

## Publication

A novel approach to parasite population genetics: experimental infection reveals geographic differentiation, recombination and host-mediated population structure in *Pasteuria ramosa*, a bacterial parasite of *Daphnia*

**JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)**

ID 2297396

**Author(s)** Andras, J. P.; Ebert, Dieter**Author(s) at UniBasel** [Ebert, Dieter](#) ;**Year** 2013**Title** A novel approach to parasite population genetics: experimental infection reveals geographic differentiation, recombination and host-mediated population structure in *Pasteuria ramosa*, a bacterial parasite of *Daphnia***Journal** Molecular Ecology**Volume** 22**Number** 4**Pages / Article-Number** 972-86**Keywords** bacteria, coevolution, *Daphnia*, Parasite, *Pasteuria*, population genetics

**Mesh terms** Animals; *Daphnia*, microbiology; Disease Resistance, genetics; Genetic Variation; Genetics, Population; Genotype; Haplotypes; Host-Pathogen Interactions; Linkage Disequilibrium; Microsatellite Repeats; *Pasteuria*, genetics; Phenotype; Ponds; Recombination, Genetic; Sequence Analysis, DNA

The population structure of parasites is central to the ecology and evolution of host-parasite systems. Here, we investigate the population genetics of *Pasteuria ramosa*, a bacterial parasite of *Daphnia*. We used natural *P. ramosa* spore banks from the sediments of two geographically well-separated ponds to experimentally infect a panel of *Daphnia magna* host clones whose resistance phenotypes were previously known. In this way, we were able to assess the population structure of *P. ramosa* based on geography, host resistance phenotype and host genotype. Overall, genetic diversity of *P. ramosa* was high, and nearly all infected *D. magna* hosted more than one parasite haplotype. On the basis of the observation of recombinant haplotypes and relatively low levels of linkage disequilibrium, we conclude that *P. ramosa* engages in substantial recombination. Isolates were strongly differentiated by pond, indicating that gene flow is spatially restricted. *Pasteuria ramosa* isolates within one pond were segregated completely based on the resistance phenotype of the host—a result that, to our knowledge, has not been previously reported for a nonhuman parasite. To assess the comparability of experimental infections with natural *P. ramosa* isolates, we examined the population structure of naturally infected *D. magna* native to one of the two source ponds. We found that experimental and natural infections of the same host resistance phenotype from the same source pond were indistinguishable, indicating that experimental infections provide a means to representatively sample the diversity of *P. ramosa* while reducing the sampling bias often associated with studies of parasite epidemics. These results expand our knowledge of this model parasite, provide important context for the large existing body of research on this system and will guide the design of future studies of this host-parasite system.

**Publisher** Blackwell**ISSN/ISBN** 0962-1083 ; 1365-294X**edoc-URL** <http://edoc.unibas.ch/dok/A6211997>**Full Text on edoc** Restricted;**Digital Object Identifier DOI** 10.1111/mec.12159**PubMed ID** <http://www.ncbi.nlm.nih.gov/pubmed/23279064>

**ISI-Number** WOS:000314220900007

**Document type (ISI)** Journal Article