Disease Ecology: The role of global change on emerging infectious diseases

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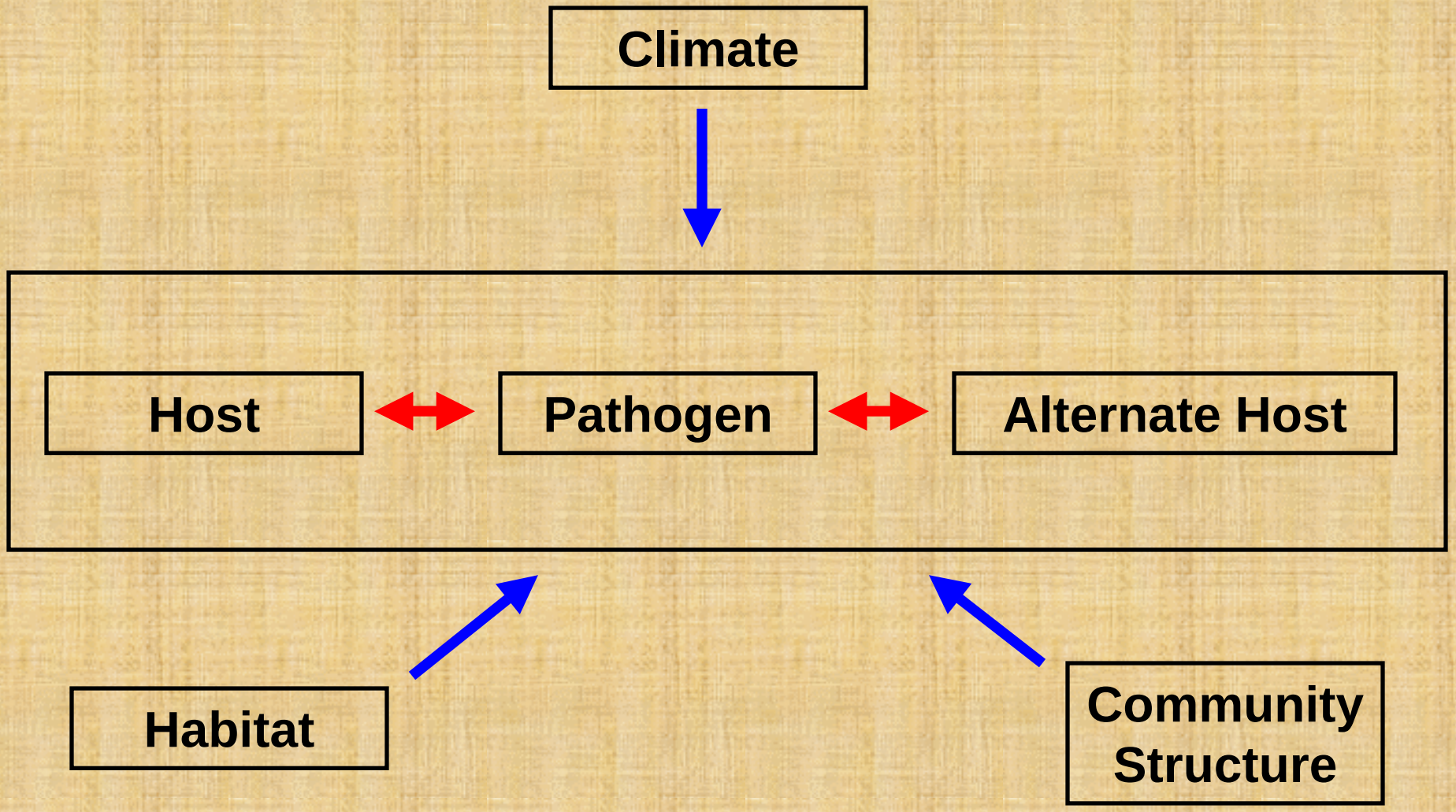
Emerging infectious diseases

- Usually zoonotic
- Appear in areas undergoing ecological transformation
- Result from adaptation to new hosts OR
- Reemerge as a result of antimicrobial resistance
- Increase in the past 2 decades

EID Institutes and Programs

- NSF/NIH Ecology of Infectious Diseases
- NEON - Detecting EID's
- KSU Biosecurity Research Institute
- KSU Food Safety Institute
- KSU Department of Plant Pathology
- KSUCVM Diagnostics and Pathobiology
- KSU TE proposal - Developing predictive epidemiological models

How do global and regional drivers affect ecosystem services like disease regulation?



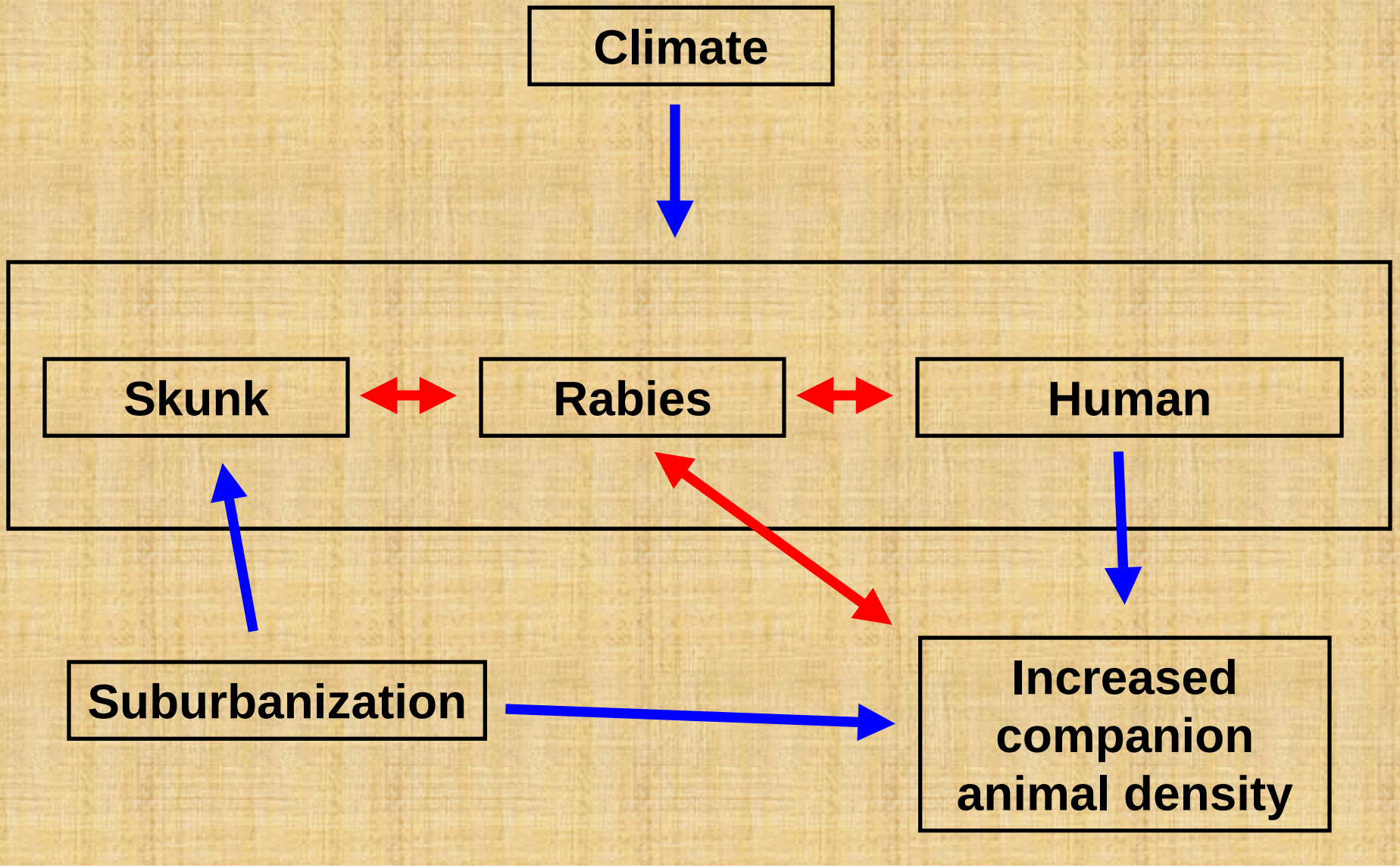
Ecological transformation

- Human induced habitat change in the Flint Hills
  - Woody encroachment
  - Suburbanization
  - Changing livestock practices
- Increases transmission rates of emerging infectious diseases

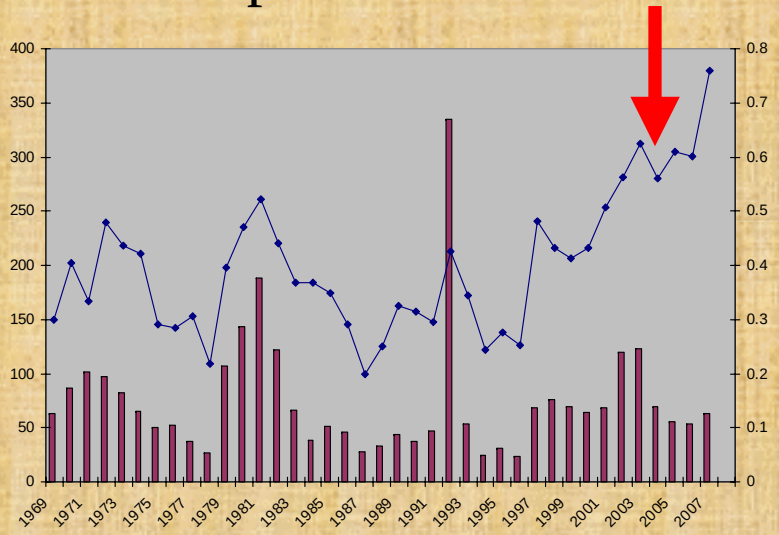
EID Research Models on KPBS

Driver	Pathogen	Host
Suburbanization	Rabies	Striped skunk
Woody encroachment	White-tailed deer	Chronic Wasting Disease
Agricultural landscape	AR Enterrococcus	Cattle Bison
Agricultural landscape	Multiple	Big bluestem Wheat

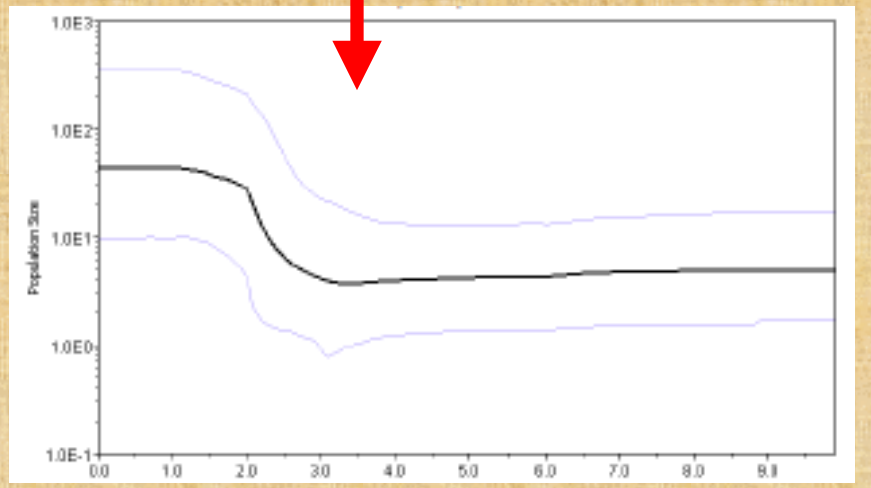
Rabies model



No. of positive animals

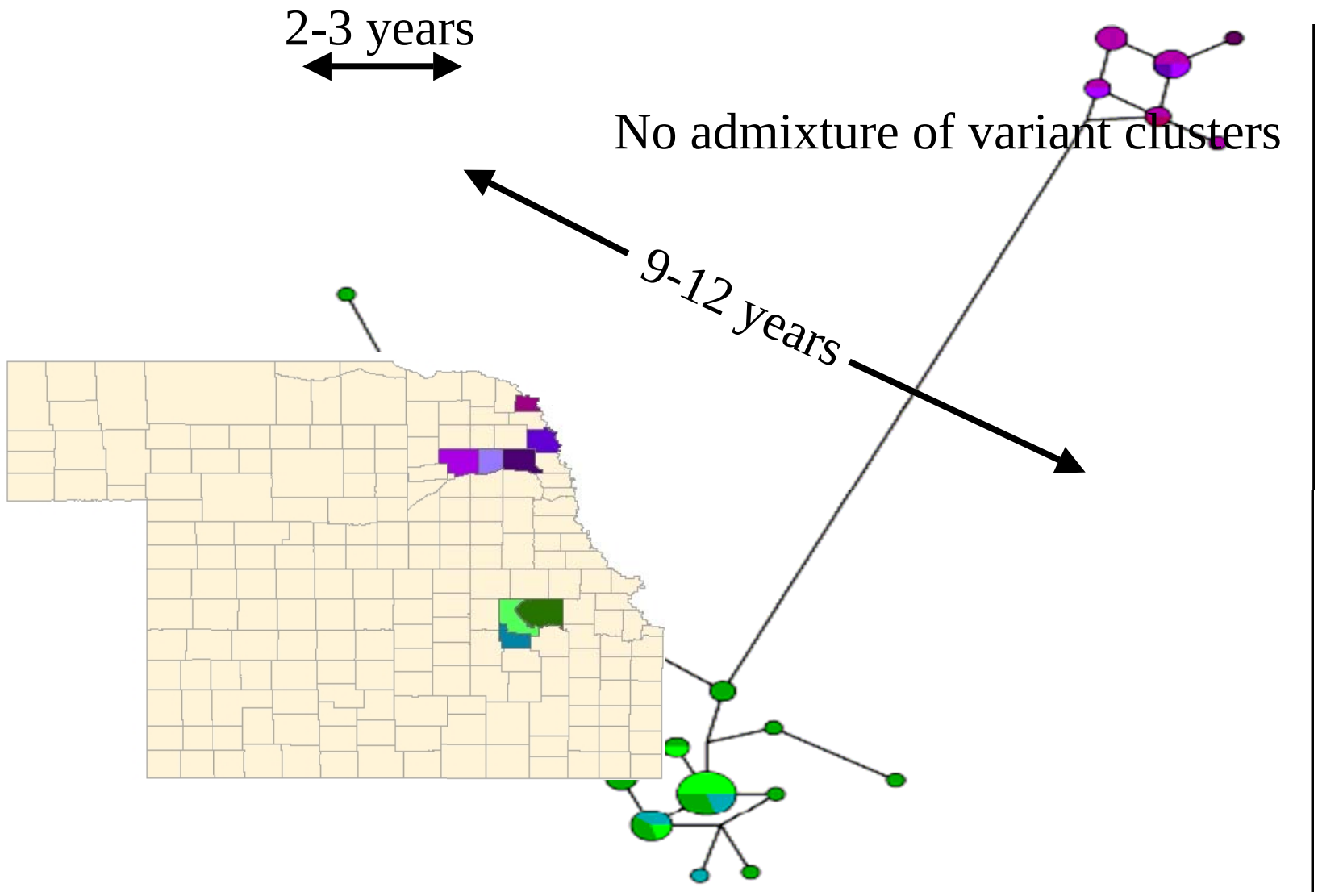


Effective number of infections



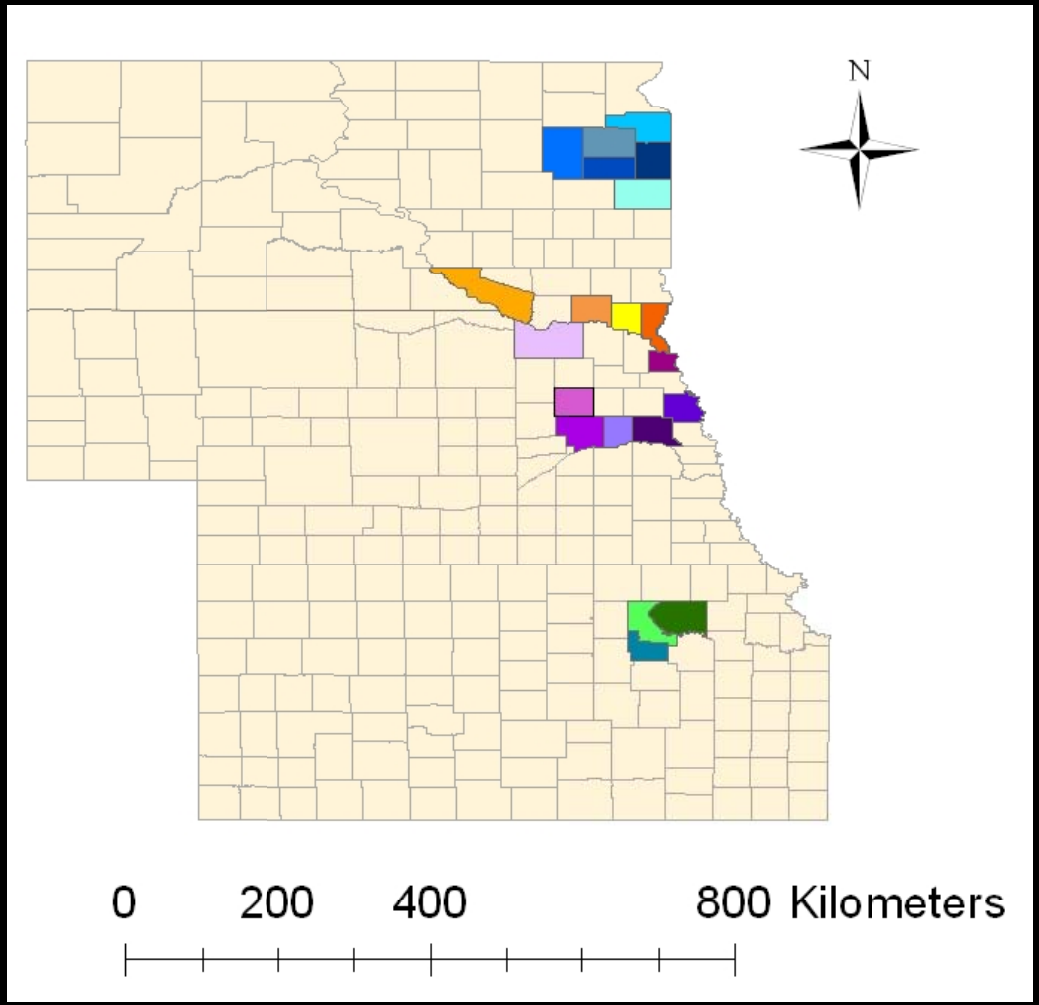
Significant periodicity at 4 and 10 years

Heather Barton, in prep.


2-3 years
No admixture of variant clusters
9-12 years

Skunk population dynamics

- Global F_{ST}= 0.02
- 11 migrants per generation
- Non-equilibrium populations
- Evidence of population bottleneck



Integrate

- Habitat use
- Land cover change
- Risk assessment

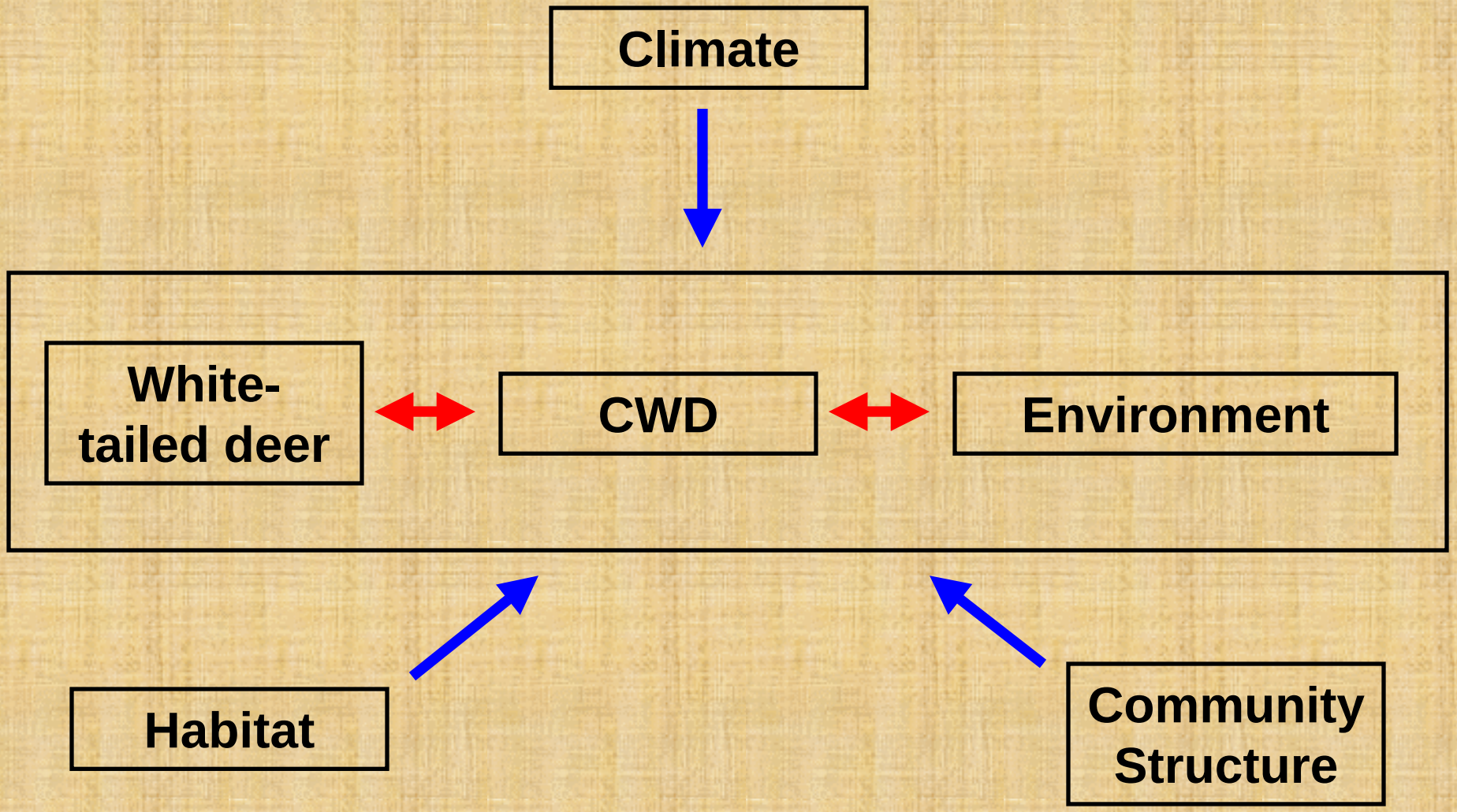
Check out Sarah Bowe's poster!!

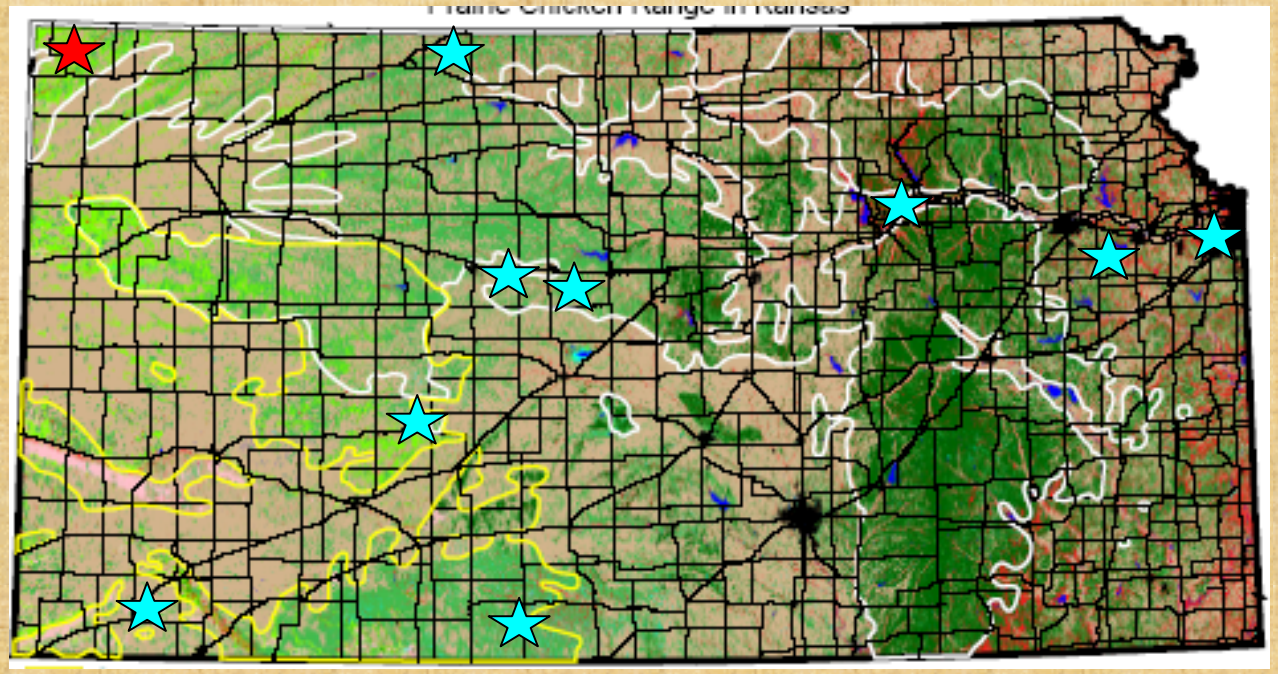
Future directions

- How do multiple infections influence epidemiology of rabies?
- How does community composition influence the evolutionary potential of rabies?
- What is the effect of temperature and precipitation on rabies evolution?

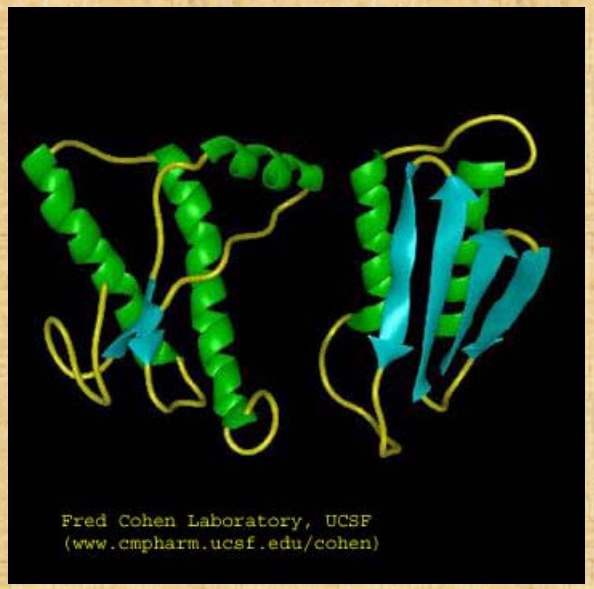
NSF – EID proposal, in prep.

Predictive model of CWD spread in Kansas based on habitat suitability and genetic susceptibility





Landscape genetic analysis of population connectivity



Frequency of susceptible genotypes

Dr. Mark Statham

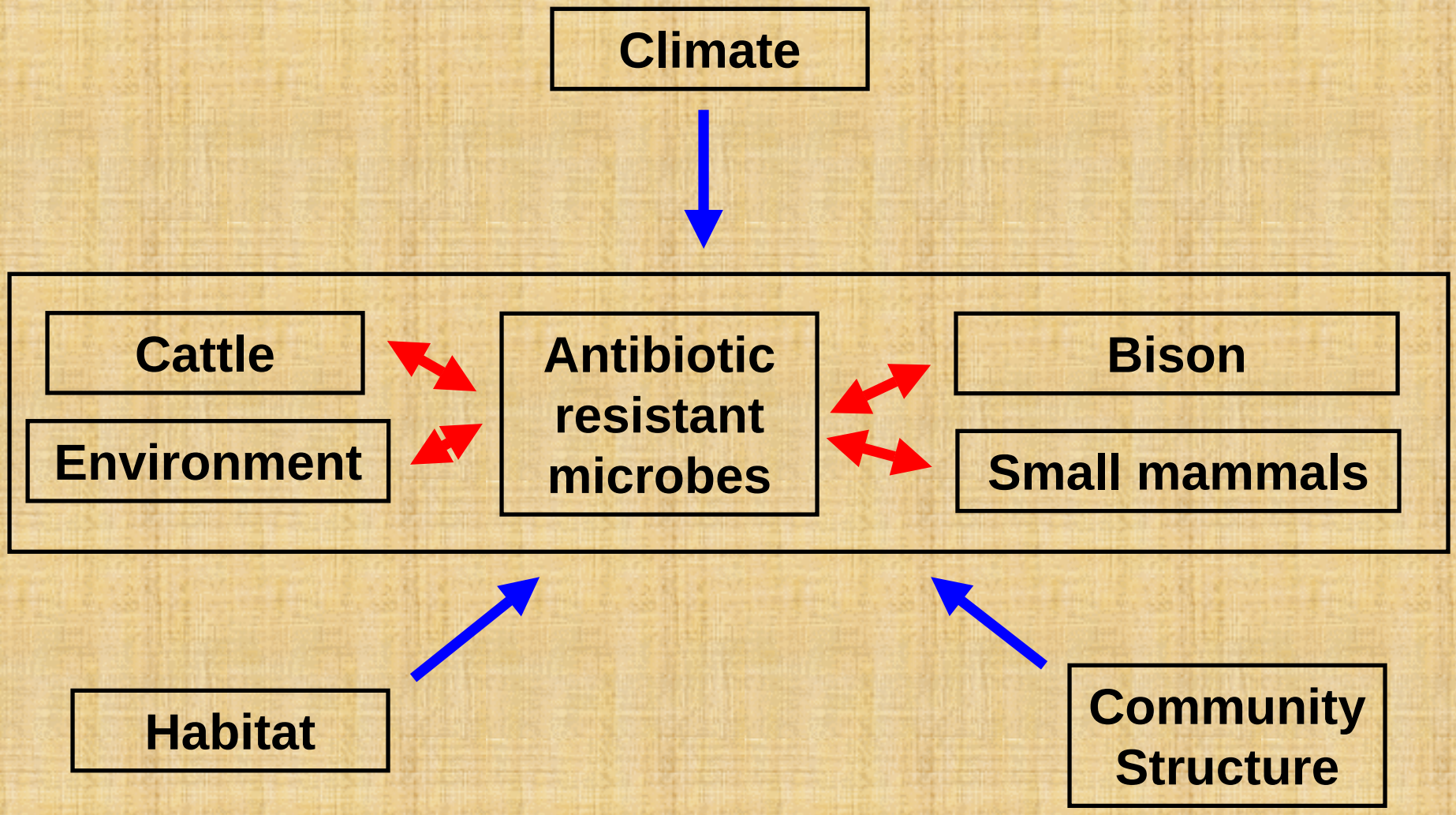
Alyssa Mattox

Future Directions

- How does population density influence relatedness, group structure, and spatial arrangement on KPBS?

How community structure contributes to the spread of antibiotic resistance

Helmut Hirt



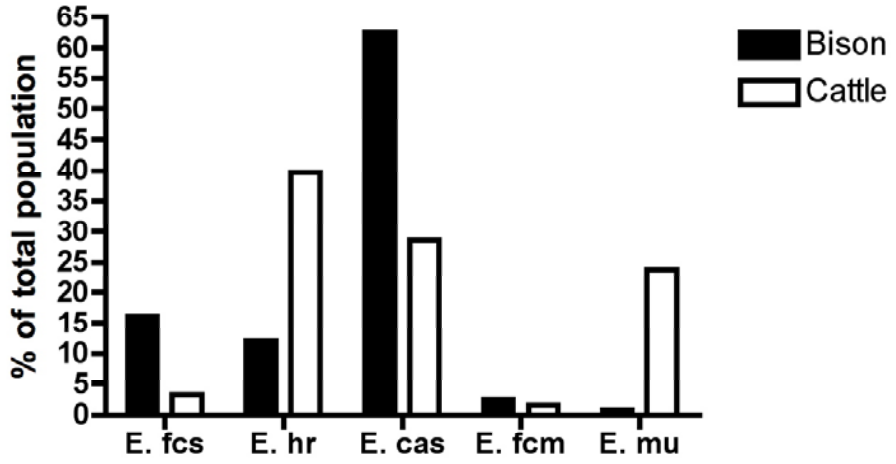
Enterococcal Species Distribution and Antibiotic Resistance

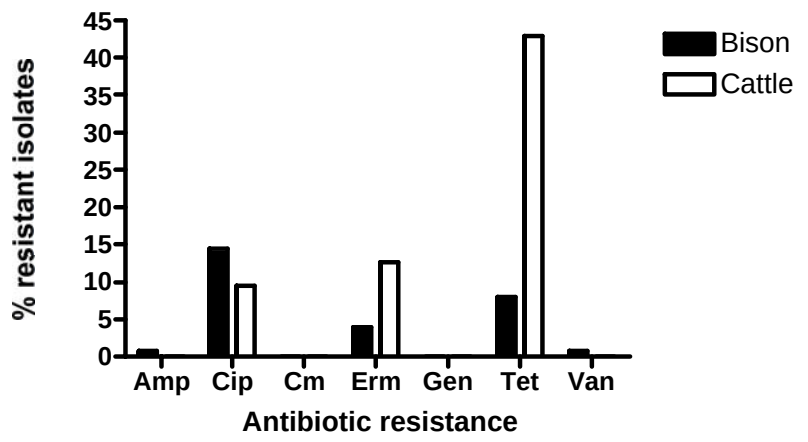
Bison - Cattle

Total isolates:

Bison: 125

Cattle: 63





Species determined by:

ddl
vanC1/C2 } Multiplex-PCR

sodA - sequencing

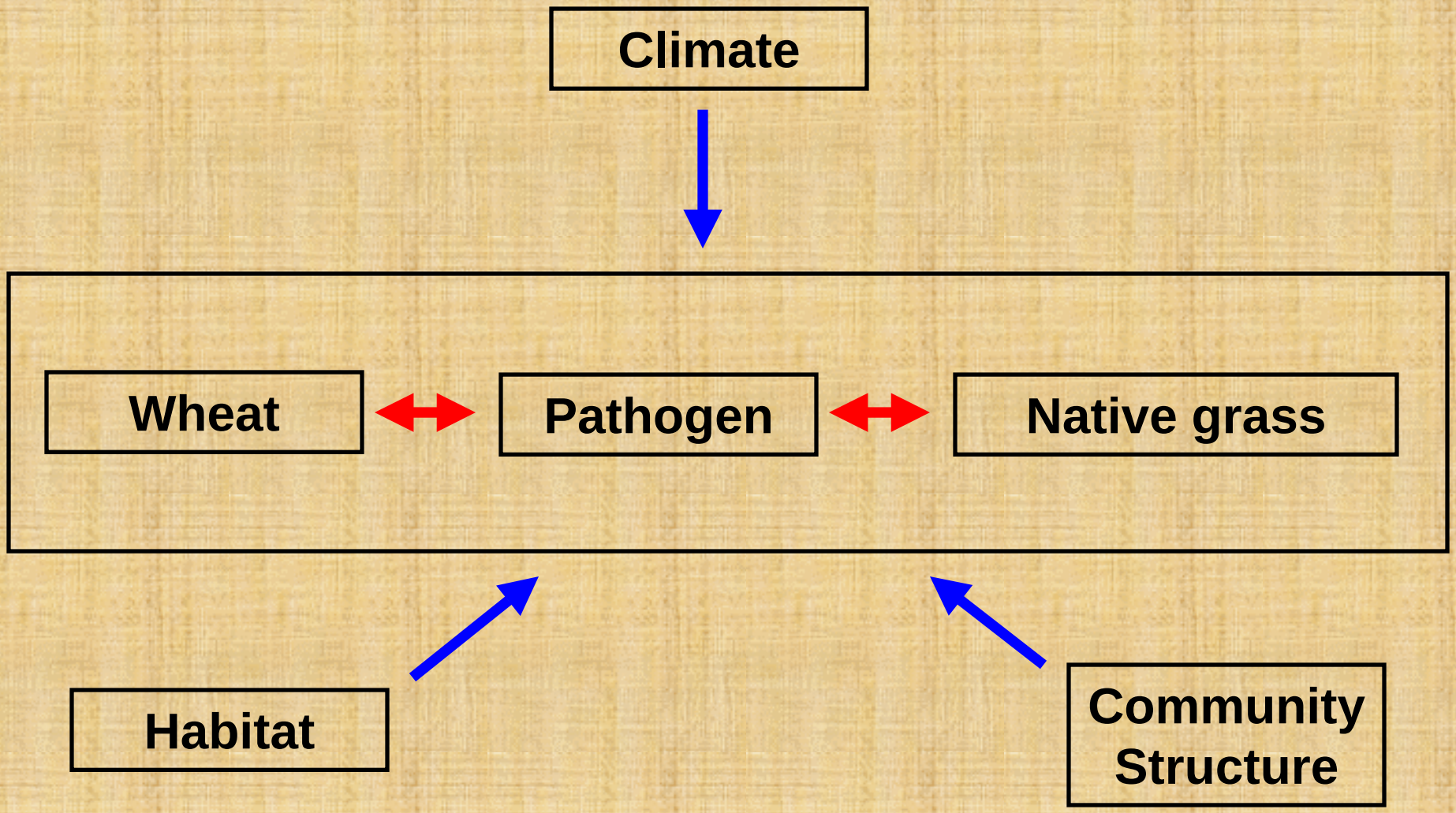
Tetracycline resistance: 8% (bison) - 42.9% (cattle)
Erythromycin resistance: 4% (bison) - 12.7% (cattle)
Ciprofloxacin resistance: 14.4% (bison) - 9.5% (cattle)

Future Directions

- Colonization patterns in individual bison over time
- Sample Konza soil, plants, water for enterococci and antibiotic resistance genes
- Sample small mammals for enterococci and resistance genes

Plant Disease Ecology

Karen Garrett



BYDV infection in native grasses

- First report of BYDV/CYDV in these grass species: percentage infection based on at least 50 plants of each species
- PAV is the most common strain in wheat, but was not recovered from the grasses at Konza Prairie
- In wheat, infection rates for the “tallgrass prairie strains” were high adjacent to prairie but fell off 30 m into wheat fields

Percentage plants infected by virus strain

Grass species	PAV	MAV	RMV	RPV	SGW
Indian grass	0	0	0	0	0
Little bluestem	0	4	2	0	58
Switchgrass	0	31	0	0	4
Big bluestem	0	59	0	0	3

Garrett et al. 2004

Cox et al, in review: Pathogen sharing and connectivity among dominant grasses

Susceptibility of native grasses to take-all

Grass species	Response
Big bluestem	Res
Little bluestem	Res
Indian grass	Res
Switchgrass	Res
Sideoats grama	Sus
Blue grama	Sus
Buffalo grass	Sus

- Native grass seedlings showed nearly complete resistance or susceptibility to the take-all pathogen
- Connectivity analysis based on spatial pattern of host species that share this and other pathogens

Summary

- National Academies Grand Challenge
- Both ecological and evolutionary responses to global change