# ABSTRACT

In a context of global change, understanding the interactions between parasites and their environment is essential to predict future infection dynamics and changes in ecosystem functioning. That said, parasite distribution patterns and drivers of infection vary in time and space, making understanding the underlying mechanisms highly complex. Comparative studies based on empirical data must therefore take into account the factors of variation involved in estimating infection parameters in natural populations. Using a multi-scale approach, we explored the sources of variation in the estimation of infection prevalence, focusing on black spot disease in littoral freshwater fish communities. Our results showed that infection prevalence is spatially heterogeneous across the landscape with evidence of infection hotspots and coldspots. Method-related sampling biases led to significant variations in prevalence estimates and spatial patterns of disease occurrence. Our results also indicated that low sampling effort tend to overestimate the prevalence of infection in the landscape, and that the sampling effort required to estimate infection prevalence depends on the sampling method employed. Water physico-chemical characteristics and local fish community structure were found to be the best predictors of small-scale infection. Furthermore, our results suggest dilution effects due to obstruction and compatibility barriers limiting cercarial survival. Several relationships between infection prevalence and environmental predictors revealed non-linearity, suggesting complex interactions. Our study contributes to the development of our understanding of the interactions between parasites and their environment, as well as potential biases in the study of infection dynamics.

**Keywords :**

Host-parasite interactions, spatial ecology, black spot disease, sampling bias, sampling effort, distribution patterns, infection drivers, littoral fish communities, freshwaters.