Yersinia

Systems Biology and Control

Edited by

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Preface

Systems biology, made possible by advances in biotechnology and bioinformatics during the last decade, is becoming an increasingly prominent methodology in infectious disease research. Systems biology can mean different things to different people, but at its core is a comprehensive, integrative, and quantitative analysis of all components of a biological system, such as an intact cell, organism, or community. The ambitious ultimate goal of systems biology is to understand how all the components interact to enable the system to function successfully in different conditions; for example, how a host responds to infection and how a microbe adapts to survive within its host or in an external ecosystem. Deciphering these dynamic biological networks is expected to disclose new molecular targets for disease control strategies. The first part of this book reviews some of the pioneering applications of systems biology to study host-pathogen interactions of the medically important *Yersinia* species. The eventual synthesis of these and future analyses should provide a more holistic perspective of *Yersinia* infection mechanisms. The epidemiology and control of plague and yersiniosis is a second focus of the book. Interestingly, infectious disease ecology has historically relied on systems analysis, in which the pathogen is but one component of a complex ecosystem. Discovery of the important elements of the ecosystem and characterizing the interactions that lead to disease outbreaks in a population represents another level of systems biology that is critical for effective public health surveillance and control measures. We thank Annette Griffin and Horizon Scientific Press for the opportunity to organize this volume and all of the authors for their outstanding contributions.

Elisabeth Carniel and B. Joseph Hinnebusch

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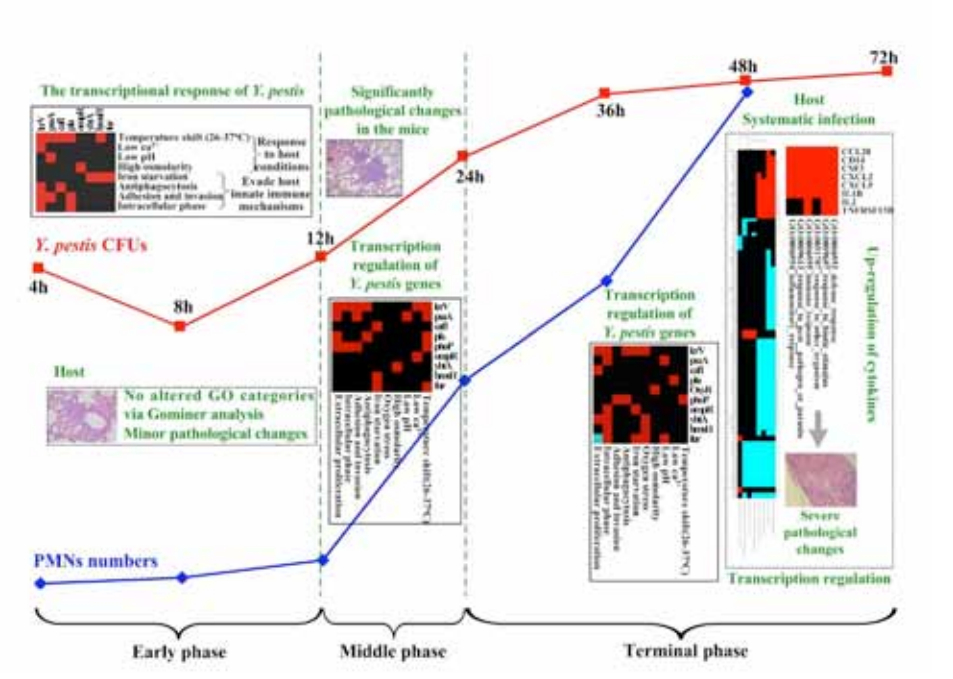

Figure 3.1 *Y. pestis*–host interaction revealed by the transcriptional responses after exposure to *Y. pestis*. The dynamics of bacterial load (red line) and PMNs numbers in lung tissue (blue line) are shown at different time points post infection. The clustered gene expression data of *Y. pestis* and of lung tissue of infected mice are shown in the solid line frame and the dotted line frame, respectively. Red represents the up-regulation and green represents the down-regulation of specific genes. This figure is drawn according to the results of Liu *et al.* (2009).

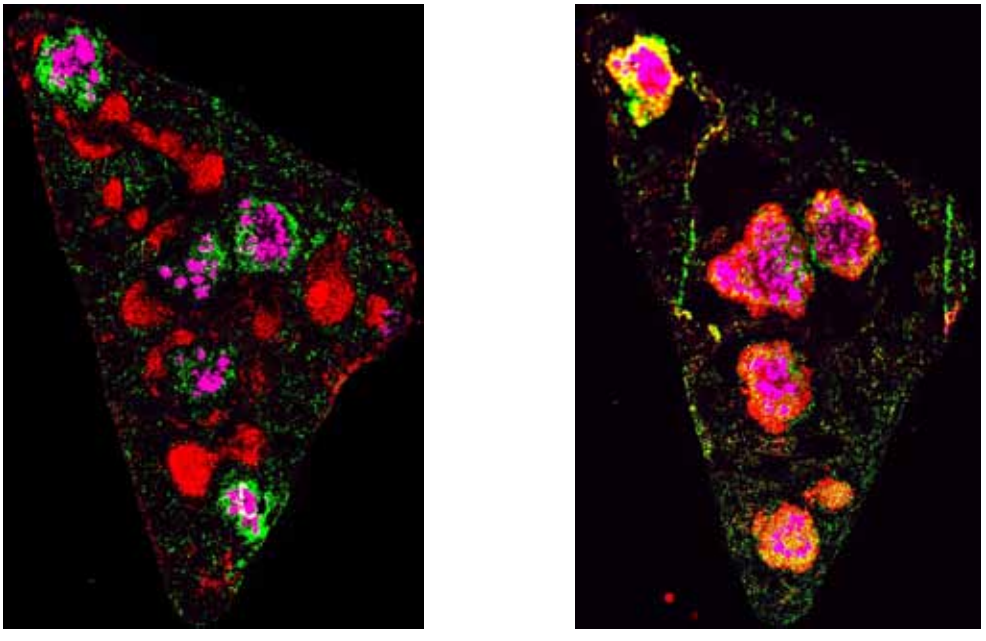

Figure 4.1 Serial cryosections of mouse spleen collected three days after intraperitoneal infection with *Y. enterocolitica* O:8 (from C57BL/6 mouse carrying the CX_3CR1-EGFP reporter gene expressed by a subpopulation of DCs and macrophages). Five abscess-like lesions/*Y. enterocolitica* microcolonies are shown. Left: *Y. enterocolitica* patches: pink; neutrophils (Ly6G+): red; CX_3CR1-positive cells: green. Right: *Y. enterocolitica* patches: pink; B lymphocytes (white pulp): red; CX_3CR1-positive cells: green (Lenk, 2011).