

1 **The leading edge of the geographic distribution of *Ixodes scapularis***
2 **(Acari: Ixodidae)**

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12 Dear Editor,

13 A recent paper by Hahn et al. (2016) modeled and mapped the geographic
14 distribution of the tick *Ixodes scapularis* Say, the primary vector of several pathogens in
15 eastern North America. Because their results indicated an unexpectedly small
16 distributional area for the species, we (Peterson and Raghavan 2017) developed a
17 partial reanalysis and showed that the model-predicted distributional extent depended to
18 a large degree on methods for thresholding models into binary results. Hahn et al.
19 (2017) then responded to our critique. Here, we present a brief further response, with
20 the aim of clarifying the aims of the overall exercise.

21 Although Hahn et al. (2016) presented some methodological variations and
22 focused on differences between the two modeling protocols, our model predictions were
23 closely similar to theirs when we followed their assumptions about thresholding. As a

24 result, we do not believe that the difference has to do with methodology, but rather with
25 conceptual framework and interpretation.

26 Hahn et al. (2017) stated that their purpose had been "... to better define the
27 leading edge of the tick's ongoing geographic expansion." We assert that they have not
28 made the appropriate assumptions to this end: that is, they accepted greater omission
29 error, which reduced the area identified as suitable to the very conservative, "rimming"
30 distributional estimate that they had originally reported. If the primary purpose is to
31 define the "leading edge" of the species' distribution, a more liberal, lower threshold
32 would be in order.

33 It is important to note that this issue is not simply one of different thresholding
34 assumptions including more or less area within model predictions. If large-scale
35 differences exist in abundances (or at least in the sampling and reporting) of tick
36 populations in marginal regions, these marginal regions (or marginally sampled regions)
37 are systematically removed by the higher thresholds that Hahn et al. (2017) advocate.
38 That is, assumptions and choices regarding thresholds on model predictions must be
39 established based on conceptual frameworks, rather than on convenience (Peterson et
40 al. 2011).

41 The definition of a fundamental ecological niche is an inclusive set of conditions
42 under which the species is able to maintain populations without immigrational subsidy
43 (Peterson et al. 2011). Clearly, the center of abundance of this species is not at the
44 western edge of its distribution, but just as clearly, the species' distribution extends
45 much farther west than the model predictions that Hahn et al. (2016) presented would
46 indicate (see numerous records in Eisen et al. 2016). The distribution of abundance of

47 the species across this distributional area is of course interesting and relevant, and can
48 be examined via other classes of models in distributional ecology (Martínez-Meyer et al.
49 2012). However, the “leading edge” of the distribution of *I. scapularis* is at a longitude of
50 about 98°W, rather than much farther to the east; this broader range is reflected in the
51 transmission of pathogens and cases of canine and human Lyme disease in many
52 regions (Bacon et al. 2008) that were indicated by the Hahn et al. (2016) models as
53 unsuitable (compare panels A and B in their Figure 3). Over the years, *I. scapularis* has
54 been collected consistently as far west as central Kansas, both by flag/dragging
55 methods and from sentinel species (e.g., white tailed deer) by us and other researchers,
56 albeit in small numbers; appropriate models aimed at locating the leading edge of the
57 distribution of the species should include these areas, as the tick is certainly present
58 and important in public health and policy-making there. Although we two are based in
59 Kansas, this discord between presence of the tick and transmission of *Borrelia* versus
60 the Hahn et al. (2016) model results has broad, sweeping public health implications: the
61 “leading edge” of the distribution of the species is in the central United States, and the
62 distribution of this tick species covers much of the eastern United States.

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