

**Publication****A Population Biology Perspective on the Stepwise Infection Process of the Bacterial Pathogen *Pasteuria ramosa* in *Daphnia*****JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)****ID** 3705185**Author(s)** Ebert, Dieter; Duneau, David; Hall, Matthew D.; Luijckx, Pepijn; Andras, Jason P.; Du Pasquier, Louis; Ben-Ami, Frida**Author(s) at UniBasel** [Ebert, Dieter](#) ; [Hall, Matthew](#) ; [Du Pasquier, Louis](#) ; [Duneau, David](#) ; [Luijckx, Pepijn](#) ;**Year** 2016**Title** A Population Biology Perspective on the Stepwise Infection Process of the Bacterial Pathogen *Pasteuria ramosa* in *Daphnia***Journal** Advances in Parasitology**Volume** 91**Pages / Article-Number** 265-+

The infection process of many diseases can be divided into series of steps, each one required to successfully complete the parasite's life and transmission cycle. This approach often reveals that the complex phenomenon of infection is composed of a series of more simple mechanisms. Here we demonstrate that a population biology approach, which takes into consideration the natural genetic and environmental variation at each step, can greatly aid our understanding of the evolutionary processes shaping disease traits. We focus in this review on the biology of the bacterial parasite *Pasteuria ramosa* and its aquatic crustacean host *Daphnia*, a model system for the evolutionary ecology of infectious disease. Our analysis reveals tremendous differences in the degree to which the environment, host genetics, parasite genetics and their interactions contribute to the expression of disease traits at each of seven different steps. This allows us to predict which steps may respond most readily to selection and which steps are evolutionarily constrained by an absence of variation. We show that the ability of *Pasteuria* to attach to the host's cuticle (attachment step) stands out as being strongly influenced by the interaction of host and parasite genotypes, but not by environmental factors, making it the prime candidate for coevolutionary interactions. Furthermore, the stepwise approach helps us understanding the evolution of resistance, virulence and host ranges. The population biological approach introduced here is a versatile tool that can be easily transferred to other systems of infectious disease.

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