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Quantitative genetics and breeding methods in autopolyploid plants

A. Gallais

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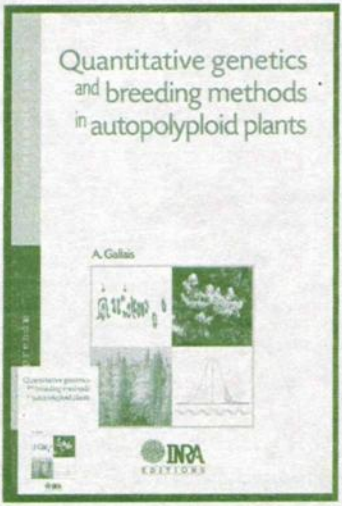

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Table 4.1a. *Analysis of variance of a randomised block design for estimating genotypic and environmental variance among clones.*

Sources of variation	*Mean squares*	*d.f.*	*Expected mean squares*
Blocks	MS_b		
Genotypes	MS_G	υ_1	$\sigma^2_{e'} + n\sigma^2_c + bn\sigma^2_G$
Plot within block	MS_c	υ_2	$\sigma^2_{e'} + n\sigma^2_c$
Residual	$MS_{e'}$		$\sigma^2_{e'}$

$\sigma^2_G = (MS_G - MS_c)/bn$, $\sigma^2_c = (MS_c - MS_{e'})/n$

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Table 4.1b. *Analysis of variance of a design with a population of clones studied in different environments.*

Sources of variation	*Mean squares*	*Expected mean squares*
Environment	MS_E	
Genotype	MS_G	$\sigma^2_{e'} + n\sigma^2_c + bn\sigma^2_{GE} + bn\ell\sigma^2_G$
Genotype × Environment	MS_{GE}	$\sigma^2_{e'} + n\sigma^2_c + bn\sigma^2_{GE}$
Plot/block/environment	MS_c	$\sigma^2_{e'} + n\sigma^2_c$
Residual	$MS_{e'}$	$\sigma^2_{e'}$

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Quantitative genetics and breeding methods in autopolyploid plants

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"Practice without theory is blind, theory without practice is powerless"

based on Kant "Critique of Pure Reason"

Preface

Why this book? At a time when so much is said about biotechnology and genomics, it may seem anachronistic to publish a book on quantitative genetics and the selection theory of autopolyploid plants. Yet the development of biotechnology and genomics does not eliminate the interest of quantitative genetics for research and applied breeding work, and furthermore, there has been no such book whereas for species with diploid behaviour, including allopolyploids, there are many. Because of their number of homologous chromosomes greater than two, which leads to particular meiosis, the population and quantitative genetics of autopolyploids differ from those of diploids. Consequently, although breeding methods may be largely the same, their modes of application must be rather different. As only two examples among many differences, there is generally no point in trying to develop pure line varieties by self-fertilisation and double crosses among inbred lines are expected to be better than single crosses.

The characteristics introduced by the autopolyploid state thus justified a book. Admittedly, it would have been better had it arrived earlier. Nevertheless we think that it will render service to quantitative geneticists and to breeders alike. It is their requests relating to the management and use of the genetic variability in autotetraploid plants which have motivated us. Given the relatively high frequency of autopolyploid wild plants and the economic importance of several autopolyploid crop species, there will always be geneticists and breeders working on these species. This book is thus for them. Publishing at the present time makes it possible to incorporate elements on genetic mapping, QTL detection and marker-assisted selection.

The expected readership is varied. It is for researchers, teachers and students faced with problems of the quantitative genetics and selection of autopolyploids. For them, we wished to give all the concepts and theoretical bases required for the understanding of the developments, though it is better, but not essential, to have some background in quantitative genetics developed for diploids and in breeding schemes. Furthermore, it is necessary to have some knowledge in statistics, such as analysis of variance with random effects, regression and correlation. We used many elements already published but, when required, original developments are given. In all circumstances demonstration of formulae is given, at least partially. That makes this book theoretical even though we have tried to complement theoretical conclusions with experimental results, when possible, and with practical schemes of selection. Nevertheless, we hope that the breeder will also find the elements needed for quantitative genetic studies, implementation of recurrent selection and varietal development methods. To help the reader, we have always sought to clearly emphasize the distinguishing features compared to the diploid state as well as the practical consequences of these.

After an introductive chapter (Chapter 1) giving some general aspects on autopolyploidy, the text is structured in six chapters grouped in three major parts. Part I and II give basic notions on the factors affecting genetic constitution of populations, whereas Part III applies these notions to the theory of plant breeding and varietal development. Part I is aimed at giving elements of population genetics for large and restricted population size, with the study of inbred populations, considering population composition and the effect of natural selection and mutation. In part II, the general model, *i.e.* Kempthorne's model, for the study of genetic variation of quantitative trait is first introduced at the level of random mating population in panmictic and linkage equilibrium (Chapter 4). The principles of quantitative trait locus (QTL) detection, with the difficulties due to autopolyploidy, is also presented. Then, in Chapter 5 using the generalized kinship and inbreeding coefficients defined in Chapter 3, quantitative genetics of inbred populations is developed, as well as the particular case of random mating after inbreeding. The last and longer part comprises two chapters. Chapter 6 gives the theory of population improvement by recurrent selection aimed at preparing varietal development. Main schemes of recurrent selection are presented and expected genetic advance is discussed at different levels of evaluation for example *per se* value, combining ability, value of derivable lines and synthetics. Marker-assisted selection is then presented as a specific case of recurrent selection. Finally Chapter 7 examines the development of each possible type of variety: clones, lines, single and double-cross hybrids and synthetics. Development of completely inbred lines and of hybrids among these lines is considered, because although it is unrealistic to develop homozygous lines by self-fertilisation, this could be realistic in some specific situations by using quadrupled haploids. Development of synthetics is particularly detailed because, as many autopolyploids are allogamous and perennial, with the difficulties for developing hybrid varieties, this type of variety is often used and indeed is a way to exploit genetic variability in such situations.

All major topics for quantitative genetics and breeding methodology of autopolyploid plants are treated. Topics not specific to autopolyploids are introduced but not fully developed. This is the case of genotype x environment interaction which is just presented when discussing broad-sense heritability and for estimating genetic variance components. Similarly, its effect on evaluation of material in recurrent selection and in varietal development is just introduced. Multitrait selection is also only introduced for indirect selection and index selection. For these two topics the reader may consult general textbooks in plant breeding. Optimisation of plant breeding, which is a crucial aspect, is briefly considered. In the same manner, we do not insist on statistical aspects for estimating variance components and heritabilities. This does not mean that these two problems are not important, but again they are not specific to the breeding of autopolyploid species, and we give references where these problems are solved.

Acknowledgments

I must first express my gratitude to Professor Yves Demarly. It is his pioneer work on quantitative genetics of autotetraploids which attracted me to work with him, when he was the head of the INRA Plant Breeding Station of Lusignan (Vienne, France). In this research station, when I was a young scientist, breeding cocksfoot and developing my thesis work on lucerne, he always stimulated my interest for quantitative genetics, more specifically for autotetraploid species. Even though I have since worked on maize quantitative genetics and breeding methodology, I have never forgotten autotetraploid genetics. The problem was to find time for writing such a book.

The writing of this book was a long endeavour. I have profited considerably from interactions with several colleagues. Joëlle Ronfort has contributed significantly to the chapter 1 and the population genetics part (chapters 2 and 3), introducing the mutational load with an approach of inbreeding depression. By her influence this part was separated from the one on quantitative genetics, making clearer, we hope, the presentation of some concepts such as gametic disequilibrium. Furthermore she has forced me to discuss more accurately some problems such as the study of structured populations. Bernadette Julier has given me many references on polyploids, more specifically on genetic mapping and QTL detection, and she has reviewed a preliminary version of chapters 1, 2, 3, 4 and 5, which was an appreciable contribution. I am extremely grateful to Joëlle and Bernadette for their suggestions and all their help. I acknowledge also Christine Dillmann, Jacques David and Jean-Pierre Henry who have accepted to discuss with me some aspects of autopolyploid population or quantitative genetics. Many thanks to Marie-Marguerite Rolland who has typewritten, with patience, duty and kindness, a part of a very complex manuscript, with complex formulae. Thank you to Joan Sobota, English lecturer at the Institut National Agronomique de Paris-Grignon who had contributed to the improvement of my English. Finally, I am deeply indebted to two very kind persons, two friends: John Hill and H. Sidney Easton. Both, despite their activities, have kindly accepted the heavy task of revising my English, and more than English, the contents, for all chapters. I imagine that they have sometimes regretted accepting such a task. Thank you John, thank you, H. Sidney. I apologize to the reader for the remaining stylistic and grammatical errors, this is only my fault. I am hoping that this will not be a problem limiting the understanding.

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