

Attempts to understand the range expansion of *Amblyomma maculatum*



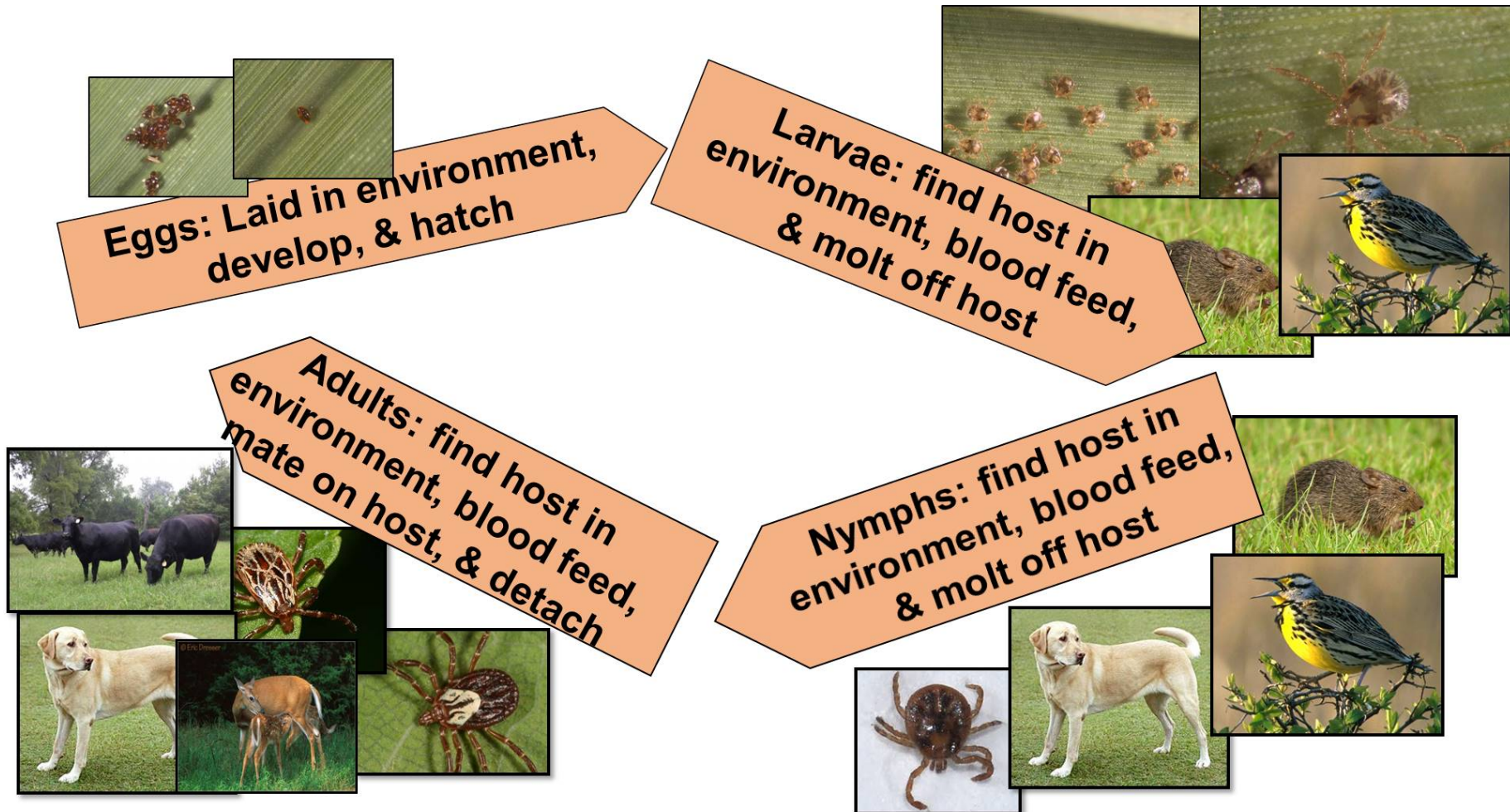
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Assistant Professor of Medical & Veterinary Entomology

Department of Entomology & Plant Pathology

February 2018, MAMCA Carolina Beach, NC

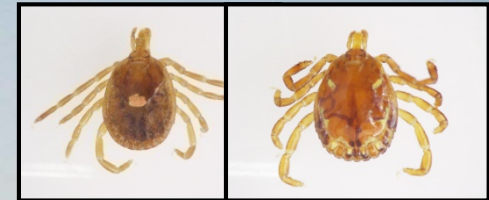
Life Cycle: 3-host tick



Investigate the tick populations & associated SFGR at a hotspot



Trout Fryxell et al. 2015 PLoS ONE
Mays et al. 2015 JME
Baldwin et al. *in prep.*
Trout Fryxell & DeBruyn *in prep.*
Trout Fryxell & Staton *in prep.*
Theuret et al. *in prep.*



***Amblyomma americanum* (AA)**



***Amblyomma maculatum* (AM)**



***Dermacentor variabilis* (DV)**

Vector Ecology Site

Ames Plantation Research & Education Center

Wildlife
Ecology
History Farming
Livestock
Education

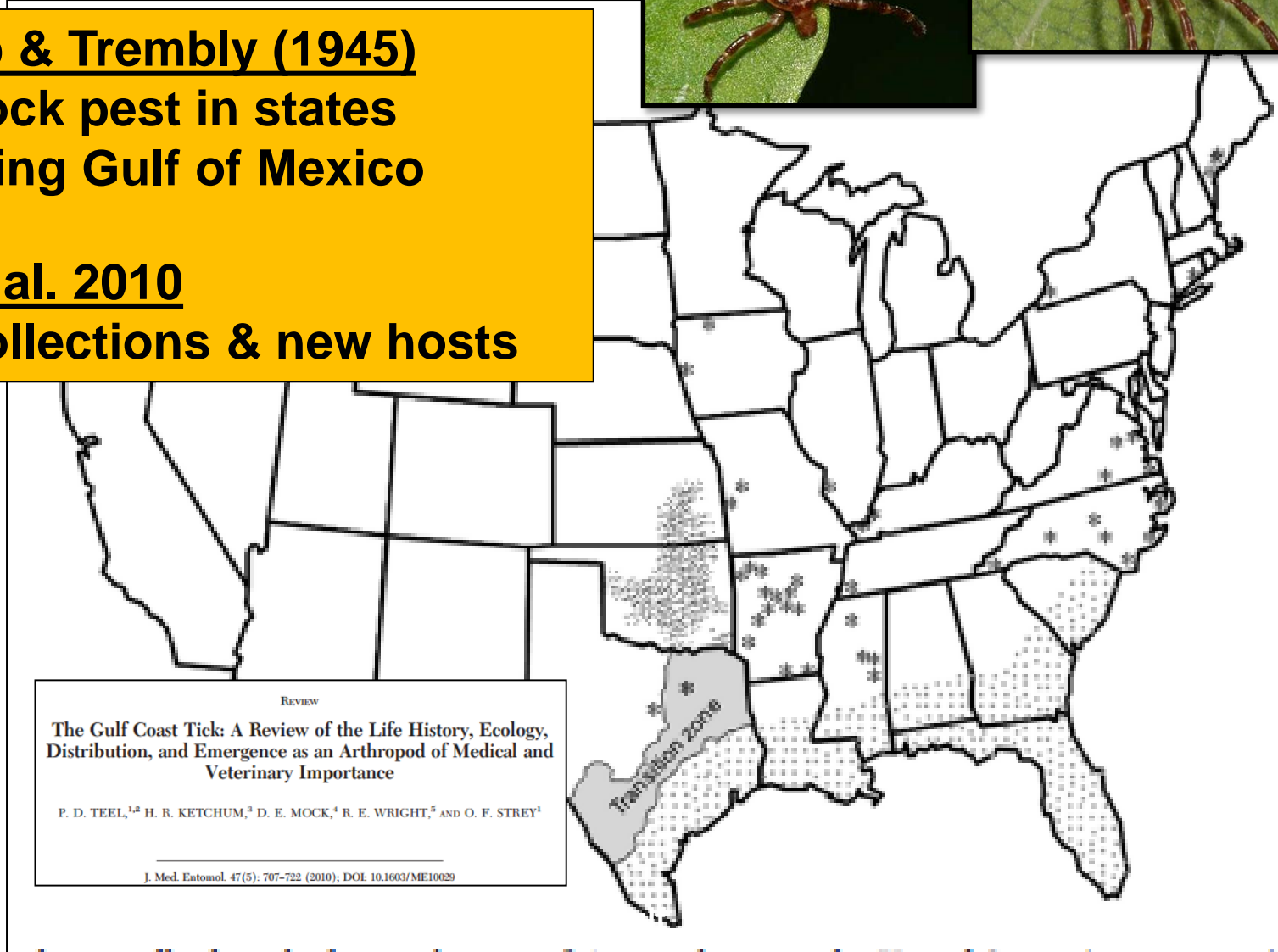


Amblyomma maculatum

Range Expansion

Bishop & Trembly (1945)
Livestock pest in states
bordering Gulf of Mexico

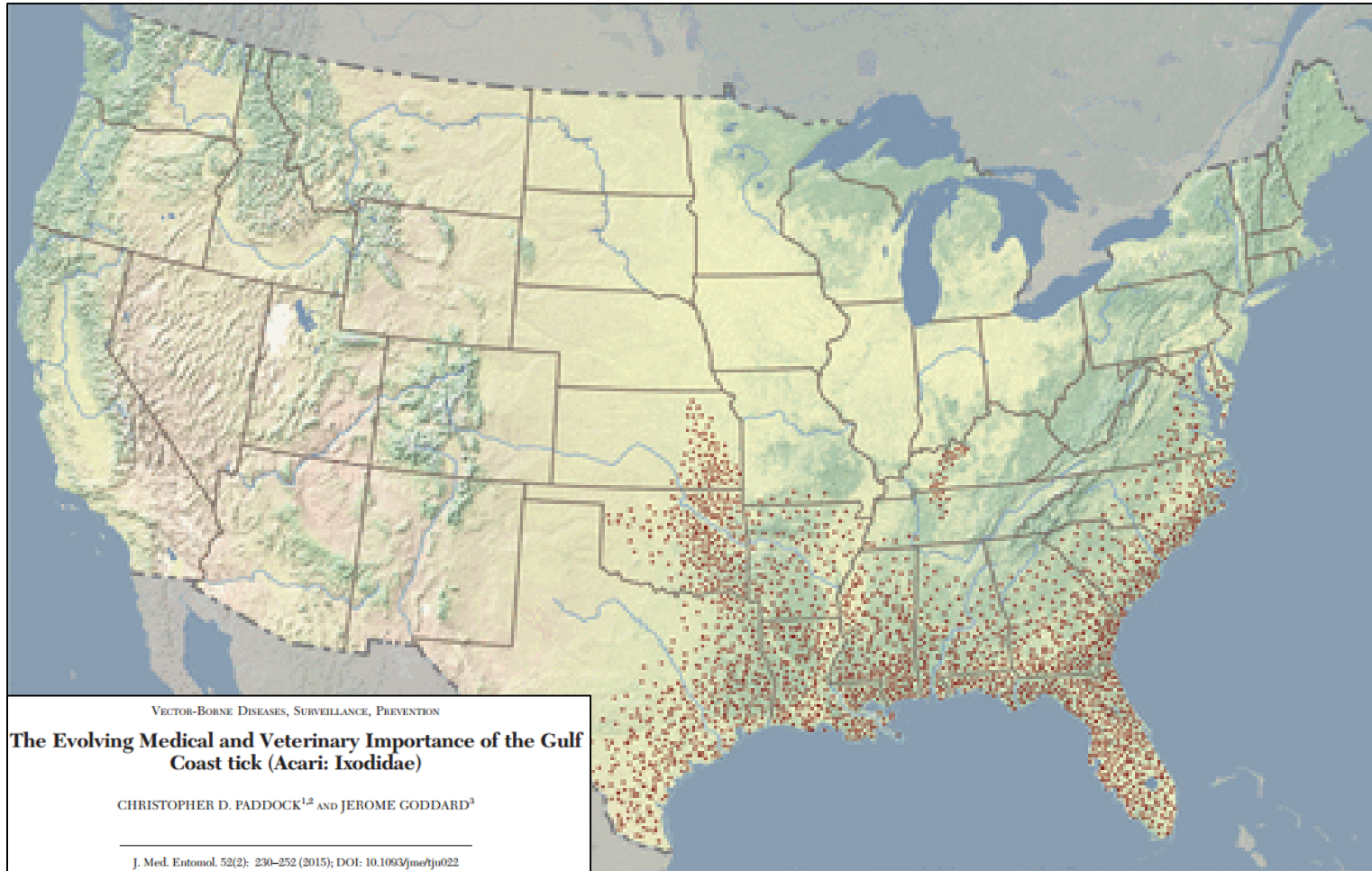
Teel et al. 2010
New collections & new hosts



REVIEW
The Gulf Coast Tick: A Review of the Life History, Ecology,
Distribution, and Emergence as an Arthropod of Medical and
Veterinary Importance
P. D. TEEL,^{1,2} H. R. KETCHUM,³ D. E. MOCK,⁴ R. E. WRIGHT,⁵ AND O. F. STREY¹
J. Med. Entomol. 47(5): 707-722 (2010); DOI: 10.1603/ME10029

Amblyomma maculatum

Range Expansion



An estimated distribution of *A. maculatum* in the United States for 2014 that interpolates contemporary data ([Wilson and Baker 1972](#), [Goddard and Norment 1983](#), [Harrison et al. 1997](#), [Clark et al. 1998](#), [Williams et al. 1999](#), [Reeves et al. 2002](#), [Barker et al. 2004](#), [Goddard and Paddock 2005](#), [Cohen et al. 2010](#), [Teel et al. 2010](#), [Trout et al. 2010](#), [Brown et al. 2011](#), [Fornadel et al. 2011](#), [Varela-Stokes et al. 2011](#), [Wright et al. 2011](#), [Pagac et al. 2014](#), and [Florin et al. 2014](#)).

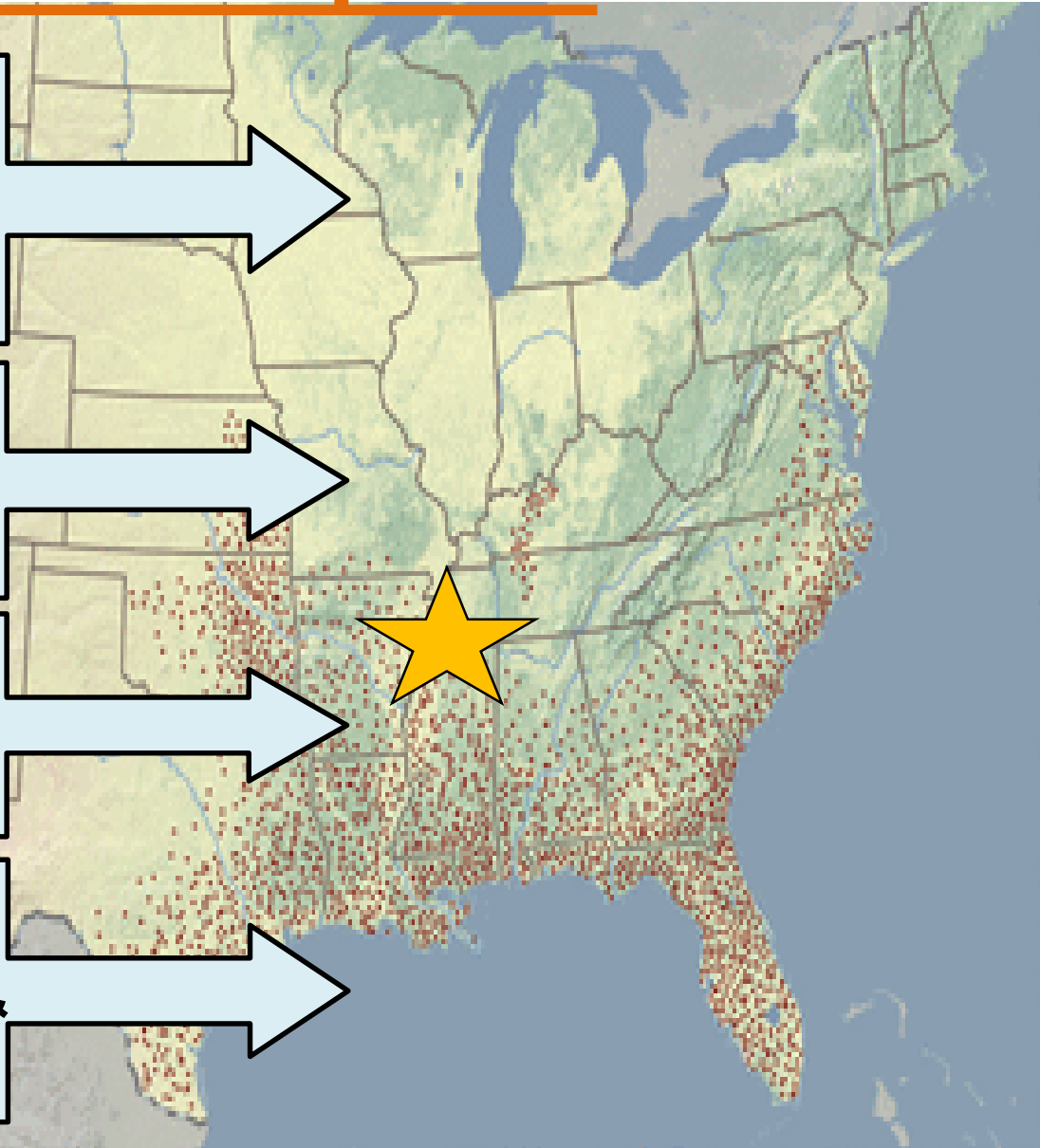
Amblyomma maculatum: Range Expansion Impact?

1) Environment
Phenology, Behavior,
Overwintering, &
Natural Enemies

2) Host Communities
Dispersal, Fecundity, &
Mating Populations

3) Microbial Communities
Synergistic, Antagonistic,
& Informative

4) Population Structure
Gene flow, Genetic drift, &
Selection pressures



1) Environment: Questing Site



GRASSLANDS



CONIFEROUS



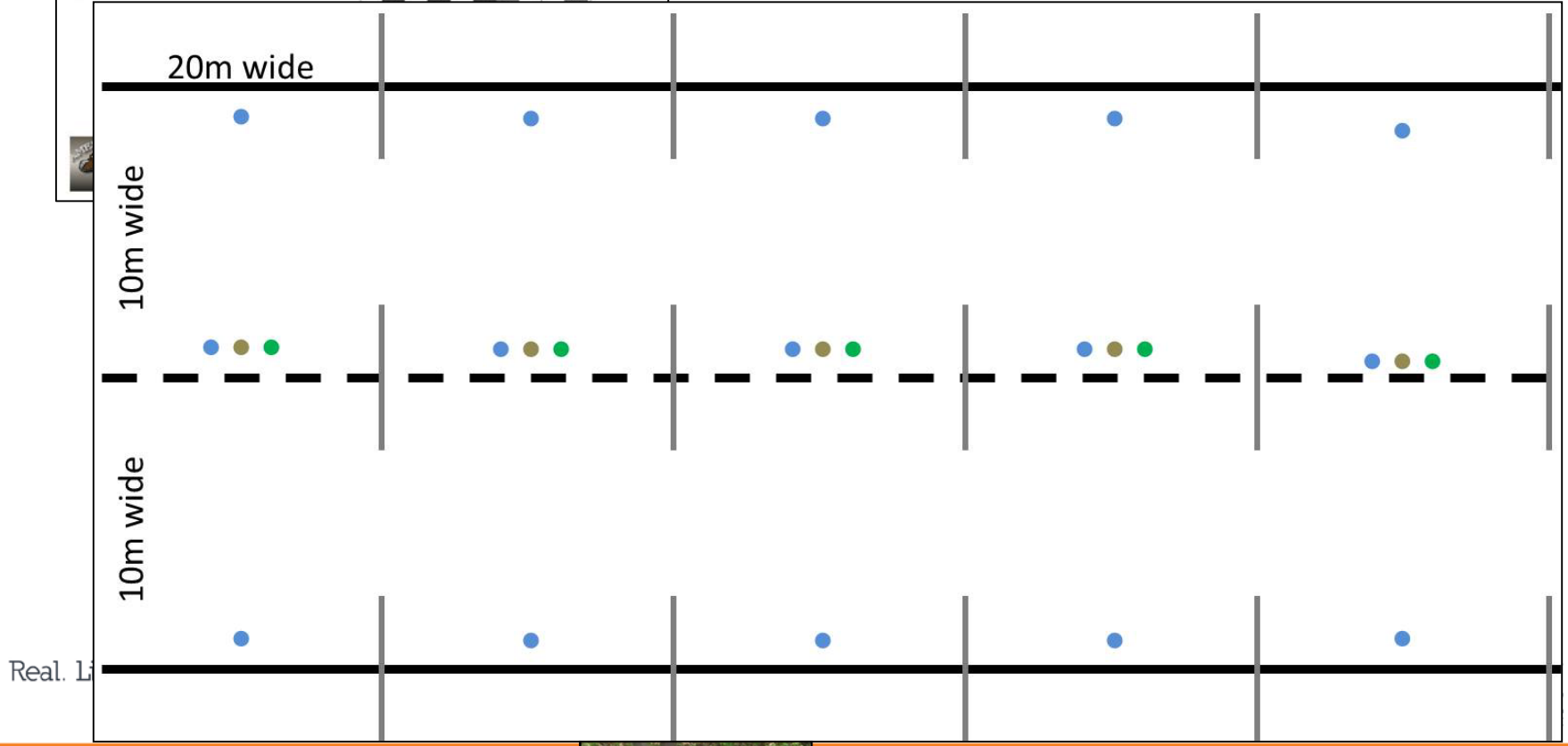
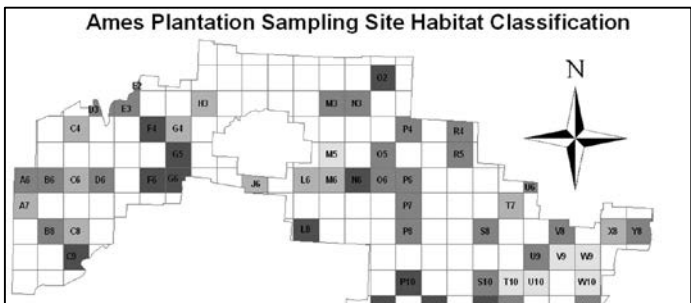
**UPLAND
DECIDIOUS**



**BOTTOMLAND
DECIDIOUS**

1) Questing Site

June 2014 @ 80 sites
Ticks samples every 20 m (300 m) (●)
Center transect: habitat
characterization
Soil (●) & Vegetation (●)



1) Questing Site



RESPONSE

PREDICTOR

Landcover Classification of Ames plantation

Amblyomma maculatum

NDVI

Habitat type x Plant Diversity

habitat type

plant diversity

plant evenness

STAT

basal area

distance to roads

$P = 0.0308$

Openness

$P = 0.0195$

Openness

GRASSLANDS

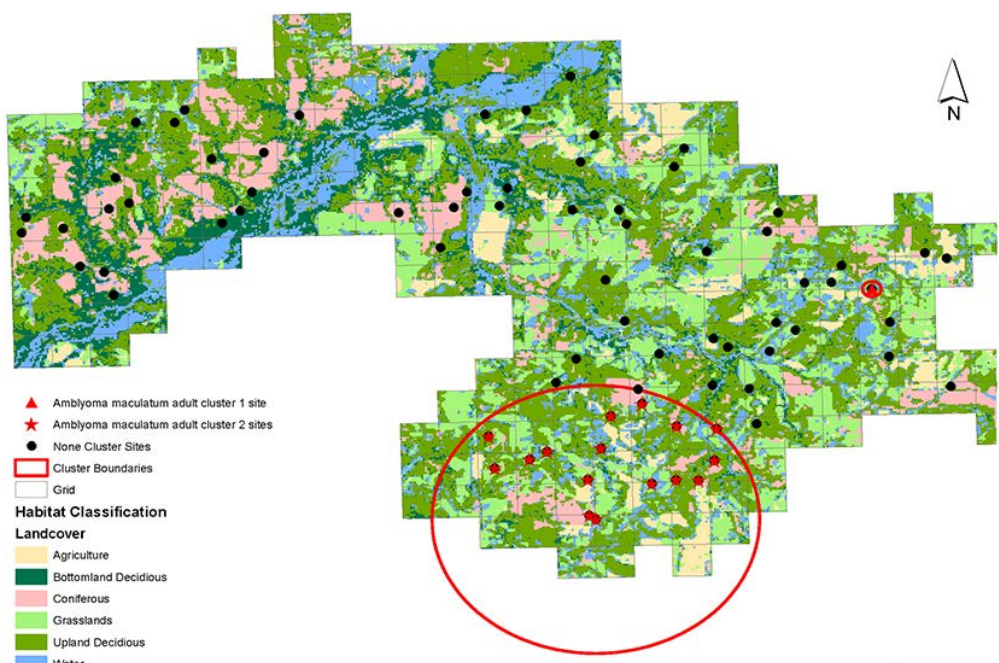


habitat type: NDVI

habitat type: soil pH

habitat type: water

Residuals



- ▲ *Amblyomma maculatum* adult cluster 1 site
- ★ *Amblyomma maculatum* adult cluster 2 sites
- None Cluster Sites
- Cluster Boundaries
- Grid
- Habitat Classification**
- Landcover**
- Agriculture
- Bottomland Deciduous
- Coniferous
- Grasslands
- Upland Deciduous
- Water

B

A

2) Host Communities

Local



Long-distance



Anthropogenic



Journal of Parasitology

31 FEBRUARY, 1945 Number 1

DISTRIBUTION AND HOSTS OF CERTAIN NORTH AMERICAN TICKS

F. C. BISHOPP¹ AND HELEN LOUISE TREMBLEY²

The Gulf Coast Tick: A Review of the Life History, Ecology, Distribution, and Emergence as an Arthropod of Medical and Veterinary Importance

P. D. TEEL,^{1,2} H. R. KETCHUM,³ D. E. MOCK,⁴ R. E. WRIGHT,⁵ AND O. F. STREY¹

J. Med. Entomol. 47(5): 707-722 (2010); DOI 10.1603/MEI10029

Population Dynamics of Immature *Amblyomma maculatum* (Acari: Ixodidae) and Other Ectoparasites on Meadowlarks and Northern Bobwhite Quail Resident to the Coastal Prairie of Texas

PETE D. TEEL, SIDNEY W. HOPKINS,¹ WILLIAM A. DONAHUE,² AND OTTO F. STREY

Department of Entomology, Texas A&M University, College Station, TX 77843

J. Med. Entomol. 35(4): 483-488 (1998)

2) Host Communities

Source (n)	2012	2013	2014	2015	2016	2017	Total
Questing (?)	20	74	17	.	.	Tbd	>111
Cattle (~700)	-	83	27	.	149	.	259
Deer (~300/yr)	0	0	-	.	.	.	0
Rodents (295)	-	7	-	.	.	Tbd	>7
Human (85)	0	30	5	1	0	6	42
Birds (295)	-	0	-
Total	20	194	49	1	149	>6	419

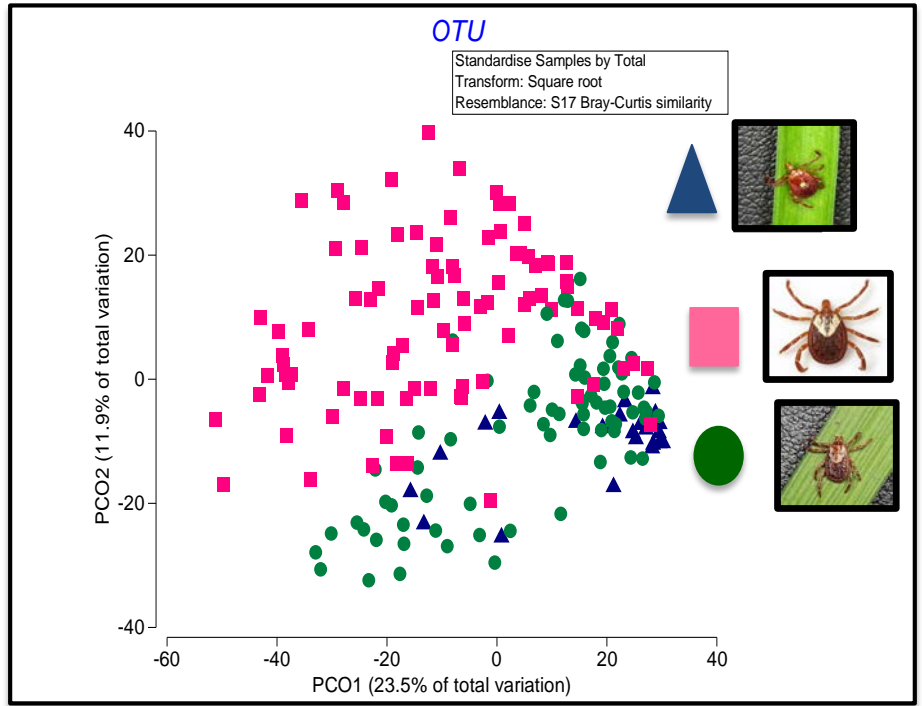
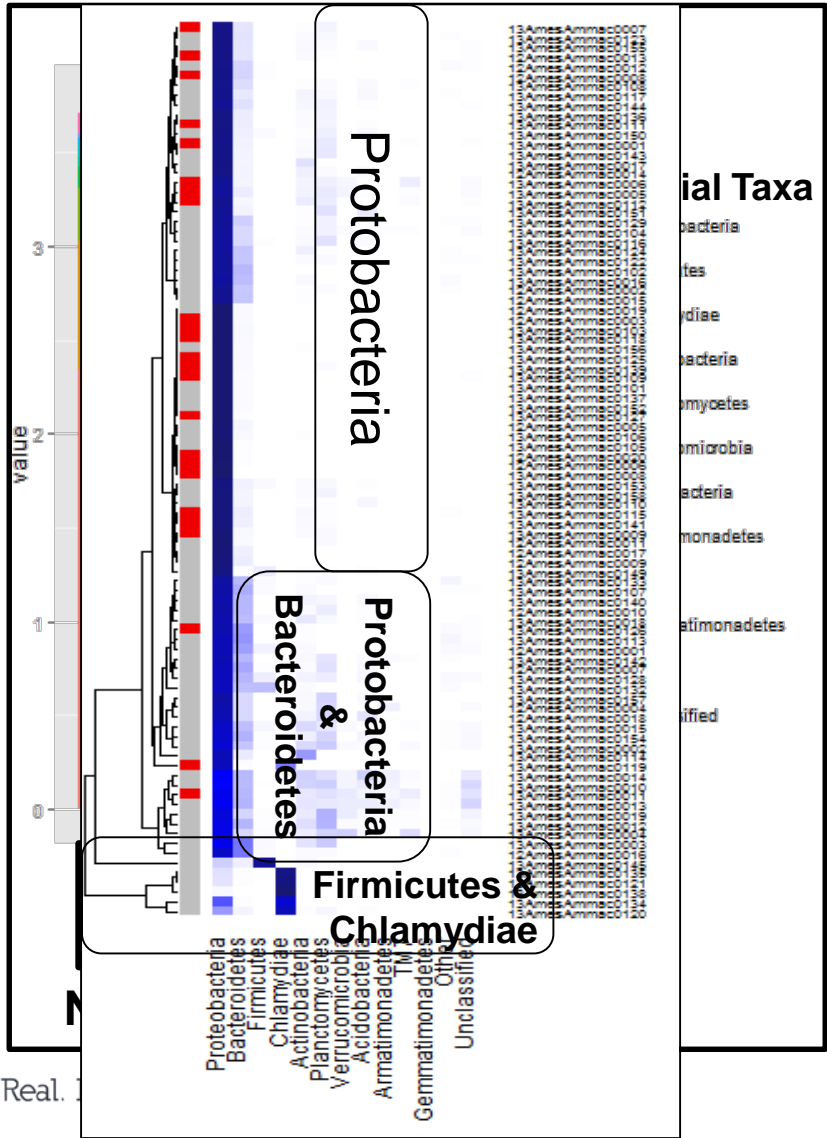
Local

Long-distance

Anthropogenic

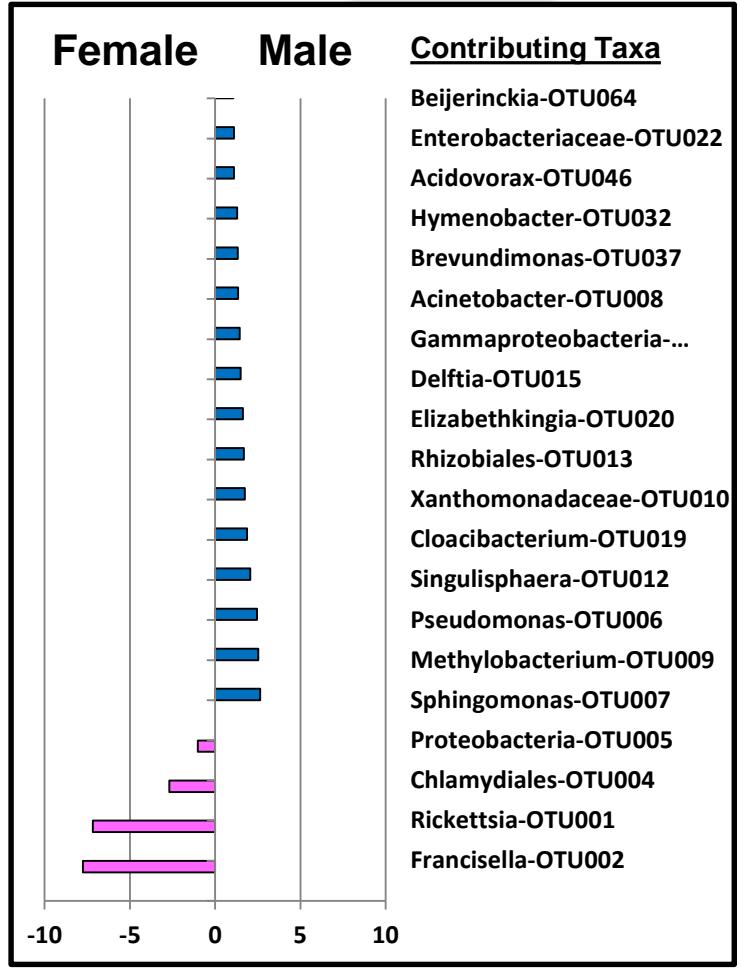
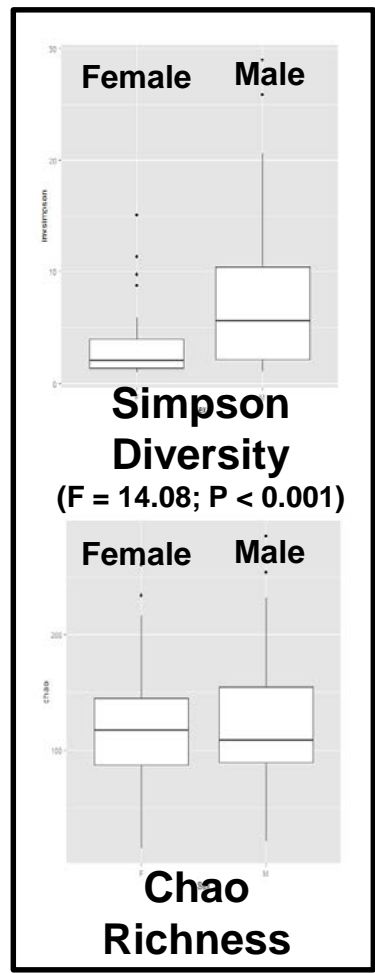
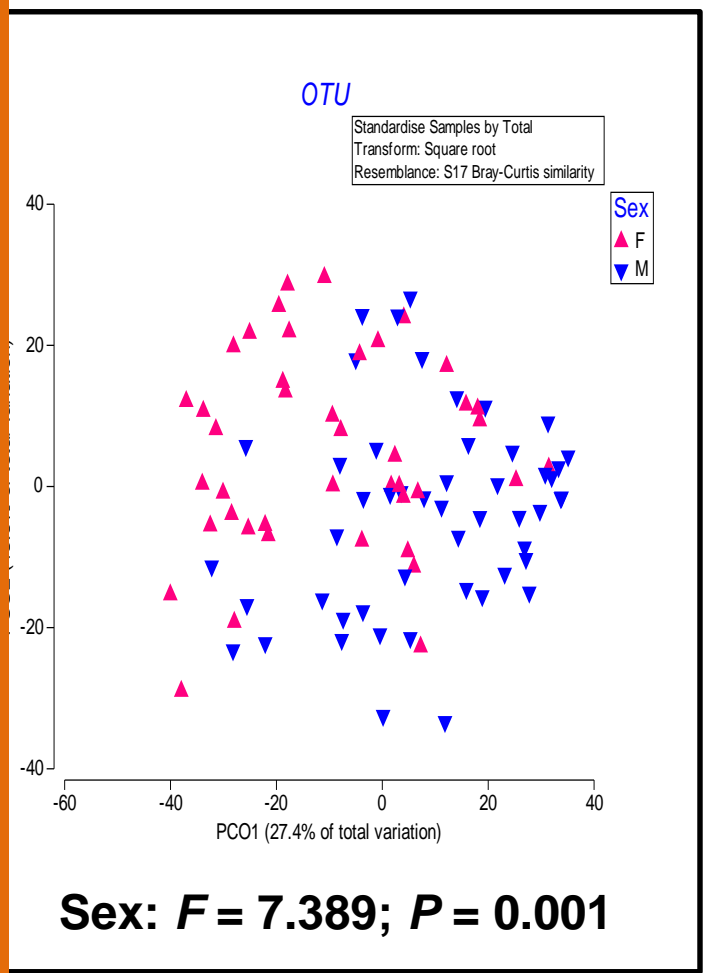


3) Microbial Communities

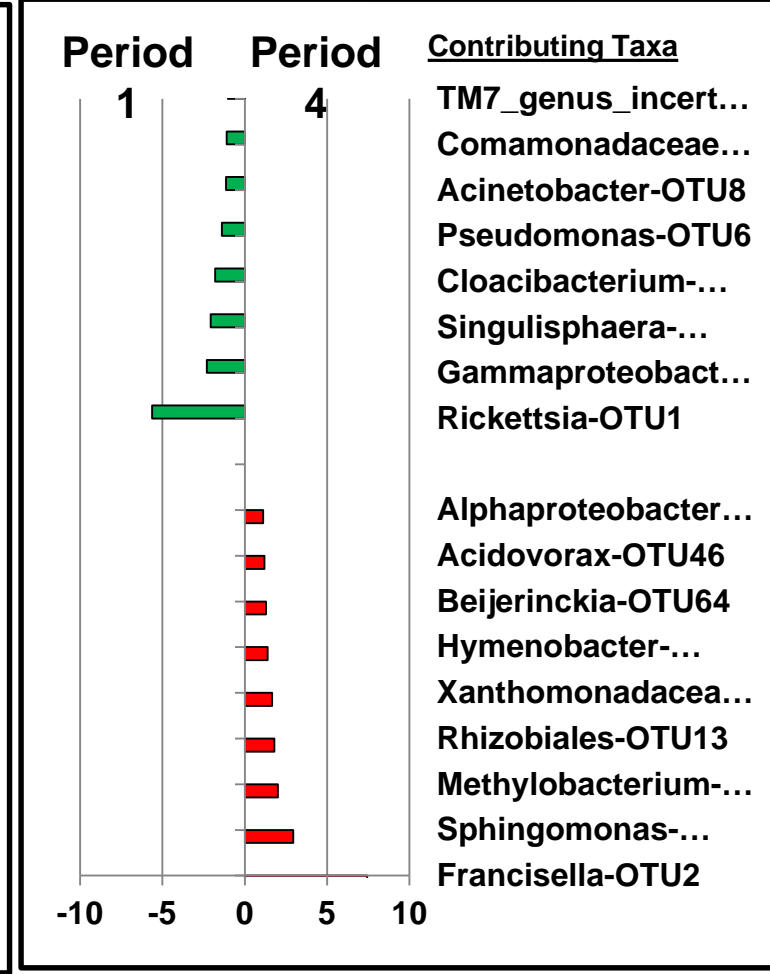
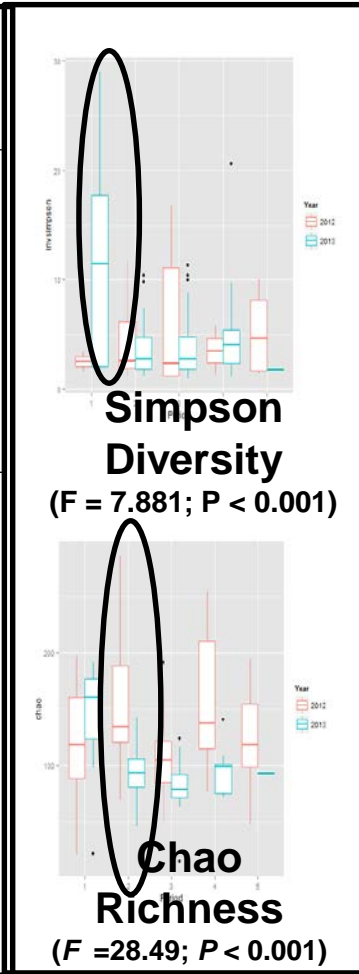
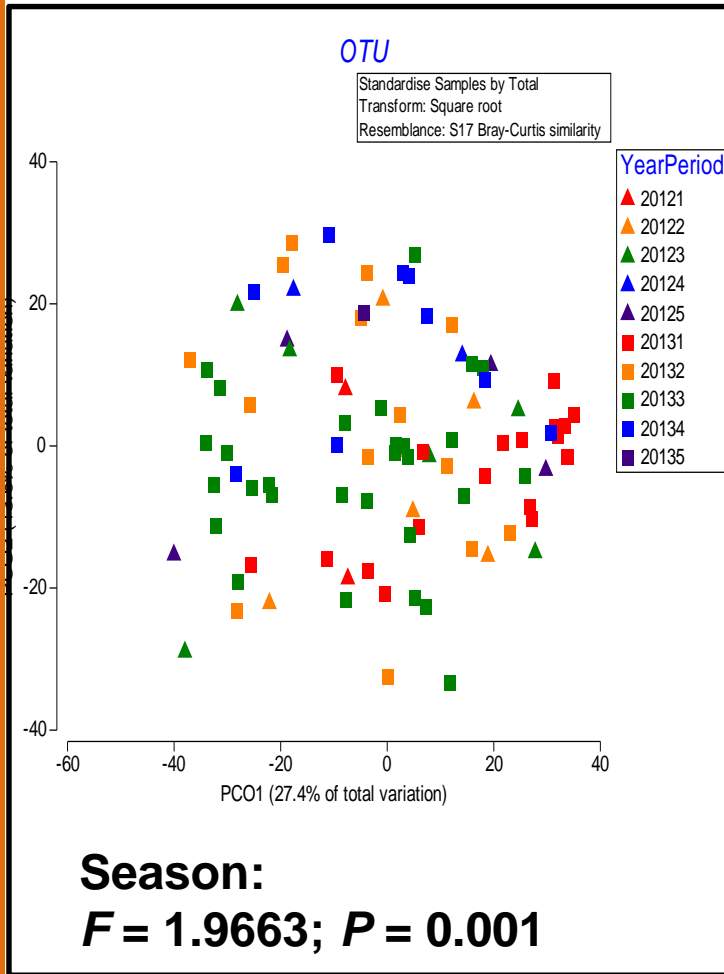


**All from Ames Plantation
Collected 2012-2014
= 3 distinct microbial communities**

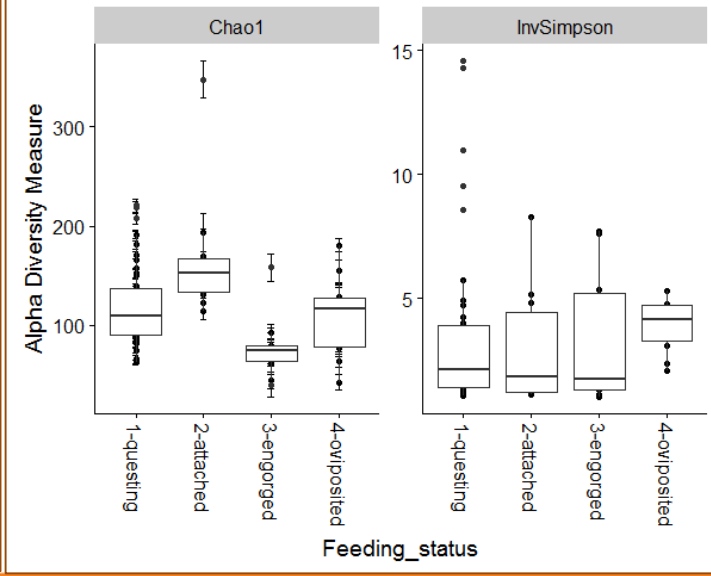
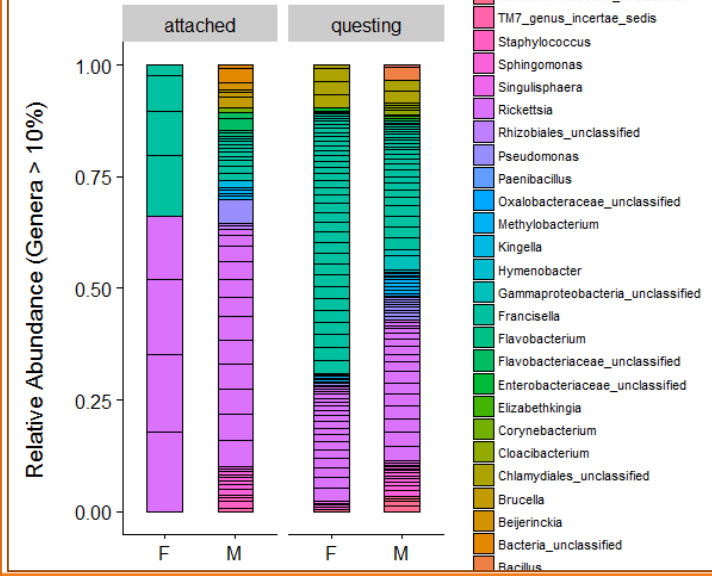
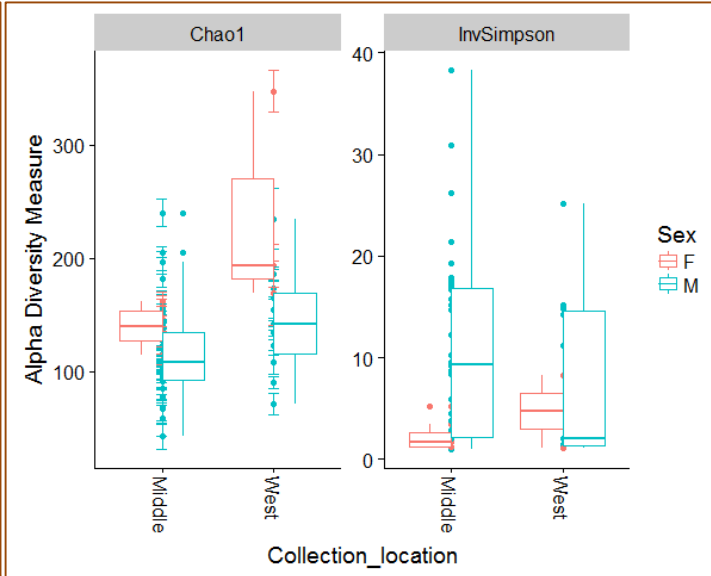
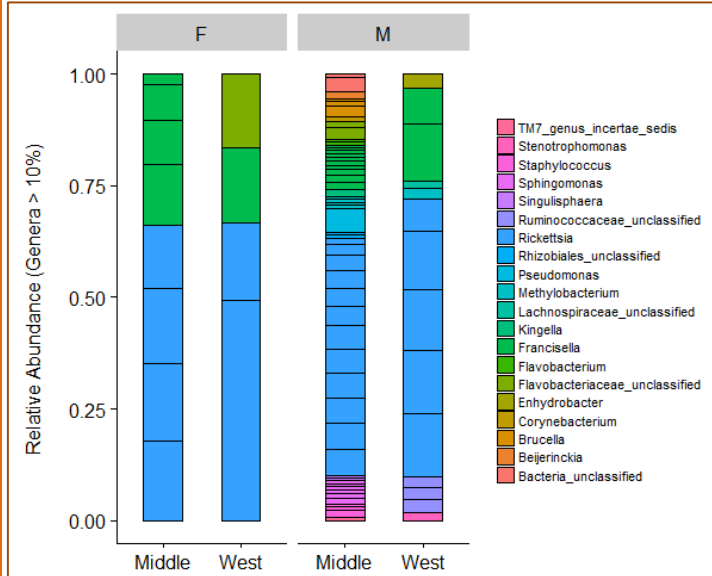
3) Microbial Communities



3) Microbial Communities



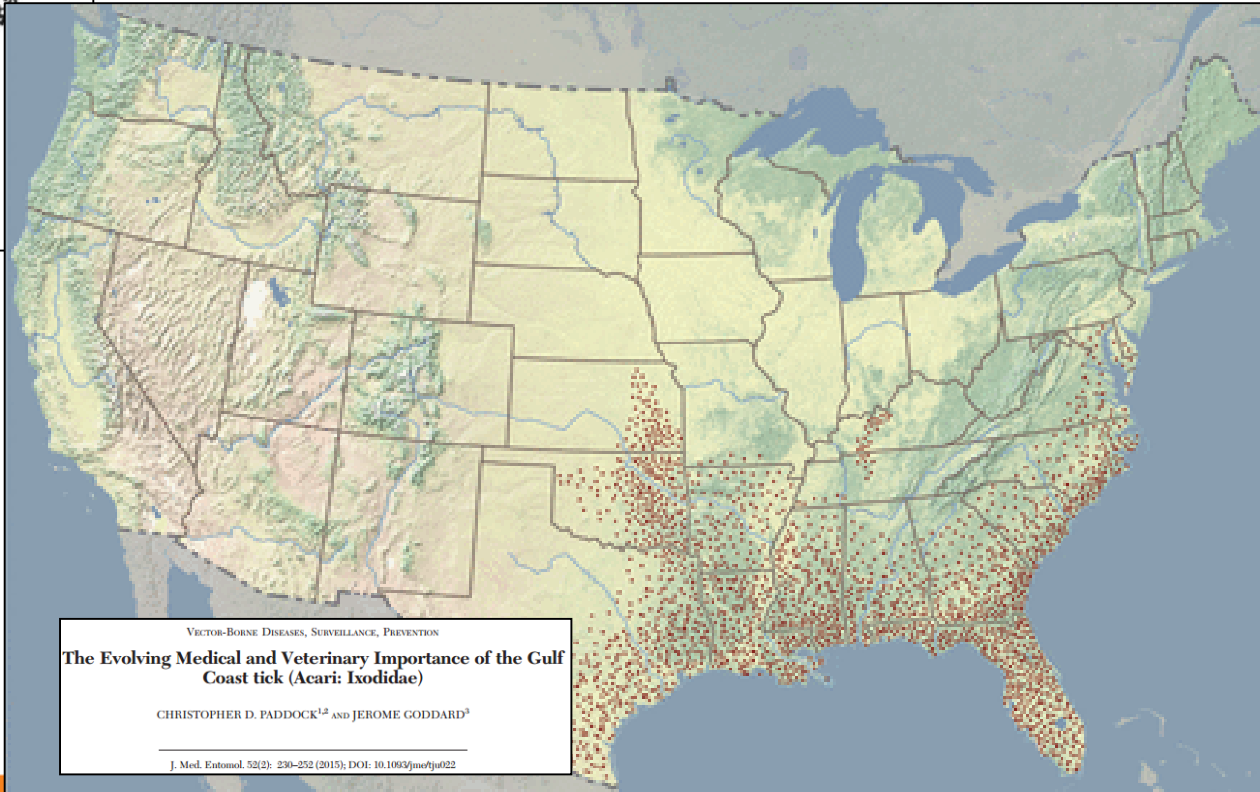
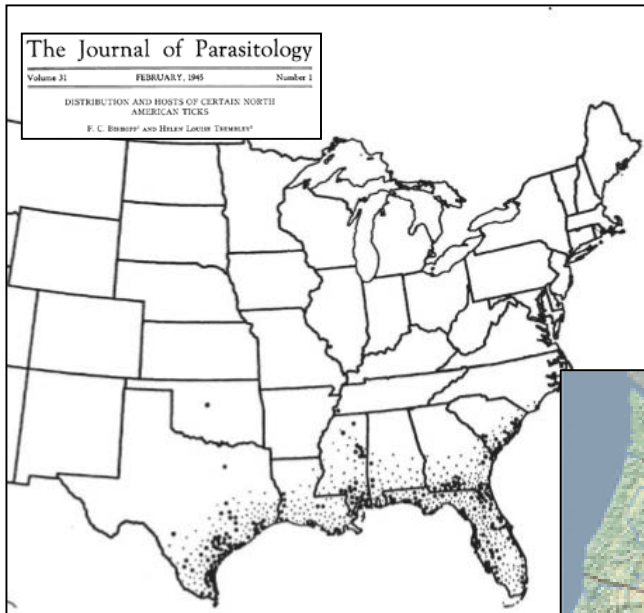
3) Microbial Communities



Microbial differences by region

& by feeding status

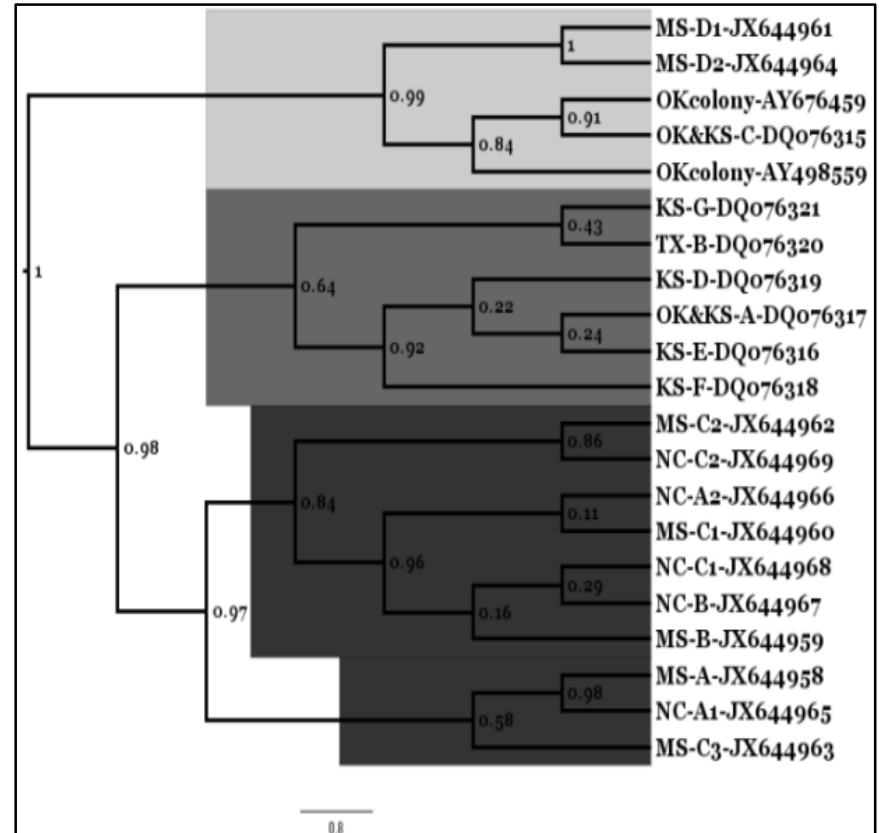
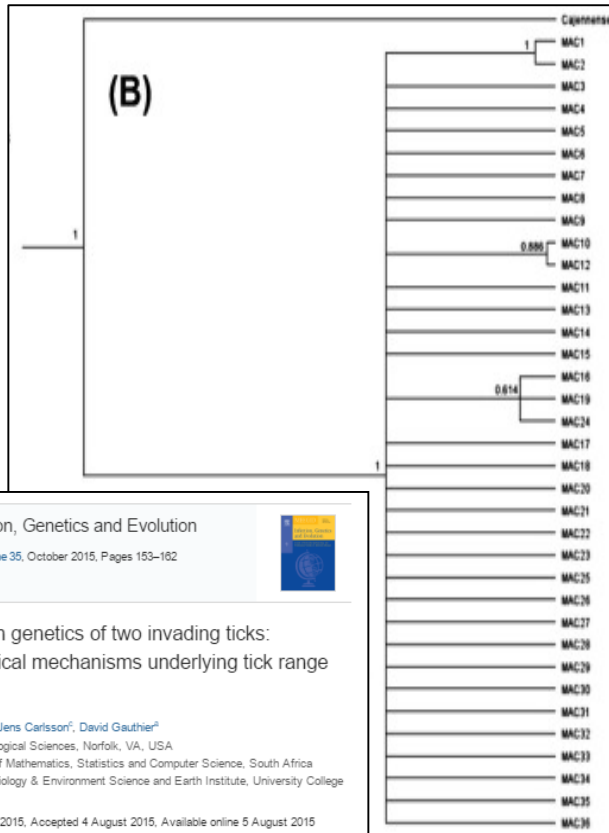
4) Population Structure



4) Population Structure

16S rDNA of ticks from
VA, KY, MS, NC, & TN =
1 population

16S rDNA from GenBank
MS, OK, KS, TX, NC, AR =
4 populations



ELSEVIER

Infection, Genetics and Evolution
Volume 35, October 2015, Pages 153–162

Comparative population genetics of two invading ticks:
Evidence of the ecological mechanisms underlying tick range
expansions

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^a Old Dominion University, Dept. of Biological Sciences, Norfolk, VA, USA
^b University of KwaZulu-Natal, School of Mathematics, Statistics and Computer Science, South Africa
^c Area 52 Research Group, School of Biology & Environment Science and Earth Institute, University College
Dublin, Belfield, Dublin, Ireland

Received 5 June 2015, Revised 29 July 2015, Accepted 4 August 2015, Available online 5 August 2015

4) Population Structure

1) 95 samples for GBS sequencing (Cornell)

- 1) Habitats: Deciduous & Grasslands
- 2) Hosts: Cattle & Humans
- 3) *ompA*: pos. & neg.

2) Optimization & Library Construction

ApeKI for optimization & Pst/MSPI for double digest

3) 100bp single end reads generated on Illumina HiSeq 2500

4) Bioinformatics

23,275,556 / 235,335,191 (9.8%) unique reads

More filtering = 8,392 biallelic SNPs w/ 4x coverage per individual
95 specimens sent, but 64 specimens produced *good* results
SNPs calling: *Ixodes scapularis* genome or UNEAK

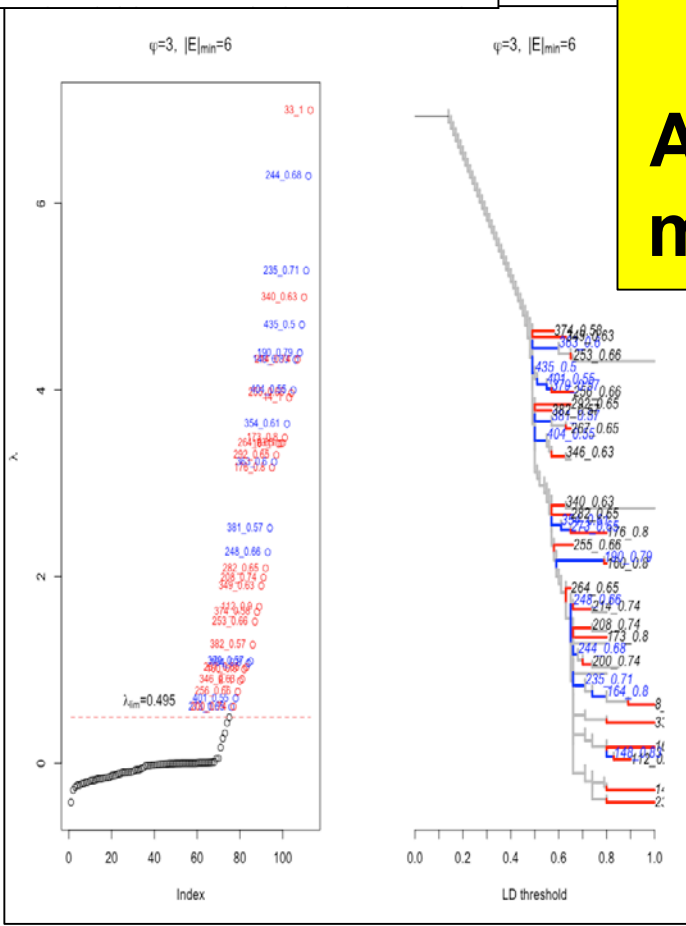
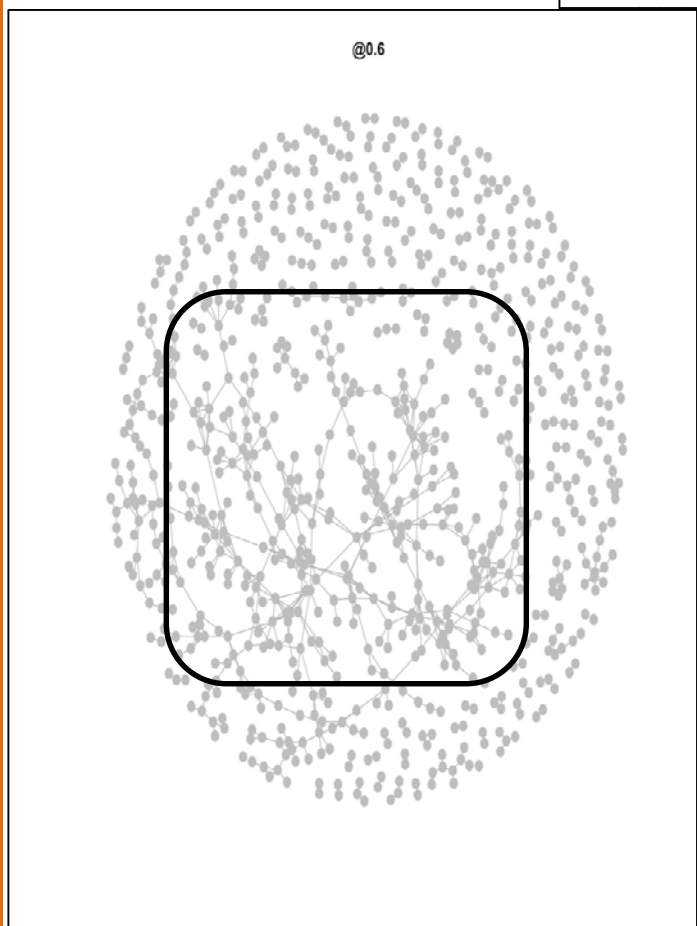
4) Population Structure

Linked SNPs via IDNA analysis

Linkage disequilibrium network analysis (LDna) gives a global view of chromosomal inversions, local adaptation and geographic structure

PETRI KEMPPAINEN,*†, CHRISTOPHER G. KNIGHT,* DEVOJIT K. SARMA,*‡, THAUNG HLAING,§ ANIL PRAKASH,‡ YAN NAUNG MAUNG MAUNG,§ PRADYA SOMBOON,¶ JAGADISH MAHANTA‡ and CATHERINE WALTON*

**Removed:
788 not in
HWE,
3 singleton,
& 98 IDNA
SNPs
Allowed 15%
missing data**

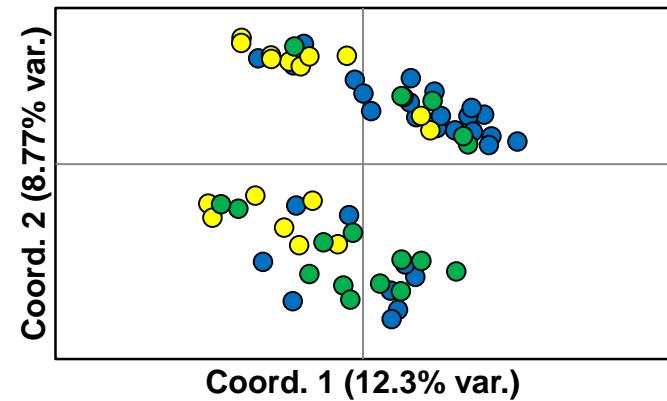
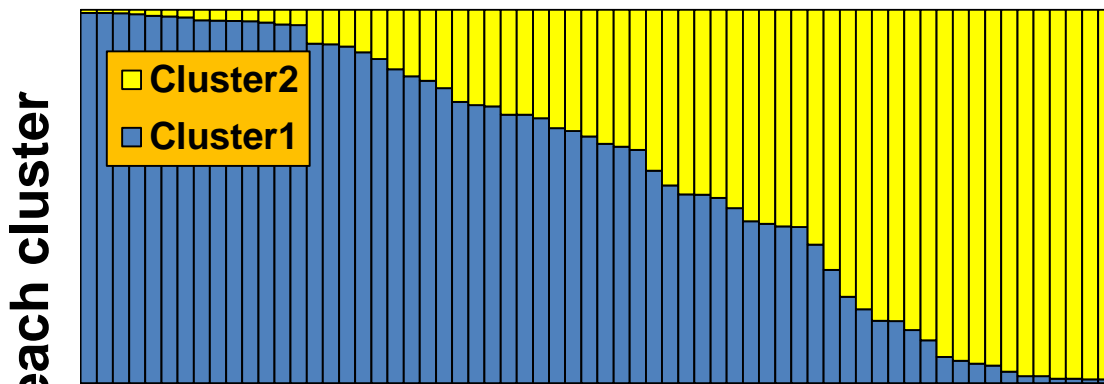


4) Population Structure

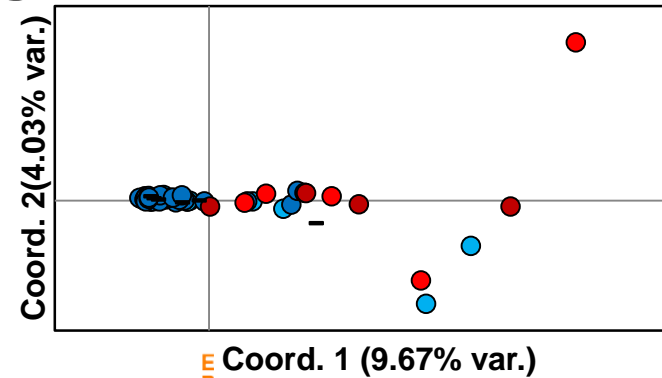
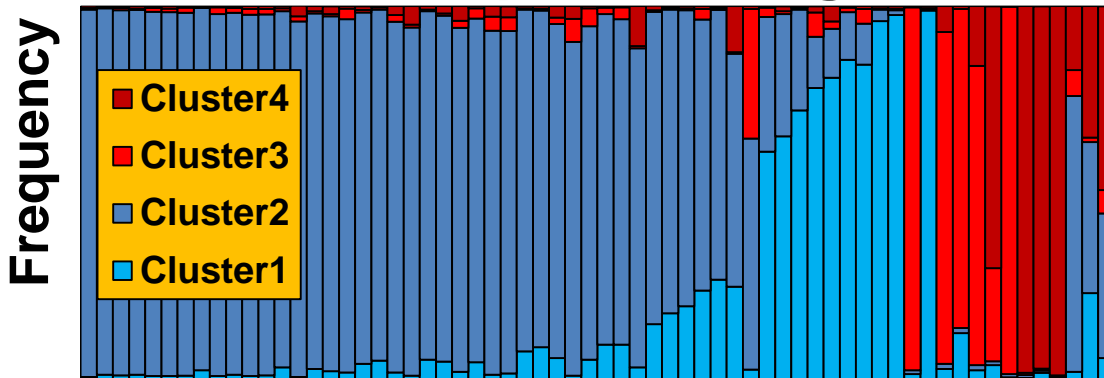


SNP Discovery Pipeline Differences

Cornell: BRC pipeline aligned to *Ix. scapularis* = 575 SNPs



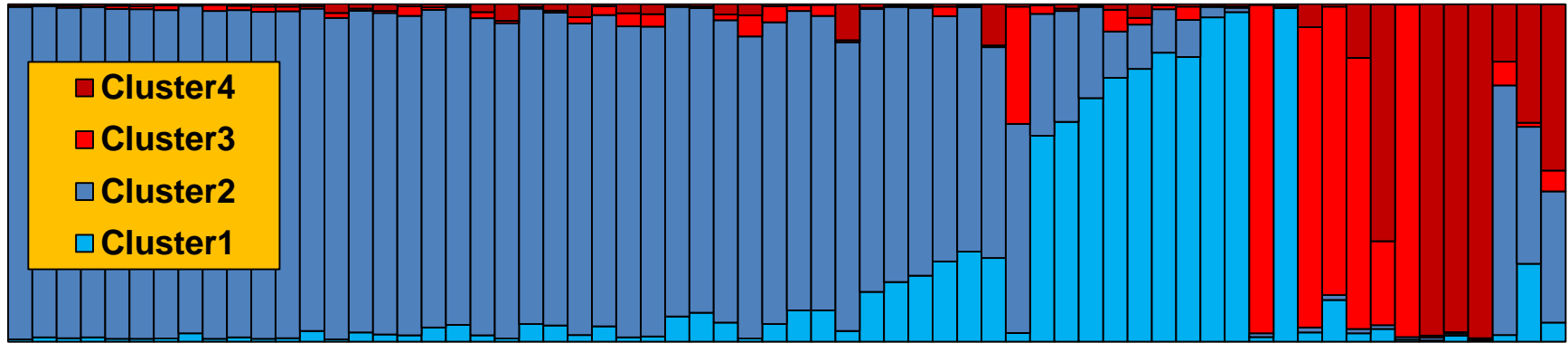
US: UNEAK Pipeline, no genome alignment = 2130 SNPs



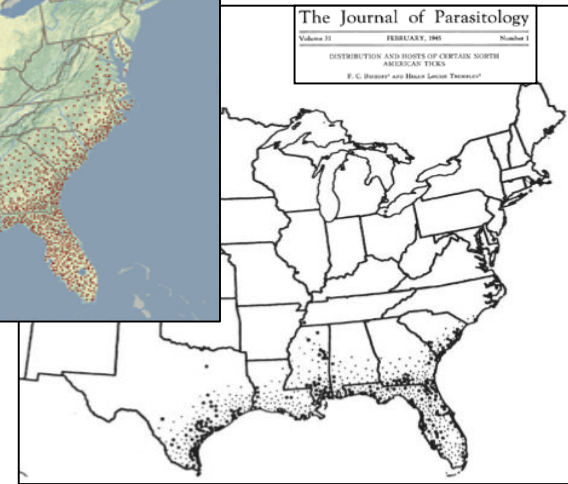
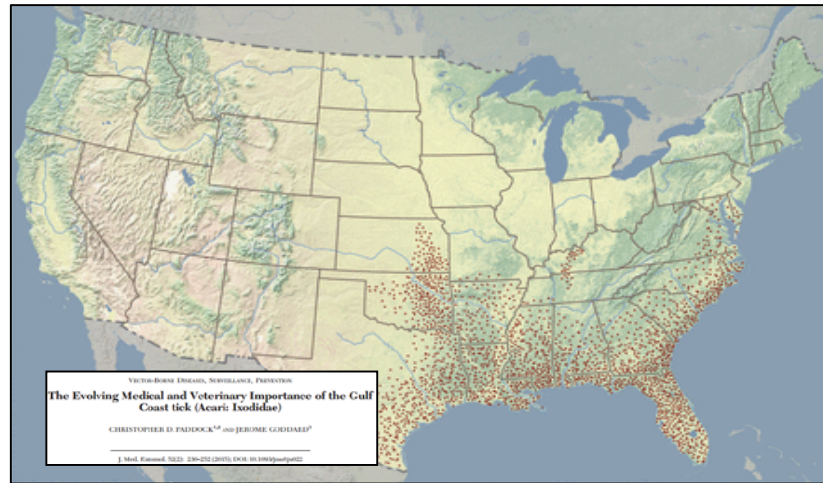
Real. Life. Solutions.™

64 individual tick specimens

4) Population Structure



Clusters do not align with phenotypes: sex, pathogen, habitat, or host



5) Summary:

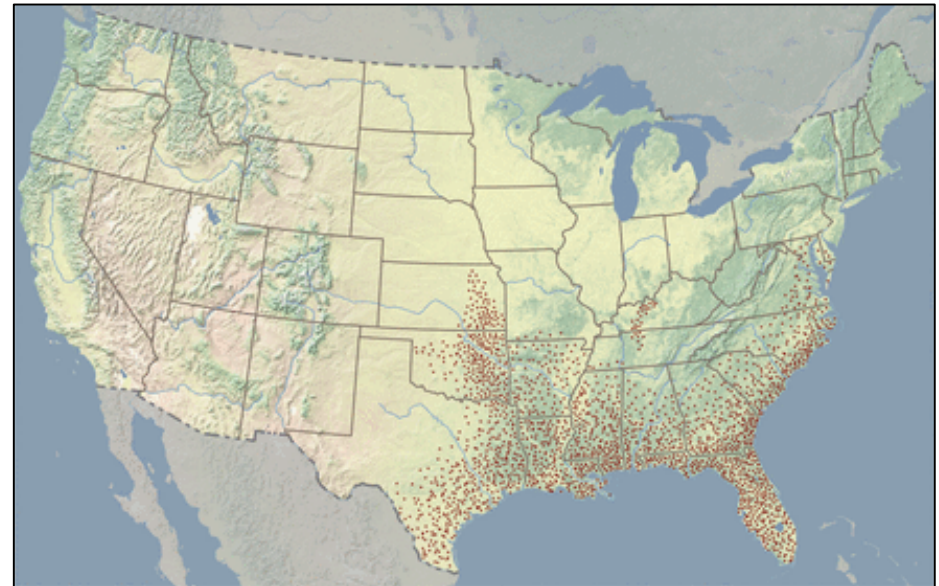
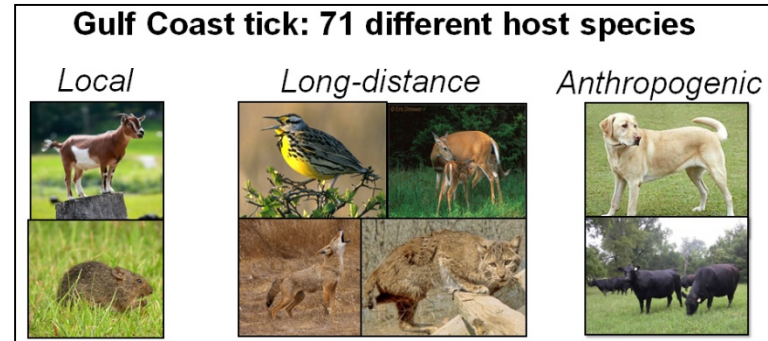
Amblyomma maculatum from western Tennessee

- **Environment**
 - Prefer grasslands; verified with low NDVI values (shrubs & grasslands)
- **Hosts**
 - Cattle > human > cotton rats = deer; None on birds (yet)
- **Microbial Communities**
 - Lots of variation (sex, infection, collection period, region, & feeding status)
- **Population Structure**
 - Established population with high rates of genetic admixture
 - Established population mixing with new population

5) Putting the Pieces Together Future Direction

Incorporate tick & data submissions from other locations
Texas (Hamer)
Oklahoma (Coburn)
Mississippi (Portugal)
Alabama (Ray)
Florida (Weeks & Hertz)

Collaborations Needed to understand Range Expansion



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COE students- Taylor, Hannah, Kim, Jeremy, & Jessica

UGs- Daniel, Drew, Casey, Megan L., Chelsea, Caitlin, Megan N.

Collaborators

EPP- Staton

FWF- Houston, Hickling, Jean-Philippe, Kyser, & Kwit

BESS- DeBruyn, Schaeffer, & Jagadamma

Vet.Med- Odoi

Memphis- Kennedy, Park, Collins, Moore

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UTIA COE Center for Veterinary Medicine

UTIA AgResearch Seed Proposal

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