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1 **A COMMUNITY ANALYSIS APPROACH TO PARASITE TRANSMISSION IN**
2 **MULTI-HOST SYSTEMS: ASSEMBLAGES OF SMALL MAMMAL PREY AND**
3 ***ECHINOCOCCUS MULTILOCULARIS* IN AN URBAN AREA IN NORTH AMERICA**

4
5 **Prey assemblage analysis and parasitic transmission**

6
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21 **ABSTRACT**

22 **Background:** *Echinococcus multilocularis* (*Em*) is a parasite with a complex life cycle whose
23 transmission involves a predator-prey interaction. Accidental ingestion of *Em* eggs by humans
24 may cause alveolar echinococcosis, a potentially fatal disease. Although previous research
25 suggested that the composition of the assemblage of prey species may play a key role in the
26 transmission, the relation between *Em* presence and the prey assemblages has never been
27 analyzed. Herein, we propose a community analysis approach, based on assemblage similarity
28 statistics, clustering, non-metric dimensional scaling and GLM modelling to analyze the
29 relationships between small mammal assemblages, environmental variables, and the prevalence
30 of *Em* in intermediate and definitive hosts in an urban area.

31 **Results:** In our study areas within the City of Calgary, Alberta (Canada), we identified three
32 main small mammal assemblages associated with different prevalence of *Em*, characterized by a
33 different proportion of species known to be good intermediate hosts for *Em*. As expected,
34 assemblages with higher proportion of species susceptible to *Em* were observed with higher
35 prevalence of parasite, whereas the total abundance *per se* of small mammals was not a predictor
36 of transmission likely due to dilution effect. Furthermore, these assemblages were also predicted
37 by simple environmental proxies such as land cover and terrain.

38 **Conclusions:** Our results indicated that the use of a community analysis approach allows for
39 robust characterization of these complex and multivariate relationships, and may offer a
40 promising tool for further understanding of parasite epidemiology in complex multi-host
41 systems. In addition, this analysis indicates that it is possible to predict potential foci of disease
42 risk within urban areas using environmental data commonly available to city planners and land
43 managers.

44

45 Keywords: Epidemiology, *Echinococcus multilocularis*, community ecology, community

46 analysis, urban parks, trophically transmitted parasite with complex life cycle, small mammals

47

48 1. BACKGROUND

49 *Echinococcus multilocularis* (*Em*) is a parasitic tapeworm that can cause human alveolar
50 echinococcosis (AE), currently considered among the most serious zoonotic diseases outside of
51 the tropics (Massolo et al., 2014). The parasite is endemic across the northern hemisphere, and
52 its distribution is expanding (Davidson et al., 2012; Massolo et al., 2014). The disease has high
53 fatality rate (i.e. > 90%) if not treated, and often requires life-long treatments (Craig, 2003). In
54 2010, it was estimated that globally there were 18,235 human cases of AE annually (Torgerson
55 et al., 2010) with an increasing trend. Only few cases were reported in North America outside of
56 Alaska, but there are indications that the risk of AE may be increasing (Massolo et al., 2014).

57 *Echinococcus multilocularis* is a trophically transmitted parasite with a complex life cycle that
58 involves two different hosts and a free-living stage. The parasite typically infects canid predators
59 such as foxes *Vulpes* spp. and coyotes *Canis latrans* (but also domestic dogs) as definitive hosts
60 (DH). The adult parasite, in the DH intestine, produces embryonated eggs which are released in
61 the environment with feces. More than 40 small mammal species (usually rodents) act as
62 intermediate hosts (IHs) by accidentally ingesting these eggs (Liccioli et al., 2013; Vuitton et al.,
63 2003) and developing the final infectious larval stage in the target organ (often the liver). The
64 life cycle is completed when infectious IHs are predated by DHs. Although climate conditions
65 likely determine the limit of the parasite distribution at the global scale, at more local scales the
66 presence and relative abundance of the IH species plays a key role in the parasite distribution and
67 transmission intensity (Giraudoux et al., 2004; Liccioli et al., 2013; Romig et al., 2017). In the
68 southern edge of its European distribution, for example, *Em* spread was deemed to be limited by
69 the presence of single species of small mammal IH (Guerra et al., 2014). Landscape and
70 environmental characteristics that define the distribution of small mammals (e.g., the proportion

71 of the landscape composed by optimal habitat for the susceptible small mammal species) can be
72 important predictors of where the intensity of the parasite transmission is high (Giraudoux et al.,
73 2004; Raoul et al., 2015).

74 However, the influence of susceptible small mammal species on the transmission of *Em* is made
75 complex by interactions among small mammal species and between predator and prey. Higher
76 population density of DH is expected to increase the transmission rate (Raoul et al., 2015). Even
77 in an area inhabited by susceptible small mammal species, parasite transmission is unlikely if
78 their relative abundance within the prey ensemble is low. The presence of other species that are
79 not susceptible to the parasite but preferred as prey by DHs will reduce the probability of *Em*
80 transmission (Baudrot et al., 2016; Guerra et al., 2014). Our previous research on the distribution
81 of small mammals and *Em* in the City of Calgary suggested that the proportion of susceptible
82 species within the small mammal community may be a key factor in determining the prevalence
83 of the parasite (Liccioli et al., 2014).

84 Despite these recent findings, so far researchers have only analyzed the effects of single
85 intermediate species variations on transmission of *Em*, and speculated on or modelled the effects
86 of the small mammal assemblages as a whole. Following up on our previous study (Liccioli et
87 al., 2014), we wanted to explore in more detail the association between small mammal
88 assemblages and *Em* transmission using an analytical approach typical of community ecology. In
89 addition, we analyzed environmental features associated with the prevalence of the parasite,
90 which may allow us to predict areas of high risks.

91 In particular, we aimed to

- 92 A. characterize the composition and structure of the various types of small mammal prey
93 assemblages in the study area;

- 94 B. explore the association between the various types of prey assemblages and *Em* infection
95 in both definitive and intermediate hosts;
- 96 C. identify the environmental proxies that are associated with the various assemblages, and
97 the environment where *Em* transmission is more likely to occur, using geographical data
98 commonly available for city planners.

99

100 2. METHODS

101 2.1 Study area and data description

102 The samples were collected in the City of Calgary (AB, Canada; 51°5'N, 114°5'W; Figure 1),
103 located in the southeastern region of Alberta in the foothills of the Canadian Rocky Mountains,
104 from June 2012 to July 2013. The city encompasses an area of 848 km² and has a population of
105 1,235,171 (The City of Calgary, 2016). The city ranges in elevation from 965 to 1304 meters
106 a.s.l., and encompasses many streams and water bodies with riparian habitats that are often
107 designated as parks and natural areas. The climate is relatively dry (annual precipitation of 412.6
108 mm) and cold, with an average annual high temperature of 10.5 °C and low temperature of -2.4
109 °C (Statistics Canada, 2017). Common habitats in parks and natural areas are grasslands in dry
110 areas, aspen forests in moderately well-drained areas, and willow shrublands in imperfectly
111 drained areas (The City of Calgary, 2014).

112 Common mammals in the city area are snowshoe hares (*Lepus americanus*), white-tailed jack
113 rabbit (*Lepus townsendii*), Richardson's ground squirrels (*Urocitellus richardsonii*), gray
114 squirrels (*Sciurus carolinensis*), southern red-backed and meadow vole (*Myodes gapperi*;
115 *Microtus pennsylvanicus*), deer mouse (*Peromyscus maniculatus*), muskrat (*Ondatra zibethicus*),
116 coyote, beaver (*Castor canadensis*), mule deer (*Odocoileus hemionus*), white-tailed deer

117 (*Odocoileus virginianus*), and less commonly red fox (*Vulpes vulpes*; The City of Calgary,
118 2014). Of these, only southern red-backed vole, meadow vole, deer mouse, beaver and muskrat
119 are currently described as IHs for *Em* (Liccioli et al., 2013), but beaver and muskrats were rarely
120 reported in the diet of urban coyotes in the City of Calgary (Liccioli et al., 2015).

121 We used data on small mammal relative abundance per site collected for the study of Liccioli et
122 al. (2014) between June 2012 and July 2013 in sites within Calgary urban parks and natural
123 areas. Specifically, these sites were located in Nose Hill Park (site NHP1 ~ NHP3), Bowmont
124 (BM1 ~ BM3), Weaselhead (WSH1 ~ WSH3), Southland lowland (SL1 & SL2), and Fish Creek
125 Provincial Park (FCPP1 ~ FCPP3; Figure 1). Samples collected in June and July 2013 were not
126 used in the study by Liccioli et al. (2014) because of their interest in seasonal pattern, but were
127 included in this study in order to increase the sample size, whereas the first trapping session in
128 June 2012 included in Liccioli et al. (2014) was removed from this study because it was
129 conducted with a different protocol (i.e. trappings were conducted for 4 nights in row instead of
130 3 due to weather condition causing most traps to misfire on the first night). The small mammals
131 sampled within these sessions totaled 1223 small mammals of 9 different species (Liccioli et al.,
132 2014).

133 We used DH prevalence estimated from 385 coyote feces collected by Liccioli et al. (2014) in
134 the same five areas between May 2012 and July 2013 (Table 1: Liccioli et al., 2014). For more
135 details on the small mammal and fecal collection methods and data analysis methods, see
136 Liccioli et al. (2014).

137

138 2.2 Assemblage analysis

139 The trap catch-rate of small mammals caught at each site were standardized by aggregating all
140 captures for each site and then divided by number of trap-nights, not counting misfires and traps
141 that caught other species (e.g. a trap that caught a deer mouse could not have caught a meadow
142 vole that same night) to represent the relative abundances of each species (Table 1). Differences
143 between species composition at each trap site were measured using the Bray-Curtis statistic
144 (Bray and Curtis, 1957), treating each trap site as statistical unit and the relative abundance for
145 each species as variable. The relative abundances were log-transformed ($\log(x+1)$) before
146 calculation of the similarity matrix (Beals, 1984).

147 The Bray-Curtis similarity was visualized through hierarchical agglomerative clustering
148 dendrogram, using group average algorithm to calculate the distance between clusters (Field et
149 al., 1982). To test the robustness of the cluster structures, clustering with single-linkage and
150 complete-linkage algorithms were also performed. In addition, hierarchical agglomerative
151 clustering was performed on data transformed to percentage of each species before calculation of
152 Bray-Curtis similarity, again using group average, single-linkage, and complete-linkage.

153 Resulting cluster structures were compared for consistency. Significance of the clusters were
154 tested using similarity profile (SIMPROF) tests (Clarke et al., 2008). The association between
155 clusters and presence of *Em* infected small mammals were statistically tested using Fisher's
156 exact test (Sokal and Rohlf, 1995).

157 To identify the general characteristics of each cluster type, we performed Canonical Correlation
158 Analysis on the principal coordinates (CAP) procedure (Anderson and Willis, 2003). This
159 procedure displays cloud of multivariate points with reference to a hypothesis set a priori by
160 finding axes that maximize the difference among groups. The procedure also tests the
161 significance in the difference among groups using permutation tests and "trace" statistics,

162 equivalent to Pillai's trace statistics in traditional multivariate analysis of variance test. Pearson
163 correlation coefficients between the abundance and proportion of each species to the CAP axes
164 were calculated and their vectors overlaid on the plot.

165 A pooled *Em* prevalence was calculated for each small mammal assemblage for each site as the
166 number of infected animals divided by the total number of small mammals caught. This pooled
167 prevalence was a simple estimate of the likelihood for a coyote to become infected by preying on
168 a specific assemblage.

169 We associated the DH prevalence estimates for the five areas to the trap sites in each area, which
170 is a reasonable assumption considering the distance between each area and territoriality of
171 coyotes. The possible exception was the FCPP3 site which was close to SL. However, because
172 SL and FCPP had similar estimate of DH prevalence, FCPP3 could be either associated with DH
173 of FCPP or SL with little difference.

174

175 2.3 Environmental analysis

176 The environmental proxies surrounding each trap site were identified using ArcGIS Desktop
177 (Release 11. Redlands, CA: Environmental Systems Research Institute). We hypothesized that
178 combination of land cover types, distance to water, and terrain features would allow us to
179 identify habitats associated with small mammal assemblages. Land cover types and distance to
180 water were obtained from a Land Cover map (updated at 2014) with 5 meter resolution (Fiera
181 Biological Consulting Ltd., 2014). Terrain features (the average aspect, slope, and "ruggedness"
182 or the standard deviation of the slope) of each trap site were calculated from a digital elevation
183 model with resolution of 0.75 arc-second, or approximately 18 meters (Natural Resources
184 Canada, 2012).

185 A multinomial logistic regression (MLR) model (Fox, 2008; Hosmer et al., 2013) associating the
186 environmental variables to assemblage types was developed. We built a set of alternative models
187 based on what we considered biologically relevant combinations, such as land cover types of
188 forest, grassland, and shrub lands and terrain features. We used focal statistics with circle of 200
189 meter radius to standardize the way we measure surrounding environment, assuming that areas
190 within 200 meter were sufficient for identifying the habitats influencing the small mammals
191 based on their home ranges while also approximating the areas covered by trap grids (Madison,
192 1980; Madison et al., 1984). We used total numbers of raster cells within 200 meter radius for
193 each land cover type as predictor variables. We used the mean value of the cells within 200
194 meter radius for the terrain variables after resampling each terrain raster to 5 meter resolution.
195 The models were then compared using the corrected AICc scores and weights (Burnham and
196 Anderson, 2002). The best performing MLR model was then applied to develop a predicted
197 distribution map of the small mammal assemblage for the entire area of the City. Because we did
198 not sample small mammals from agricultural areas, and because the agricultural areas were at the
199 periphery of the city, we removed agricultural areas from the final map. Similarly, because small
200 mammals are known to avoid mowed grass (Bowers and Dooley, 1993), and because in one
201 experimental trapping we found no small mammal in a field of mowed grass adjacent to a
202 naturally wooded area, we also removed areas classified as manicured grass. Final map was
203 resampled to 50 meters resolution to be used for an agent-based simulation of the transmission of
204 *Em* in future study.

205 All the statistical analysis, except for the MLR were performed using software Primer ver.6 with
206 PERMANOVA+ add-on (Anderson et al., 2008). MLR was performed using SPSS ver.24 (IBM
207 Corps. 2016).

208

209 **3. RESULTS**210 3.1 Assemblage analysis

211 To reduce the noise on the community analysis, least chipmunk, northern pocket gopher, and
212 house mice were removed from relative abundance data prior to the calculation of the Bray-
213 Curtis similarity matrix because of their minimal abundance in the data. The hierarchical
214 clustering of the small mammal assemblage identified three major assemblage types using an
215 arbitrary cut-off line of 45% similarity, although SIMPROF test failed to detect significance
216 ($p=0.678$, Figure 2a).

217 Cluster 1 consisted of three BM sites, where Liccioli et al. (2014) found two IHs positive for *Em*,
218 and estimated highest prevalence among DH. Cluster 2 consisted of three NHP sites, FCPP1,
219 SL1, WSH2 and WSH3. Liccioli et al. (2014) found positive IHs in three sites and estimated
220 moderately high prevalence among DH in NHP. The remaining sites WSH1, SL2, FCPP2, and
221 FCPP3 constituted cluster 3. Liccioli et al. (2014) found no positive IH in these sites and
222 estimated low prevalence of DH in these areas (Table 1). Fisher's exact test on the *Em* positive
223 cases of small mammals and the three clusters could not detect any significant difference ($p =$
224 0.136).

225 Clustering with complete-linkage algorithm also grouped trap sites into the same three clusters (p
226 $= 0.695$, Figure 2b). The same pattern was not observed with single-linkage, where trap sites
227 successively joined groups instead of grouping into distinct clusters (not shown, $p = 0.718$).
228 Similar, but slightly different cluster patterns were observed when group-average and complete-
229 linkage clustering algorithms were performed on percentage of species ($p = 0.144$ and 0.136
230 respectively, result of group-average shown in Figure 2c). With percentage of species, cluster 3

231 was smaller and consisted of only two sites, but BM still formed a single cluster. Clustering
232 percentage data with single-linkage algorithm showed less distinct a pattern, but BM sites still
233 grouped into a single cluster ($p = 0.127$). All the following analyses are based on relative-
234 abundance data and clusters based on group-average algorithm.

235 Conversely, CAP procedure of the small mammal assemblages, using the three clusters identified
236 as grouping factors (Figure 3), highlighted the significant difference between the three clusters
237 (trace statistics 1.6536, $p = 0.001$). Vectors representing the correlation between the CAP axes
238 and the abundances of each species overlaid in Figure 3a indicated that all the species were more
239 abundant in cluster 2. Vectors indicating the correlation of the CAP axes to the proportion of
240 each species and (Figure 3b) indicated that cluster 1 assemblages (particularly BM 1 and BM2)
241 were dominated by deer mice, whereas cluster 3 sites (SL2 and FCPP2) were characterized by
242 shrews.

243

244 3.2 Environmental proxies for assemblages

245 The best MLR model selected by AICc used north-south aspect and ruggedness as predictor
246 variables, with AICc of 18.722 and classified 13 out of 14 trap sites correctly (Table 2). When
247 this model was applied to the natural areas of the City of Calgary, 1209 ha (6.96%) were
248 predicted to be habitat for cluster 1, 8164 ha (47.02%) for cluster 2, and 7991 ha (46.02%) for
249 cluster 3 (Figure 4; see supplementary material for parameter estimates).

250

251 **4. DISCUSSION**

252 Using a community ecology analytical approach, we identified three assemblage types of small
253 preys of coyotes, the main carnivore species in urban settings in Calgary, Alberta (Canada).

254 More importantly, we highlighted an association between these assemblages and the presence of
255 *Echinococcus multilocularis* in wild hosts. Finally, we identified potential environmental proxies
256 calculated from land use data readily available for urban settings that could be associated with
257 parasite within this sylvatic cycle. Our results provided evidence to support recent theoretical
258 models that emphasized the role of complexity of host community in transmission of tropically
259 transmitted parasites (Baudrot et al., 2016).

260

261 4.1 Small prey assemblages and *Echinococcus multilocularis*

262 Our clustering analysis using Bray-Curtis similarity identified three clusters. Although the
263 clusters structures were not statistically significant by SIMPROF test possibly due to small
264 sample size, similar structure were observed in both relative abundances and percentage of
265 species, and with different clustering algorithms, providing some confidence in classifying the
266 small mammal assemblages to the three assemblage types. Assemblage 1 consisting of BM sites
267 seemed to be highly susceptible to the transmission of *Em*, while assemblage 3 seemed to be
268 least susceptible to *Em* transmission.

269 In our study area, the three small mammal species of most interest due to their known
270 susceptibility to *Em* are deer mice, meadow voles, and southern red-backed voles (Liccioli et al.,
271 2013a). Particularly interesting was the correlation of proportion of deer mice to assemblage 1,
272 where the prevalence among DH was high (Figure 3b). This is consistent with conclusions drawn
273 by Liccioli et al. (2014) that proportion of susceptible species is the key factor in the
274 transmission of the parasite. However, even though assemblage 1 and 2 had about same
275 proportion of susceptible species, assemblage 1 was associated with higher prevalence in both

276 DH and IH. Compared to assemblage 1, assemblage 2 had higher abundance of most species of
277 small mammals (Figure 3a). Therefore we suspect that higher abundance of small mammals in
278 general, both susceptible and non-susceptible, led to dilution of exposure and reduced
279 transmission (Baudrot et al., 2016).

280 Any inference drawn from this cluster analysis is limited by the samples size - an issue
281 associated with the low prevalence at which the parasite occurs in intermediate hosts, which
282 likely caused the lack of statistical significance for the Fisher's exact test on the assemblage
283 types and the presence of positive IHs. However, the patterns observed were in agreement with
284 the theoretical studies (Baudrot et al., 2016; Raoul et al., 2015).

285

286 4.2 The urban small mammal assemblages and their landscape proxies

287 In our study, the terrain features (north-facing aspect and ruggedness) turned out to be better
288 predictors of assemblage types than land cover types and were selected for the best MLR model.
289 This was probably because the land cover classification was too coarse for the habitats of small
290 mammals. While land cover types were good indicator of where the natural land covers were
291 (because we collected samples only from natural areas), terrain features were probably better
292 indicators of subtle differences in habitats (Franklin, 1995). For example, assemblage 2 seemed
293 to be associated positively with north-facing aspect and negatively with ruggedness
294 (supplementary Table). These terrain features may be better predictors of vegetation types that
295 prefer moist environment. Distance to water was not selected in the model, probably because
296 most sites were close to water, and the only site that differed for this variable (NHP3) had
297 species composition resembling other sites.

298 Interestingly, the predicted distribution of the small mammal assemblage type 1 was
299 characterizing most of BM and a fair portion of NHP (Figure 4). The prevalence of *Em* in these
300 two areas were higher than the other three areas (Liccioli et al., 2014) and in agreement with our
301 inference that assemblage 1 contributed most to the transmission of the parasite, and possibly
302 explains why NHP had higher prevalence even though all three NHP sites were in assemblage 2.
303 However, the predicted distribution of assemblage 1 also covered large area of FCPP, where the
304 prevalence of *Em* was estimated to be low, both in DH and IH (Liccioli et al., 2014).

305 Another possible explanation for the observed pattern of *Em* prevalence would be the availability
306 to coyotes of food sources other than small mammals, which was not quantified in our study.
307 Coyote diet in our study area includes deer and lagomorphs, fruits and vegetable matters, and
308 anthropogenic food sources (Liccioli et al., 2015). Abundance of deer in the area is expected to
309 be particularly important in winter, when they are more frequently consumed and the parasite
310 prevalence in IH is highest (Liccioli et al., 2015; Liccioli et al., 2014). Large and/or connected
311 parks such as NHP, FCPP, and WSH would likely be used by deer more frequently than smaller,
312 less connected parks such as BM and SL.

313 The feeding and marking behavior of coyotes (i.e., DHs) can also be important for the
314 transmission of the parasite. Although the small mammal assemblages and environmental
315 proxies in and around each site may provide some clues on the parasite transmission, coyotes are
316 known to have wide home ranges and readily travel through urban areas (Gehrt, 2007; Lamy,
317 2015). To estimate transmission of parasites and their spatial patterns, analysis of small mammal
318 assemblages alone is not sufficient. Studies on spatial behavior of coyotes, using simulations
319 such as agent-based models, would provide further understanding of the spatial patterns of *Em*

320 transmission. Such studies would also allow testing if changes in small mammal assemblages
321 could exert significant effects on parasite transmission.

322

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334

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- 412
- 413

414 **LIST OF TABLES**

415 Table 1. This table summarizes the data on small mammal assemblages composition extracted
416 from (Liccioli et al., 2014) collected in 2012-2013 in city parks and natural areas in the
417 City of Calgary (Alberta, Canada). In table are reported the catch rate for each species
418 (indicated by genus names) for every hundred trap-nights, the presence of *Echinococcus*
419 *multilocularis* (1= present, 0 = absent) and prevalence (%) among intermediate hosts (IH),
420 and prevalence among definitive hosts (DH) at each site. The species of small mammals
421 are: Deer mouse (*Peromyscus maniculatus*), Meadow vole (*Microtus pennsylvanicus*),
422 Shrews (*Sorex* sp.), Southern red-backed vole (*Myodes gapperi*), Western jumping mouse
423 (*Zapus princeps*), Thirteen-lined ground squirrel (*Spermophilus decemlineatus*), Least
424 chipmunk (*Tamias minimus*), Northern pocket gopher (*Thomomys talpoides*), and House
425 mouse (*Mus musculus*).

426
427 Table 2. Comparison of multinomial logistic regression models predicting various types of
428 assemblages of small mammals developed from data collected in 2012-2013 in city parks
429 and natural areas in the City of Calgary, (Alberta, Canada). The values k , Δ_i , and w_i
430 indicate number of parameters estimated, difference in AICc, and relative weights of AICc,
431 respectively. Although the model with north-south aspect and ruggedness performed best
432 in terms of AICc, N-S aspect and slope model, N-S aspect, slope, and ruggedness model
433 performed comparably well.

434

435

436 **LIST OF FIGURES**

437 Figure 1. Study sites for the characterization of the small mammal assemblages in urban Calgary,
438 AB, Canada in 2012-2013, showing the location of five areas in Urban Calgary and
439 detailed map of Bowmont, Southland Lowlands, and Weaselhead. Bowmont (BM),
440 Fishcreek Provincial Park (FCPP), Nose Hill Park (NHP), Southland Lowlands (SL), and
441 Weaselhead (WSH).

442
443 Figure 2. Dendrograms derived from the Bray-Curtis similarity of small mammal assemblages in
444 five parks and natural areas in urban Calgary, AB, Canada, 2012-2013. a) Dendrogram
445 using abundance data and group-average clustering algorithm. The dashed line indicates
446 the cluster cut-off line of 45% similarity. Symbols for each site indicate the prevalence of
447 definitive hosts (EmDH) and presence (1) or absence (0) of infected small mammals
448 (EmIH). b) Dendrogram using abundance data and complete-linkage clustering algorithm.
449 Note how it is similar to the dendrogram using group-average algorithm. c) Dendrogram
450 using proportion data and group-average clustering algorithm. Note how all BM sites are in
451 single cluster and all NHP sites and most sites are in another cluster, similar to the
452 dendrogram using abundance data.

453
454 Figure 3. Plot of the Canonical Correlation Analysis on the principal coordinates (CAP) of small
455 mammal assemblages in five parks and natural areas in urban Calgary, AB, Canada, 2012-
456 2013, using the cluster as a grouping factor. The cluster 1 is on the lower right corner,
457 cluster 2 is on the lower left corner, and cluster 3 is on the center to the top of the plot. The

458 45% similarity contour line is drawn based on the dendrogram in Figure 2a. a) Vectors
459 were overlaid showing the correlation with the abundances of each species to each cluster.
460 The red vector shows the correlation with the abundance of all the susceptible species
461 combined. b) Vectors were overlaid showing the correlation with the proportion of each
462 species to each cluster. The red vector shows the correlation with the proportion of all the
463 susceptible species.

464

465 Figure 4. Map showing the geographic distribution of three small mammal assemblage types
466 predicted for the City of Calgary area by a multinomial logistic regression (MLR) model
467 associating the environmental variables to assemblage types, developed from data collected
468 in 2012 and 2013 (Liccioli et al., 2014). Note how large portion of BWM and NHP were
469 classified as assemblage 1 as expected, but also large portion of FCPP, where it was not
470 expected.

471

472 **Table 1.**

<u>Site</u>	<u>Peromyscus</u>	<u>Microtus</u>	<u>Sorex</u>	<u>Myodes</u>	<u>Zapus</u>	<u>Thomomys</u>	<u>Spermophilus</u>	<u>Tamias</u>	<u>Mus</u>	<u>IH presence (Prevalence %)</u>	<u>DH Prevalence (%)</u>
BM1	2.9530	0.1030	0.1545	0.1545	0	0	0	0	0.1545	1 (1.43)	
BM2	1.2318	0.0462	0.2304	0	0.3682	0	0	0	0	1 (2.44)	63.07
BM3	0.8246	0.0462	0.5969	0	0.0923	0	0	0	0	0	
FCPP1	0.8836	3.8810	0.7804	0.0524	0	0	0	0	0	0	
FCPP2	0.1284	0.7653	0.5963	0	0.2138	0	0	0	0	0	6.23
FCPP3	0	0.3745	0.8696	0	0	0	0	0	0.0626	0	
NHP1	2.0658	3.2526	1.6213	0	0	0	0	0	0	1 (0.93)	
NHP2	1.4470	2.4053	0.8836	0	0.4178	0	0	0	0	1 (1.00)	17.28
NHP3	1.5603	1.9081	0.2874	0	0.4304	0	0	0	0	0	
SL1	1.6618	4.0874	3.4752	0	0	0.0367	0	0	0.0367	1 (0.38)	5.42
SL2	0.4288	1.0230	2.4780	0	0	0.0861	0	0	0	0	
WSH1	0.9620	0.7610	0.6098	0.1021	0.2041	0	0.3058	0	0	0	
WSH2	2.0045	1.1976	0.9752	2.5111	0.9009	0	0	0.1513	0	0	6.22
WSH3	2.0101	3.2258	1.5980	2.6622	0.3407	0	0	0.1706	0	0	

473

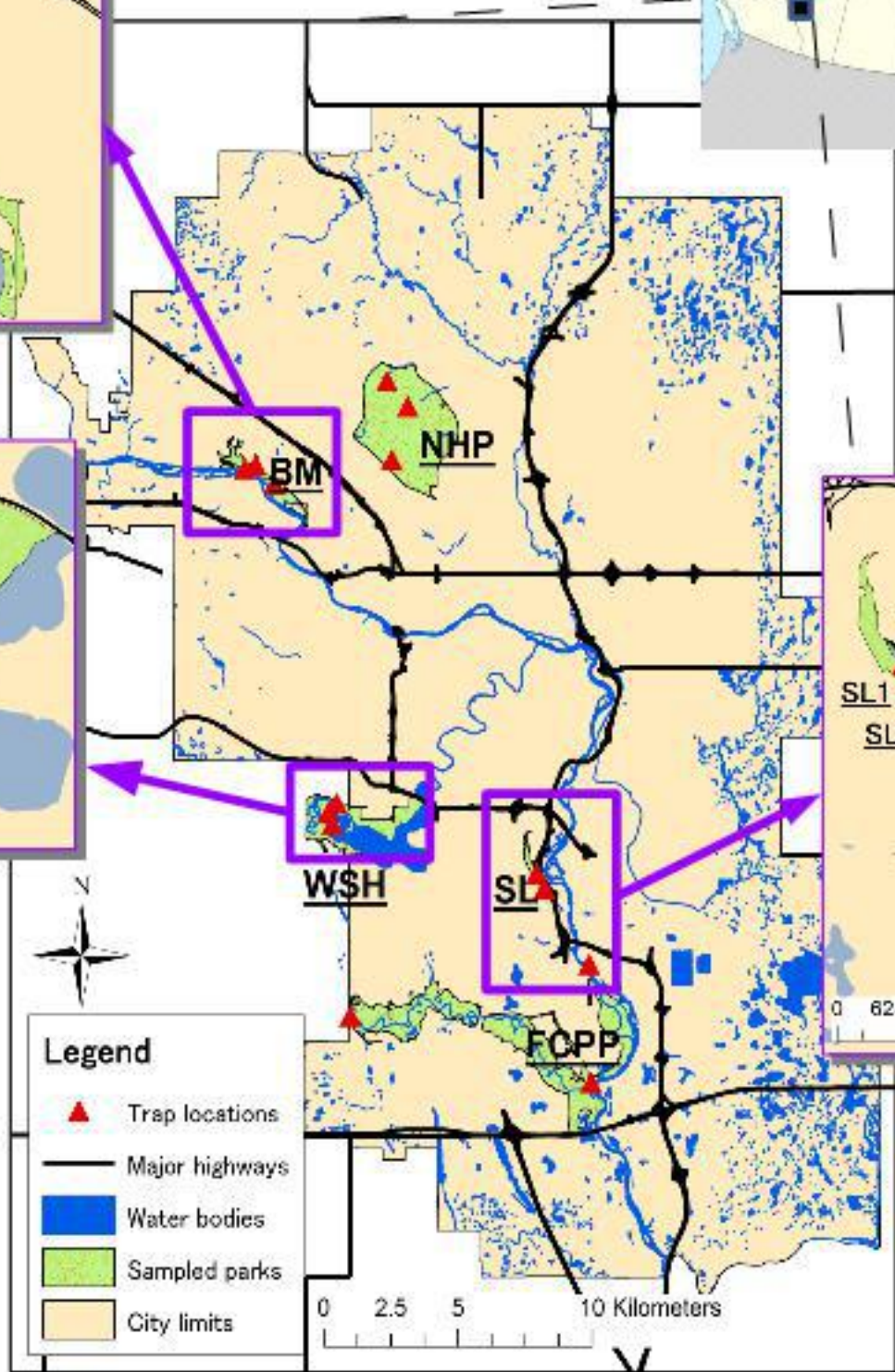
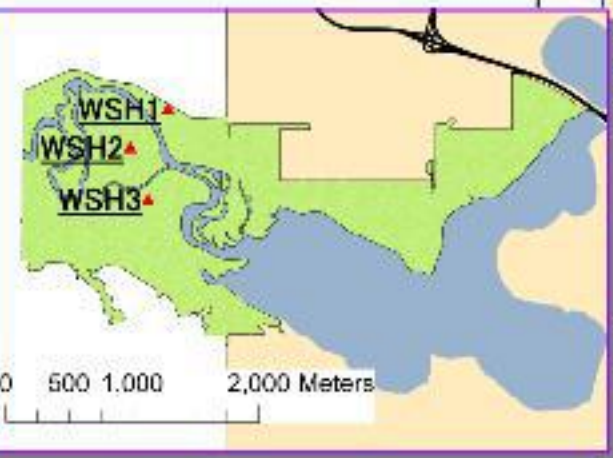
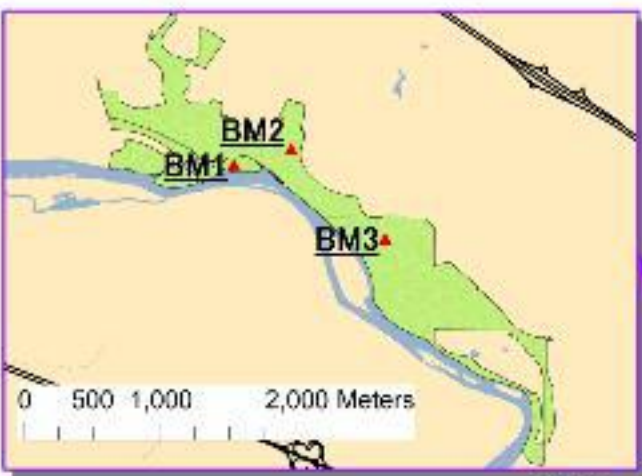
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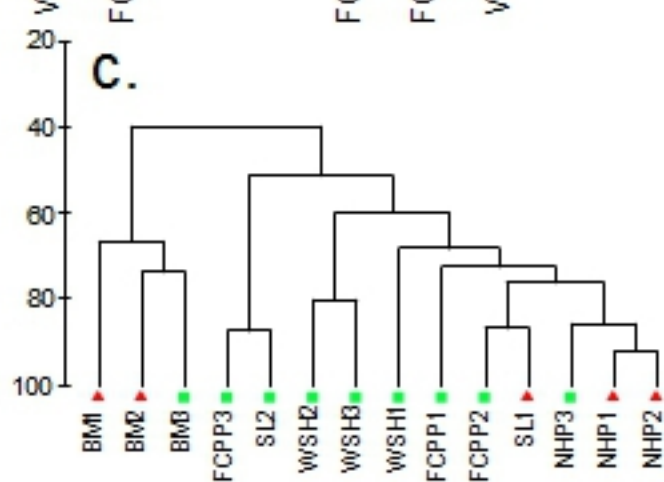
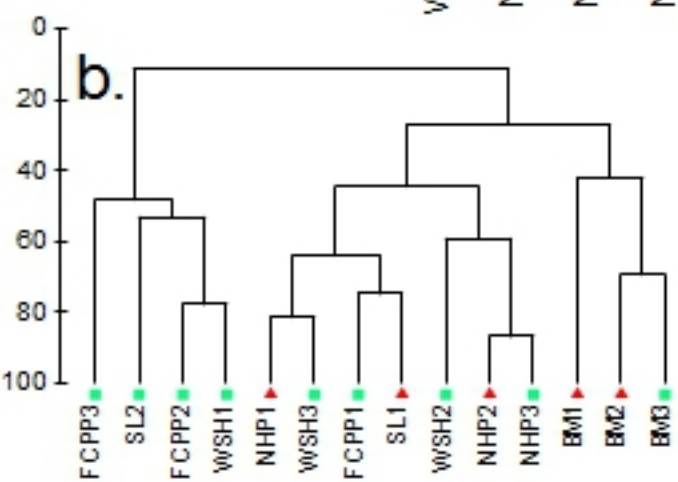
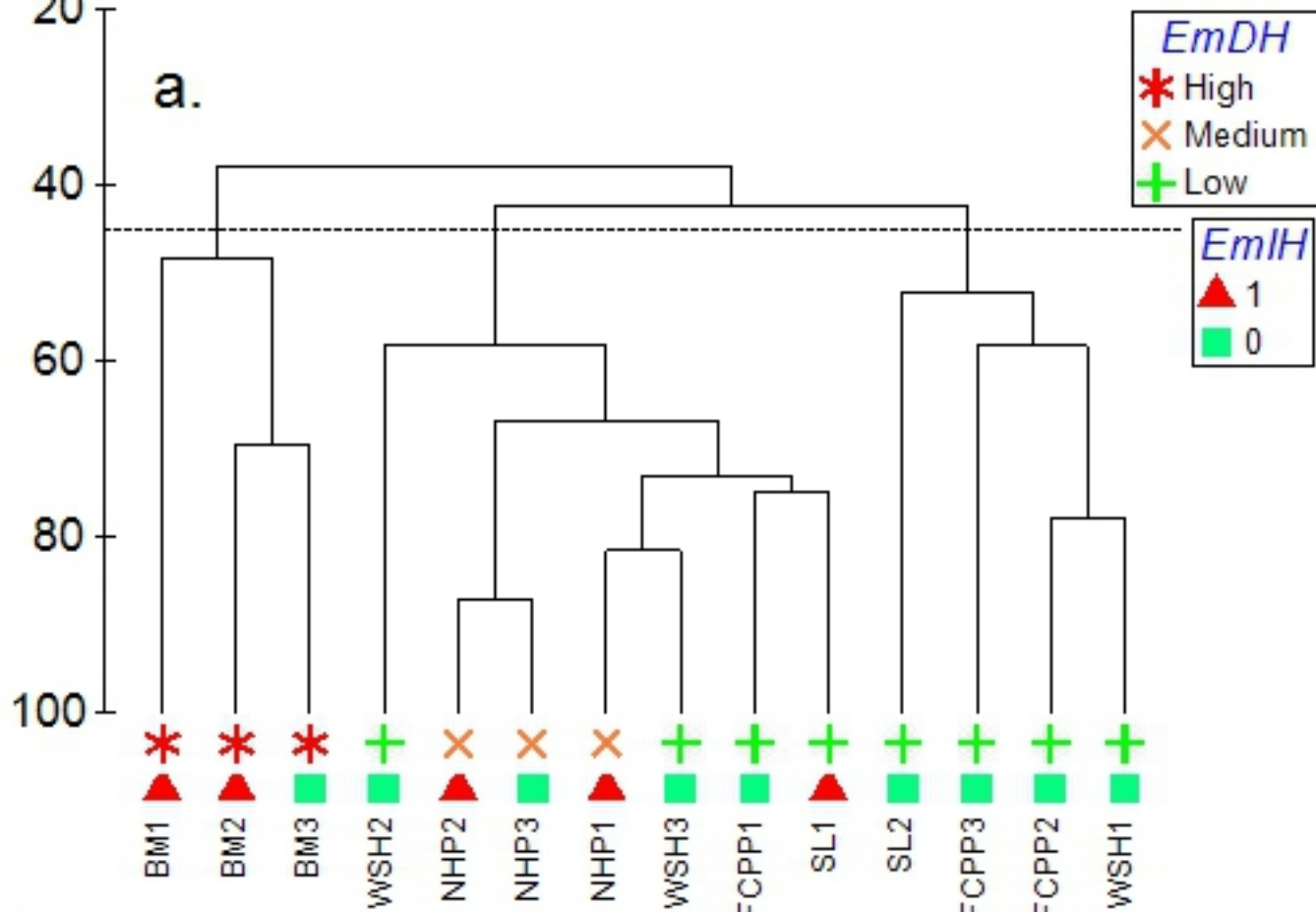
476 Table 2.

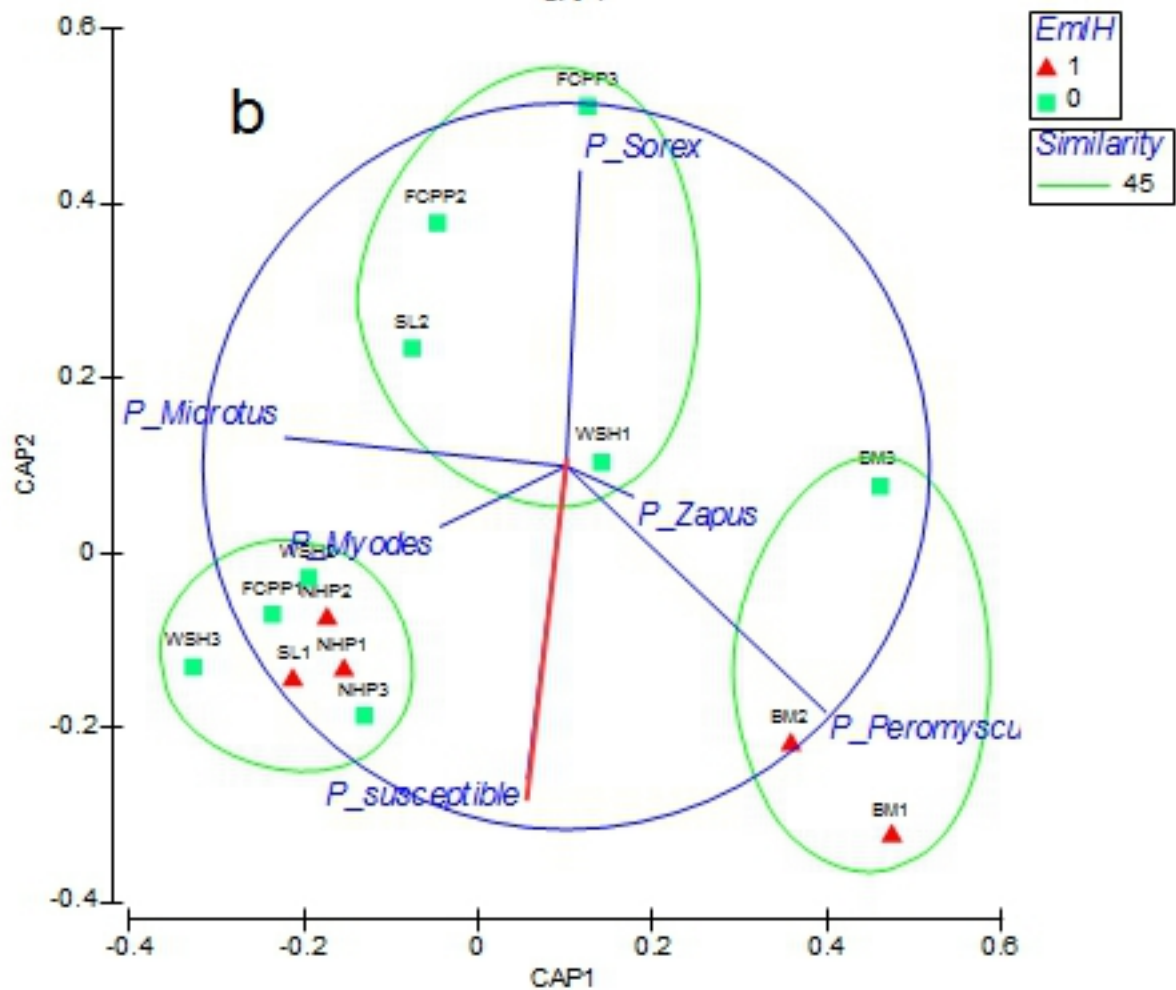
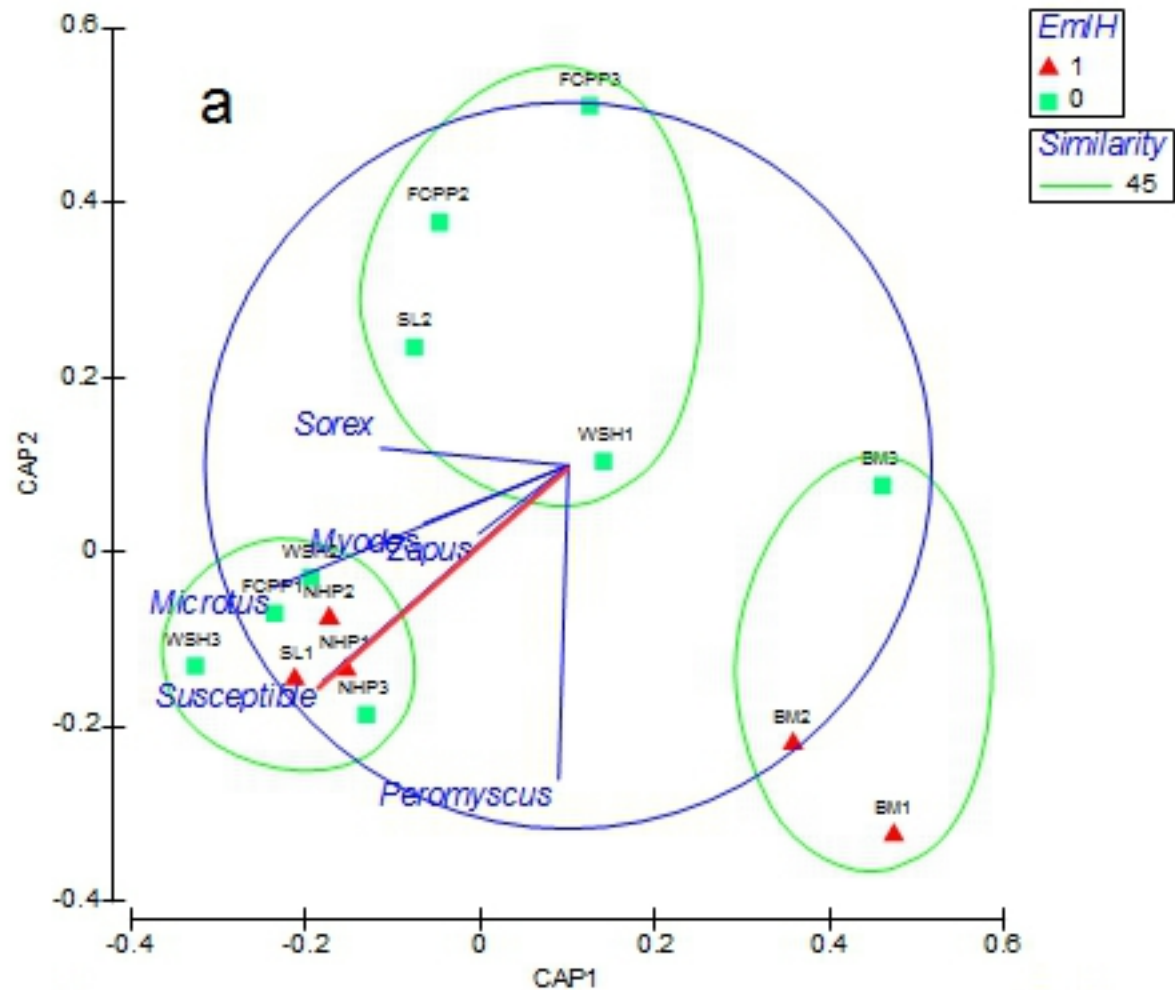
<u>Model</u>	<u>k</u>	<u>-2 * log likelihood</u>	<u>Classification accuracy (%)</u>	<u>AICc</u>	<u>Δ_i</u>	<u>w_i</u>
N-S Aspect & Ruggedness	3	4.322	92.9	18.722	0	0.4857
N-S Aspect & Slope	3	5.616	92.9	20.016	1.2940	0.2543
N-S Aspect & Ruggedness & Slope	4	0	100	20.4444	1.7224	0.2053
N-S Aspect only	2	14.06	78.6	23.1509	4.4289	0.0530
Slope only	2	22.887	57.1	31.9779	13.2559	0.0006
Ruggedness & Slope	3	18.586	64.3	32.9860	14.2640	0.0004
Intercept only	1	29.805	50	33.3023	14.5803	0.0003
Ruggedness only	2	24.532	50	33.6229	14.9009	0.0003

477



- Legend**
- ▲ Trap locations
 - Major highways
 - Water bodies
 - Sampled parks
 - City limits





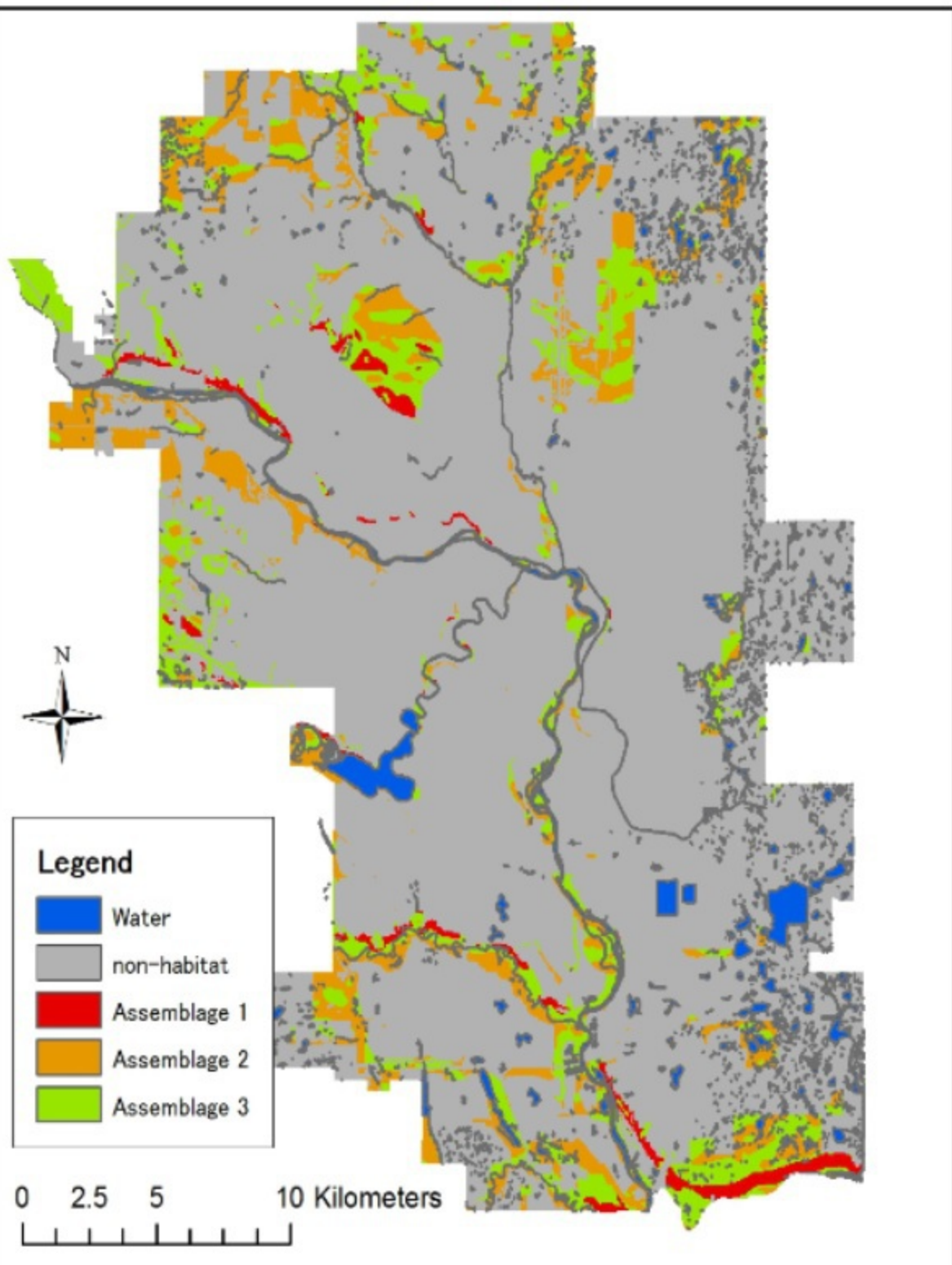
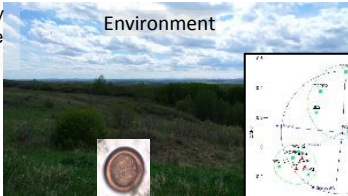


Photo by
Kensuke
Mori



Environment



Parasite egg



Intermediate Host Community



Definitive Host



Coyote Photo by
Alessandro
Massolo

Small Mammal
Photos by Phil
Myers, Creative
commons



Parasite