Climate change influences on the geographic distributional potential of the spotted fever vectors *Amblyomma maculatum* and *Dermacentor andersoni*

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Amblyomma maculatum (Gulf Coast tick), and *Dermacentor andersoni* (Rocky Mountain wood tick) are two North American ticks that transmit spotted fevers associated *Rickettsia*. *Amblyomma maculatum* transmits *Rickettsia parkeri* and *Francisella tularensis,* while *D. andersoni* transmits *R. rickettsii*, *Anaplasma marginale*, *Coltivirus* (Colorado tick fever virus), and *F. tularensis*. Increases in temperature causes mild winters and more extreme dry periods during summers, which will affect tick populations in unknown ways. Here, we used ecological niche modeling (ENM) to assess the potential geographic distributions of these two medically important vector species in North America under current condition and then transfer those models to the future under different future climate scenarios with special interest in highlighting new potential expansion areas. Current model predictions for *A. maculatum* showed suitable areas across the southern and Midwest United States, and east coast, western and southern Mexico. For *D. andersoni*, our models showed broad suitable areas across northwestern United States. New potential for range expansions was anticipated for both tick species northward in response to climate change, extending across the Midwest and New England for *A. maculatum*, and still farther north into Canada for *D. andersoni*.

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Abstract

Amblyomma maculatum (Gulf Coast tick), and *Dermacentor andersoni* (Rocky Mountain wood tick) are two North American ticks that transmit spotted fevers associated *Rickettsia*. *Amblyomma maculatum* transmits *Rickettsia parkeri* and *Francisella tularensis,* while *D. andersoni* transmits *R. rickettsii*, *Anaplasma marginale*, *Coltivirus* (Colorado tick fever virus), and *F. tularensis*. Increases in temperature causes mild winters and more extreme dry periods during summers, which will affect tick populations in unknown ways. Here, we used ecological niche modeling (ENM) to assess the potential geographic distributions of these two medically important vector species in North America under current condition and then transfer those models to the future under different future climate scenarios with special interest in highlighting new potential expansion areas. Current model predictions for *A. maculatum* showed suitable areas across the southern and Midwest United States, and east coast, western and southern Mexico. For *D. andersoni*, our models showed broad suitable areas across northwestern United States. New potential for range expansions was anticipated for both tick species northward in response to climate change, extending across the Midwest and New England for *A. maculatum*, and still farther north into Canada for *D. andersoni*.

Keywords

Gulf Coast tick, Rocky Mountain wood tick, Ecological niche modeling, Climate change, GCMs, RCPs, North America.

Manuscript to be reviewed

Introduction

Beside the tick *Dermacentor variabilis*, *Amblyomma maculatum* (Gulf Coast tick), and *D. andersoni* (Rocky Mountain wood tick) are three North American ticks that transmit spotted fever (Boorgula et al. 2020; CDC 2018; CDC 2019). Spotted fever rickettsioses (spotted fevers) are a group of bacterial pathogens that cause disease to humans by exposure to infected ticks or mites (CDC 2019). In the United States, there are several spotted fevers: Rocky Mountain spotted fever (RMSF), which is the most documented spotted fever, caused by *Rickettsia rickettsii*; *R. parkeri* rickettsiosis caused by *Rickettsia parkeri*; rickettsialpox caused by *R. akari*; and Pacific Coast tick fever caused by *R. philippi* (CDC 2019). *Amblyomma maculatum* transmits *R. parkeri*, and *Francisella tularensis* which cause diseases in humans, and *Hepatozoon americanum*, which causes health problems in dogs (Sonenshine 2018). *Dermacentor andersoni* transmits *R. rickettsii*, *Anaplasma marginale*, *Coltivirus* (Colorado tick fever virus), and *Francisella tularensis* (Alkishe et al. 2021; Dantas-Torres et al. 2012).

Amblyomma maculatum and *D. andersoni* have different geographic distributions: *A. maculatum* occurs throughout the southern states of the Gulf Coast and Mid-Atlantic states (Cumbie et al. 2020), whereas *D. andersoni* occurs throughout the Rocky Mountain region, Nevada, California, and southwestern Canada (British Columbia, Alberta, and Saskatchewan; ADW 2021). Those different geographic ranges are associated with different climate conditions for each tick species (Fig. 1). *Amblyomma maculatum* is found in different months in different states with fall and winter considered as low-activity seasons for this species (Nadolny & Gaff 2018), whereas *D. andersoni* is found in hot and dry areas in summer (Wilkinson 1967).

60   Climate warming is warming North America dramatically. Mean global temperature

61 has increased more than 1°C owing to anthropogenic greenhouse gas emissions

62 (Djalante 2019). This increasing temperature has caused mild winters with increasing rain

63 more than snow during winter, and more extreme drier periods during summers

64 (Wuebbles et al. 2017). Increasing temperature can also affect vector disease survival,

65 abundance, and activity as well as transmission dynamics, re-emergence of vector-borne

66 diseases, and geographic expansions (Rocklöv & Dubrow 2020).

67   Here, we used ecological niche modeling (ENM) to assess the geographic

68 potential of these two medically important vectors of diseases in North America under

69 current conditions and then transfer those models to the future under different scenarios,

70 with special interest in highlighting potential range new expansion areas. We also assess

71 the model uncertainty for projected future models to highlight areas with high versus low

72 confidence of geographic expansions.

73

74

75 **Methods**

76 **Data preparation**

77   We obtained totals of 255 and 586 occurrence points for *A. maculatum* and *D.*

78 *andersoni*, respectively. Those data were obtained from various sources: Global

79 Biodiversity Information Facility (GBIF; http://www.gbif.org), VectorMap

80 (http://vectormap.si.edu/), and BISON (https://bison.usgs.gov) (sources summarized in

81 supplementary file; S1). We followed Cobos et al. (2018) in cleaning the data to remove

82 errors that clearly fall outside of the known geographic distribution of the species,

83 duplicate records, and localities with missing or meaningless coordinates such as zero

84 degrees latitude and zero degrees longitude (0°N, 0°E), or georeferencing errors (records

85 in ocean and far from coast). We used the spTthin R package to reduce the data spatially

86 based on a 50 km distance filter for several reasons: based on precision of the occurrence

87 points in the area, environmental heterogeneity that present in the area, and to avoid

88 problems with autocorrelation (Aiello-Lammens et al. 2015). In the end, we had 93 and

89 82 occurrence points for *A. maculatum* and *D. andersoni*, respectively. We divided the

90 final occurrence data randomly into two sets: 50% for model calibration and 50% for

91 evaluation steps involved in model calibration. For producing final models, we used the

92 entire cleaned occurrence points.

93

94 **Delineate the calibration area**

95   The accessible area (**M)** is the set of places to which the species has had access

96 over relevant time periods, and depends on the dispersal of the species from populations

97 (Barve et al. 2011). Since the movement of tick species is associated with the movement

98 of host species, we assumed ample dispersal abilities for the ticks (Nadolny & Gaff 2018;

99 Sonenshine 2018). As such, we created 200 km buffer areas around the known

100 occurrence points for each species (Fig. 1).

101

102 **Environmental variables**

103   For the current time, bioclimatic variables were downloaded from WorldClim

104 version 1.4, at 10' spatial resolution (Hijmans et al. 2005) (available at

105 http://www.worldclim.org). We removed variables 8, 9, 18, and 19 because of known

106 spatial artefacts (Escobar 2020). The 15 remaining variables were masked to the

107 calibration area (**M**) for each species. We then used principal component analysis (PCA)

108 to reduce dimensionality and multicollinearity among those variables. After having PCA

109 results, we created 11 sets of environmental variables that represent all possible

110 combinations of the first four principal components to test them with other parameter

111 settings to choose best models during model calibration, following Cobos et al. (2019)

112 (see below).

113   For future climatic conditions, we used five general circulation models (GCMs)

114 under two representative concentration pathway scenarios (RCP 4.5, and RCP 8.5).

115 Future climate data layers were downloaded from the Climate Change, Agriculture and

116 Food Security (CCAFS) database at 10' resolution (available at: http://www.ccafs-

117 climate.org/data_spatial_downscaling). GCMs used were (1) National Center for

118 Atmospheric Research (NCAR_CCSM4); (2) Met Office Hadley Centre (HadGEM2); (3)

119 Model for Interdisciplinary Research on Climate (MIROC5); (4) Institut Pierre Simon

120 Laplace (IPSL_CM5A); and (5) Russian Institute for Numerical Mathematics Climate

121 Model Version 4 (INM_CM4). GCM choice was based on frequency of use in other such

122 research applications, and on full availability of scenarios for both RCP scenarios.

123

124 **Ecological niche modeling and model transfers**

125   The combination of 11 sets of environmental variables, 15 feature classes (all

126   combinations of linear = l, quadratic = q, product = p, hinge = h), and 17 regularization

127   multiplier values (0.1 to 1 at intervals of 0.1, and 2 to 10 at intervals of 1) resulted in 2805

128   candidate models for each species. We evaluated candidate models based on statistical

129   significance (partial ROC, $P \leq$ 0.05; Peterson et al. 2008), predictive performance

130   (omission rates, <5%; Anderson et al. 2003), and a criterion of minimum complexity

131   (Akaike Information Criterion corrected for small sample sizes, AICc; Warren & Seifert

132   2011). Specifically, we used differences between particular AICc values and the minimum

133   values (ΔAICc < 2) to select best model parameter settings with which to produce final

134   models.

135

136   **Final models**

137   For creating final models, we used the complete set of occurrences and the

138   parameterizations selected during model calibration. We created 10 bootstrap replicates,

139   and transferred the models across North America (Mexico, United States and Canada)

140   under current and future scenarios. We calculated medians of all replicate medians from

141   final predictions for each calibration area in which final models were produced to

142   summarize model results. Then, we binarized models using a threshold of allowable

143   omission error rate (E) of 5%, assuming that as a percentage of data may have included

144   errors that misrepresented environments used by the species.

145   We calculated differences in suitable areas between current and the two future

146   scenarios RCP (4.5, and 8.5). For representing changes of suitable areas, we used the

147 agreement of changes (stable, gain, loss) among the five GCMs per RCP scenario.

148 Simply, for each RCP scenario, we took all projections to future conditions based on

149 distinct GCMs and compared against the current projection, and quantified the agreement

150 of gain and loss of suitable areas, as well as the stability of suitable and unsuitable

151 conditions. All modeling analysis steps were done in R 3.5.1 (R Core Team. 2018) using

152 Maxent 3.4.1 (Phillips et al. 2017), implemented in the kuenm package (Cobos et al.

153 2019).

154

155 **Uncertainty in model projections**

156   We used the mobility-oriented parity metric (MOP, considering the nearest 5% of

157 reference cloud) (Owens et al. 2013) to assess strict extrapolation risk. We also

158 calculated variance arising from distinct sources (replicates, parameter settings, GCMs,

159 and RCPs) in our model projections (Peterson et al. 2018). Both model variability and

160 strict extrapolation were represented geographically following Owens et al. (2013) and

161 Cobos et al. (2019), respectively.

162

163 **Results**

164 **Model calibration results**

165   From among 2805 candidate models for each of *A. maculatum* and *D. andersoni*,

166 2728 and 2554 were significantly better than random expectations, respectively (pROC

167 test, $p \leq 0.05$). Of these models, 2129 and 761 met the omission rate criteria, (i.e., OR $\leq$

168   0.05) respectively. Based on AICc, 55 and two models were selected as best models for

169   *A. maculatum* and *D. andersoni,* respectively. For *A. maculatum*, models performed better

170   with the variables in set 1 (PC1, PC2, PC3, PC4), set 2 (PC1, PC2, PC3), set 3 (PC1,

171   PC2, PC4), and set 6 (PC1, PC2), whereas for *D. andersoni* variables in sets 4 (PC1,

172   PC3, PC4) and 7 (PC1, PC3).

173

174   **Current and future potential distribution**

175   ***Amblyomma maculatum***

176   Current model predictions for *A. maculatum* showed suitable areas across the

177   southern United States (Florida, Georgia, South and North Carolina, Virginia, West

178   Virginia, Maryland, Delaware, Kentucky, Tennessee, Arkansas, Alabama, Mississippi,

179   Louisiana, Oklahoma, and Texas), and in the Midwest (Missouri; eastern Kansas;

180   southern Illinois, Indiana, and Ohio), and restricted areas of northeastern states (New

181   Jersey and Pennsylvania). Suitable areas extend to include areas in western states

182   (Arizona, California, Oregon, and Washington), although those areas are not likely

183   accessible to the species (Fig. 2). Our models also showed suitable areas for the species

184   across parts of eastern, western, and southern Mexico (Quintana Roo) (Fig. 2).

185   Future model transfers showed stable suitable areas (i.e., suitable in current time

186   and in the future time) across the South, Midwest, and the Northeast, in the of United

187   States (Fig. 2). Areas of range reduction (loss) were in restricted areas in Kansas,

188   Oklahoma, and Texas. Range expansion (gain) was anticipated in the northeastern

189   (Pennsylvania, New York, Connecticut, Rhode Island, Massachusetts, Vermont, New

190   Hampshire, Maine) and midwestern states (Kansas, Missouri, Nebraska, Iowa, Illinois,

191   Indiana, Ohio, Michigan, Wisconsin) (Fig. 2). In general, we noted greater agreement

192   among models in terms of losses and gains in the RCP 8.5 scenario compared to RCP

193   4.5.

194

195   ***Dermacentor andersoni***

196   Current-time range predictions for *D. andersoni* showed broad suitable areas

197   across Washington, Idaho, Oregon, California, Montana, Nevada, Utah, Wyoming, and

198   Colorado, in cases where this species is known to occur in the United States. Climatically

199   suitable areas extended across the Midwest, and Northeast and in some southeastern

200   states (Fig. 3), although these areas are not likely accessible to the species. Currently

201   suitable areas were also observed in parts of central and western Canada (British

202   Columbia, Alberta, Saskatchewan, and restricted areas in Manitoba) (Fig. 3).

203   Future model transfers showed stable suitable areas across the states listed

204   above, with some degree of reduction in suitable areas in the western states including

205   much of Washington, Oregon, California, Nevada, Arizona, New Mexico, and Utah, and

206   restricted areas in Colorado, Idaho, and Montana (Fig. 3). Predictions for the two RCP

207   scenarios showed closely similar patterns of range stability, expansion, and loss, with

208   more agreement among models in the RCP 8.5 scenario (Fig 3).

209

210   **Model uncertainty**

211   MOP results for *A. maculatum* showed that strict extrapolative areas among future

212   scenarios were concentrated in northern parts in North America, particularly in Canada,

213   and in some restricted areas of the United States and southern Mexico (Fig. 2). Model

214   variability results showed almost no variation coming from replicates and RCPs, but high

215   contribution to variation from GCMs and parameter choice (Supplementary material; Fig.

216   S3).

217   In *D. andersoni*, we noted high agreement of strictly extrapolative areas in both

218   southern and northern North America, and in lesser degree in the eastern United States

219   and Canada (Fig. 3). High model variability came mainly from parameter choice in the

220   eastern United States; we noted low variation deriving from GCMs, RCPs, and replicates

221   (Supplementary material; Fig. S4).

222

223   **Discussion**

224   The geographic distributions of *A. maculatum* and *D. andersoni* are much wider

225   today than they were in the recent past. For example, *A. maculatum* has expanded its

226   geographic range from the southeastern United States to become well established in the

227   Northeast in Connecticut (Molaei et al. 2021), and in the Midwest in southern Illinois

228   (Jolley 2020). Beside the movement of tick adults for long distances via their hosts to new

229   areas, immature *A. maculatum* can also access new areas with the help of migratory

230   birds; larvae and nymphs can move thousands of miles during bird migratory seasons

231   from the southern United States north to southern Canada (Florin et al. 2014; Teel et al.

232   2010). Cuervo et al. (2021) showed similar suitable ranges using current time predictors,

233   and demonstrated that levels of niche conservatism differed among different members of

234   *A. maculatum* group (*A. tigrinum* and *A. triste*).

235   This study is the first to assess the geographic distributions of the spotted fever

236   vectors *A. maculatum* and *D. andersoni* in North America under current and future climate

237   conditions. We included uncertainty analyses (MOP analysis and model variability) in our

238   future model projections to detect areas with strict extrapolation, and to assess variation

239   coming from multiple sources, such as different GCMs and RCPs. We considered only

240   abiotic climatic variables such as temperature and precipitation as predictors that may

241   influence the geographic distributions of those tick species.

242   Our models predicted that suitable areas for *A. maculatum* will remain stable in

243   most southern and Midwestern states, whereas few reductions in suitable areas were

244   anticipated only in western parts of Texas, Oklahoma, and Kansas (Fig. 2). Most

245   importantly, our models predicted newly suitable areas northward in the United States

246   successfully, to cover areas that were recently discovered to hold new populations in

247   Connecticut and Illinois (Jolley 2020; Molaei et al. 2021) (Fig. 4). For *D. andersoni*, our

248   models showed broader suitable areas beyond its known range (from Washington state

249   to Colorado). Midwestern and eastern states; however, most of the anticipated reduction

250   in ranges were in areas not known to hold this tick species. Most of the anticipated

251   expansions in range were in northward in Canada (Fig. 3).

252   Our projections suggested higher potential of *A. maculatum* to invade new areas

253   outside its native range mainly in the southeastern United States. For *D. andersoni*,

254   suitable areas were mostly in northern North America (United States and Canada). We

255 also noted more extensive strict extrapolative areas for *D. andersoni* than *A. maculatum*,

256 especially in the eastern United States, which suggested caution about interpreting those

257 areas as suitable for *D. andersoni* (Fig. 3).

258   Several significant limitations and caveats regarding predictions emerging from

259 ecological niche modeling that should be considered. First, a species faces dispersal

260 limitations and biotic interactions that may prevent it from occupying the full suitable area

261 that corresponds to its fundamental ecological niche. Second, the variation in spatial

262 precision associated with different occurrence data records, which can cause problems

263 for model results. Third, data availability in which biases in sampling in regions more than

264 others can cause biases in model output (Peterson 2014). All these points have been

265 considered in the design of our methodology to achieve the most robust model possible.

266   In the United States, numbers of documented spotted fever cases have increased

267 in recent years, especially in 2017, with 6248 new cases (CDC 2021). Previous analyses

268 have noted overlap between reported cases in some states and suitable areas for spotted

269 fever vectors including *Dermacentor variabilis* (Alkishe et al. 2021; Boorgula et al. 2020).

270 Spotted fever case data collected by the Centers for Disease Control and Prevention, and

271 used by Alkishe et al. (2021) however, were lacking in full detail on the type of pathogen

272 and associated tick species, which made it difficult to interpret the source of the infection.

273   In summary, using ecological niche modeling allowed us to highlight suitable areas

274 of two medically important tick species in North America. We showed the potential for

275 expansion of those tick vectors into new areas that were not suitable in the past with

276 emphasis on the newly discovered dispersal of A. maculatum to those newly suitable

277 areas in Illinois and Connecticut. We also showed the uncertainty and variability that can

278 come from projection models to different times and places. These results help to

279 recognize the uncertainty and source of variability in predicting suitability.

280

281 **Author Contributions**

282 AA and ATP designed the work; AA performed the analysis; AA and ATP wrote the

283 manuscript.

284

285 **Conflict of interest statement**

286 The authors declare that there is no conflict of interest.

287

288 **Funding**

289 This research was supported by a grant from the National Science Foundation (OIA-

290 1920946).

291

292 **Acknowledgments**

293 AA thanks Amel Dwebi and Yosr Alkishe for their support during this work. We also

294 thank Gengping Zhu and one anonymous reviewer for their comments, which allowed

295 us to improve the manuscript.

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408   **Figure 1.** Occurrence points and calibration areas for *Amblyomma maculatum* (blue dots

409   and blue buffer) and *Dermacentor andersoni* (red dots and red buffer) in geographic and

410   environmental space.

411

412   **Figure 2.** Left panel: Potential suitable areas of *Amblyomma maculatum* based on

413   binarized (5% threshold) models under current conditions (in blue and gray), and future

414   (blue = no longer suitable, red = newly suitable) conditions. Right panel: agreement in

415   strict extrapolation areas among the five general circulation models. Results are

416   presented for RCP 4.5 (top) and RCP 8.5 (bottom).

417

418   **Figure 3.** Left panel: Potential suitable areas of *Dermacentor andersoni* based on

419   binarized (5% threshold) models under current conditions (in blue and gray), and future

420   (blue = no longer suitable, red = newly suitable) conditions. Right panel: agreement in

421   strict extrapolation areas among the five general circulation models. Results are

422   presented for RCP 4.5 (top) and RCP 8.5 (bottom).

423

424   **Figure 4.** Detail of figure 2, showing the most recent confirmed established populations

425   of *Amblyomma maculatum* in counties of Illinois and Connecticut in the United States

426   (light blue boundaries) (Jolley 2020; Molaei et al. 2021). Gray indicates suitable areas

427   under current and future conditions. Red color indicates newly suitable areas with climate

428   change.

Figure 1

Figure 1

Occurrence points and calibration areas for *Amblyomma maculatum* (blue dots and blue buffer) and *Dermacentor andersoni* (red dots and red buffer) in geographic and environmental space.
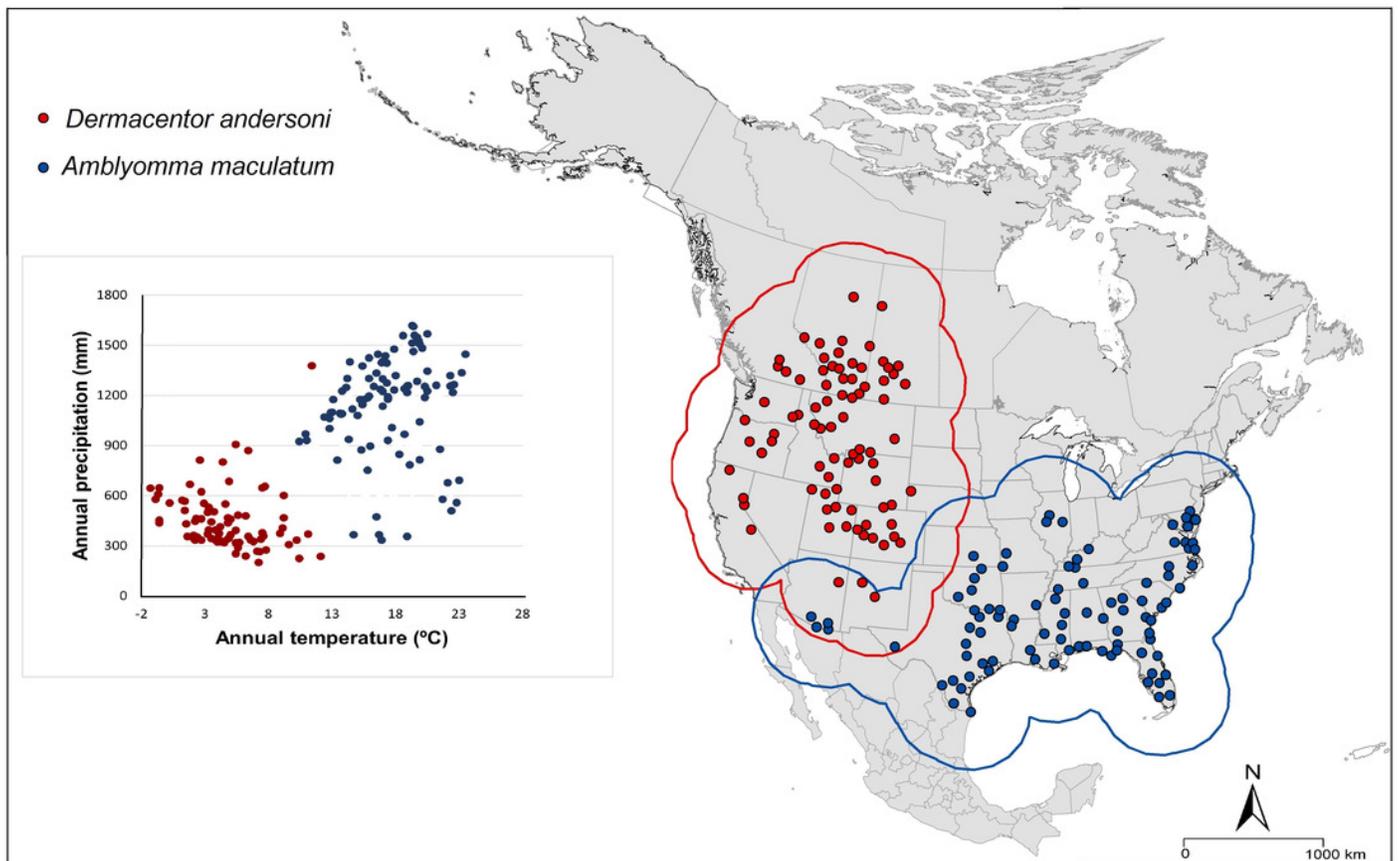
Figure 2

Figure 2

Left panel: Potential suitable areas of *Amblyomma maculatum* based on binarized (5% threshold) models under current conditions (in blue and gray), and future (blue = no longer suitable, red = newly suitable) conditions. Right panel: agreement in strict extrapolation areas among the five general circulation models. Results are presented for RCP 4.5 (top) and RCP 8.5 (bottom).
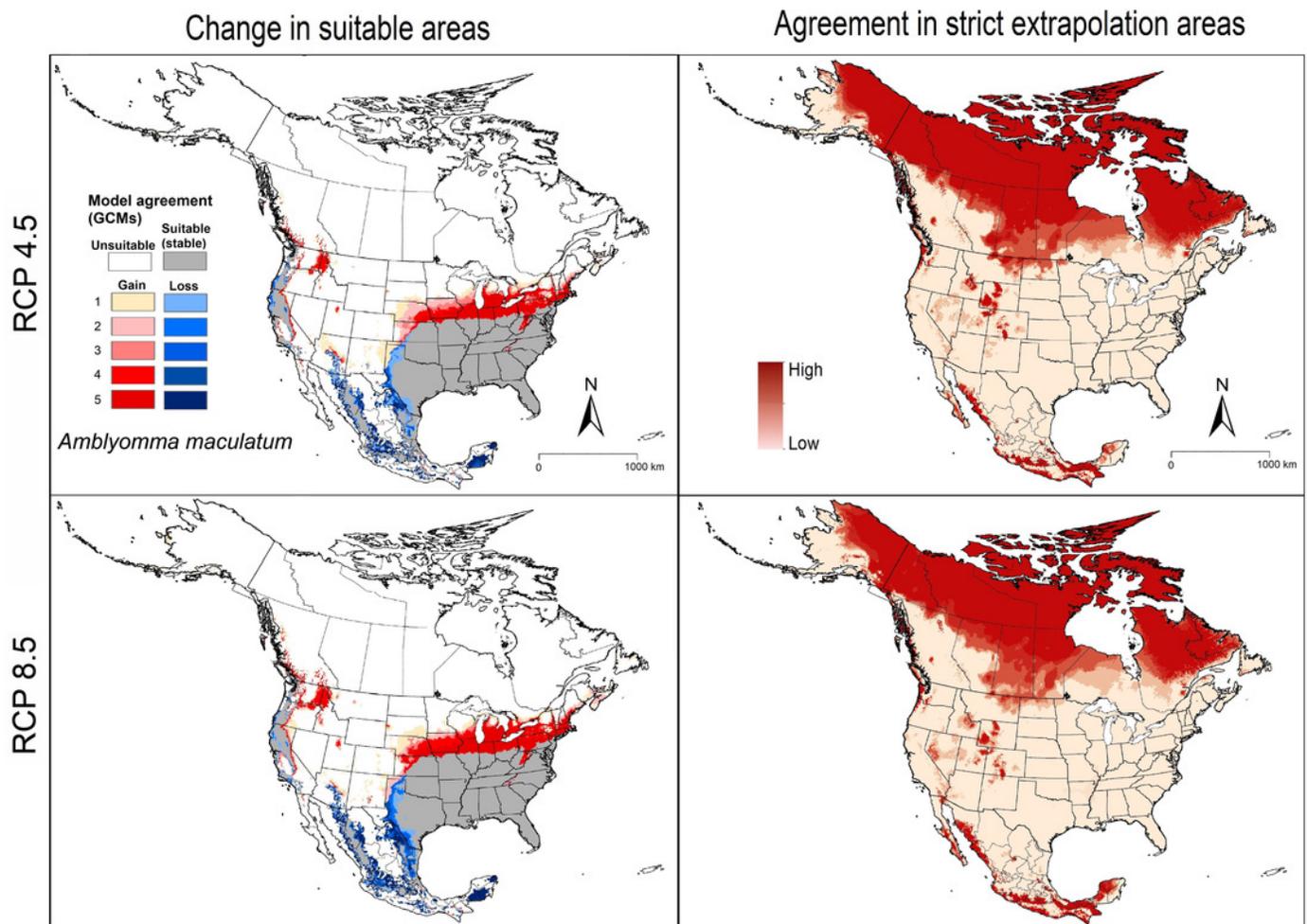
Figure 3

Figure 3

Left panel: Potential suitable areas of *Dermacentor andersoni* based on binarized (5% threshold) models under current conditions (in blue and gray), and future (blue = no longer suitable, red = newly suitable) conditions. Right panel: agreement in strict extrapolation areas among the five general circulation models. Results are presented for RCP 4.5 (top) and RCP 8.5 (bottom).
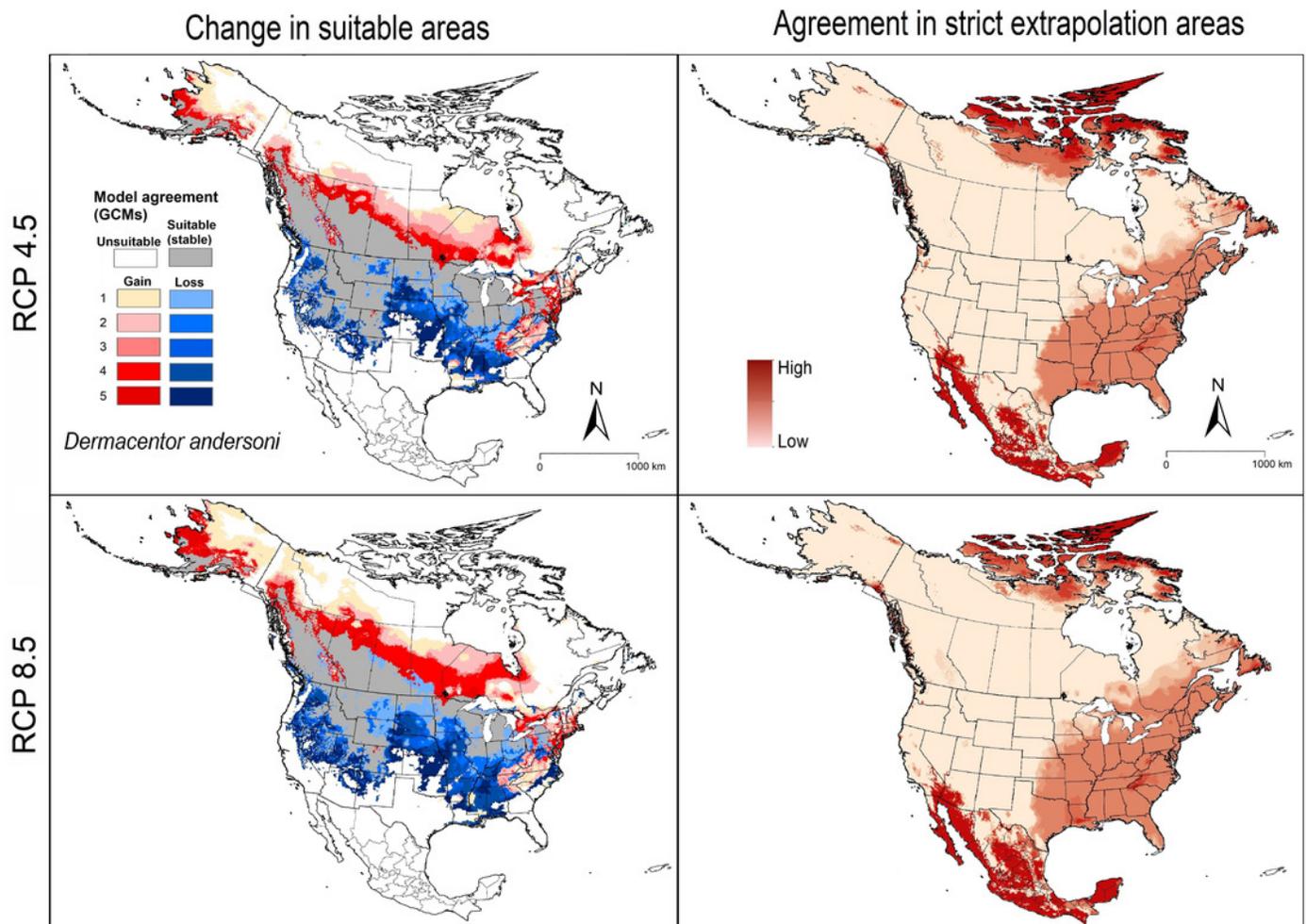
Figure 4

Figure 4

Detail of figure 2, showing the most recent confirmed established populations of *Amblyomma maculatum* in counties of Illinois and Connecticut in the United States (light blue boundaries) (Jolley 2020; Molaei et al. 2021). Gray indicates suitable areas under current and future conditions. Red color indicates newly suitable areas with climate change.