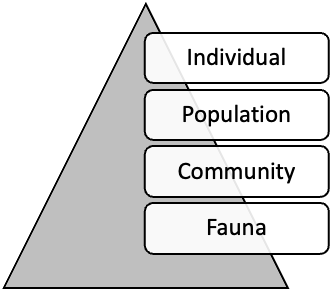
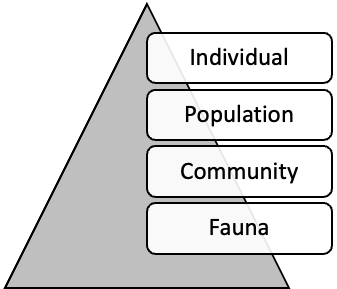
**1 | INTRODUCTION**

**[PAR1]** Often neglected in ecological studies (Morley, 2012; Scholz & Choudhury, 2014), parasites are a key component of natural communities and Biodiversity-Ecosystem-Functioning (Dobson & Hudson, 1986; Frainer et al., 2018; Lafferty et al., 2008; Marcogliese, 2004; Minchella & Scott, 1991; Pascal et al., 2020; Poulin, 1999). They are inevitably vulnerable to environmental changes as they depend on and co-evolute with free-living species (Gandon et al., 2008; Mostowy & Engelstädter, 2010). Yet, their spatial distribution patterns and networks are still misunderstood as general rules are hard to uncover (Poulin, 2007). One of the first steps to clarify those context-dependencies is to address the importance of spatial scaling for the estimation of infection parameters in biotic communities (here prevalence of infection).

**[PAR2]** Infection patterns are variable across taxa, time and space (Happel, 2019; Poulin, 2006; Poulin & Dick, 2007; Thieltges & Reise, 2007; Villalba-Vasquez et al., 2018; Young & Maccoll, 2017). Even so, literature currently fails to disentangle the processes explaining variations in parasitic infection across scale as metacommunities’ species filtering is widely scale-dependent (Bolnick et al., 2020). Scaling is relevant above all in parasite ecology given the hierarchical organization of both parasite and host component (Fig1). Considering the complexity of host-parasite systems, there are still many biological scale combinations that need to be investigated. For example, component communities (see Bush et al., 1997) of metazoan parasites in fish host-populations have been the focus of many studies in the past decades regarding spatiotemporal patterns (e.g. Carney & Dick, 2000; González & Poulin, 2005; Pérez-del-Olmo et al., 2009; Villalba-Vasquez et al., 2018). Conversely, species-specific infection patterns in host-community remains largely unexplored in fish species across spatial scales. Thus, host-parasite associations are well-suited models to investigate the implications of scaling on infection estimates.



Parasite

Host

Fig1.

As a matter of fact, scale-dependance have been raised on abundance and distribution patterns of metazoan parasite infection in freshwater (Poulin, 1998).

**[PAR3]** Since current literature lacks consistency, it remains unclear whether infection patterns result from stochastic events or determinist filtering (Carney & Dick, 2000; González & Poulin, 2005; Kennedy, 2009; Poulin, 2007; Poulin & Valtonen, 2002). Even though, the search for uncovering processes shaping host-parasite dynamics must not be put to an end. Studies have shown that both biotic and abiotic components can be correlated to variation of infection metrics at various spatial scales (Altman & Byers, 2014; Falke & Preston, 2021; Lagrue et al., 2011; Lagrue & Poulin, 2015; Poulin & Morand, 1999; Thieltges et al., 2008). Individual characteristics such as sex (Zuk & McKean, 1996), age/size (Marcogliese et al., 2001; Poulin, 2000) and genetic (Williams-Blangero et al., 2012) drives host susceptibility leading to source of variations in infection estimates and patterns. On a larger scale, communities’ properties such as species richness and populations’ densities can create a “dilution effect” by reducing encounter or success of infection (Ahn & Goater, 2021; Buck & Lutterschmidt, 2017; Dargent et al., 2013; Lagrue & Poulin, 2015). Local habitat characteristics have also been correlated to variation in parasitological metrics and communities. In American eels (*Anguilla rostrata*), parasite diversity decrease when pH is below 5.4 and Digenean trematodes are absent below 4.7 (Marcogliese & Cone, 1997). Lentic water bodies with dense vegetation display higher prevalence and abundance of *Posthodiplostomum cuticola* in fish than rivers and steep banks reservoirs (Ondrackova et al., 2004), suggesting that local habitat and morphometry are drivers of encounter filtering. Furthermore, systems’ spatial features (e.g., watershed, connectivity) act as large scale filtering by limiting dispersal (Bolnick et al., 2020) thus creating infection patchiness in the landscape. Happel (2019) provided evidence for consistent geographical pattern in prevalence of the black spot disease between watersheds. Bolnick et al. (2020) also found a small effect of waterways distance between waterbodies on parasite communities of threespine stickleback (*Gasterosteus aculeatus*). With this in mind, a complete ecological perspective on host-parasite systems must incorporate abiotic, biotic and spatial drivers to highlight mechanism shaping patterns as some filters are scale-dependent (Bolnick et al., 2020; Cohen et al., 2016). Still, we lack crucial information on how patterns and predictors of infection parameters change across scale to properly monitor and managed parasitic disease.

**[PAR4]** Here, we test the effect of spatial scale on infection prevalence estimates across different sampling methods using data on the black spot disease in littoral fish communities across 15 lakes varying in morphometric attributes and local conditions. We analyze infection prevalence data at the host-community level for scaling-dependencies through three spatial scale levels (regional, local and fine-scale) in order to investigate **(i)** the effect of random sampling effort on regional prevalence estimation through different sampling methods **(ii)** the distribution of observed local prevalence estimations and **(iii)** the importance of ecological predictors on infection prevalence on a manageable scale (i.e., transect).

**[PAR5]** For regional scale estimates we used random prevalence accumulation curves by resampling across lakes. This approach allows us to compare regional-scale prevalence estimates (and associated variance) among different sampling methods along a gradient of increasing sampling effort (or area sampled). Akin to interpretations of species-area relationships, the accumulation curves can show evidence for scale-invariance (“flat curve” – infection prevalence does not change with increasing sampled area because it is well mixed across samples) or for spatial patchiness (“non-linear curve” – the number of infected individuals sampled and the number of individual sampled increase at different rates). Observed estimates in wild fish populations can be influenced by sampling design elements such as sample size (Poulin, 2013), sampling method (Wilson et al., 1993) and timing of sampling (Hutchins et al., 2021). Consequently, sampling design elements must be considered when studying scale-dependencies of infection estimates. Patterns of regional-scale estimates from random sampling can be caused by different underlying local patterns of infection. For instance, a regional prevalence of 20% could be caused by all lakes being at 20% or by all lakes being at 20% on average (e.g., half at 0% and half at 40%). Thus, investigating local-scale patterns is important to bring the necessary nuances on the regional-scale estimates and to infer processes properly. For example, frequency distributions of infection parameters are useful to understand infection dynamics in the landscape (Hess et al., 2002; McGeoch & Gaston, 2002). The final step was to test a suit of deterministic environmental predictors underlying scale-dependent processes to understand the observed infection prevalence and explore whether some indicators could be useful for management of parasite infection in fish communities. Investigating wide-ranging predictors has the potential to enlighten processes driving infection patchiness (herein infection hotspots) within a system that appears homogenous (Bolnick et al., 2020). The shapes and strength of the relationships between infection parameters and drivers are a key element to better understand the mechanisms behind infection patterns (Poulin et al., 2011). Our goal here was not to make predictions on spatial distribution of the parasitic infection but disentangle how patterns are shaped through a scaling perspective to make monitoring and management of parasitic infection in freshwaters easier.

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