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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 km<sup>2</sup> 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  $k$ ,  $\Delta_i$ , 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

474

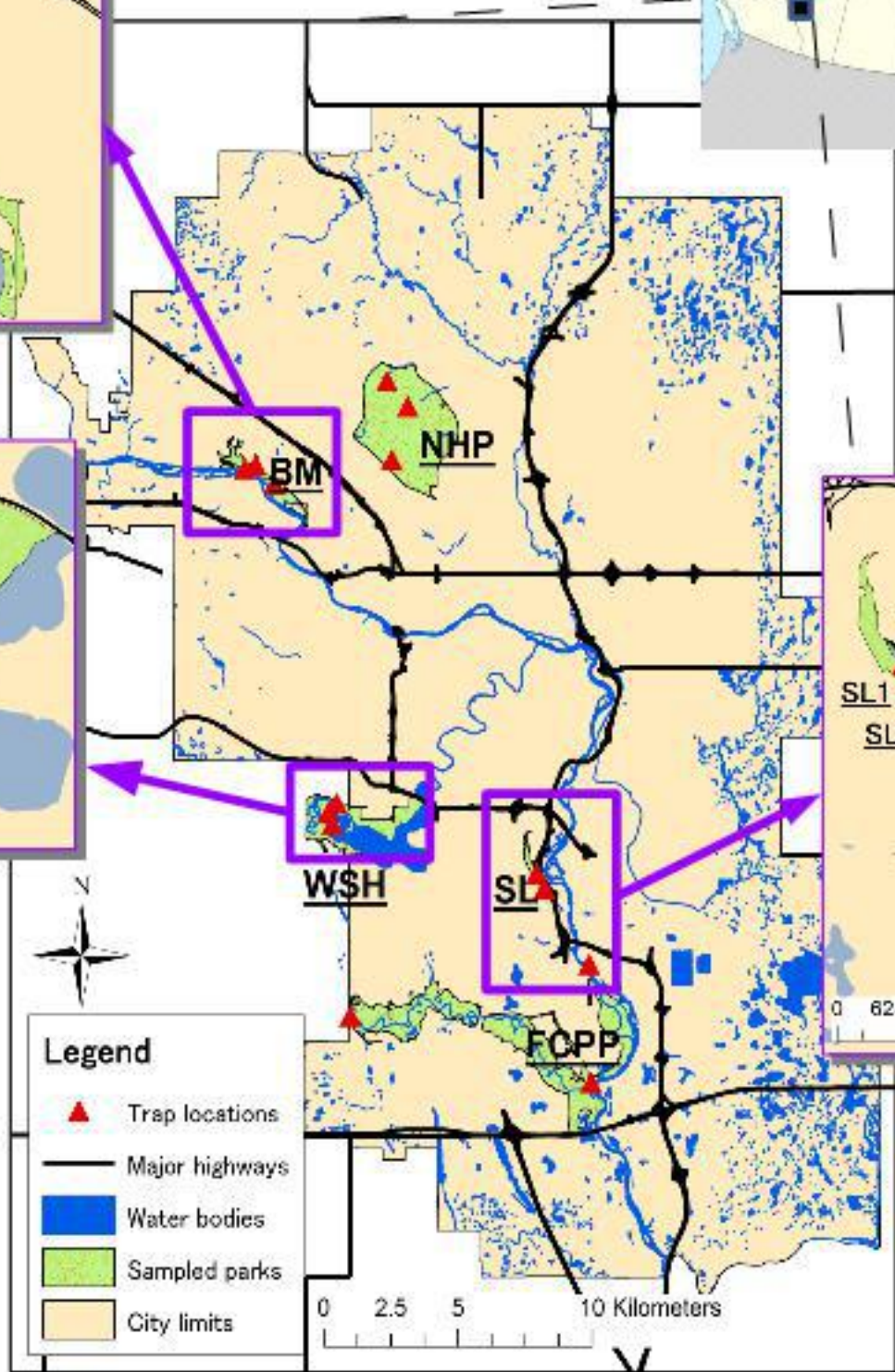
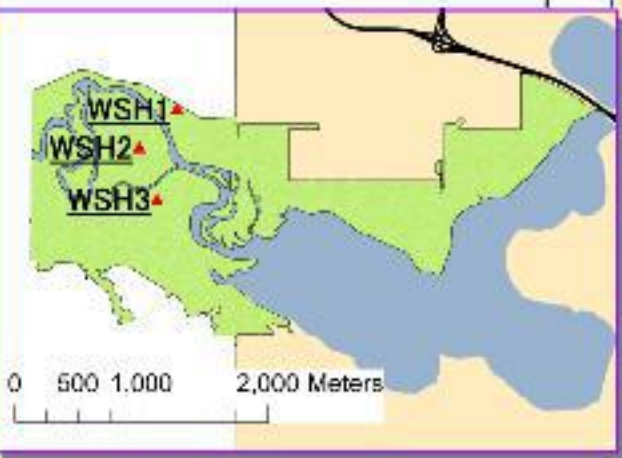
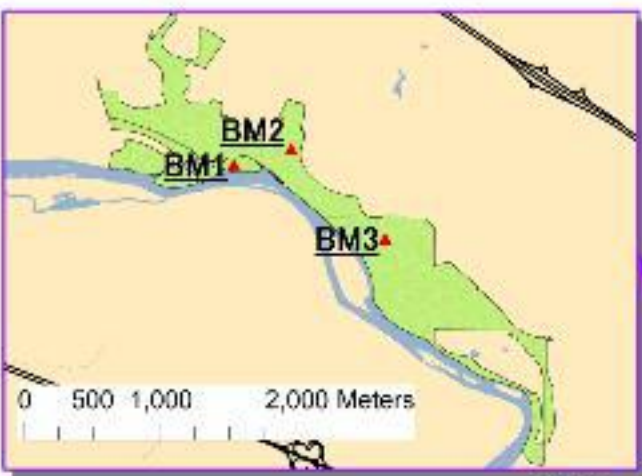
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476 Table 2.

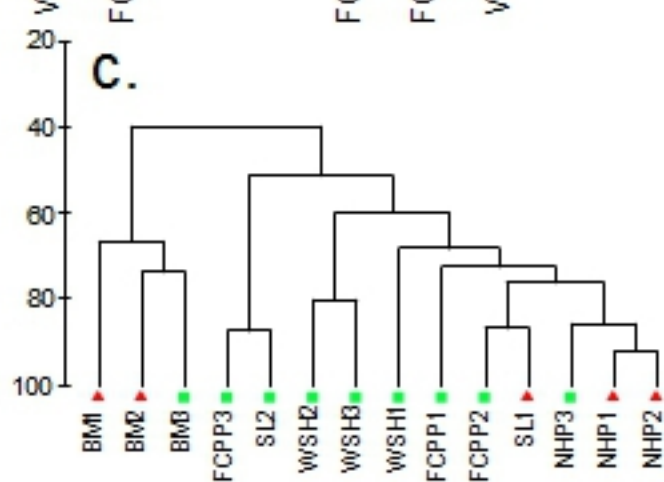
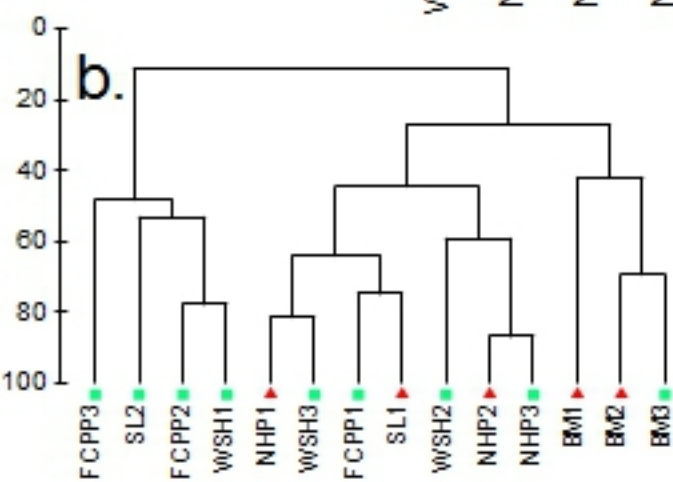
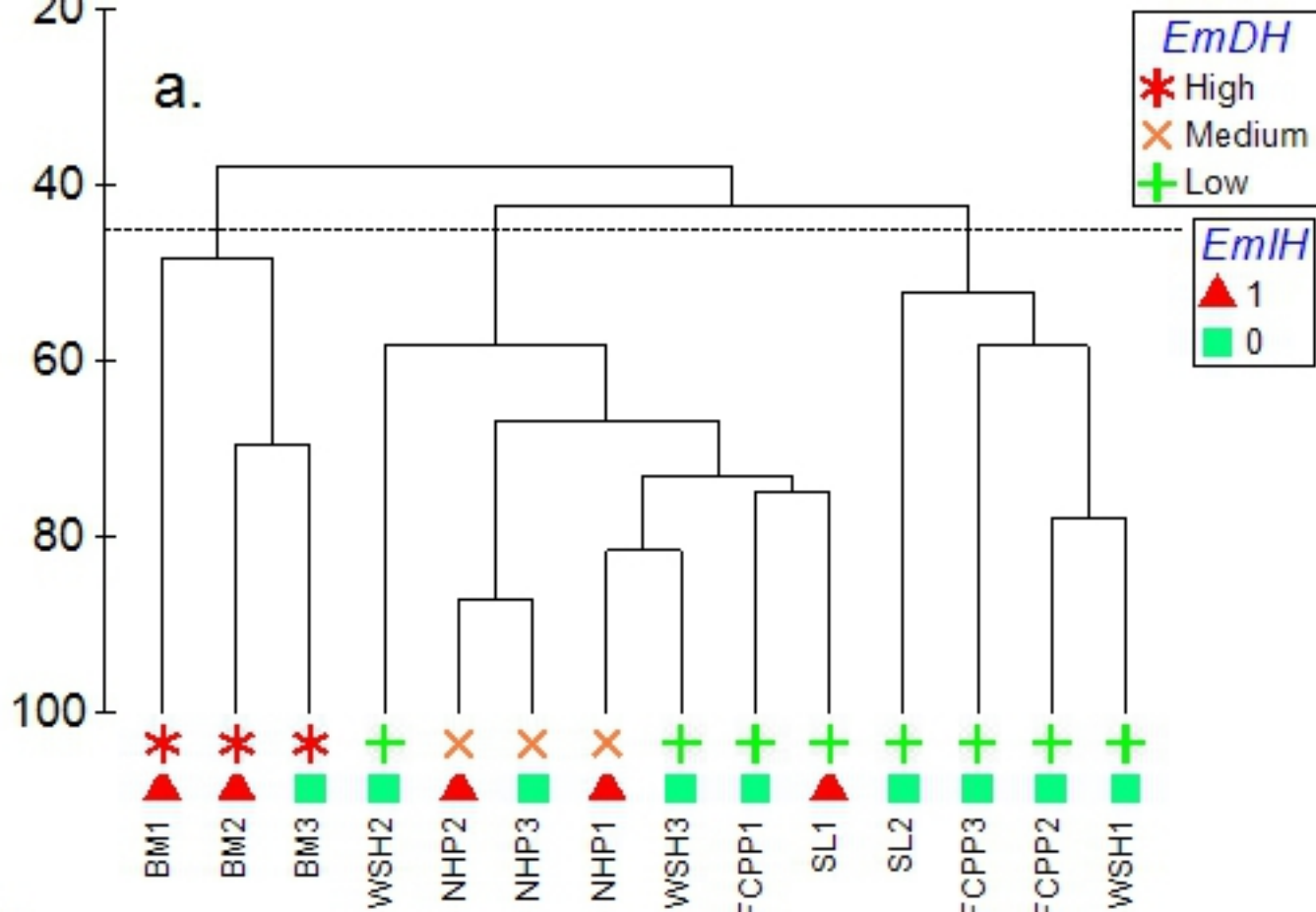
<u>Model</u>	<u>k</u>	<u>-2 * log likelihood</u>	<u>Classification accuracy (%)</u>	<u>AICc</u>	<u><math>\Delta_i</math></u>	<u><math>w_i</math></u>
N-S Aspect & Ruggedness	3	4.322	92.9	18.722	0	0.4857
N-S Aspect & Slope	3	5.616	92.9	20.016	1.2940	0.2543
N-S Aspect & Ruggedness & Slope	4	0	100	20.4444	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

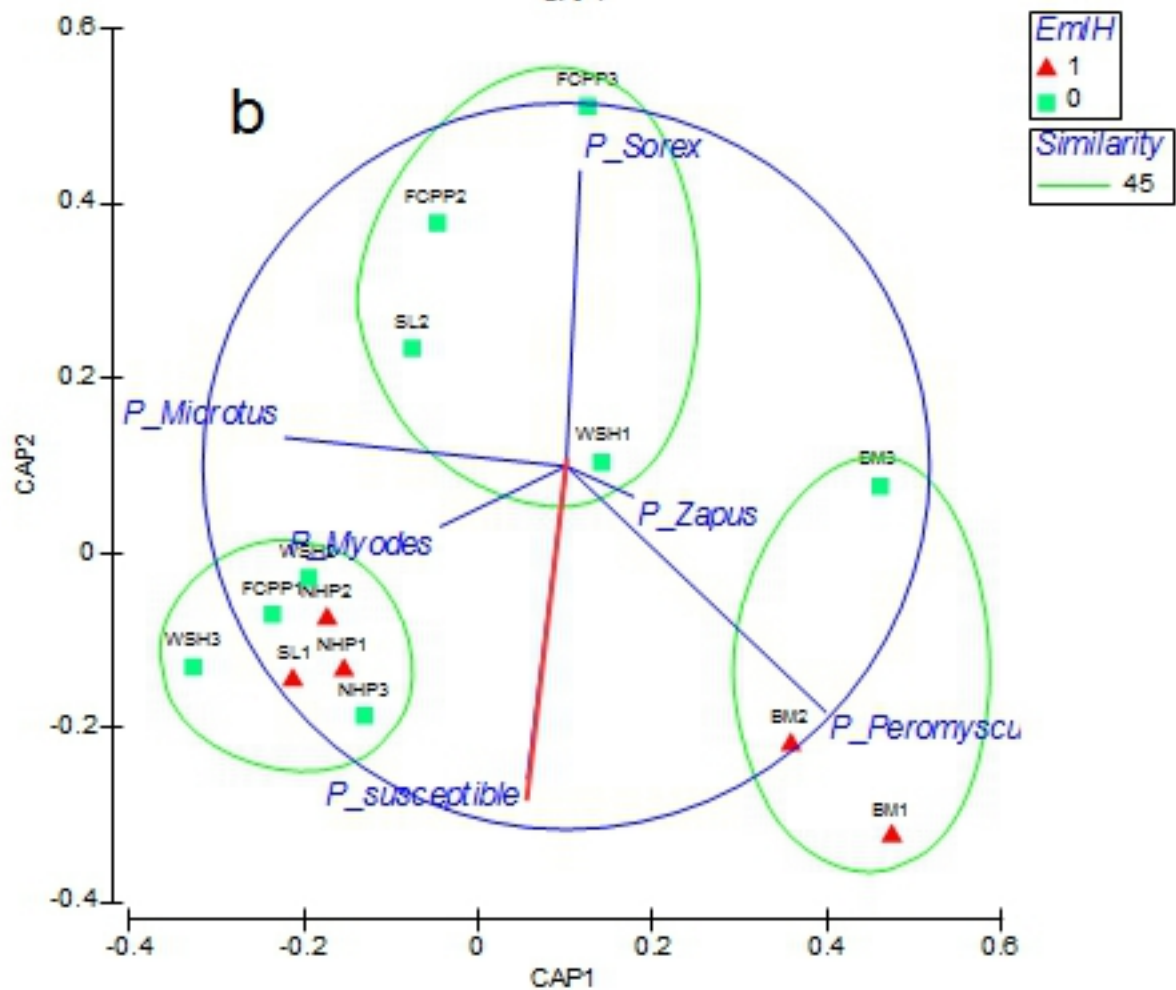
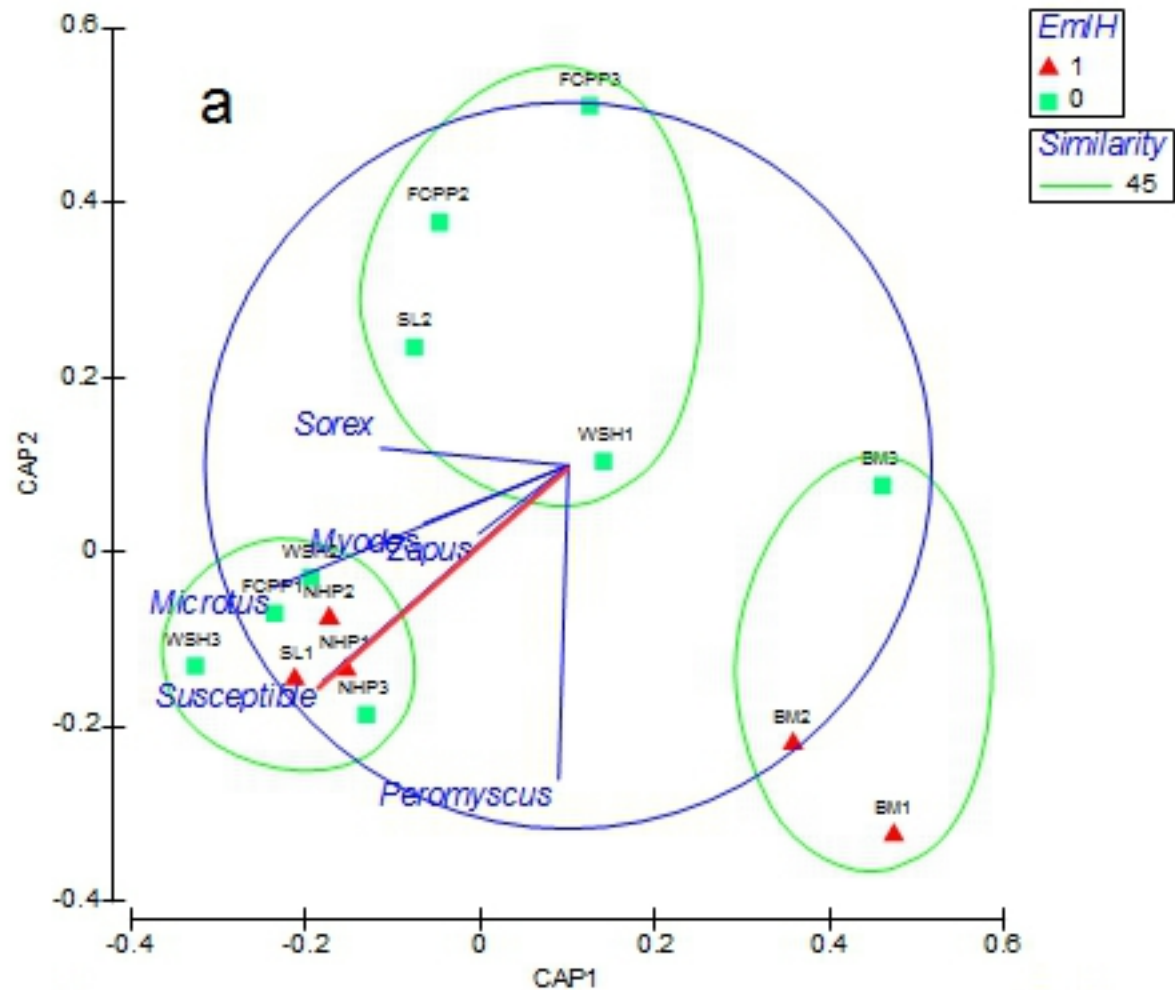
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- Legend**
- ▲ Trap locations
  - Major highways
  - Water bodies
  - Sampled parks
  - City limits







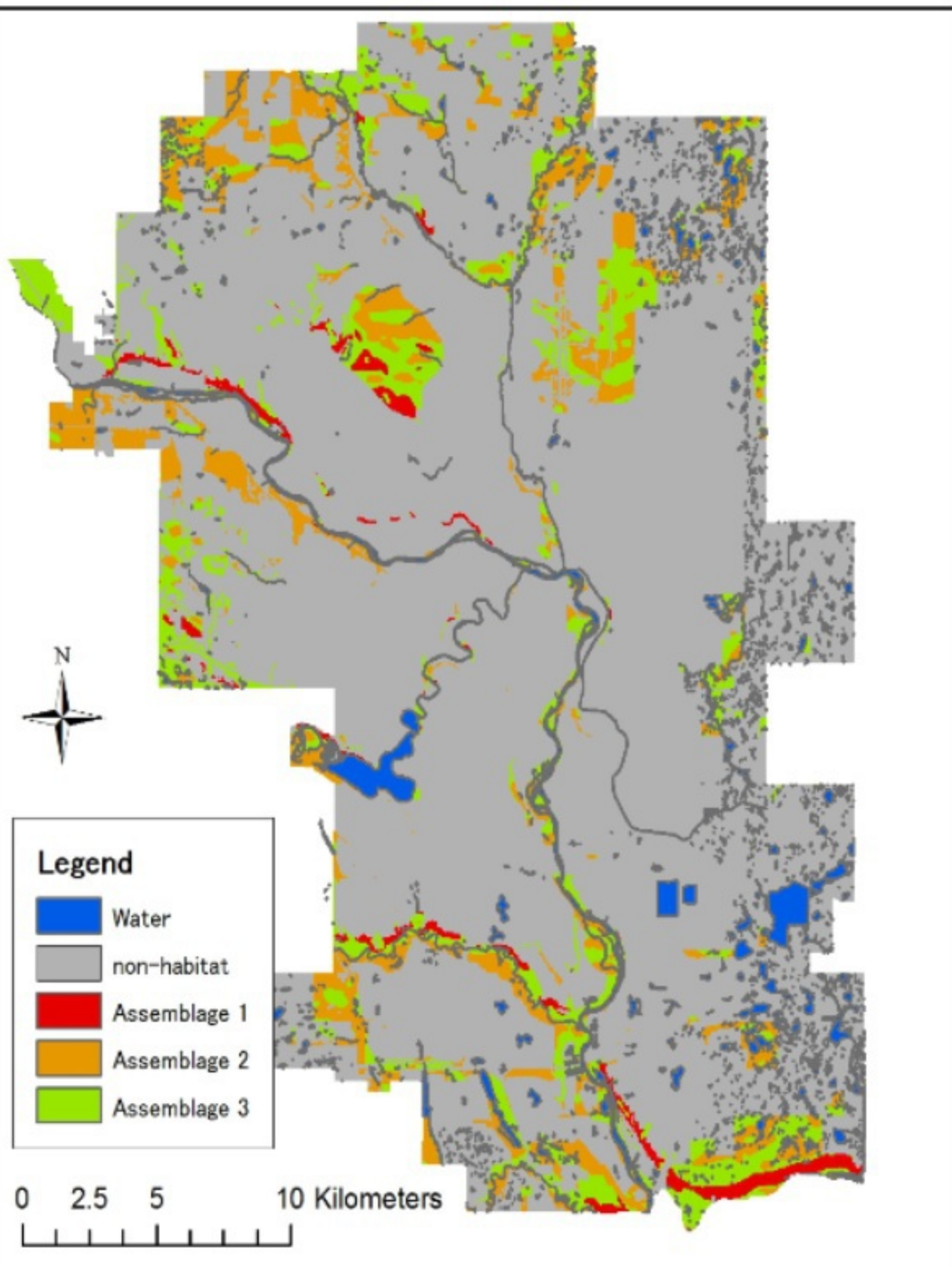
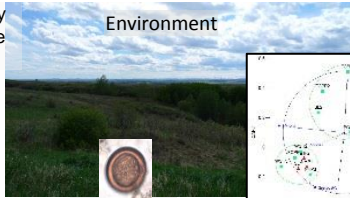


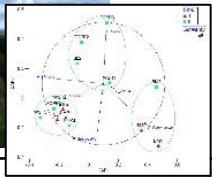
Photo by  
Kensuke  
Mori



Environment



Parasite egg



Intermediate Host Community

Small Mammal  
Photos by Phil  
Myers, Creative  
commons

Definitive Host



Coyote Photo by  
Alessandro  
Massolo



Parasite

