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Autore	Campbell, Mary K.
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Altri autori (Persone)	Altieri, Fabio Farrell, Shawn O.
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Note generali	Includes 55 p. of answers and exercises, glossary and index Orig.Tit.: Biochemistry
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2. Record Nr.	UNINA9910789124303321
Titolo	Campylobacter ecology and evolution / / edited by Samuel K. Sheppard ; associate editor, Guillaume Meric
Pubbl/distr/stampa	Norfolk, England : , : Caister Academic Press, , [2014] ©2014
ISBN	1-908230-98-3
Descrizione fisica	1 online resource (377 p.)
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Soggetti	Campylobacter Campylobacter - Ecology Campylobacter - Evolution
Lingua di pubblicazione	Inglese
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Livello bibliografico	Monografia
Note generali	"Medical microbiology and infectious diseases, Swansea University, Swansea UK."
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Contents; Current books of interest; Contributors; Foreword; Preface; Part I: Mechanisms of Evolution; 1: A Candidate Hopeful Monster in the Genus <i>Campylobacter</i> ; Introduction; Hybridization by horizontal gene transfer; 2: Learning About Recombination in <i>Campylobacter</i> ; Introduction; Estimating recombination from population data; Estimating recombination from closely related isolates; Discussion; 3: Within-host Evolution of <i>Campylobacter jejuni</i> ; Introduction; Phenotypic changes of <i>Campylobacter jejuni</i> after host passage; Genotypic changes of <i>Campylobacter jejuni</i> during host passage; Conclusions Future studies4: Concerted Evolution in <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> ; Concerted evolution; Duplicated genes in <i>Campylobacter</i> ; Unresolved questions; 5: Genome and Transcriptome Evolution in the Genus <i>Campylobacter</i> ; Introduction; Characteristics of <i>Campylobacter</i> genome sequences; Transcriptome evolution in the genus <i>Campylobacter</i> ; Conclusions; 6: Repetitive DNA: A Major Source of Genetic Diversity in <i>Campylobacter</i> Populations?; Introduction; Types, prevalence and mutability of SSRs in <i>Campylobacter</i> genomes; Variation in SSRs has functionally important phenotypic effects Combinatorial consequences of multiple phase-variable genesInfluence of mutational, selective and population forces on the diversity of

phase-variable genotypes; Modelling phase-variable genes and selection for mutational rates; Experimental issues connected with phase variation; Summary; Future perspectives; Part II: Adaptations to Host Colonization; 7: *Campylobacter* Strategies for Colonizing the Host Gastrointestinal Tract; Introduction; Carbon sources utilized by *Campylobacter* to support growth in vivo; Mucins and the mucous layer; Conclusions and future trends

8: The Intricate Relationship Between *Campylobacter* and Mucus The structure and function of intestinal mucus; The ecology of *C. jejuni* in intestinal mucus; Mucus as a source of glycans; *Campylobacter jejuni* commensalism in chickens; Conclusions and future directions; 9: *Campylobacter* Association with the Human Host; Introduction; Adhesion, invasion and translocation; Bacterial factors influencing adhesion and invasion of *C. jejuni*; Do all campylobacters invade to the same extent?; Conclusion; 10: Siderophore-mediated Iron Acquisition for *Campylobacter* Infection; Introduction

Iron sources in the intestine: an ecological view Enterobactin-mediated iron acquisition; Salmochelin-mediated iron acquisition; Hydroxamate siderophore-mediated iron acquisition; Conclusion and future directions; 11: Genetic Mechanisms Involved in *Campylobacter jejuni* Survival Under Oxidative Stress Conditions; The *C. jejuni* survival conundrum; Oxidative stress overview; *C. jejuni* mechanisms for countering oxidative stress; Oxidative stress regulation in *C. jejuni*; Discussion and future perspectives; 12: Oxidative Stress Survival During *Campylobacter* Transmission and Infection

*Campylobacter jejuni* transmission and aerotolerance

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#### Sommario/riassunto

Members of the genus *Campylobacter* are commonly found in the gastrointestinal tract of mammals and birds, and can be commensal or pathogenic in nature. For example, *Campylobacter jejuni* can be a harmless commensal organism in poultry and other avian and animal hosts, but in humans, it is pathogenic and the most common cause of bacterial gastroenteritis worldwide. In recent years, the application of DNA sequencing and 'omics' technologies to large numbers of isolates has allowed *Campylobacter* research to advance rapidly, revealing fascinating new insights into the cellular biology and evolution

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