

BOOK REVIEW

Estatística genômica aplicada a populações derivadas de cruzamentos controlados

Ivan Schuster and Cosme Damião Cruz

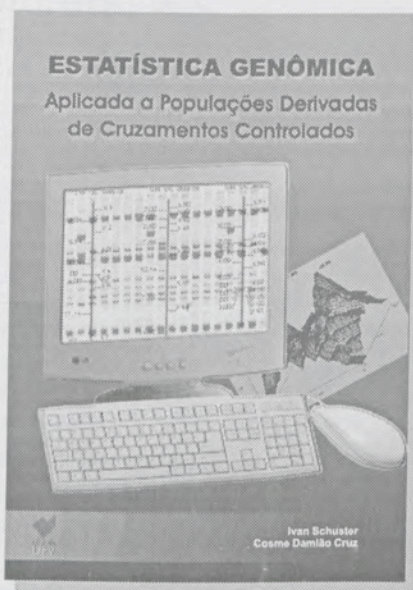
By Heyder Diniz Silva¹*

From the 80s onwards, modern molecular markers techniques along with the dissemination and evolution of personal computers (PCs) have made the study of polymorphisms at the DNA level possible and provoked a true revolution in genetics and plant improvement. The construction of saturated genetic maps and consequently the identification and localization of the genes involved in the genetic control of most economical traits has since then become reality. This entails an exponential growth of the volume of information and quantity of data to be evaluated in improvement programs and genetic studies, which calls for the development of more adequate statistical tools to analyze the type of information actually available. A new science, the **genomics**, was born, which merges the various areas of genetics (mendelian genetics, cytogenetics, molecular genetics, population genetics and quantitative genetics) with statistics and with information technology and automatized study and genome sequencing systems. One faces the fact that today's specialists in genetics and improvement need a broad knowledge in several scientific areas. Along this line, the publication **Estatística genômica**

aplicada a populações derivadas de cruzamentos controlados (**Genomical statistics applied to populations derived from controlled crossings**), by Ivan Schuster and Cosme Damião Cruz, two noted professionals in genetics

and improvement with great theoretical knowledge and hands-on experience, fills in a gap in the Portuguese literature. The underlying concepts and methodologies are described together with the use of genomics in a single volume. In a didactic and logical organization, this exceptional book tackles from the elementary concepts of genetics and statistics up to the construction of genetic maps and gene mapping involved in the genetic control of quantitative traits (QTL - Quantitative Trait Loci). The text of 568 pages, divided in 10 chapters, is illustrated by a series of examples that enable the reader to understand and follow the presented theory more easily. Moreover, the authors provide

software Gqmol (www.uf.br/gqmol/gqmol.htm) in whose procedures the entire methodology discussed in the book is applied. This is a reading experience that whoever wishes to become acquainted with this new science, genomics, must not miss out on.



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