

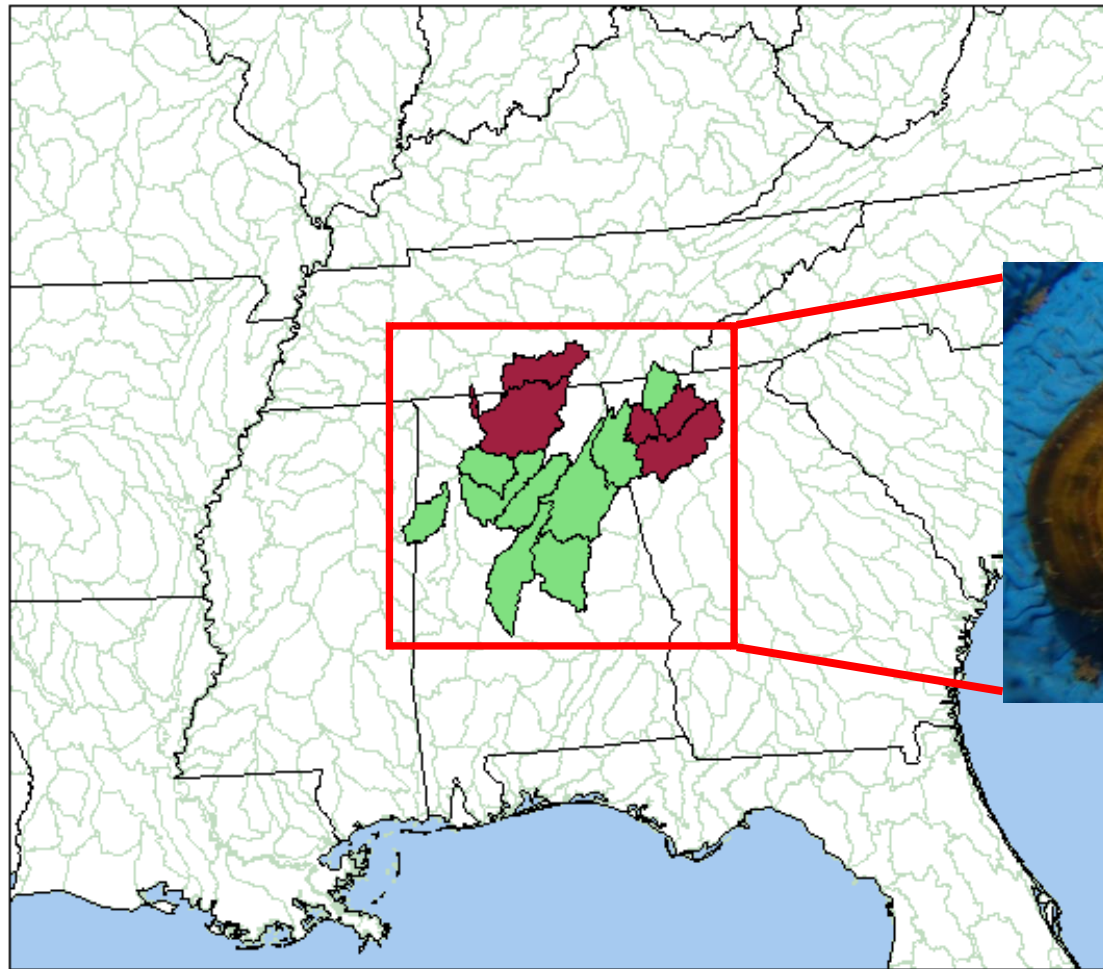
# COMPARISON OF THE DIGESTIVE GLAND MICROBIOME BETWEEN TWO WILD POPULATIONS OF VILLOSA NEBULOSA

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# Alabama rainbow (*Villosa nebulosa*)



*Villosa nebulosa*  
Alabama Rainbow

Map created April 2010

Administrative Boundary  
Hydrological Unit  
Current Distribution  
Extirpated/Possibly Extirpated

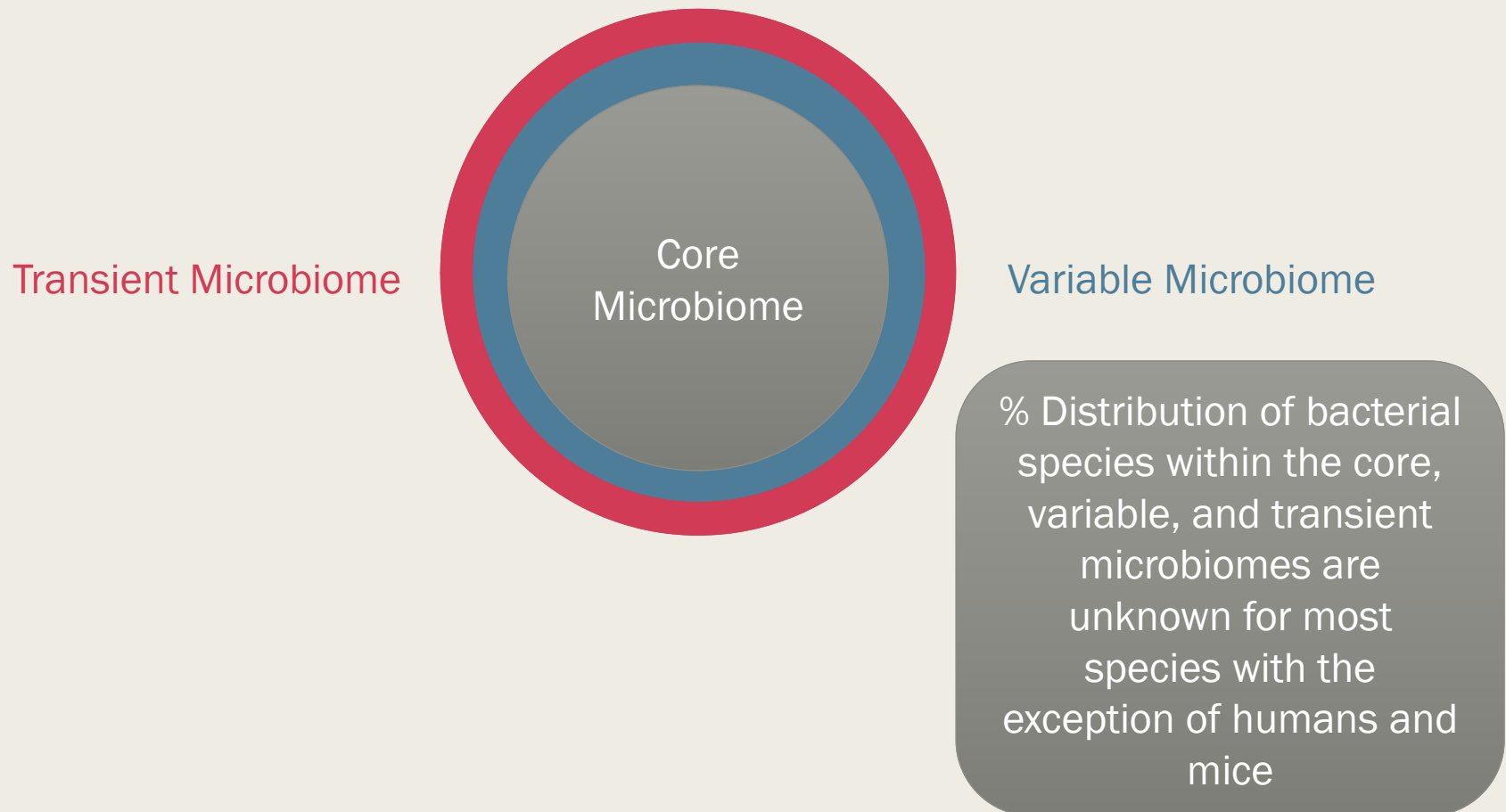
100 0 100 Kilometers

  
NatureServe

# Collaboration between AU & AABC



Core microbiome: the group of bacteria that is common in all individuals from a species





# Host-microbiome interactions

- Hologenome concept of evolution
  - *Symbionts are important in host health*
  - *Holobiont: the host and all of its' symbiotic microbes*
  - *Hologenome: the host and microbial genomes of the holobiont*
- Microbiome in conservation efforts of aquatic invertebrates (Bahrndorff et al. 2016)
  - *Microbiome of culture animals  $\neq$  microbiome of wild animals*
    - Fitness becomes affected in mussels held in captivity



# Objectives

- 1) *To compare the digestive gland microbiome between wild and cultured Alabama rainbows, including two geographically distinct populations.*
- 2) *To determine the contribution of environmental microbes to the core microbiome of Alabama rainbows.*

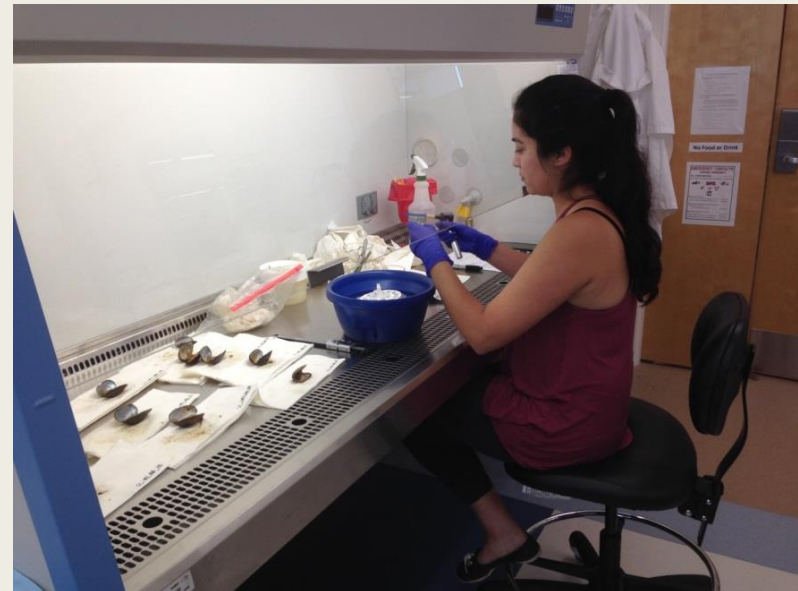
# Materials and Methods

- Wild Alabama rainbows
  - 9 individuals from Shoal Creek
  - 2 individuals from Flannigan Creek
- Cultured Alabama rainbows from AABC
  - 5 individuals derived from Shoal Creek populations
  - 5 individuals derived from Flannigan Creek populations
- Water and sediment samples were also collected at these sites.



# Materials and Methods

- Samples: digestive gland, water, and sediments
- DNA extraction using standard protocols
- The pool of 16S rRNA genes present in each sample were sequenced using MiSeq Illumina.
- Sequences were ascribed to Operational Taxonomic Units (OTUs): proxy for bacterial species at 97% sequence similarity based on information deposited in Greengenes & GenBank.
- Data analysis
  - MOTHUR
  - PRIMER 6





# Results

	Sequences	OTUs	Good's coverage	Shannon evenness
Mussels	842,236	4,865	0.98	0.452
Water	423,430	5,391	0.94	0.632
Sediment	517,488	16,044	0.93	0.856

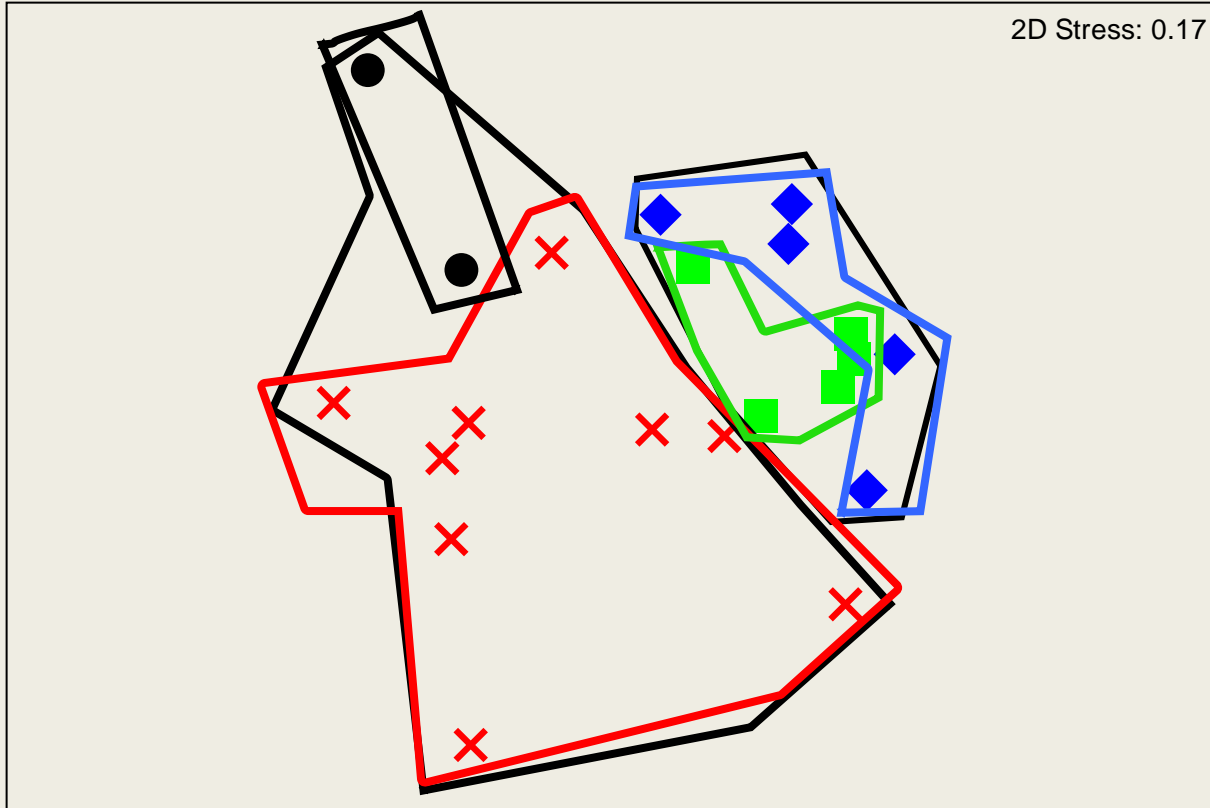
# Cultured vs. wild Alabama rainbows

Standardise Samples by Total  
Resemblance: S17 Bray Curtis similarity

2D Stress: 0.17

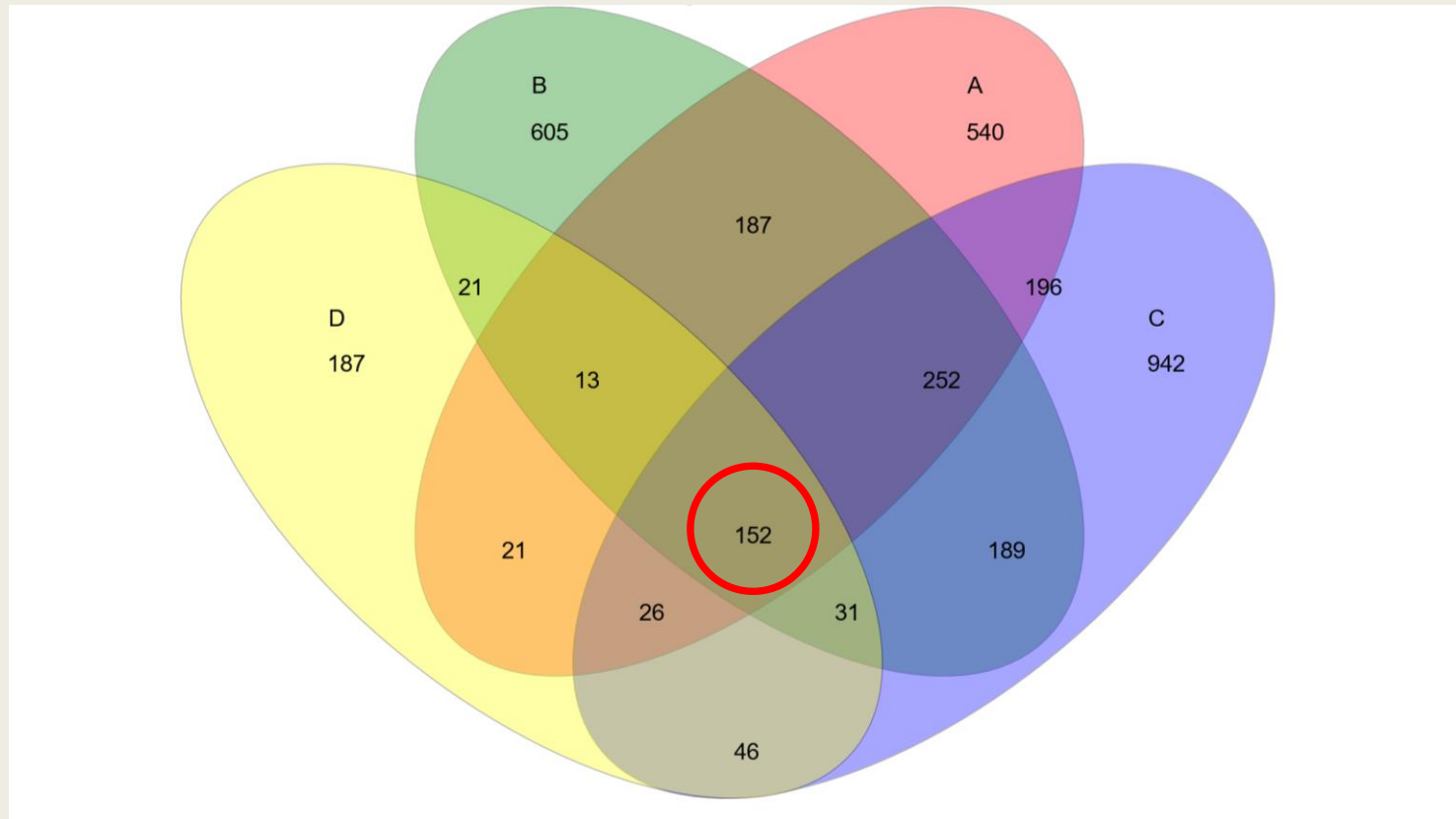
*Group*

- Cultured - Shoal Creek
- ◆ Cultured - Flannigan Creek
- ✕ Wild - Shoal Creek
- Wild - Flannigan Creek





# Core microbiome between mussel groups

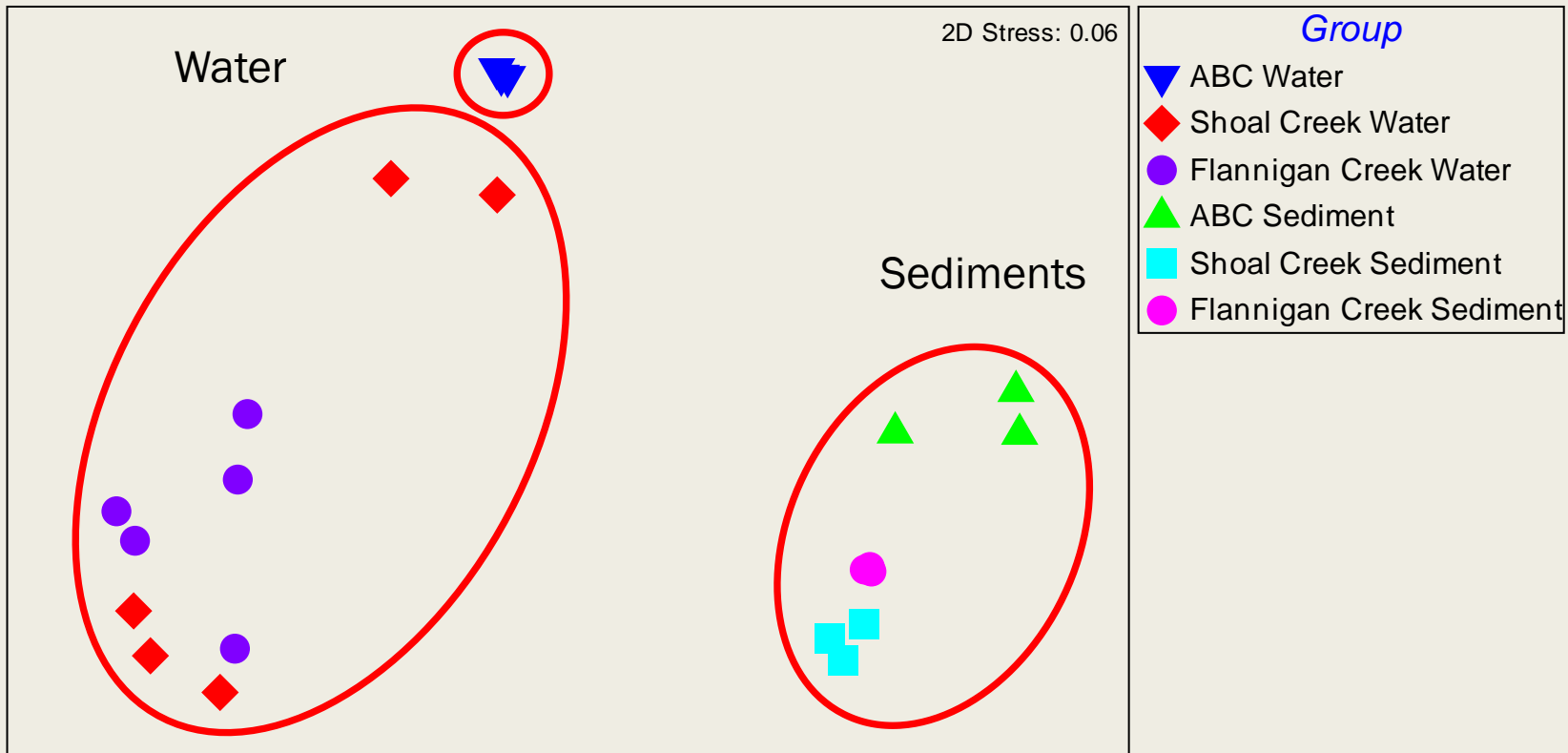


A = Cultured Shoal Creek  
B = Cultured Flannigan Creek  
C = Wild Shoal Creek  
D = Wild Flannigan Creek



# Creeks vs. AABC environmental factors

Standardise Samples by Total Resemblance: S17 Bray Curtis similarity



# Conclusions

- Microbial communities between cultured and wild mussels were significantly different.
- Rearing environment exerted a stronger effect than population.
- A core microbiome exists within the digestive gland of *V. nebulosa*.
- Microbial communities in sediments from all three locations were not statistically different.
- Microbial communities in water samples were less diverse than sediment communities.

# Acknowledgements

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- AABC



**AUBURN**

SCHOOL OF FISHERIES,  
AQUACULTURE AND AQUATIC SCIENCES