The Potential Distribution of Ornithodoros hermsi, a Vector of Tick-borne Relapsing Fever Spirochetes, in Western North America Tammi L. Johnson^{1,2}, Robert J. Fischer², and Tom G. Schwan² HEAD

¹Montana Ecology of Infectious Diseases, Organismal Biology and Ecology, Division of Biological Sciences, University of Montana ²Rocky Mountain Laboratories, National Institute of Allergy and Infectious Disease, National Institutes of Health

INTRODUCTION

• Tick-borne relapsing fever (TBRF) in western North America is caused by infection with Borrelia hermsii, a highly motile spirochete bacteria (Davis 1940).

The University of **Montana**

- TBRF is maintained in an enzootic cycle involving • rodents and the nidiculous tick vector Ornithorodos *hermsi* (Davis 1940).
- The geographic distribution of TBRF in North America has been broadly defined, based largely on investigations of reported human cases, elevation, and host distribution (Schwan et al. 2007).
- Despite the ubiquity of potential hosts across the landscape, cases of TBRF are clustered in distinct foci, suggesting that there may be constraints beyond just the presence of a suitable host for the tick vector.

MOTIVATION

- A more thorough understanding of the relationship between *O. hermsi* and environmental conditions is necessary to understand the distribution of the tick, thereby defining areas of potential human risk of infection with *B. hermsii*.
- Maxent has been widely used to predict the distribution of various species and enables modelers to utilize small number of presence only records.
- Vial (2009) suggests that because soft ticks occupy a stable microclimate, the broad-scale analyses applied to hard ticks should not be applicable to them. Because so little is known about the ecology and behavior of soft ticks, macroclimate-scale analyses, as performed here, may be useful to accurately define the distribution of these ticks and other nidiculous (nest-dwelling) species.

OBJECTIVES

- Assess the utility of niche models on a nidiculous species.
- Present the first detailed distribution map of *O. hermsi.*
- Evaluate the effect of climate on the distribution of *O. hermsi.* Evaluate the potential to use the proposed distribution map as a risk assessment tool for medical practitioners and direction for future researchers.
- Assess the effect of climate change on the proposed distribution.



Acknowledgements: TLJ received funding for her dissertation research from an NSF IGERT fellowship and an pre-doctoral IRTA fellwoship funded by the division of Intramural Research, NIAID, NIH.





METHODS

- Maxent evaluates the suitability of each grid cell as a function of environmental variables at that cell (Phillips et al. 2004, 2006)
- 40 presence points, 75% for training and 25% withheld for testing the model
- 9 Bioclim variables and elevation @ 30 arc-sec (~1km) resolution

Current Predicted Distribution



Annual T Range .5.2%



Fig. 2 Top – Current predicted occurrence/ecological suitability of *O. hermsi*. Probability of occurrence increases as the shading becomes darker.



CSIRO



Fig. 2 Bottom – Predicted occurrence/ecological suitability of *O. hermsi* in 2050. Probability of occurrence increases as the shading becomes darker.

RESULTS

- Average training AUC = 0.982 (SD = 0.003)
- Average testing AUC = 0.957 (SD = 0.029)
- 90% of presence points (37 out of 40) in areas with high predicted probability of occurrence (Fig. 2)

 Climate change predicted to decrease highly suitable areas (Table 1, Fig. 2)

Table 1. Area (km²) of each probability class for the predicted distribution of *O. hermsi*. Climatic requirements identified for current environmental conditions were projected onto future climate change models to predict the probability distribution of the tick in the year 2050. Three climate change models under the conservative (B2) emissions scenario were used: 1) the Canadian Centre for Climate Modelling and Analysis (CCCMA), 2) the Commonwealth Scientific and Industrial Research Organisation (CSIRO), and 3) the Hadley Centre for Climate Prediction and Research (HADCM).

Probability of Predicted Distribution	Current km ²	CCCMA	CSIRO
		<u>B2</u> km²	<u>B2</u> km²
< 0.05	5,148,611	1,952,027	1,834,023
0.05-0.25	1,695,386	3,367,906	4,858,090
0.25-0.50	594,298	1,889,005	873,315
0.50-0.75	331,531	593,862	245,842
> 0.75	115,205	82,231	73,761

CONCLUSIONS

- Like other vector-borne diseases, the spatial distribution of TBRF is likely limited by the environmental restrictions of *O*. hermsi.
- Cool moist habitats had highest predicted probability.
- High probabilities occurred in known TBRF endemic areas and additional areas.
- Additional potential foci identified in ID, OR, CA, and Baja California, Mexico.
- Unlike many other vector-borne diseases, the distribution of TBRF is predicted to decrease with global climate change.
- In 2050, suitable climates will be less abundant and located at higher elevations in ID, WY and CO.
- Ecological niche modeling may be a useful tool for nidiculous species.

REFERENCES

- Davis, G. E. 1940. Ticks and relapsing fever in the United States. Public Health Reports 55: 2347–2351. Phillips S.J., M. Dudík, and R.E. Schapire. 2004. A maximum entropy approach to species distribution modeling. In Proceedings of the Twenty-First International Conference on Machine Learning pp. 655–662. Phillips, S.J., R.P. Anderson, and R.E. Schapire. 2006. Maximum entropy modeling of species geographic distributions. Ecological Modelling 190:231–259.
- Schwan, T.G., S.J. Raffel, M.E. Schrumpf, and S.F. Porcella. 2007. Diversity and distribution of Borrelia hermsii. Emerging Infectious Diseases 13:436–442.
- Vial, L. 2009. Biological and ecological characteristics of soft ticks (Ixodida: Argasidae) and their impact for predicting tick and associated disease distribution. Parasite 16:191–202.





• Five climate variables contributed > 75% to model fit (Fig. 1)

HADCM			
<u>B2</u> km ²			
2,947,951			
4,126,808			
618,408			
176,356			
15,508			