Local environment and sampling bias drive parasite prevalence estimates in freshwater fish communities

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October 20, 2024

Abstract

Parasite occurrence and infection estimates vary through time and space, making understanding the underlying drivers highly complex. Comparative studies based on empirical data must consider the factors of variation involved in estimating infection metrics in natural populations to make appropriate and reliable comparisons. 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 sampled across 15 lakes in Québec, Canada. Our results show 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 efforts tend to overestimate the prevalence of infection in the landscape, and that the sampling effort required to estimate an accurate infection prevalence depends on the sampling method employed. Physico-chemical characteristics of the sites and local fish community structure were found to be the best drivers of infection at smaller spatial scales. Furthermore, our results suggest dilution effects due to obstruction and compatibility barriers limit the survival of the free-living cercaria parasite lifestage. Several relationships between infection prevalence and environmental drivers revealed non-linearity, suggesting complex interactions. Examining infection prevalence data at various spatial scales revealed method-induced biases, sampling effort effect and environment driven relationships underscoring the importance of context-dependencies and scale-dependencies in studies on host-parasite interactions.

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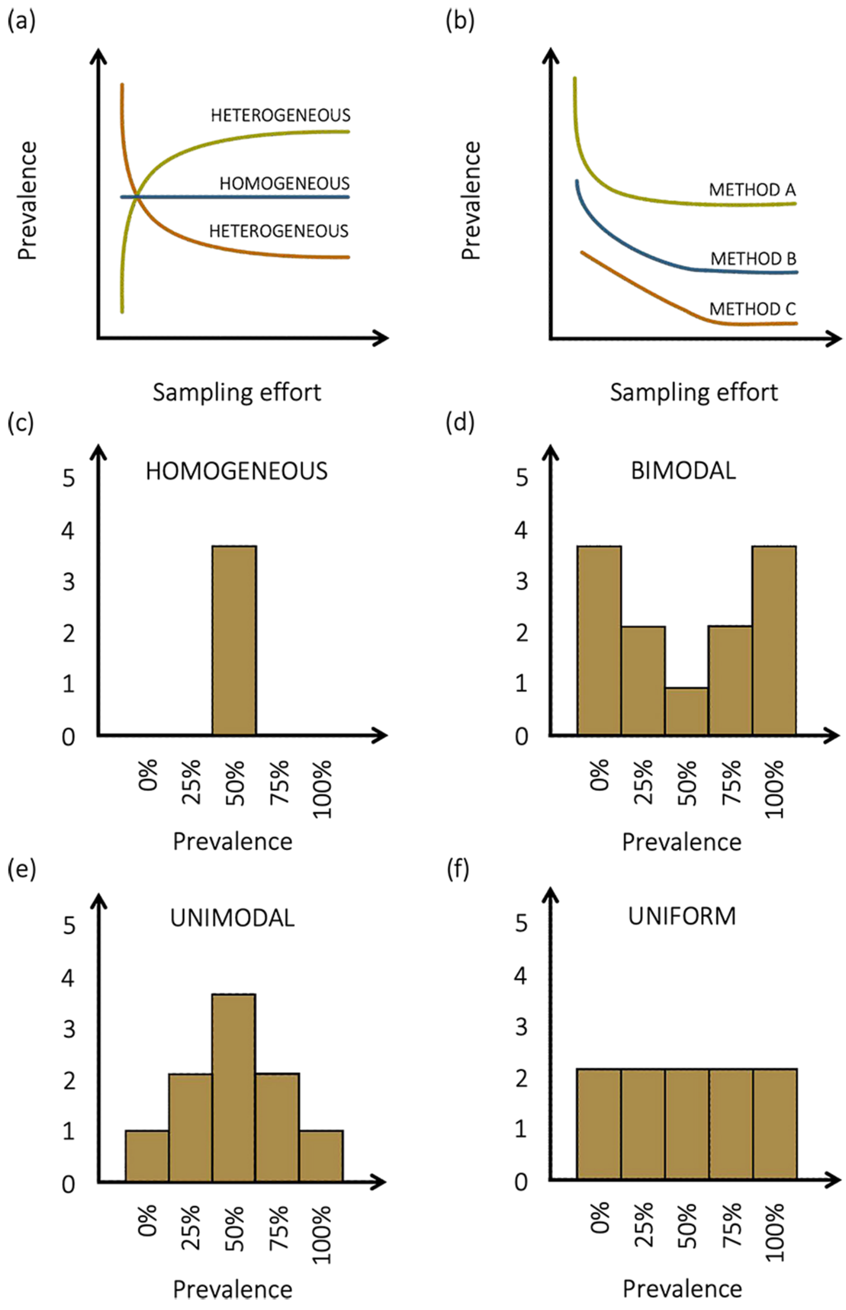
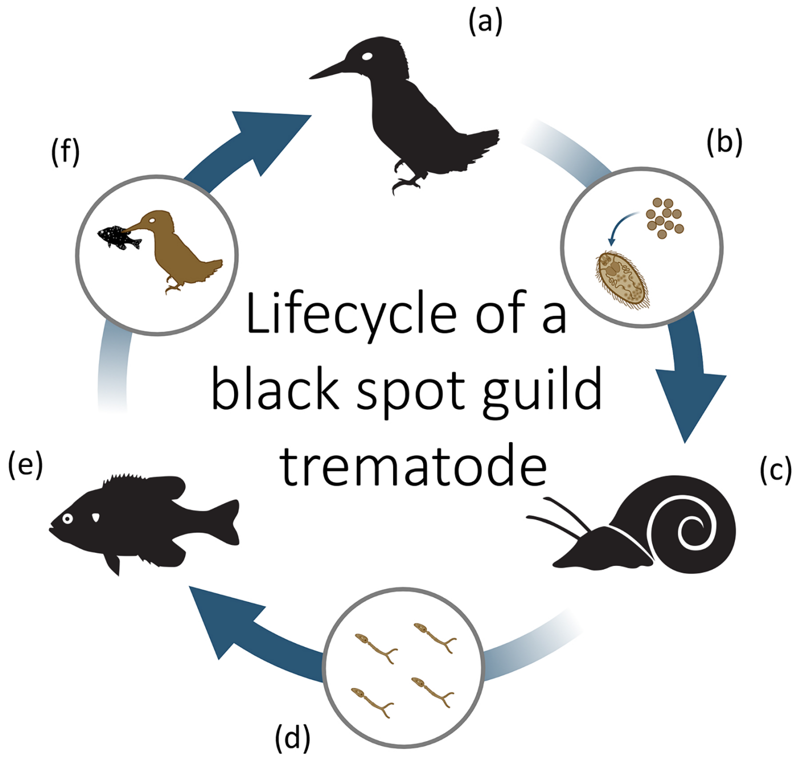
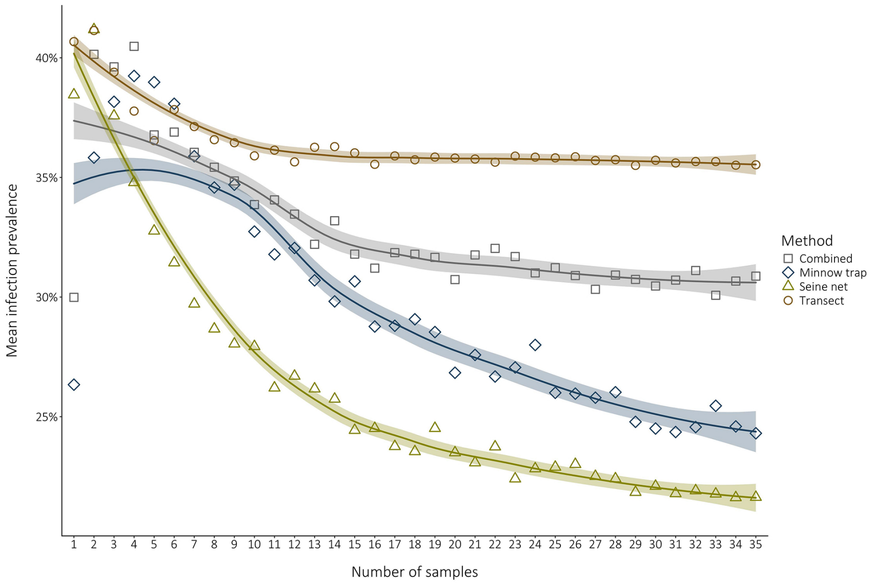
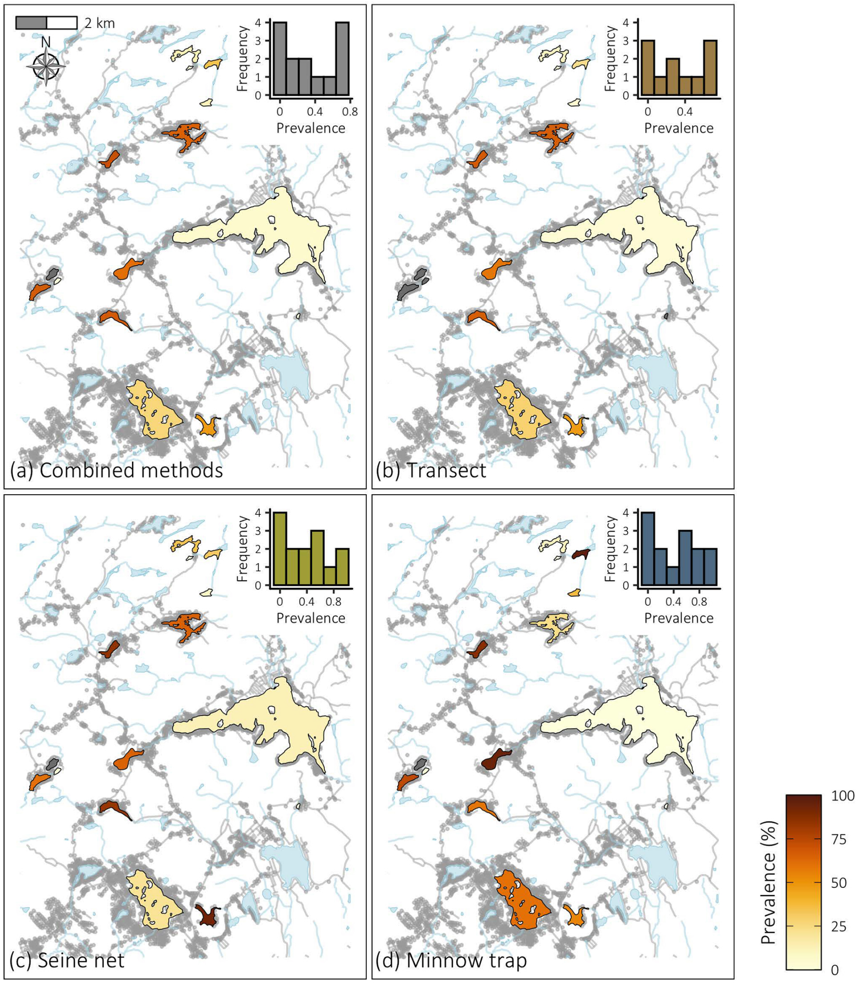
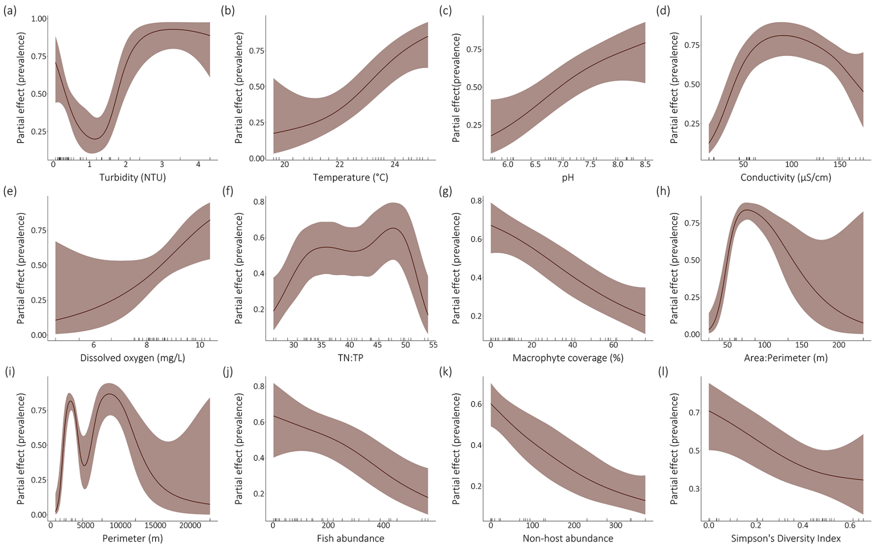

(a)
Prevalence
HETEROGENEOUS
HOMOGENEOUS
HETEROGENEOUS
Sampling effort
(b)
Prevalence
METHOD A
METHOD B
METHOD C
Sampling effort
(c)
HOMOGENEOUS
0
1
2
3
4
5
0%
25%
50%
75%
100%
Prevalence
(d)
BIMODAL
0
1
2
3
4
5
0%
25%
50%
75%
100%
Prevalence
(e)
UNIMODAL
0
1
2
3
4
5
0%
25%
50%
75%
100%
Prevalence
(f)
UNIFORM
0
1
2
3
4
5
0%
25%
50%
75%
100%
Prevalence


(a)
(b)
(c)
(d)
(e)
(f)
Lifecycle of a black spot guild trematode


Mean infection prevalence
40%
35%
30%
25%
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35
Number of samples
Method
□ Combined
◇ Minnow trap
△ Seine net
○ Transect


2 km
N
Frequency
0
1
2
3
4
0
0.4
0.8
Prevalence
(a) Combined methods
Frequency
0
1
2
3
0
0.4
Prevalence
(b) Transect
Frequency
0
1
2
3
4
0
0.4
0.8
Prevalence
(c) Seine net
Frequency
0
1
2
3
4
0
0.4
0.8
Prevalence
(d) Minnow trap
Prevalence (%)
100
75
50
25
0


(a)
Partial effect (prevalence)
1.00
0.75
0.50
0.25
0
1
2
3
4
Turbidity (NTU)
(b)
Partial effect (prevalence)
0.75
0.50
0.25
0.00
20
22
24
Temperature (°C)
(c)
Partial effect(prevalence)
0.75
0.50
0.25
6.0
6.5
7.0
7.5
8.0
8.5
pH
(d)
Partial effect (prevalence)
0.75
0.50
0.25
50
100
150
Conductivity (µS/cm)
(e)
Partial effect (prevalence)
0.75
0.50
0.25
0.00
6
8
10
Dissolved oxygen (mg/L)
(f)
Partial effect (prevalence)
0.8
0.6
0.4
0.2
30
35
40
45
50
55
TN:TP
(g)
Partial effect (prevalence)
0.8
0.6
0.4
0.2
0
20
40
60
Macrophyte coverage (%)
(h)
Partial effect (prevalence)
0.75
0.50
0.25
0.00
50
100
150
200
Area:Perimeter (m)
(i)
Partial effect (prevalence)
0.75
0.50
0.25
0.00
0
5000
10000
15000
20000
Perimeter (m)
(j)
Partial effect (prevalence)
0.8
0.6
0.4
0.2
0
200
400
Fish abundance
(k)
Partial effect (prevalence)
0.6
0.4
0.2
0
100
200
300
Non-host abundance
(l)
Partial effect (prevalence)
0.7
0.5
0.3
0.0
0.2
0.4
0.6
Simpson's Diversity Index