments, Special Designs and Applications** Alpha Science Int'l Ltd.

This text provides a guide to the experimental and analytical methodologies available to study quantitative traits, a review of the genetic control of quantitative traits, and a discussion of how this knowledge can be applied to breeding problems and evolution.

*Crossover* World Scientific

Crossover is a laboratory manual and computer program that work together to teach the principles of genetics. Designed to complement regular textbooks and classroom instruction, Crossover consists of thirty-five modules that can be tailored to fit genetics courses at several levels. Examples, interactive computer models, problems, and self-tests all help students understand difficult concepts and learn the basic mathematical skills needed to study contemporary theories of genetics, evolution, and breeding. The easy-to-use tutorial system lets students work at their own pace. Features include: \* In-depth investigations of meiosis, genetic ratios, linkage mutation, natural selection, Hardy-Weinberg equilibrium, artificial selection, quantitative genetics, breeding methods, mating designs, plant patent law, and the use of molecular markers \* A computer model that allows students to manipulate genetic parameters and compare outcomes. Students can observe evolution and artificial selection in action \* A "Major Concepts" section at the beginning of each chapter to

help students focus on the important material to be learned \* A visual, easy-to-understand presentation of material \* Exercises based on genetic data and analyses from actual research projects \* Several stages of complexity within each area of instruction. \* Instant grading of exercises \* "Suggested Readings" at the end of each chapter to direct the student to related books, articles, and computer programs.

**Marker-Assisted Plant Breeding: Principles and Practices** International Potato Center

A new approach was developed for analyzing diallel tests with SAS PROC MIXED and PROC IML. The new method can estimate variance components, obtain BLUE (best linear unbiased estimators) of fixed effects and BLUP (best linear unbiased predictors) of random genetic effects simultaneously. A new formula based on BLUP was further developed to predict individual tree breeding values. This new analytical method was validated using computer simulation and was compared with other existing programs. To analyze disconnected diallel mating designs with more than one diallel, simulated data generated with known parameters were analyzed using BLUP to compare three alternative models, which include diallel as fixed effect (Model 1), random effect (Model 2) or no diallel effect (Model 3). Both Model 1 and Model 3 produced unbiased GCA (general combining ability) variance estimates, while Model 2 resulted in downward biased GCA variance estimate. The accuracy of BLUP prediction for three models was very close, with Model 3 slightly better than the other two. Statistical approaches were also evaluated for combining multiple disconnected diallel test series in a given region. The best GCA sample variance prediction in the class of linear combination of local variance estimates was derived. Simulation study showed that a checklot adjustment was very critical to improve the prediction of genetic values obtained using BLUP analysis. Additional adjustment with improved GCA sample variance prediction could improve the correlation slightly beyond checklot adjustment. Analysis of annual measurement through age 8 from a total of 275 parents, 690 full-sib families from 23 diallel tests of loblolly pine in Northern, Coastal and Piedmont test regions showed: 1) dominance variance was small (20-40% of total genetic variance) relative to additive variance; 2) heritability increased over time, and the magnitude of heritabilities for diameter at breast height (DBH) and volume was comparable with the.

**Diversity Study Based on Quality Traits and RAPD Markers and Investigation of Heterosis in Ethiopian Mustard** Newnes

This book discusses special modifications and extensions of designs that arise in certain fields of application such as genetics, bioinformatics, agriculture, medicine, manufacturing, marketing, etc. Well-known and highly-regarded contributors have written individual chapters that have been extensively reviewed by the Editor to ensure that each individual contribution relates to material found in Volumes 1 and 2 of this book series. The chapters in Volume 3 have an introductory/historical component and proceed to a more advanced technical level to discuss the latest results and future developm.

**Mendelian to Molecular Approaches** Springer

A 2 x 2 x 2N confounded diallel mating design (2 series, 2 males, N females per male per series) was used to obtain estimates of the genetic parameters in body weight traits in a noninbred population of New Hampshire chickens grown on 18% and 24% protein rations. Individual selection also was

applied to evaluate the reliability of the genetic parameters obtained under each protein level. The analysis showed an extremely large contribution of series effects to the total variation in the traits which was attributed to the environmental influences from one series to the other and to the maternal environment. The component of variance due to series x male interaction was found to be small or zero under the 24% protein ration. An optimal environment may have given certain genotypes a greater opportunity to adapt to the environment. The higher estimates of the component of variance of series x female interaction for one-day body weight suggests the influence of maternal effects from one series to the other and from one dam to the other. Generally, estimates for the component of variance of male effects were higher under the 18% protein ration than under the 24% protein ration. Conversely, the component of variance of female effects showed higher values under the 24% protein ration than under 18% protein ration for most of the traits considered.

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**Hybridization of Crop Plants** New India Publishing Agency

This book is open access under a CC BY 4.0 license. This book provides a fresh, updated and science-based perspective on the current status and prospects of the diverse array of topics related to the potato, and was written by distinguished scientists with hands-on global experience in research aspects related to potato. The potato is the third most important global food crop in terms of consumption. Being the only vegetatively propagated species among the world's main five staple crops creates both issues and opportunities for the potato: on the one hand, this constrains the speed of its geographic expansion and its options for international commercialization and distribution when compared with commodity crops such as maize, wheat or rice. On the other, it provides an effective insulation against speculation and unforeseen spikes in commodity prices, since the potato does not represent a good traded on global markets. These two factors highlight the underappreciated and underrated role of the potato as a dependable nutrition security crop, one that can mitigate turmoil in world food supply and demand and political instability in some developing countries. Increasingly, the global role of the potato has expanded from a profitable crop in developing countries to a crop providing income and nutrition security in developing ones. This book will appeal to academics and students of crop sciences, but also policy makers and other stakeholders involved in the potato and its contribution to humankind's food security.

**Combining-ability determinations for incomplete mating designs** Springer Science & Business Media  
This book fills the gap between textbooks of quantitative genetic theory, and software manuals that provide details on analytical methods but little context or perspective on which methods may be most appropriate for a particular application. Accordingly this book is composed of two sections. The first section (Chapters 1 to 8) covers topics of classical phenotypic data analysis for prediction of breeding values in animal and plant breeding programs. In the second section (Chapters 9 to 13) we provide the concept and overall review of available tools for using DNA markers for predictions of genetic merits in breeding populations. With advances in DNA sequencing technologies, genomic data, especially single nucleotide polymorphism (SNP) markers, have become available for animal and plant breeding programs in recent years. Analysis of DNA markers for prediction of genetic merit is a relatively new and active research area. The algorithms and software to implement these algorithms are changing rapidly. This section represents state-of-the-art knowledge on the tools and

technologies available for genetic analysis of plants and animals. However, readers should be aware that the methods or statistical packages covered here may not be available or they might be out of date in a few years. Ultimately the book is intended for professional breeders interested in utilizing these tools and approaches in their breeding programs. Lastly, we anticipate the usage of this volume for advanced level graduate courses in agricultural and breeding courses.

**Biometrical genetics** Springer

To respond to the increasing need to feed the world's population as well as an ever greater demand for a balanced and healthy diet there is a continuing need to produce improved new cultivars or varieties of plants, particularly crop plants. The strategies used to produce these are increasingly based on our knowledge of relevant science, particularly genetics, but involves a multidisciplinary understanding that optimizes the approaches taken. Principles of Plant Genetics and Breeding, 2nd Edition introduces both classical and molecular tools for plant breeding. Topics such as biotechnology in plant breeding, intellectual property, risks, emerging concepts (decentralized breeding, organic breeding), and more are addressed in the new, updated edition of this text. Industry highlight boxes are included throughout the text to contextualize the information given through the professional experiences of plant breeders. The final chapters provide a useful reference on breeding the largest and most common crops. Up-to-date edition of this bestselling book incorporating the most recent technologies in the field Combines both theory and practice in modern plant breeding Updated industry highlights help to illustrate the concepts outlined in the text Self assessment questions at the end of each chapter aid student learning Accompanying website with artwork from the book available to instructors

**Encyclopedia of Animal Cognition and Behavior** John Wiley & Sons

Systematic treatment of the commonly employed crossed and nested classification models used in analysis of variance designs with a detailed and thorough discussion of certain random effects models not commonly found in texts at the introductory or intermediate level. It also includes numerical examples to analyze data from a wide variety of disciplines as well as any worked examples containing computer outputs from standard software packages such as SAS, SPSS, and BMDP for each numerical example.

*Breeding for Quantitative Traits in Plants* Springer

Maize is used in an endless list of products that are directly or indirectly related to human nutrition and food security. Maize is grown in producer farms, farmers depend on genetically improved cultivars, and maize breeders develop improved maize cultivars for farmers. Nikolai I. Vavilov defined plant breeding as plant evolution directed by man. Among crops, maize is one of the most successful examples for breeder-directed evolution. Maize is a cross-pollinated species with unique and separate male and female organs allowing techniques from both self and cross-pollinated crops to be utilized. As a consequence, a diverse set of breeding methods can be utilized for the development of various maize cultivar types for all economic conditions (e.g., improved populations, inbred lines, and their hybrids for different types of markets). Maize breeding is the science of maize cultivar development. Public investment in maize breeding from 1865 to 1996 was \$3 billion (Crosbie et al., 2004) and the return on investment was \$260 billion as a consequence of applied maize breeding, even without full understanding of the genetic basis of heterosis. The principles of

quantitative genetics have been successfully applied by maize breeders worldwide to adapt and improve germplasm sources of cultivars for very simple traits (e.g. maize flowering) and very complex ones (e.g., grain yield). For instance, genomic efforts have isolated early-maturing genes and QTL for potential MAS but very simple and low cost phenotypic efforts have caused significant and fast genetic progress across genotypes moving elite tropical and late temperate maize northward with minimal investment. Quantitative genetics has allowed the integration of pre-breeding with cultivar development by characterizing populations genetically, adapting them to places never thought of (e.g., tropical to short-seasons), improving them by all sorts of intra- and inter-population recurrent selection methods, extracting lines with more probability of success, and exploiting inbreeding and heterosis. Quantitative genetics in maize breeding has improved the odds of developing outstanding maize cultivars from genetically broad based improved populations such as B73. The inbred-hybrid concept in maize was a public sector invention 100 years ago and it is still considered one of the greatest achievements in plant breeding. Maize hybrids grown by farmers today are still produced following this methodology and there is still no limit to genetic improvement when most genes are targeted in the breeding process. Heterotic effects are unique for each hybrid and exotic genetic materials (e.g., tropical, early maturing) carry useful alleles for complex traits not present in the B73 genome just sequenced while increasing the genetic diversity of U.S. hybrids. Breeding programs based on classical quantitative genetics and selection methods will be the basis for proving theoretical approaches on breeding plans based on molecular markers. Mating designs still offer large sample sizes when compared to QTL approaches and there is still a need to successful integration of these methods. There is a need to increase the genetic diversity of maize hybrids available in the market (e.g., there is a need to increase the number of early maturing testers in the northern U.S.). Public programs can still develop new and genetically diverse products not available in industry. However, public U.S. maize breeding programs have either been discontinued or are eroding because of decreasing state and federal funding toward basic science. Future significant genetic gains in maize are dependent on the incorporation of useful and unique genetic diversity not available in industry (e.g., NDSU EarlyGEM lines). The integration of pre-breeding methods with cultivar development should enhance future breeding efforts to maintain active public breeding programs not only adapting and improving genetically broad-based germplasm but also developing unique products and training the next generation of maize breeders producing research dissertations directly linked to breeding programs. This is especially important in areas where commercial hybrids are not locally bred. More than ever public and private institutions are encouraged to cooperate in order to share breeding rights, research goals, winter nurseries, managed stress environments, and latest technology for the benefit of producing the best possible hybrids for farmers with the least cost. We have the opportunity to link both classical and modern technology for the benefit of breeding in close cooperation with industry without the need for investing in academic labs and time (e.g., industry labs take a week vs months/years in academic labs for the same work). This volume, as part of the Handbook of Plant Breeding series, aims to increase awareness of the relative value and impact of maize breeding for food, feed, and fuel security. Without breeding programs continuously developing improved germplasm, no technology can develop improved cultivars. Quantitative Genetics in Maize Breeding presents principles and

data that can be applied to maximize genetic improvement of germplasm and develop superior genotypes in different crops. The topics included should be of interest of graduate students and breeders conducting research not only on breeding and selection methods but also developing pure lines and hybrid cultivars in crop species. This volume is a unique and permanent contribution to breeders, geneticists, students, policy makers, and land-grant institutions still promoting quality research in applied plant breeding as opposed to promoting grant monies and indirect costs at any short-term cost. The book is dedicated to those who envision the development of the next generation of cultivars with less need of water and inputs, with better nutrition; and with higher percentages of exotic germplasm as well as those that pursue independent research goals before searching for funding. Scientists are encouraged to use all possible breeding methodologies available (e.g., transgenics, classical breeding, MAS, and all possible combinations could be used with specific sound long and short-term goals on mind) once germplasm is chosen making wise decisions with proven and scientifically sound technologies for assisting current breeding efforts depending on the particular trait under selection. Arnel R. Hallauer is C. F. Curtiss Distinguished Professor in Agriculture (Emeritus) at Iowa State University (ISU). Dr. Hallauer has led maize-breeding research for mid-season maturity at ISU since 1958. His work has had a worldwide impact on plant-breeding programs, industry, and students and was named a member of the National Academy of Sciences. Hallauer is a native of Kansas, USA. José B. Miranda Filho is full-professor in the Department of Genetics, Escola Superior de Agricultura Luiz de Queiroz - University of São Paulo located at Piracicaba, Brazil. His research interests have emphasized development of quantitative genetic theory and its application to maize breeding. Miranda Filho is native of Pirassununga, São Paulo, Brazil. M.J. Carena is professor of plant sciences at North Dakota State University (NDSU). Dr. Carena has led maize-breeding research for short-season maturity at NDSU since 1999. This program is currently one of the few public U.S. programs left integrating pre-breeding with cultivar development and training in applied maize breeding. He teaches Quantitative Genetics and Crop Breeding Techniques at NDSU. Carena is a native of Buenos Aires, Argentina.

<http://www.ag.ndsu.nodak.edu/plantsci/faculty/Carena.htm>

*Plant Breeding* Springer Science & Business Media

Plants have been successfully selectively bred for thousands of years, culminating in incredible yields, quality, resistance and so on that we see in our modern day crops and ornamental plants. In recent years the techniques used have been rapidly advanced and refined to include molecular, cell and genetic techniques. An Introduction to Plant Breeding provides comprehensive coverage of the whole area of plant breeding. Covering modes of reproduction in plants, breeding objectives and schemes, genetics, predictions, selection, alternative techniques and practical considerations. Each chapter is carefully laid out in a student friendly way and includes questions for the reader. The book is essential reading for all those studying, teaching and researching plant breeding.

*Statistical and Biometrical Techniques in Plant Breeding* Springer Science & Business Media

Various forms of the diallel crosses play an important role in evaluating the breeding potential of genetic material in plant and animal breeding. In this paper we give the simple method of construction of partial diallel cross design through partially balanced incomplete block design as auxiliary design with the method of analysis and also see the importance of partial diallel cross

design through partially balanced incomplete block design when large number of inbred line exist in plant and animal breeding experiment. We compare the efficiencies of our proposed designs with other existing designs for partial diallel cross in the literature and found that several our designs have higher A- and D-efficiency in comparison to the existing designs. The result provides a new partial diallel cross designs for plant and animal breeding experiments.

*Genetic Data Analysis for Plant and Animal Breeding* Cuvillier Verlag

Marker-assisted plant breeding involves the application of molecular marker techniques and statistical and bioinformatics tools to achieve plant breeding objectives in a cost-effective and time-efficient manner. This book is intended for beginners in the field who have little or no prior exposure to molecular markers and their applications, but who do have a basic knowledge of genetics and plant breeding, and some exposure to molecular biology. An attempt has been made to provide sufficient basic information in an easy-to-follow format, and also to discuss current issues and developments so as to offer comprehensive coverage of the subject matter. The book will also be useful for breeders and research workers, as it offers a broad range of up-to-the-year information, including aspects like the development of different molecular markers and their various applications. In the first chapter, the field of marker-assisted plant breeding is introduced and placed in the proper perspective in relation to plant breeding. The next three chapters describe the various molecular marker systems, while mapping populations and mapping procedures including high-throughput genotyping are discussed in the subsequent five chapters. Four chapters are devoted to various applications of markers, e.g. marker-assisted selection, genomic selection, diversity analysis, finger printing and positional cloning. In closing, the last two chapters provide information on relevant bioinformatics tools and the rapidly evolving field of phenomics.

*Advances in Molecular Breeding Toward Drought and Salt Tolerant Crops* New Age International

Latest figures suggest that approximately 20% of the world's population of six billion is malnourished because of food shortages and inadequate distribution systems. To make matters worse, it is estimated that some 75 billion metric tons of soil are removed annually from the land by wind and soil erosion, much of it from agricultural land, which is thereby rendered unsuitable for agricultural purposes. Moreover, out of a total land area under cultivation 96 of approximately 1.5 x 10<sup>10</sup> ha, some 12 x 10<sup>9</sup> ha of arable land are destroyed and abandoned worldwide each year because of unsustainable agricultural practices. Add to this the fact that the world population is increasing at the rate of a quarter of a million per day, and the enormity of the task ahead becomes apparent. To quote the eminent wheat breeder E. R. Sears, It seems clear that plant geneticists can look forward to an expanded role in the 21st century, particularly in relation to plant improvement. The success of these efforts may go a long way towards determining whether the world's increasing billions of humans will be adequately fed. Food for an ever-increasing population will have to be produced not only from an ever-diminishing, but from what will become an ever-deteriorating land resource unless justifiable environmental concerns are taken into account.

*Partners in Research for the 21st Century : Program Report 1999-2000* Springer Nature

This comprehensive book provides a detailed account of the plant breeding methodology, covering particularly pre- and post-Green Revolution era. It elaborates on plant breeding and gene manipulation, utilization of self-incompatibility in developing hybrids, different plant breeding

methods for development of crop varieties and hybrids in self- and cross-pollinated crops, nature of gene action and genotype-environment interaction. The text discusses gene manipulation in the crop plant and transfer of genes from wild species to cultivated crops, application of biotechnology in plant breeding, and genetic engineering and transgenic molecular markers as breeding tools and their limitations. It concludes with a discussion on physiologic breeding approach and new plant

ideotype concepts which are new and emerging areas of interest in plant breeding research. The book will be of immense use to undergraduate and postgraduate students of Agricultural Sciences and Botany for their course study. Besides, research scholars and professionals will also find the book as an excellent source of reference.

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