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Crossover

Concepts and Applications in Genetics, Evolution, and Breeding : an Interactive Computer-based Laboratory Manual

Univ of Wisconsin Press 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.

A Bibliography of Theoretical Population Genetics

A Survey of Statistical Design and Linear Models

North-Holland This book comprises of papers presented at an International Symposium on Statistical Design and Linear Models, held in Colorado, 1973.

Research Paper NE.

Genetic Evaluation of Rapid Height Growth in Pot- and Nursery-grown Scotch Pine

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.

Southern Cooperative Series

Domestication of Radiata Pine

Springer In nature, radiata pine is very localised and an obscure tree species despite the romantic character of much of its natural habitat. That obscure status and the lack of any reputation as a virgin timber slowed its due recognition as a commercial crop. Nevertheless, it has become a major plantation forest crop internationally. It has become the pre-eminent commercial forest species in New Zealand, Chile and Australia, with important plantings in some other countries. It consequently features prominently in the international trade in forest products, in addition to its importance in domestic markets of grower countries. Very fast growth, considerable site tolerances, ease of raising in nurseries and transplanting, and ease of processing and using its wood for a range of products and purposes, have made it the utility softwood of choice almost everywhere it can be grown satisfactorily. Abundant genetic variation and its amenability to other management inputs created special opportunities for its domestication. The story of its domestication forms a classic case history in the development of modern commercial forestry, with trailblazing in both genetic improvement and plantation management; this inevitably meant a learning process that provided instructive lessons, especially for tree breeders dealing with some other species. Paradoxically, the plantation monocultures have played and can continue to play an important role in protecting natural forests and other forms of biodiversity. Given the attractions of growing radiata pine, there were inevitably cases of overreach in planting it, with lessons to be learnt. Economic globalisation has meant globalisation of pests and disease organisms, and the scale on which radiata pine is grown has meant is has been the focus of various biotic alarms, none of which have proved catastrophic. Temptations, remain, however, to pay less than due attention to some aspects of risk management. The chapter structure of the book is based on historical periods, beginning long before any important human influences, and ending with a look into what the future might hold for the species and its role in human and ecological sustainability. Almost throughout, there has been complex interplay between the technical aspects, local social and economic factors, various types of institution, the enthusiasm and drive of

some very influential individuals, and tides of economic ideology, threads that needed to be woven together to do the story justice.

Tree Breeding and Genetics in New Zealand

Springer Dothistroma pini changed New Zealand commercial forestry dramatically. Tree breeding became concentrated on a very few species and development of selection methods and breeding strategies changed in response to the new challenges. Tree-Breeding and Genetics in New Zealand provides a critical historical account of the work on provenance research and tree breeding, often with the wisdom of hindsight, and it tracks the development of breeding strategy, especially for P. radiata, Douglas-fir and the most important eucalypt species, E. regnans, E. fastigata and E. nitens. The book is a compendium of abstracts and summaries of all publications and reports on tree improvement in New Zealand since the early 1950s, with added critical comment by the author on much of the work. It is intended for other tree breeders internationally, for interested NZ foresters and for graduate students studying genetics and tree breeding.

Canadian Journal of Forest Research

Journal Canadien de la Recherche Forestière

Quantitative Genetics in Maize Breeding

Springer Science & Business Media 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 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

Progeny Testing of Forest Trees

Proceedings of Workshop on Progeny Testing, June 15-16, 1982, Auburn, Alabama

Plant Breeding

John Wiley & Sons

Publications

Genomic Selection: Lessons Learned and Perspectives

Frontiers Media SA Genomic selection (GS) has been the most prominent topic in breeding science in the last two decades. The continued interest is promoted by its huge potential impact on the efficiency of breeding. Predicting a breeding value based on molecular markers and phenotypic values of relatives may be used to manipulate three parameters of the breeder's equation. First, the accuracy of the selection may be improved by predicting the genetic value more reliably when considering the records of relatives and the realized genomic relationship. Secondly, genotyping and predicting may be more cost effective than comprehensive phenotyping. Resources can instead be allocated to increasing population sizes and selection intensity. The third, probably most important factor, is time. As shown in dairy cattle breeding, reducing cycle time by crossing selection candidates earlier may have the strongest impact on selection gain. Many different prediction models have been used, and different ways of using predicted values in a breeding program have been explored. We would like to address the questions: i. How did GS change breeding schemes of

different crops in the last 20 years? ii. What was the impact on realized selection gain? iii. What would be the best structure of a crop-specific breeding scheme to exploit the full potential of GS? iv. What is the potential of hybrid prediction, epistasis effect models, deep learning methods and other extensions of the standard prediction of additive effects? v. What are the long-term effects of GS? vi. Can predictive breeding approaches also be used to harness genetic resources from germplasm banks in a more efficient way to adapt current germplasm to new environmental challenges? This Research Topic welcomes submissions of Original Research papers, Opinions, Perspectives, Reviews, and Mini-Reviews related to these themes: 1. Genomic selection: statistical methodology 2. The (optimal) use of GS in breeding schemes 3. Practical experiences with GS (selection gain, long-term effects, negative side effects) 4. Predictive approaches to harness genetic resources Concerning point 1): If an original research paper compares different methods empirically without theoretical considerations on when one or the other method should be better, the methods should be compared with at least five different data sets. The data sets should differ either in crop, genotyping method or its source, for instance from a breeding program or gene bank accessions. Concerning point 2): Manuscripts addressing the use of GS in breeding schemes should illustrate breeding schemes that are run in practice. General ideas about schemes that may be run in the future may be considered as 'Perspective' articles. Conflict of Interest statements: - Topic Editor Valentin Wimmer is affiliated to KWS SAAT SE & Co. KGaA, Germany. - Topic Editor Brian Gardunia is affiliated to Bayer Crop Sciences and has a collaboration with AbacusBio, and is an author on patents with Bayer Crop Sciences. The other Topic Editors did not disclose any conflicts of interest. Image credit: CIMMYT, reproduced under the CC BY-NC-SA 2.0 license

Dissertation Abstracts International The sciences and engineering. B Quantitative Genetics and Crop Breeding

New India Publishing Agency 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.

Radiata Pine Breeding Manual

Biometrics

Advanced Generation Breeding of Forest Trees

Proceedings of a Workshop on Advanced Generation Breeding, Current Status and Research Needs June 6-7, 1984, Baton Rouge, Louisiana

Issues in Forestry Research and Application: 2013 Edition

ScholarlyEditions Issues in Forestry Research and Application: 2013 Edition is a ScholarlyEditions™ book that delivers timely, authoritative, and comprehensive information about Applied Forestry. The editors have built Issues in Forestry Research and Application: 2013 Edition on the vast information databases of ScholarlyNews.™ You can expect the information about Applied Forestry in this book to be deeper than what you can access anywhere else, as well as consistently reliable, authoritative, informed, and relevant. The content of Issues in Forestry Research and Application: 2013 Edition has been produced by the world's leading scientists, engineers, analysts, research institutions, and companies. All of the content is from peer-reviewed sources, and all of it is written, assembled, and edited by the editors at ScholarlyEditions™ and available exclusively from us. You now have a source you can cite with authority, confidence, and credibility. More information is available at http://www.ScholarlyEditions.com/.

Silvae Genetica

Zeitschrift Für Forstgenetik und Forstpflanzenzüchtung

Proceedings ...

Implications of population genetics and molecular biology; What have we learned from laboratory species? Theory of response and limits to selection; Results and theory with plants; Results and theory with animals; Mixed model theory in quantitative genetics;

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

Southern Cooperative Series Bulletin

Cooperative Forest Genetics Research Program

Progress Report

Evaluating Microfiche Readers

A Handbook for Librarians

Washington : Council on Library Resources

Plant Breeding Abstracts

Selection and Breeding Programs in Aquaculture

Springer Science & Business Media Although aquaculture as a biological production system has a long history, systematic and efficient breeding programs to improve economically important traits in the farmed species have rarely been utilized until recently, except for salmonid species. This means that the majority of aquaculture production (more than 90 %) is based on genetically unimproved stocks. In farm animals the situation is vastly different: practically no terrestrial farm production is based on genetically unimproved and undomesticated populations. This difference between aquaculture and livestock production is in spite of the fact that the basic elements of breeding theory are the same for fish and shellfish as for farm animals. One possible reason for the difference is the complexity of reproductive biology in aquatic species, and special consideration needs to be taken in the design of breeding plans for these species. Since 1971 AKVAFORSK, has continuously carried out large scale breeding research projects with salmonid species, and during the latest 15 years also with a number of fresh water and marine species. Results from this work and the results from other institutions around the world have brought forward considerable knowledge, which make the development of efficient breeding programs feasible. The genetic improvement obtained in selection programs for fish and shellfish is remarkable and much higher than what has been achieved in terrestrial farm animals.

Proceedings - Southern Forest Tree Improvement Conference

Cooperative Forest Genetics Research Program; Progress Report

Forest Tree Improvement

Comprehensive Dissertation Index: Agriculture

Forest Genetics

Comprehensive Dissertation Index, 1861-1972: Mathematics and statistics

Amélioration Des Arbres--un Effort Coopératif

Proceedings of the ... Meeting of the Canadian Tree Improvement Association

Plant Breeding Symposium DSIR 1986

Peanut Science

Agronomy Abstracts

Includes abstracts of the annual meetings of the American Society of Agronomy; Soil Science Society of America; Crop Science Society of America (- of its Agronomic Education Division).

The Indian Journal of Genetics & Plant Breeding

Official Publication of the Indian Society of Genetics & Plant Breeding