

# Genomic approaches to evaluate population structure of Mississippi River Basin Silver Carp

Michael Sovic, PhD  
Freedom Genomics LLC  
Email: [freegenllc@gmail.com](mailto:freegenllc@gmail.com)

Guoqing Lu, PhD  
University of Nebraska at Omaha  
Email: [glu3@mail.unomaha.edu](mailto:glu3@mail.unomaha.edu)

 @MikeSovicOSU

 Mike Sovic

 The Data Point 

# Outline

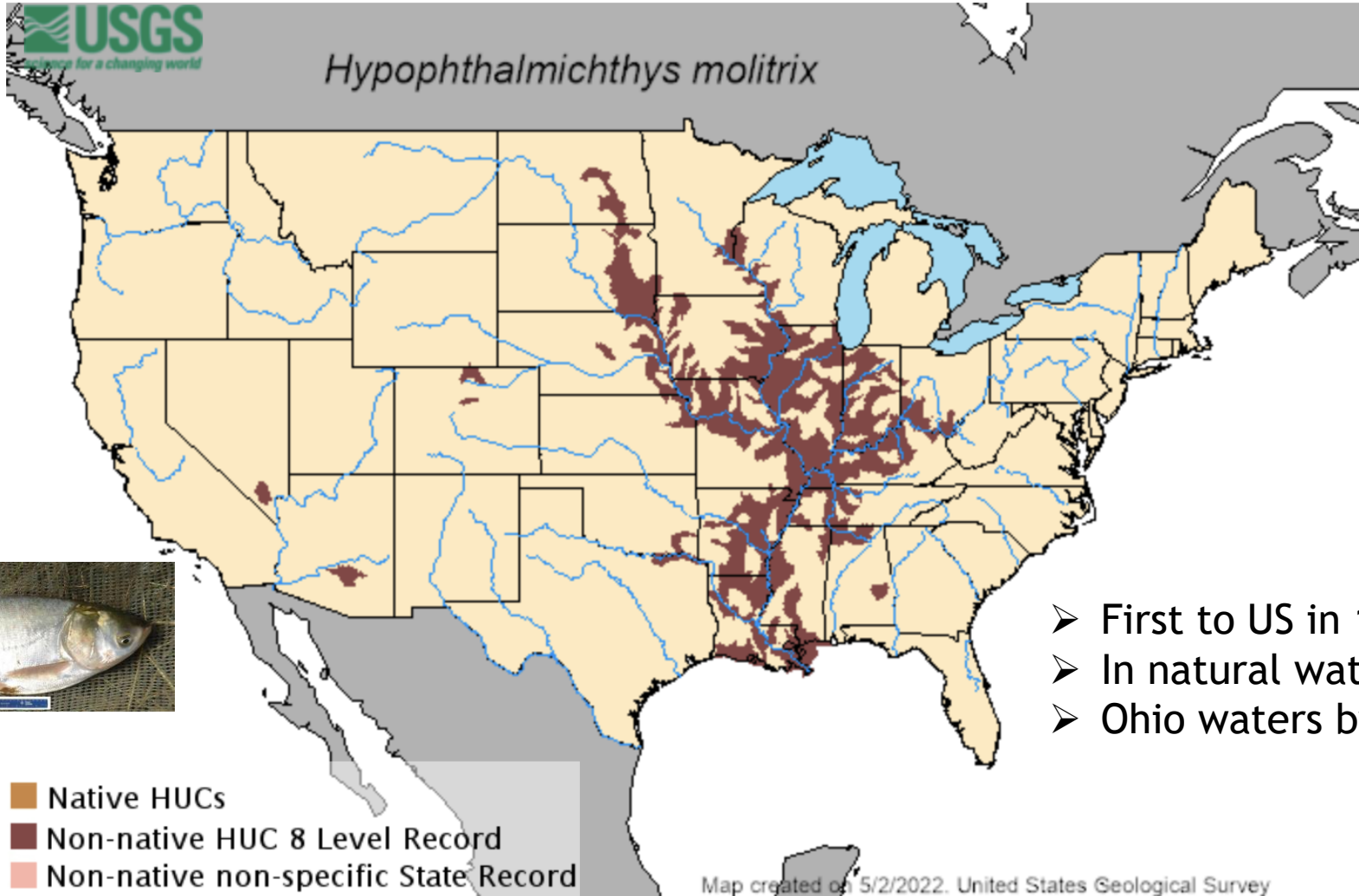
- ▶ Project Overview
- ▶ Population genetics/genomics for identifying population structure
  - ▶ How does it work?
  - ▶ Influencing Factors (pop size, time, gene flow, hybridization)
- ▶ 3 Project Phases
  - ▶ ID of genetic markers
  - ▶ Preliminary test of population structure
  - ▶ Full analysis

# Outline

- ▶ **Project Overview**
- ▶ Population genetics/genomics for identifying population structure
  - ▶ How does it work?
  - ▶ Influencing Factors (pop size, time, gene flow, hybridization)
- ▶ **3 Project Phases**
  - ▶ ID of genetic markers
  - ▶ Preliminary test of population structure
  - ▶ Full analysis



## *Hypophthalmichthys molitrix*



- Native HUCs
- Non-native HUC 8 Level Record
- Non-native non-specific State Record

Map created on 5/2/2022. United States Geological Survey

- First to US in 1970's
- In natural waters by 1980
- Ohio waters by 2012



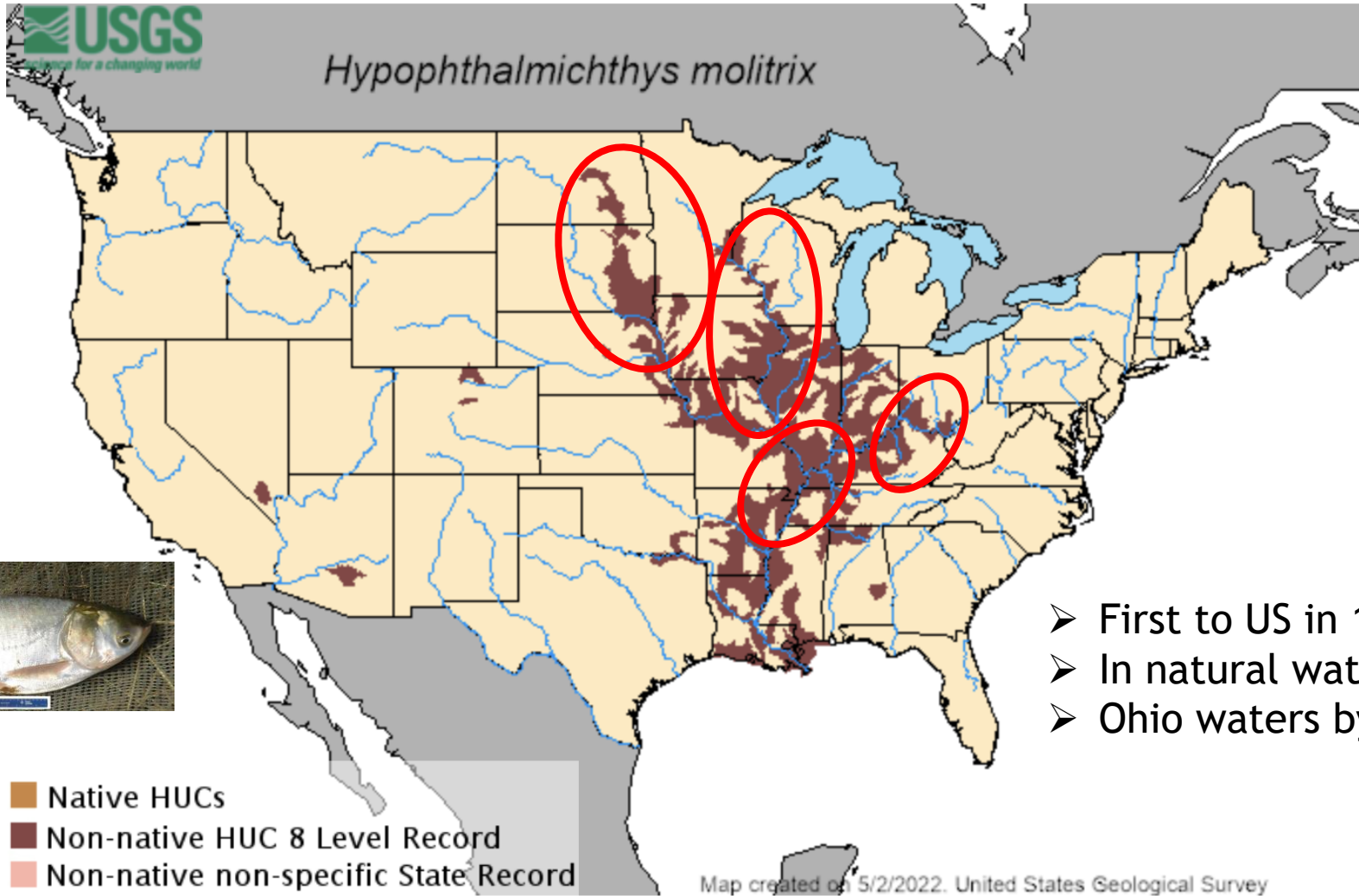
# Mississippi River Basin Panel on Aquatic Nuisance Species (MRBP)

*Question:* Can population structure (inferred through genetics) give insight into spawning locations for targeted management?





# *Hypophthalmichthys molitrix*



- Native HUCs
- Non-native HUC 8 Level Record
- Non-native non-specific State Record

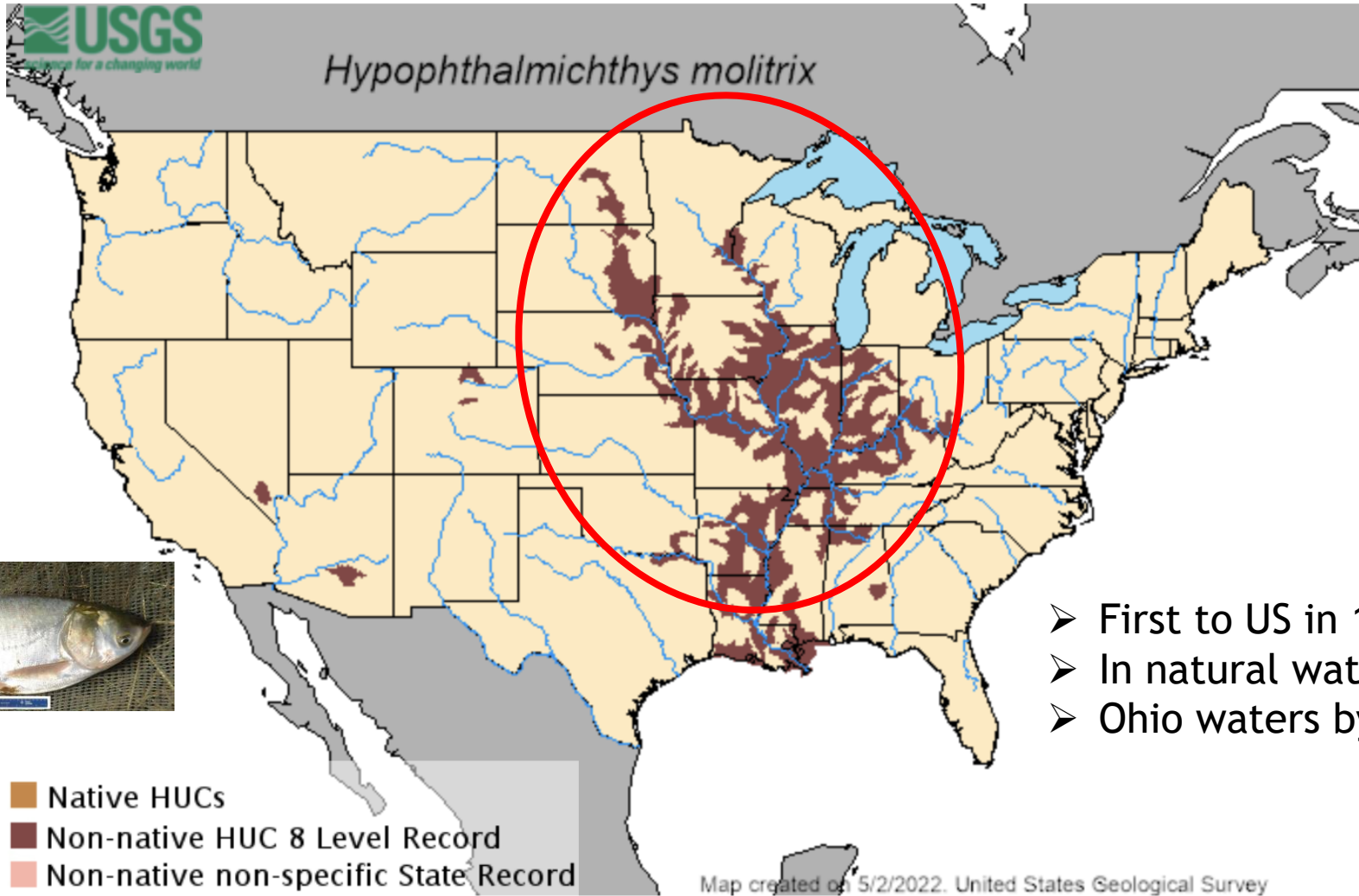
- First to US in 1970's
- In natural waters by 1980
- Ohio waters by 2012

Map created on 5/2/2022. United States Geological Survey





# *Hypophthalmichthys molitrix*



- Native HUCs
- Non-native HUC 8 Level Record
- Non-native non-specific State Record

- First to US in 1970's
- In natural waters by 1980
- Ohio waters by 2012

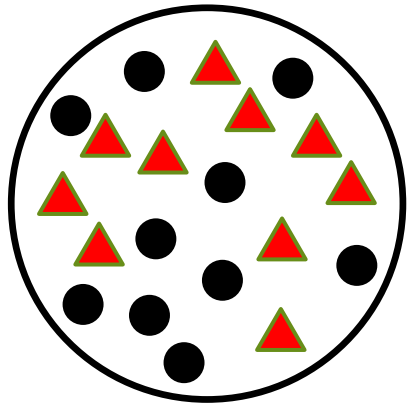


# Outline

- ▶ Project Overview
- ▶ Population genetics/genomics for identifying population structure
  - ▶ How does it work?
  - ▶ Influencing Factors (pop size, time, gene flow, hybridization)
- ▶ 3 Project Phases
  - ▶ ID of genetic markers
  - ▶ Preliminary test of population structure
  - ▶ Full analysis



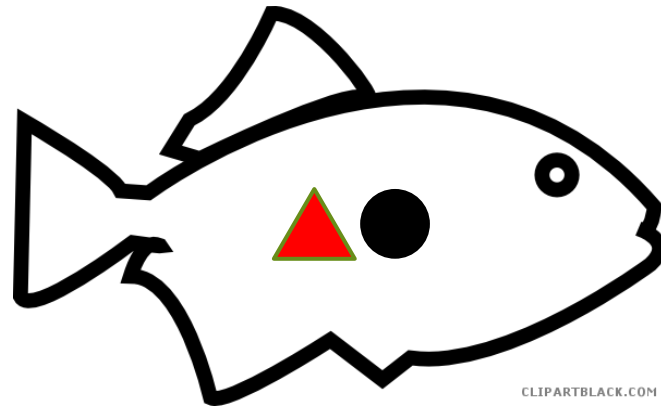
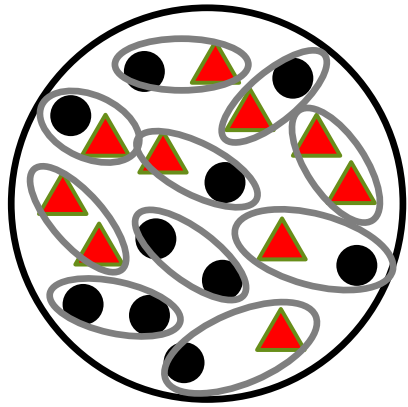
# One Genetic Marker With 2 Alleles (T/A)



Single pond (population)  
with 10 fish - looking at  
one genetic marker (20  
alleles)

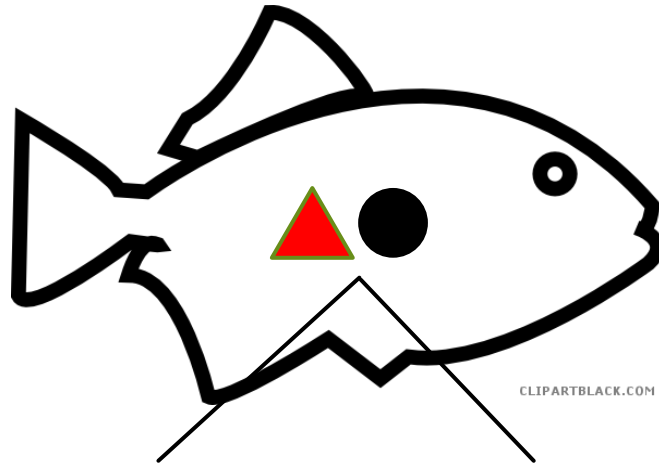
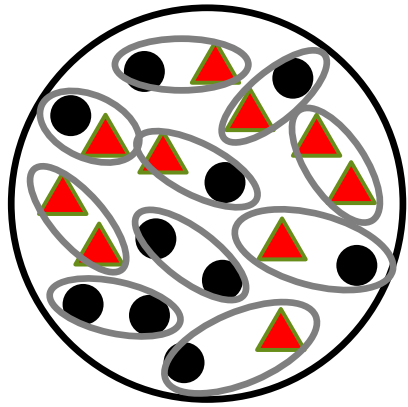
# One Genetic Marker With 2 Alleles (T/A)

Alleles actually occur  
within diploid  
individuals



# One Genetic Marker With 2 Alleles (T/A)

Alleles actually occur  
within diploid  
individuals

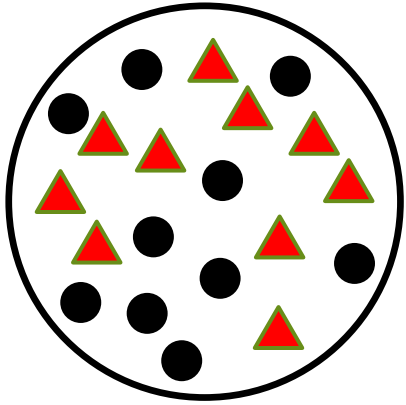


ATACGACCAGGGTATTTAC.....A.....AGGACCCCATTTACAAACCAT  
ATACGACCAGGGTATTTAC.....T.....AGGACCCCATTTACAAACCAT

~800 million bases (Silver Carp)

# One Genetic Marker With 2 Alleles (T/A)

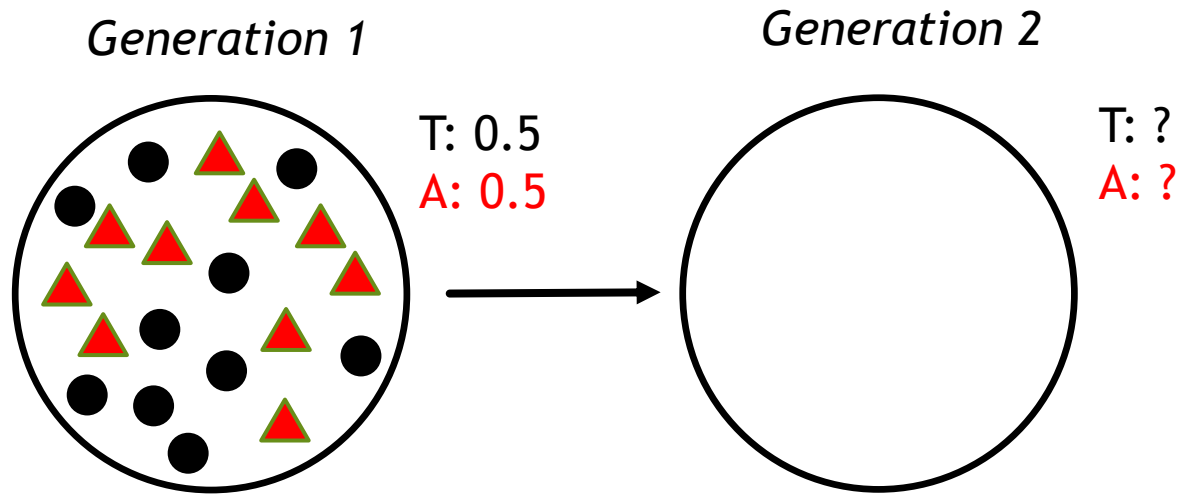
Generation 1



T: 0.5  
A: 0.5

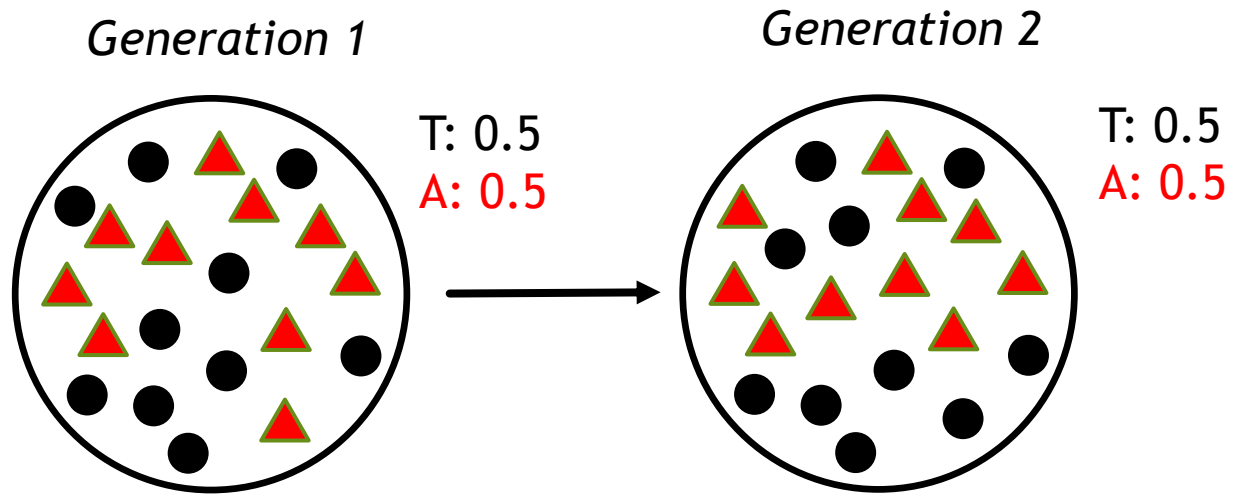
Single pond with 10 fish  
(20 alleles)

# One Genetic Marker With 2 Alleles (T/A)



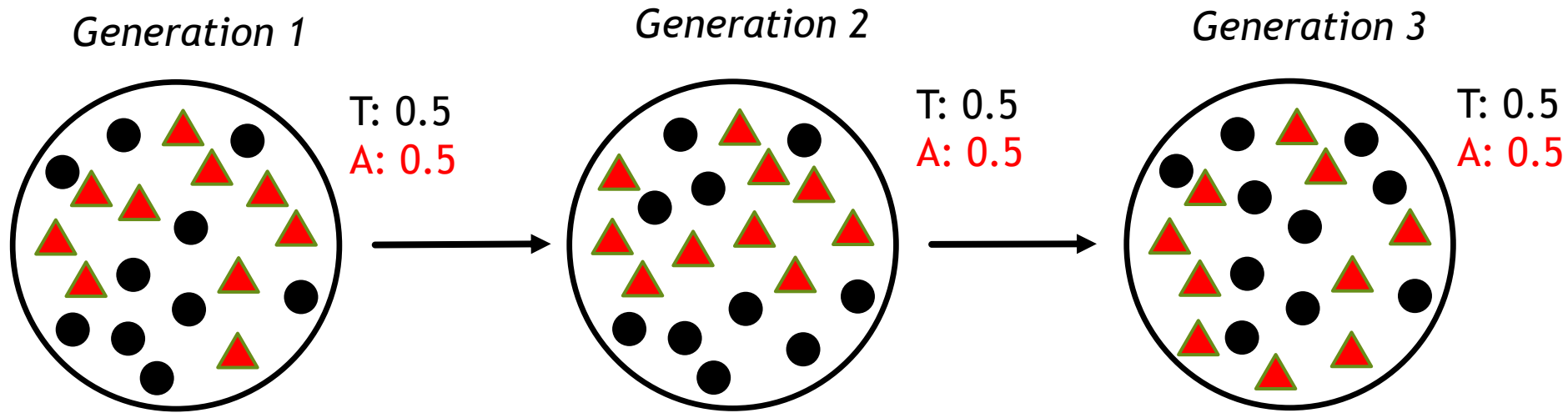
***Expectation***

# One Genetic Marker With 2 Alleles (T/A)



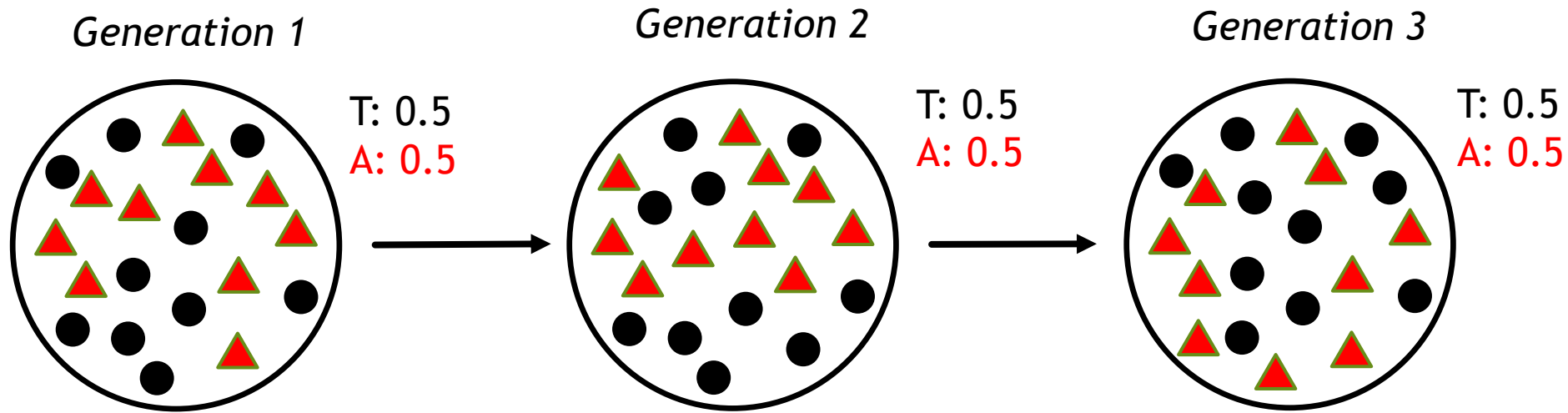
***Expectation***

# One Genetic Marker With 2 Alleles (T/A)



***Expectation***

# One Genetic Marker With 2 Alleles (T/A)



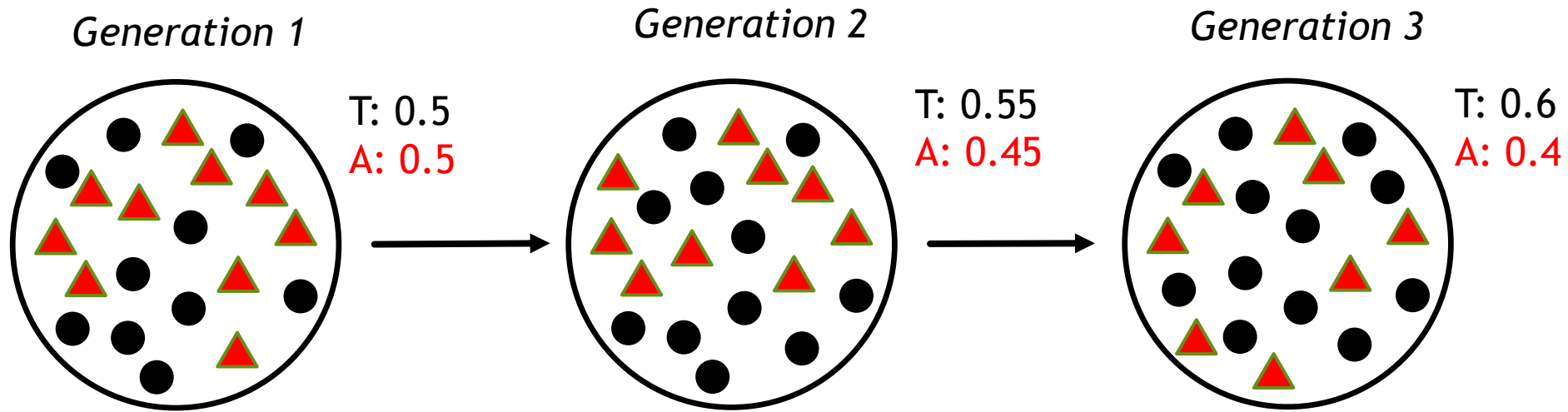
**Stochastic/Random Process!!**

***Expectation***





# One Genetic Marker With 2 Alleles (T/A)

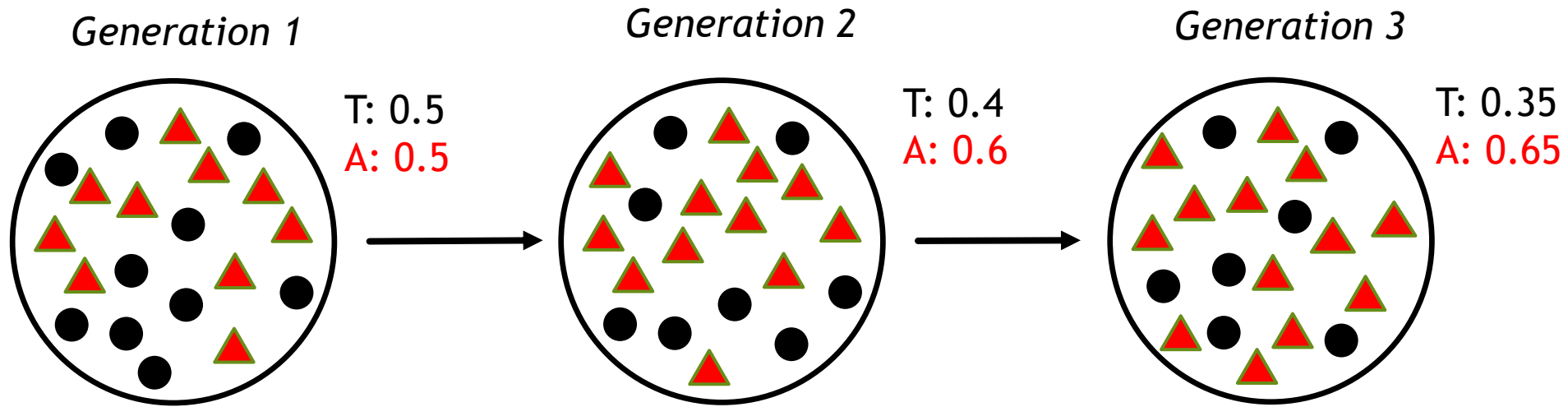


**Genetic Drift**

***Hypothetical Outcome #1***



# One Genetic Marker With 2 Alleles (T/A)

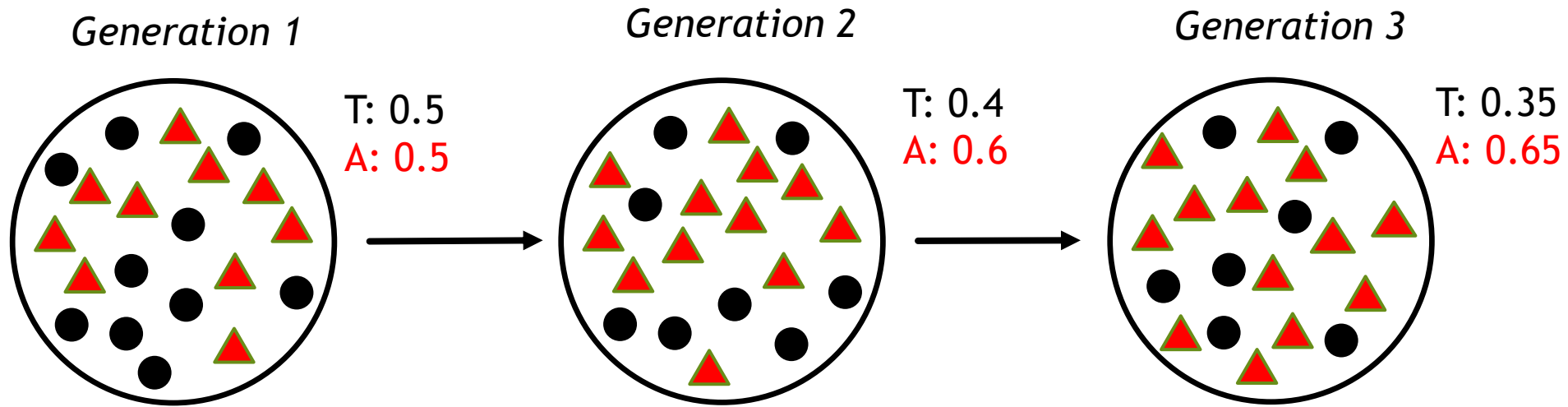


**Genetic Drift**

***Hypothetical Outcome #2***



# One Genetic Marker With 2 Alleles (T/A)



Process happens independently every generation at millions of markers in the genome.



# Possible Scenarios

T: 0.5  
A: 0.5

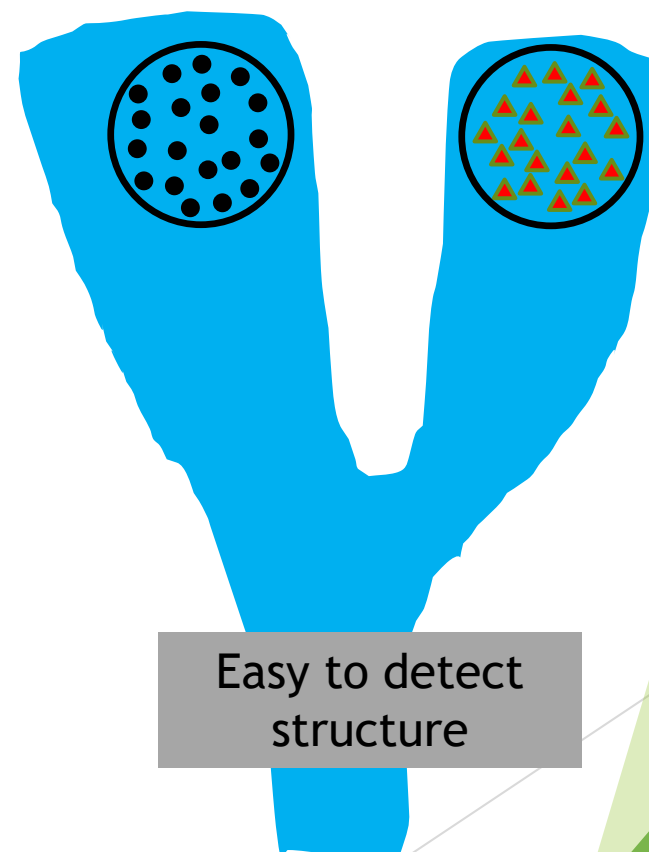
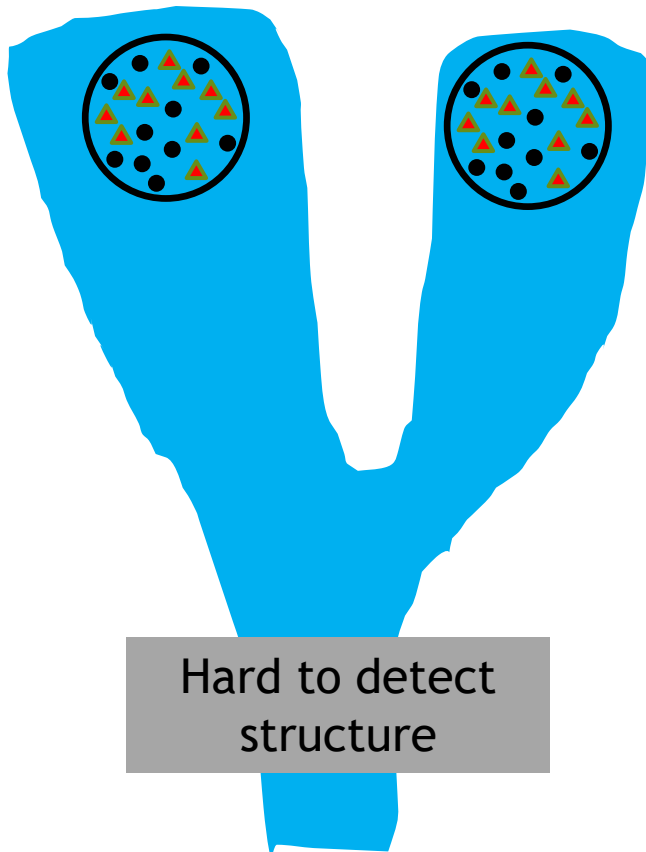
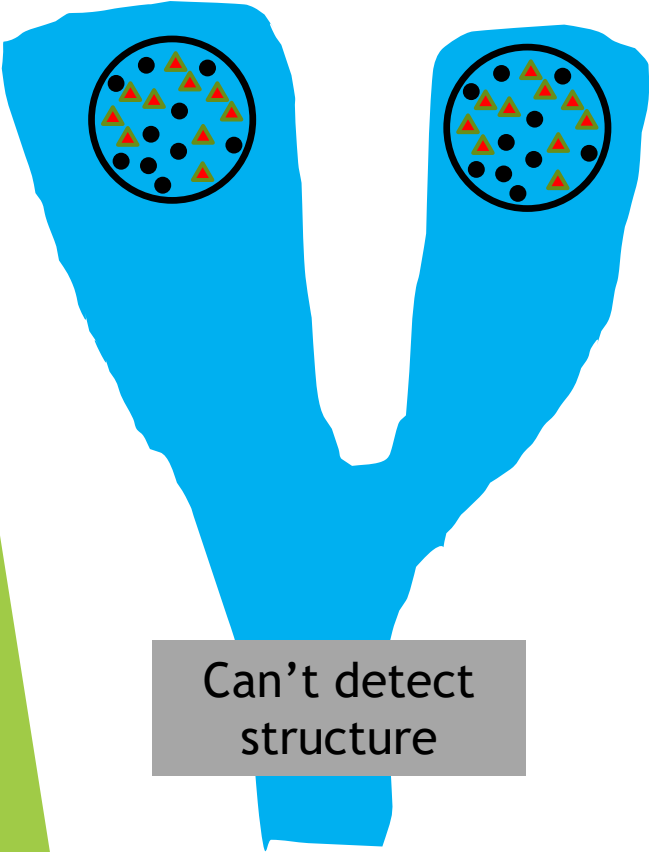
T: 0.5  
A: 0.5

T: 0.52  
A: 0.48

T: 0.49  
A: 0.51

T: 1  
A: 0

T: 0  
A: 1





# Factors That Affect Differentiation

<50 generations?

↑ Time ~ ↑ Differentiation

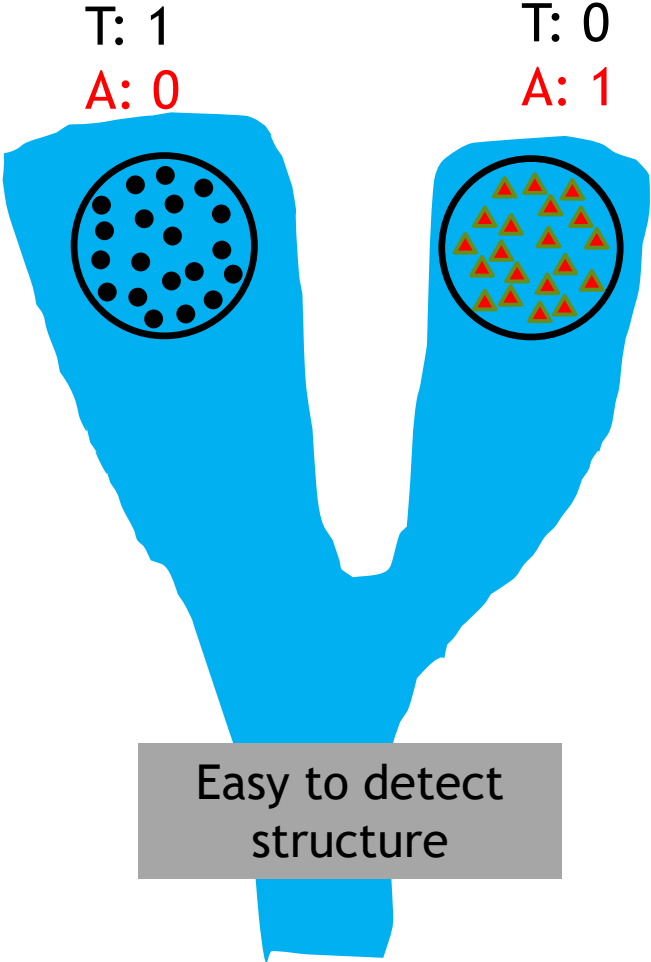
Fairly high?

↓ Migration ~ ↑ Differentiation

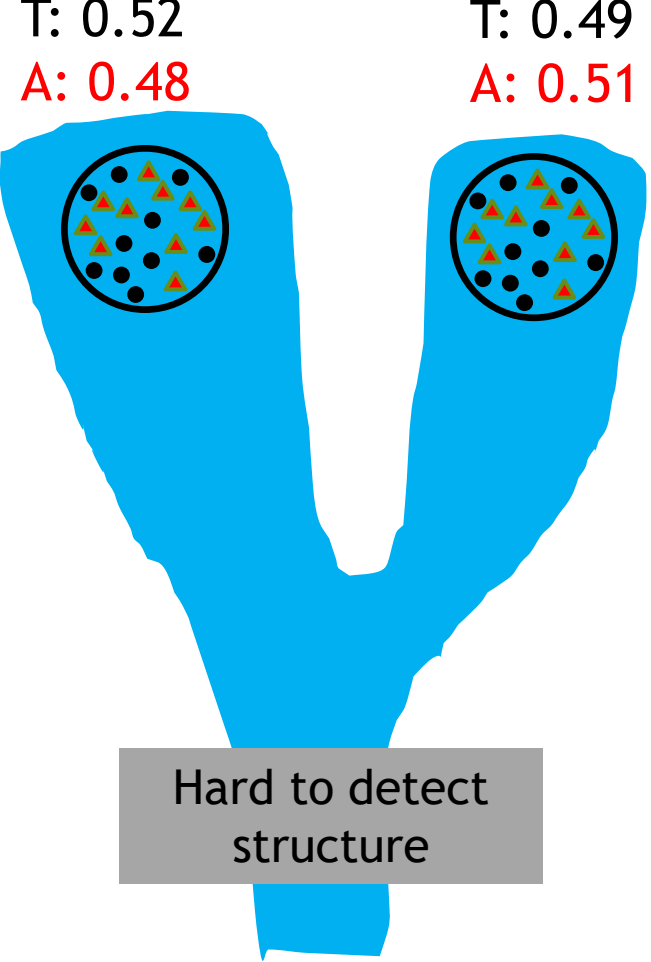
????

↓ Pop Size ~ ↑ Differentiation

# Best-Case Scenario



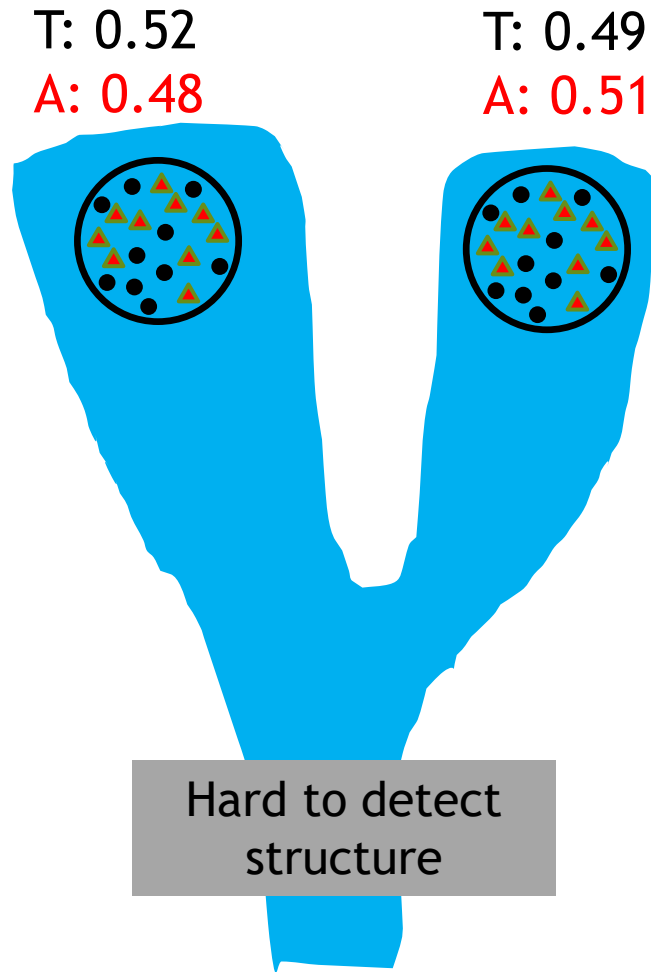
# Likely Scenario



**GENETICS**  
**VS**  
**GENOMICS**

# Likely Scenario

Genomic methods allow us to generate data from large numbers of genetic markers (1000's, potentially up to millions in some cases).



# Genomic Method: RadSeq

- Allows us to consistently sample the same genomic positions from multiple individuals (without sequencing the entire genome)
- Customizable with respect to the number of genetic markers analyzed
- Tradeoff between number needed for inference and sequencing cost.

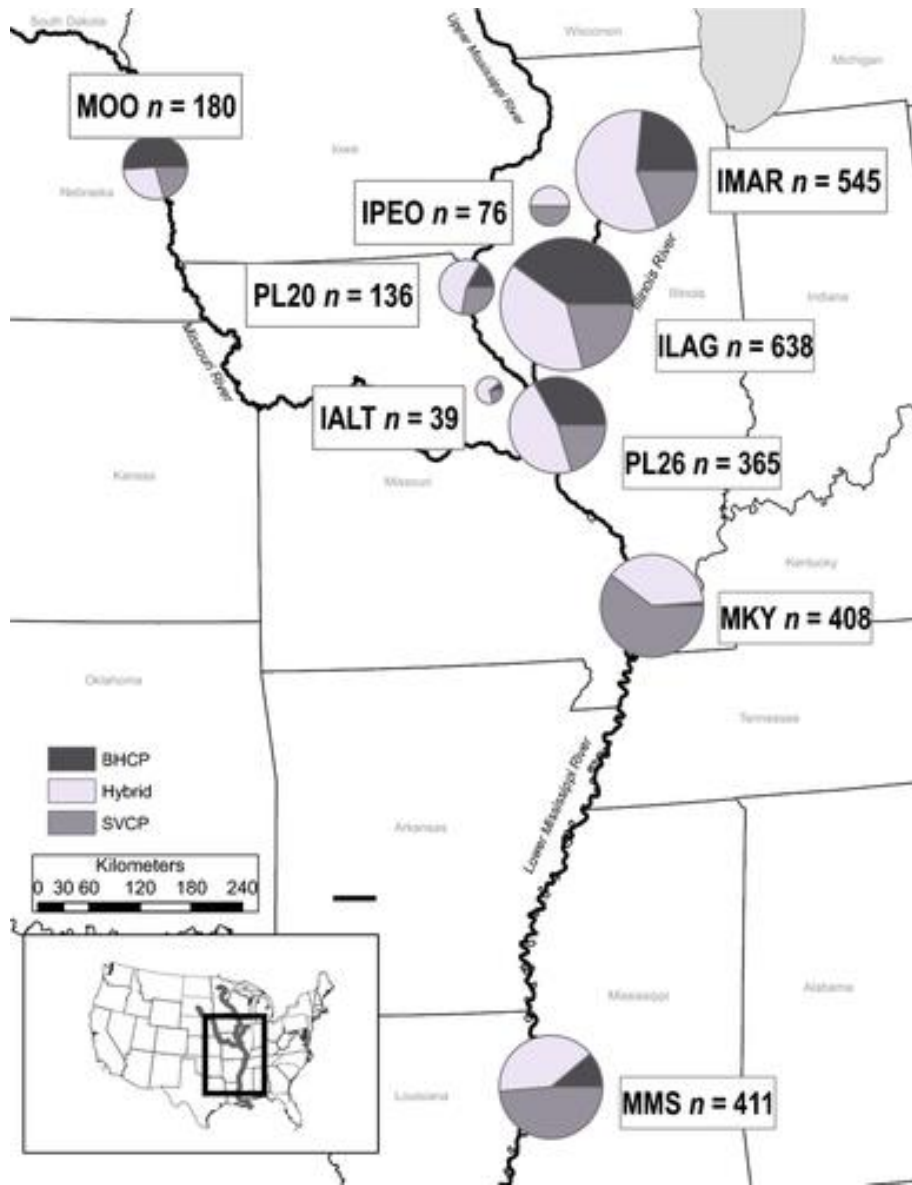


# Outline

- ▶ Project Overview
- ▶ Population genetics/genomics for identifying population structure
  - ▶ How does it work?
  - ▶ Influencing Factors (pop size, time, gene flow, hybridization)
- ▶ **3 Project Phases**
  - ▶ ID of genetic markers
  - ▶ Preliminary test of population structure
  - ▶ Full analysis

# Project Plan

| Phases  | Completion Date    |
|---|--------------------|
| 1. Develop database of informative genomic markers/protocol to generate data. (N ~10)   | In Process         |
| 2. Assess population structure of silver carp at 3 geographically distant locations. (N ~100)   | September 30, 2022 |
| 3. If population structure is identified in Phase 2, perform comprehensive analysis of silver carp population genetic structure throughout the Mississippi River Basin by including all populations of interest. (N >300) | June 30, 2023      |



## Phases 1,2 Sampling

- ILAG - Illinois River LaGrange Reach 20
- IMAR - Illinois River Marseilles 20
- MKY - Mississippi River (near Laketon, KY)
- PL20 - Pool 20 of Mississippi River (near Keokuk, IA) 17
- PL26 - Pool 26 of Mississippi River (near Alton, IL) 20
- MOO - Missouri River (near Omaha, NE) 20

Lamer et al. 2010. North American Journal of Fisheries Management 30:1452-1461.

# Phase 3 and Beyond

## WISH LIST of Collection locations:

- Invasion Fronts
  - Middle Ohio - Markland Pool
  - Tennessee River above Pickwick
  - Cheetam Reservoir on Cumberland River
  - MS River Pool 8 - Duane has samples and collecting more
  - MO River below Gavins Point dam
  - IL River Dresden Island pool
  - White River - north end, lowhead dam
  - AR River - Little Rock area
  - Red River - below Texoma
  - Tenn-Tom waterway - enough fish?
- Established Areas
  - 1-3 more sites Ohio River
  - Kentucky Lake
  - Barkley Lake
  - MS River above Lock and Dam 19, below pool 8 (all pools combined)
  - MS River between pools 26 and 19
  - MS River St. Louis area
  - MO River below mouth of Platte
  - MO River below KS River
  - Little Sioux River
  - MO River, Jefferson City - Osage stretch
  - IL River - Peoria Pool
  - IL River - near mouth of IL River
  - Atchafalaya River
  - Lower MS River - 2 more sites

# More Information

Chris Steffen

Aquatic Nuisance Species Coordinator

Kansas Department of Wildlife and Parks

o: (620) 342-0658 | [ksoutdoors.com](http://ksoutdoors.com)

c: (785) 230-2033 | [ProtectKSWaters.org](http://ProtectKSWaters.org)

Email: [Chris.Steffen@KS.GOV](mailto:Chris.Steffen@KS.GOV)



Guoqing Lu, PhD

University of Nebraska at Omaha

Email: [glu3@mail.unomaha.edu](mailto:glu3@mail.unomaha.edu)

Michael Sovic, PhD

Freedom Genomics LLC

Email: [freegenllc@gmail.com](mailto:freegenllc@gmail.com)

Stephen F. Spear, PhD

U.S. Geological Survey

Upper Midwest Environmental Sciences Center

Email: [sfspear@usgs.gov](mailto:sfspear@usgs.gov)