

'[This] timely textbook ... combines a description of the theory and methods underlying quantitative trait variation in populations with data examples and applications from modern genome technologies. It is an excellent introduction to the field.'

PETER M. VISSCHER, University of Queensland, Australia

'A masterful tour through both evolutionary and applied quantitative genetics ... provides a fruitful and unusual blend of population and quantitative genetics.'

MICHAEL WHITLOCK, University of British Columbia, Canada

'I welcome Caballero's text for new generations of students coming up to speed in this important and challenging field ... will also serve as a valuable resource for established practitioners of quantitative genetics.'

RUTH G. SHAW, University of Minnesota, USA

Quantitative genetics is the study of continuously varying traits, which make up the majority of biological attributes of evolutionary and commercial interest. This book provides a much-needed up-to-date, in-depth, yet accessible text for this field. In lucid language, the author guides readers through the main concepts of population and quantitative genetics and their applications. Written to be approachable even to those without a strong mathematical background, applied examples, a glossary of key terms, and problems and solutions support students in grasping important theoretical developments and their relevance to real-world biology. This is an engaging, must-have textbook for advanced undergraduate and postgraduate students. Given its applied focus, it also equips researchers in genetics, genomics, evolutionary biology, animal and plant breeding and conservation genetics with the understanding and tools for genetic improvement, comprehension of the genetic basis of human diseases and conservation of biological resources.

Cover illustration: Front Figure – fitness curve (broken line) which determines the probability of survival as a function of the values of a quantitative trait under stabilizing selection; the less intense the selection, the wider the fitness curve. The solid line gives the density function for the trait.

Background figure (on both front and back covers), and also back figure – the regression slope of offspring values on parental values for a quantitative trait provides an estimate of the heritability.

Back figure – restriction of the increase in the homozygosity for deleterious alleles (ordinate) through generations (abscissa) because of genetic purging in a small population.

CAMBRIDGE
UNIVERSITY PRESS
www.cambridge.org

ISBN 978-1-108-72235-3



9 781108 722353 >