

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.

Acknowledgement

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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. Wu and A. C. MARRINSON¹

(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 (DIAFIXED.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 DIAFIXED.SAS output includes (1) hypothesis testing for GCA and

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Diallel Crosses Analysis Using Sas

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Diallel Crosses Analysis Using Sas:

Genomics Data Analysis for Crop Improvement Priyanka Anjoy, Kuldeep Kumar, Girish Chandra, Kishor

Gaikwad, 2024-01-09 This book addresses complex problems associated with crop improvement programs using a wide range of programming solutions for genomics data handling and sustainable agriculture. It describes important concepts in genomics data analysis and sequence-based mapping approaches along with references. The book contains 16 chapters on recent developments in several methods of genomic data analysis for crop improvements and sustainable agriculture, all authored by eminent researchers who are experts in their fields. These chapters focus on applications of a wide range of key bioinformatics topics including assembly, annotation, and visualization of next-generation sequencing (NGS) data, expression profiles of coding and noncoding RNA, statistical and quantitative genetics, trait-based association analysis, quantitative trait loci (QTL) mapping, and artificial intelligence in genomic studies. Real examples and case studies in the book will come in handy when applying the techniques. The relative scarcity of reference materials covering bioinformatics applications, as compared with the readily available books, also enhances the utility of this book. The targeted readers of the book are scientists, researchers, and bioinformaticians from genomics and advanced breeding in different areas. The book will appeal to the applied researchers engaged in crop improvements and sustainable agriculture by using bioinformatics tools, students, research project leaders, and practitioners from the various marginal disciplines and interdisciplinary research. *Asian Regional Maize Workshop, 10. Maize for Asia - Emerging Trends and Technologies. Proceedings of The Asian Regional Maize Workshop; Makassar, Indonesia; 20-23 October, 2008* ,

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