

especially, the Halla population, because of its unique genetic structure. Finally, we can anticipate a restoration program for populations destroyed by natural and/or man-made disturbances. Some populations, such as Daekyo in this study have been severely disturbed recently, by the construction of a ski resort and other activities. In this case, we can collect seeds, grow seedlings and transplant them back to the disturbed sites. If the seedlings survive and mature, this would help maintain an effective population size.

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Analysis of Half-diallel Mating Design with Missing Crosses: Theory and SAS Program for Testing and Estimating GCA and SCA Fixed Effects

By H. X. Wu¹ and A. C. Matheson¹

(Received 17th January 2000)

Abstract

The half-diallel mating design, particularly a series of disconnected half-diallels has been widely adopted as a mating design for estimating genetic parameters and for future selection in many commercially important tree species. Standard commercial statistical packages do not allow direct specification of the linear model associated with the half-diallel design and therefore are not capable of analysing diallel

mating designs, even for balanced diallel matings (no missing crosses). Published special computer programs for diallel analyses do not provide an adequate solution for GCA and SCA fixed effects in diallels with missing crosses. This paper presents the least squares theory for analysing half-diallel mating designs with missing crosses, and a SAS computer program (DLAFIXED.SAS), developed to test the significance of GCA and SCA effects and estimate the GCA and SCA fixed effects. The program is flexible enough to accommodate different number of parents, multiple environments and missing individual trees as well as missing whole plots. The DLAFIXED.SAS output includes (1) hypothesis testing for GCA and

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Analysis Of Diallel Mating Designs Nc State University

Rodney Mauricio



Analysis Of Diallel Mating Designs Nc State University:

A Survey of Statistical Design and Linear Models Jagdish Narain Srivastava, 1975 This book comprises of papers presented at an International Symposium on Statistical Design and Linear Models held in Colorado 1973 **Genetic Evaluation of Rapid Height Growth in Pot- and Nursery-grown Scotch Pine** Maurice E. Demeritt, 1985 S2 Genetic 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

Research Paper NE. , 1985 **Canadian Journal of Forest Research. Journal Canadien de la Recherche Forestière** , 2005 **Proceedings** , 1973 *Comprehensive Dissertation Index, 1861-1972: Mathematics and statistics* Xerox University Microfilms, 1973 *Radiata Pine Breeding Manual* Alastair Colin Matheson, Alan Gordon Brown, 1983

Crossover Jack E. Staub, 1994 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

Annual Report - N.C. State University-Industry Cooperative Tree Improvement Program N.C. State University-Industry Cooperative Tree Improvement Program,1991

Plant Breeding Jack Brown,Peter Caligari,Hugo Campos,2014-10-20 This book Plant Breeding has its bases in an earlier text entitled An Introduction to Plant Breeding by Jack Brown and Peter Caligari first published in 2008 The challenges facing today's plant breeders have never been more overwhelming yet the prospects to contribute significantly to global food security and farmers quality of life have never been more exciting and fulfilling Despite this there has been a worrying decline in public funding for plant breeding related research and support for international centers of germplasm development and crop improvement In part this has resulted in a serious reduction in the number of young people interested in devoting their professional careers to plant breeding as well as the number of universities offering plant breeding courses or conducting relevant research in plant breeding The authors aim in writing this book is to provide an integrated and updated view of the current scientific progress related to diverse plant breeding disciplines within the context of applied breeding programs This excellent new book will encourage a new generation of students to pursue careers related to plant breeding and will assist a wider audience of agricultural students agronomists policy makers and those with an interest in agriculture in gaining insight about the issues affecting plant breeding and its key role in improving the quality of life of people and in securing sufficient food at the quality required and at an affordable price With comprehensive coverage including questions designed for students and an accompanying website containing additional material to help in the study of the subject Plant Breeding is an ideal text for all those studying plant and crop sciences and a convenient reference source for professionals working in the area All libraries within universities and research establishments where biological and agricultural sciences are studied and taught should have multiple copies of this book

U.S. Forest Service Research Paper SE. Southeastern Forest Experiment Station (Asheville, N.C.),1965

Handbook of Formulas and Software for Plant Geneticists and Breeders Manjit S. Kang,2024-11-15 A simple solution to complicated statistical techniques and formulas The Handbook of Formulas and Software for Plant Geneticists and Breeders is an up to date reference source that eliminates the need for hand calculations of complicated genetic formulas and equations Contributions from members of the C1 Division of the Crop Science Society of America include computer program codes not found in Statistical Analysis System SAS and other commonly available statistical packages The book provides an invaluable shortcut to sorting through piles of literature in search of programs that may have been published in abbreviated forms or never at all The Handbook of Formulas and Software for Plant Geneticists and Breeders puts full fledged program codes of specialized statistical and genetics related software programs at your fingertips It shows practicing geneticists breeders and students how to use specialized software through practical examples The book is an excellent research and teaching tool in quantitative genetics and plant breeding providing definitions of key terms and information on how to obtain

desired software and key references It also includes an extensive listing of programs available for linkage and mapping software that can be accessed through the Internet The Handbook of Formulas and Software for Plant Geneticists and Breeders presents among others programs related to genotype by environmental interaction GEI and stability analysis genetic diversity estimation best linear unbiased predictors BLUPs principal component and additive main effects and multiplicative interaction AMMI analyses quantitative trait loci by environment QTL x E analysis GGE biplot analysis diallel analyses path analysis trend analysis field plot technique The Handbook of Formulas and Software for Plant Geneticists and Breeders is essential for academics and researchers working in genetics breeding and genomics and as a supplement for coursework in quantitative genetics and plant breeding

Quantitative Genetics in Maize Breeding Arnel R. Hallauer, Marcelo J. Carena, J.B. Miranda Filho, 2010-09-28

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 Jos B Miranda Filho is full professor in the Department of Genetics Escola Superior de Agricultura Luiz de Queiroz University of S o 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 S o 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 the 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>

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Plant Breeding Abstracts ,1995 *Publication - National Academy of Sciences-National Research Council* ,1963 **Genetics of Adaptation** Rodney Mauricio,2005-07-20 An enduring controversy in evolutionary biology is the genetic basis of adaptation Darwin emphasized many slight differences as the ultimate source of variation to be acted upon by natural selection In the early 1900 s this view was opposed by Mendelian geneticists who emphasized the importance of macromutations in evolution The Modern Synthesis resolved this controversy concluding that mutations in genes of very small effect were responsible for adaptive evolution A decade ago Allen Orr and Jerry Coyne reexamined the

evidence for this neo Darwinian view and found that both the theoretical and empirical basis for it were weak Orr and Coyne encouraged evolutionary biologists to reexamine this neglected question what is the genetic basis of adaptive evolution In this volume a new generation of biologists have taken up this challenge Using advances in both molecular genetic and statistical techniques evolutionary geneticists have made considerable progress in this emerging field In this volume a diversity of examples from plant and animal studies provides valuable information for those interested in the genetics and evolution of complex traits **Forest Science** ,2014 **The Annual Report of the Peanut Collaborative Research Support Program (CRSP)** Peanut Collaborative Research Support Program,1993

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