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Book review

Quantitative Trait Loci Analysis in Animals

JI Weller
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Most traits of economic importance in livestock and of medical importance in man are quantitative in nature, and hence the ability to unravel the genetics of quantitative traits is of major importance. Before the arrival of genetic markers, animal breeders had developed very effective tools to analyse quantitative trait variation. This knowledge was very effectively exploited through the prediction and selection of animals with high breeding values using statistical tools and information obtained from phenotypes and the pedigree alone and this had led to great improvements in the efficiency of livestock production. So effective were the tools developed by animal breeders that many questioned the value of dissecting and exploiting the individual quantitative trait loci (QTL) using marker information. However, traits such as disease resistance and meat quality can be difficult to improve by the traditional methods and direct genomic selection could add significantly to genetic progress for such traits. Thus over the last 10 years there has thus been a rapid growth of studies designed to map and ultimately identify genes underlying quantitative variation in animals.

Joel Weller has been at the forefront of developing methods for QTL analysis in livestock (as well as making significant contributions in other areas of livestock genetics). Thus it is welcome to see his textbook on the analysis of QTL in animals, which presents much of the published material relevant to QTL detection by linkage in a coherent and accessible manner. The text takes the reader from setting the scene with the historical perspective through QTL mapping in inbred line crosses to QTL mapping using the various study designs possible in livestock. In a series of further chapters the book explores issues such as statistical power to detect QTL and optimisation of experimental designs, the setting significance thresholds and methods for fine mapping of QTL and multiple trait QTL analysis. Four chapters at the end explore selection in livestock, including theory and simulation studies in marker assisted selection and introgression.

The book focuses mainly on the theoretical aspects of QTL analysis and results of simulation studies. There is little discussion of actual results or summaries of conclusions so far. There is also little discussion of the various software available for QTL analysis, thus the book will be of more interest to the theoretically minded, rather than the practitioner who wants to get their hands dirty with analysis. The 'animal' in the title does not include humans, so there is little direct mention of developments specifically applied in studies of man. The biggest omission as far as livestock are concerned is that the book stops short of mapping applications that utilise disequilibrium at the population level and this must be an area where many QTL studies in livestock will be undertaken in future.

I would not agree with all of the conclusions presented in the book. For example the use of canononical transformation in multiple trait analyses has significant drawbacks and the interpretation of the false discovery rate criteria for assessing detected QTL has to be treated with care. Overall, however, there is much of value here and the book is certainly a must-have for anyone involved in the statistical analysis of QTL studies in livestock. It will also be of value to those interested in QTL analysis generally or in animal breeding and livestock genetics and a useful textbook for advanced undergraduate and postgraduate students. Experimentalists should not expect to be able to plunge straight into data analysis having read this book, but an understanding based on this text would be of great value in helping them avoid the pitfalls that can often trap the unwary in such a statistical subject as QTL analysis.

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