3-2018

Review of *Genome-Wide Association Studies: From Polymorphism to Personalized Medicine*

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The Quarterly Review of Biology Mar 2018, Volume 93, Issue 1, p. 50

GENOME-WIDE ASSOCIATION STUDIES: FROM POLYMORPHISM TO PERSONALIZED MEDICINE.

Edited by Krishnarao Appasani; Forewords by Stephen W. Scherer and Peter M. Visscher. Cambridge and New York: Cambridge University Press. $185.00. xxxi + 391 p. + 24 pl.; ill.; index. ISBN: 978-1-107-04276-6. 2016.

Genome-wide association studies (GWAS) has become a powerful tool in the area of quantitative genetics to map the relationship between trait and genomic variations. This volume provides a great resource for beginners to learn about the recent advances in GWAS and for domain experts to identify the gaps in the area. The first part of the volume lays out the statistical background of GWAS. I really liked the article by Yang et al., Introduction to Statistical Methods in Genome-Wide Association Studies. In this chapter, the authors talked about the missing heritability issue and introduced ways to calculate heritability using the traditional pedigree-based method and GWAS method that was developed by J. Yang et al. (2011. *American Journal of Human Genetics* 88:76–82). They discussed the linear mixed model (LMM) approach in conducting GWAS and also introduced how to predict the disease risk using the obtained information. At the end, they pointed to future directions by providing some thoughts on the challenges for mapping traits with highly polygenic genetic architecture.

Since the beginning of GWAS, thousands of single nucleotide polymorphisms (SNPs) associated with diseases in human genetics have been identified using GWAS. In Part II, this volume provides some case studies by Kilpeläinen on body mass index GWAS and by Ozaki and Tanaka on myocardial infarction, plus many other excellent examples. These case studies are very typical GWAS projects that allow readers to learn the details about the experimental design, results interpretation, and for troubleshooting or thinking about their own research projects. In addition to mapping the disease and SNP association, this volume also explored the area of the functional genomics, which is a very promising future direction. By functional genomics, I mean the study of microRNA, DNA methylation, and gene expression.

In Part III, the authors discussed the potential roles of those functional genomic elements in determining the risk of diseases. In particular, I enjoyed reading the chapter eQTL Mapping by Chen et al. In eQTL mapping, the phenotypic trait becomes gene expression instead of disease measured via RNA-seq or other cost-effective methods, such as microarray. As described in the article, the understanding of the genetic control of gene expression will help to close the gap between association loci identified through GWAS and the molecular mechanisms for these disease-associated loci. I liked this article because the authors provided a table of methods and software for data processing and gene expression analysis. This is particularly useful because as a researcher, I really want to apply the technology to my own studies. The provided software and case studies can guide readers through the procedures and will easily allow a researcher to finish a project on their own. I think this book will be a reliable guide for anyone who wants to learn and understand GWAS. I hope other readers will enjoy the book as much as I did.

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