Paleomicrobiology

Didier Raoult • Michel Drancourt
Editors

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Past Human Infections

Springer

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Cover Photo: Detail of a painting by Michel Serre featuring 1720 Marseilles' plague epidemics (Musée des Beaux-Arts, Marseilles, France)

ISBN: 978-3-540-75854-9 e-ISBN: 978-3-540-75855-6

Library of Congress Control Number: 2007939832

Cover design: WMXDesign GmbH, Heidelberg, Germany

Printed on acid-free paper

5 4 3 2 1 0

springer.com

Preface

Almost 15 years ago, initial reports of the molecular detection of *Mycobacterium tuberculosis* DNA in ancient human skeletons of individuals suspected of having tuberculosis launched paleomicrobiology as an emerging field of research at the intersection of microbiology and evolution, history and anthropology. Refinements in experimental protocols together with strict criteria for determining the authenticity of data now allow the molecular diagnosis of past infections such as plague, tuberculosis, leprosy, typhoid fever, bartonelloses and influenza. Pioneering studies have compared the genotypes of organisms responsible for infection in past centuries with modern strains in order to gain a better understanding of microbe evolution. Paleomicrobiology provides historians and anthropologists with demonstrative data with which to analyse mass burials and past epidemics and their impact on human populations. These data help to resolve controversies regarding the aetiology of past epidemics such as the Black Death. Continuing progress in analytical techniques may allow further diagnoses of epidemics of as yet unknown aetiology and increased insight into the epidemiology of past infections. Looking backwards to past epidemics using modern tools and concepts will in turn help to understand the continuous evolution of microbes and of their direct and indirect relationships with humans.

This book summaries, for the first time, the concepts and techniques used to explore past epidemics and infections, and serves to illustrate the fruitful dialogue between historians, anthropologists and microbiologists through selected examples of research in the field of paleomicrobiology.

September 2007

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Abbreviations

aDNA	ancient DNA
AR	absolute risk
BSA	bovine serum albumin
clyA	cytolysin A
CSD	cat scratch disease
DR	Direct Repeat
Fr1	unique fraction 1
GMS	Grocott-Gomori methenamine silver
H&E	hematoxylin and eosin
HIV	Human Immunodeficiency Virus
HPLC	high performance liquid chromatography
HSV	Herpes simplex virus
INRAP	Institut National de Recherches Archéologiques Preventives
MIRU	mycobacterial interspersed repetitive units
MS	mass spectroscopy
MST	multiple spacers typing
MTB	*Mycobacterium tuberculosis*
MTC	*Mycobacterium tuberculosis* complex
narG	nitrate reductase 1
osmC	osmotically inducible protein C
PAS	periodic acid-Schiff
PCR	polymerase chain reaction
PFGE	pulsed-field gel electrophoresis
PTB	*N*-phenacylthiazolium bromide
RFLP	restriction fragment length polymorphism
RR	relative risk
RT-PCR	reverse-transcription-polymerase chain reaction
SARS	severe acute respiratory syndrome
SNP	single nucleotide polymorphism
TB	tuberculosis
UV	ultraviolet
VNTR	variable number tandem repeats
WWI	First World War