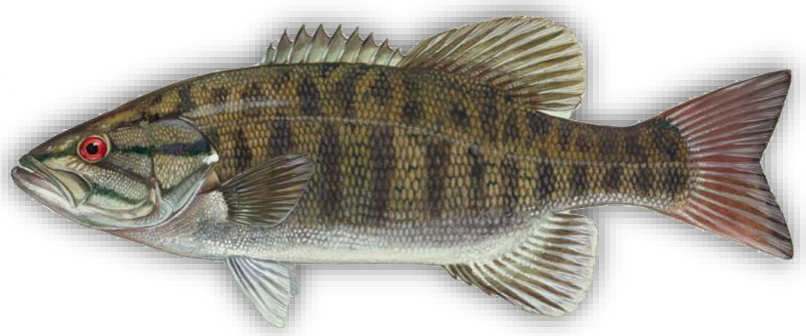
Comparing genetic and direct measures of smallmouth bass dispersal.

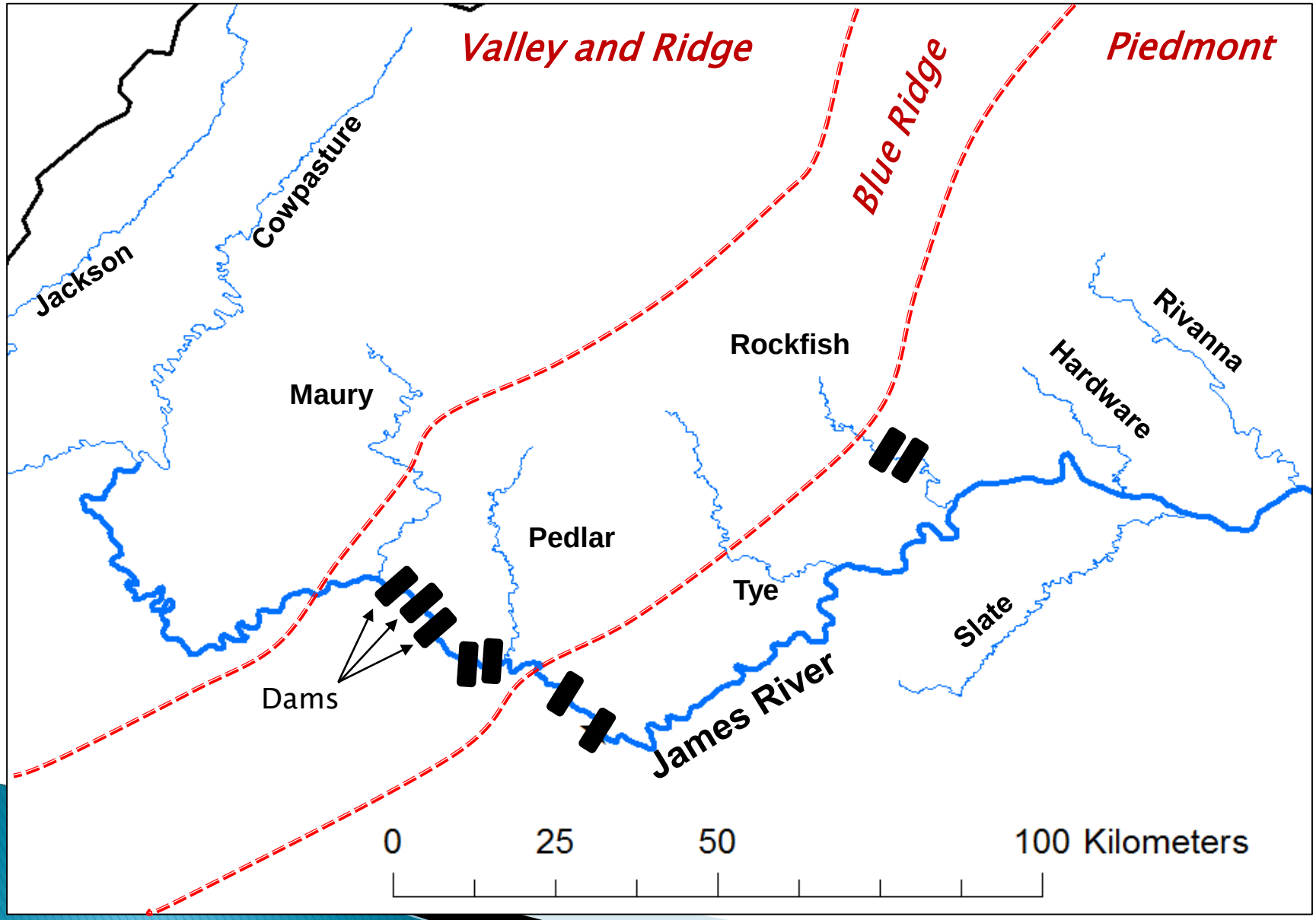


Robert Humston, Eric Hallerman, Garrett Muckleroy, Juli Sorenson, Scott Smith

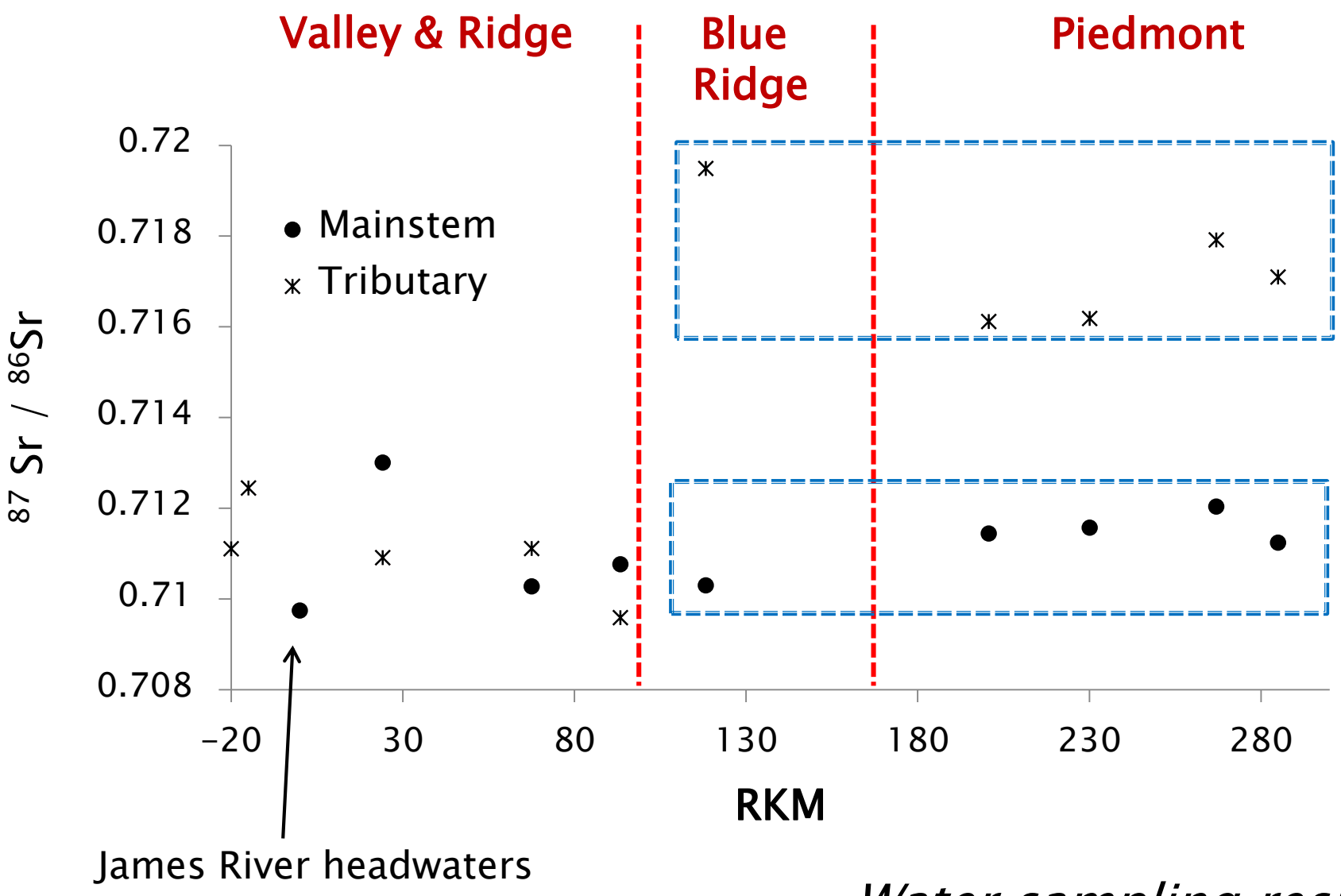
Research Questions and Context

- Non-native in Virginia, introduced in 1800's, now a flagship recreational fishery.
  - Recruitment exchange between mainstem / tributary habitats
- Expansion of SMB range with warming climate
  - Understanding dispersal / movement ecology

Study Methods

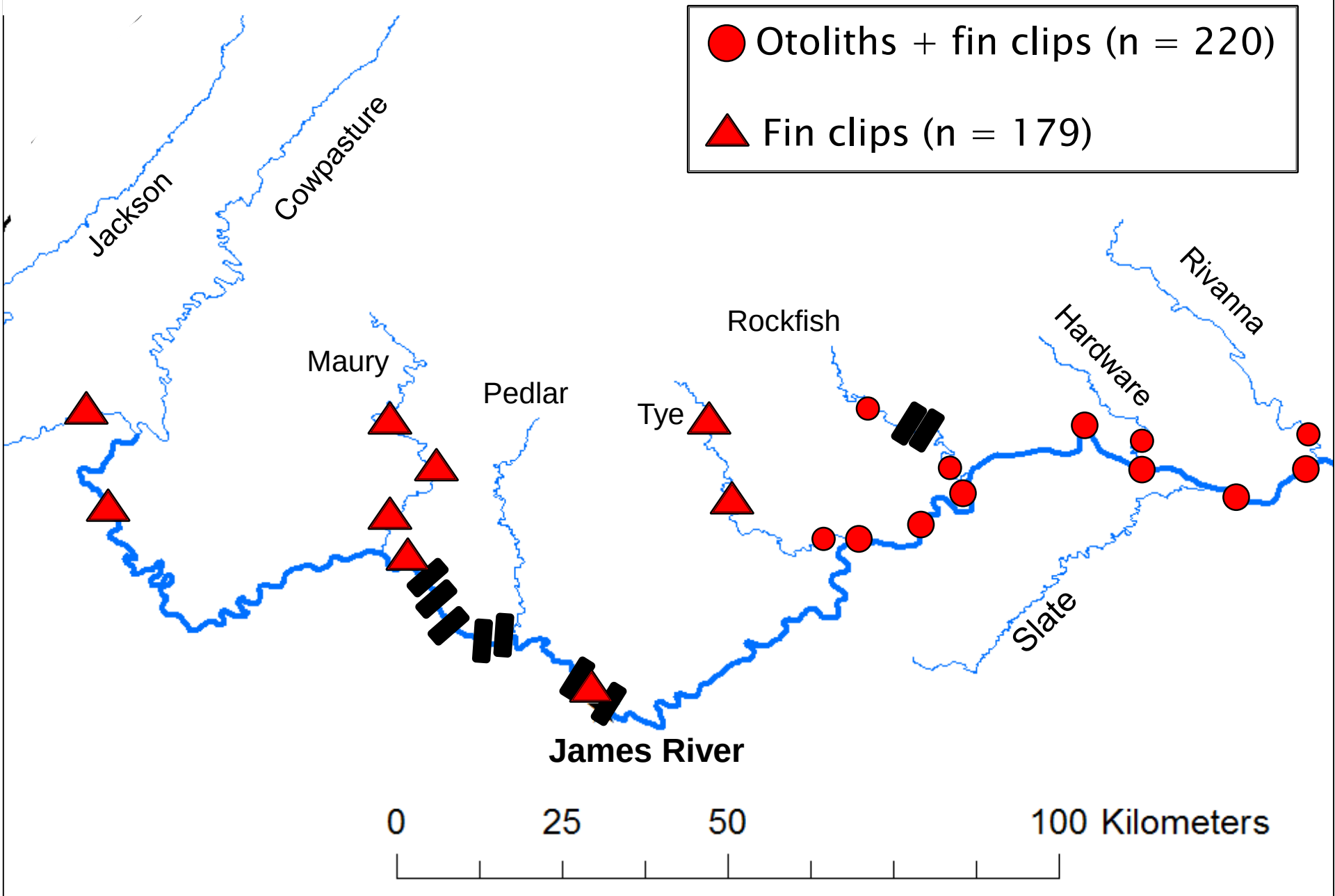


Regional Geology and Geochemistry



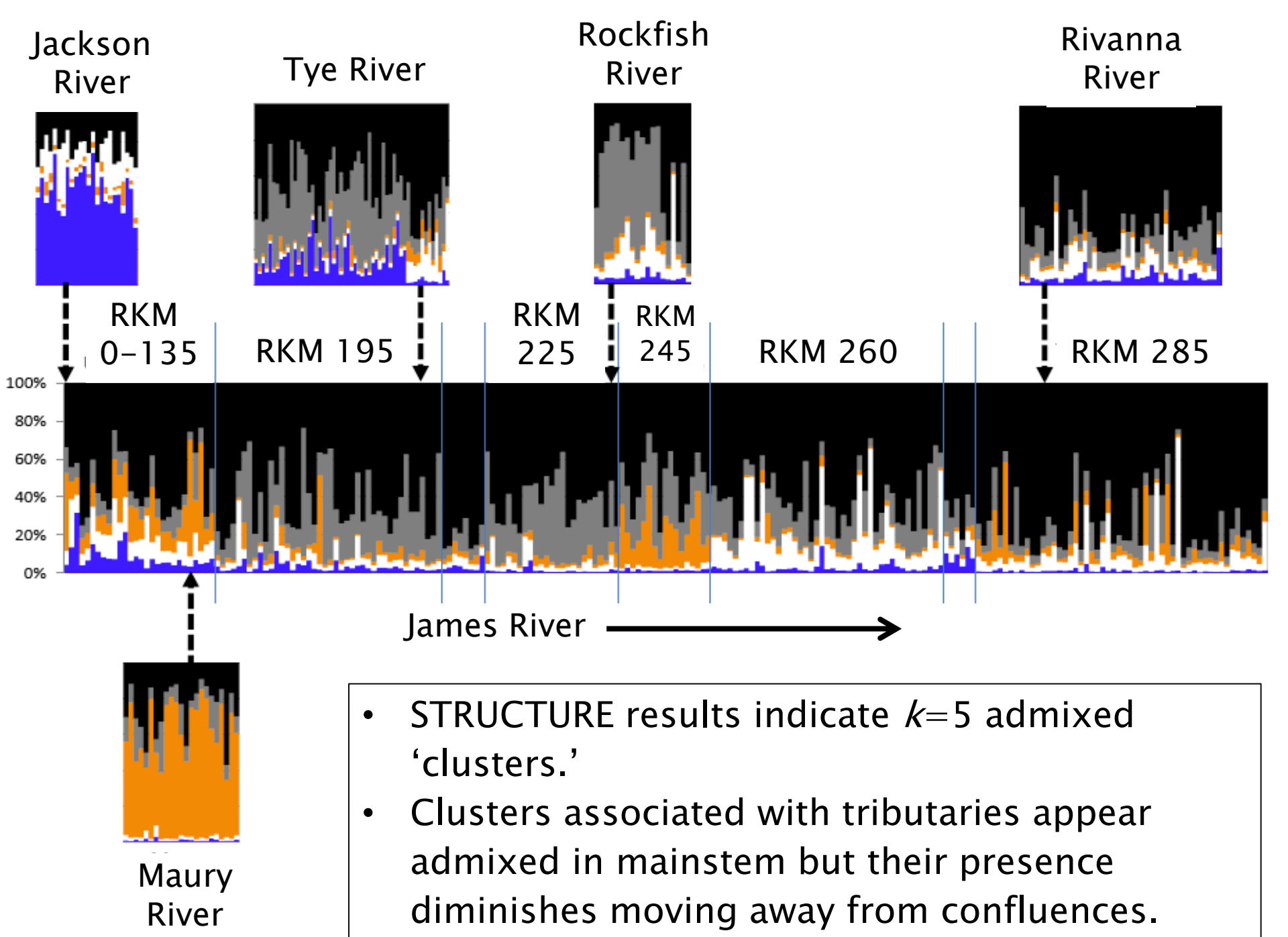
Water sampling results

Sample Collections



Genetic Data and Analyses

- Otolith chemistry provides minimal info on movement in mainstem ('longitudinal' movement).
- Genetic data provide inference on spatial structure within mainstem and between main / tribs.
- 13 microsatellite markers analyzed:
  - Structure
  - Isolation by distance



- STRUCTURE results indicate *k*=5 admixed 'clusters.'
- Clusters associated with tributaries appear admixed in mainstem but their presence diminishes moving away from confluences.

Isolation by Distance

Tests for spatial correlation between geographic and genetic distance:

1) Mantel tests (matrix correlation)

2) Linear regression

6																	
20	14																
39	33	19															
50	44	30	11														
60	54	40	21	10													
76	70	56	37	26	16												
2.5	8.5	22.5	41.5	52.5	62.5	78.5											
22	16	2	21	32	42	58	20.5										
78	72	58	39	28	18	2	76.5	56									
30	36	50	69	80	90	106	27.5	48	104								
52	58	72	91	102	112	128	49.5	70	126	22							
38	32	18	37	48	58	74	35.5	16	72	32	54						
44	38	24	43	54	64	80	41.5	22	78	34	48	6					
45	39	25	44	55	65	81	42.5	23	79	35	47	7	1				
71	77	91	110	121	131	147	73.5	93	149	81	103	109	115	116			
109	115	129	148	159	169	185	111.5	131	187	119	141	147	153	154	38		
207.5	213.5	227.5	246.5	257.5	267.5	283.5	210	229.5	285.5	217.5	239.5	245.5	251.5	252.5	136.5	98.5	
219	225	239	258	269	279	295	216.5	237	293	209	231	237	243	244	148	110	11.5
144.9	150.9	164.9	183.9	194.9	204.9	220.9	142.4	162.9	218.9	114.9	117.1	146.9	140.9	139.9	73.9	35.9	122.4	113.9

Pairwise geographic distance matrix

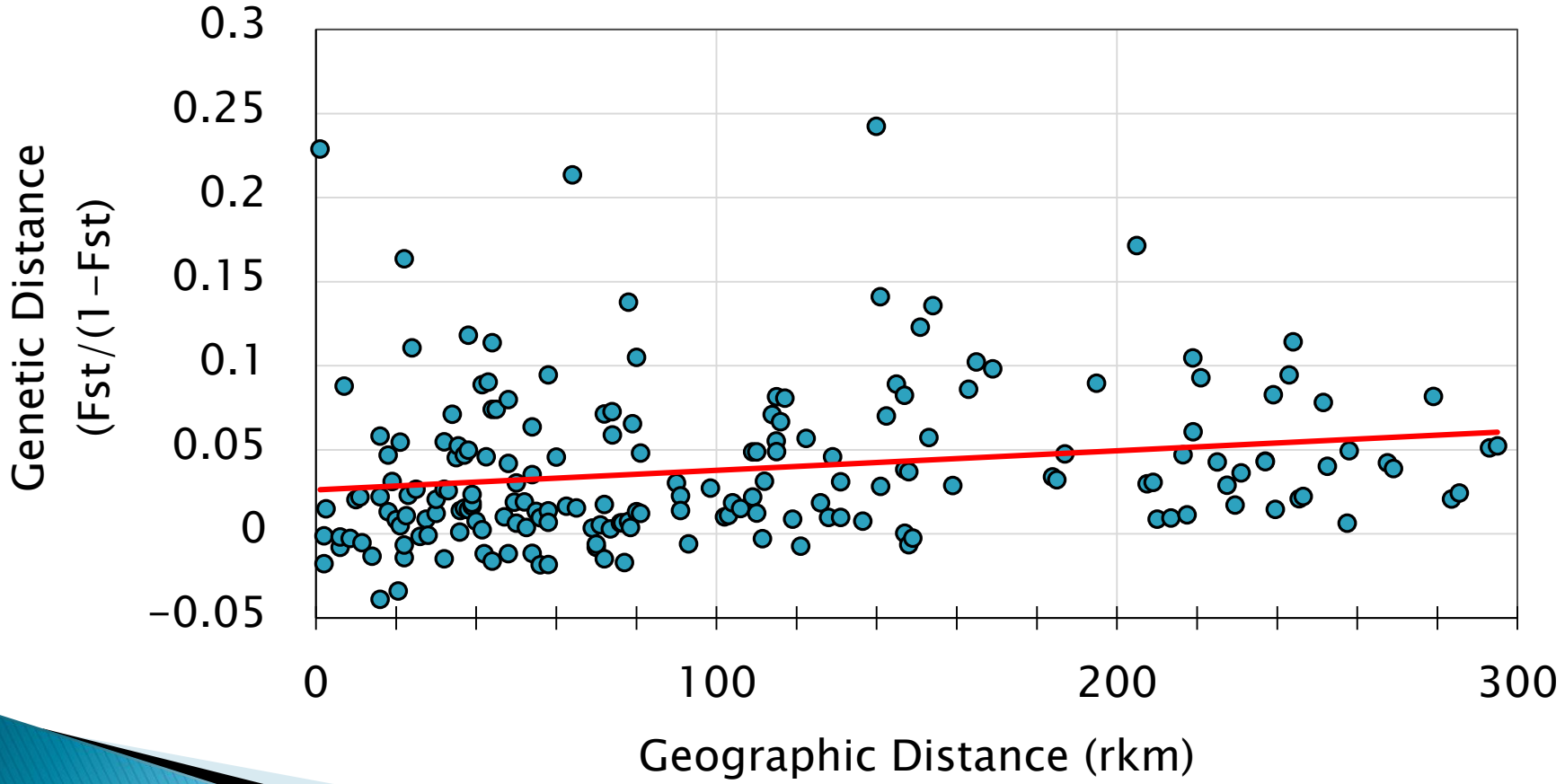
Pairwise genetic distance matrix

-0.01																		
0.01	-0.01																	
0.02	0.03	0.03																
0.01	-0.02	0.01	0.02															
0.05	-0.01	0.01	0.05	0.02														
0.01	-0.01	0.01	0.02	0.00	0.02													
0.01	0.00	0.01	0.00	0.00	0.02	0.00												
-0.01	-0.04	-0.02	0.00	-0.01	-0.01	-0.02	-0.03											
0.01	-0.01	0.01	0.02	0.00	0.01	0.00	0.01	-0.02										
0.02	0.01	0.03	0.00	0.01	0.03	0.02	0.01	-0.01	0.02									
0.02	0.01	0.02	0.02	0.01	0.03	0.01	0.02	-0.01	0.02	-0.01								
0.05	0.05	0.05	0.05	0.04	0.09	0.06	0.05	0.06	0.07	0.03	0.04							
0.07	0.12	0.11	0.09	0.06	0.21	0.11	0.09	0.16	0.14	0.07	0.08	0.00						
0.07	0.02	0.03	0.11	0.01	0.02	0.05	0.05	0.02	0.07	0.05	0.01	0.09	0.23					
0.01	-0.02	0.01	0.01	-0.01	0.03	0.00	0.00	-0.01	0.00	0.01	0.01	0.05	0.08	0.07				
0.02	0.05	0.05	-0.01	0.03	0.10	0.03	0.00	0.01	0.05	0.01	0.03	0.04	0.06	0.14	0.01			
0.03	0.01	0.03	0.02	0.01	0.04	0.02	0.01	0.02	0.02	0.01	0.01	0.02	0.08	0.04	0.01	0.03		
0.06	0.04	0.08	0.05	0.04	0.08	0.05	0.05	0.04	0.05	0.03	0.04	0.04	0.09	0.11	0.04	0.05	-0.01	
0.09	0.12	0.10	0.03	0.09	0.17	0.09	0.07	0.09	0.10	0.06	0.08	0.08	0.14	0.24	0.07	0.00	0.06	0.07

Isolation by Distance – Sampling Locations

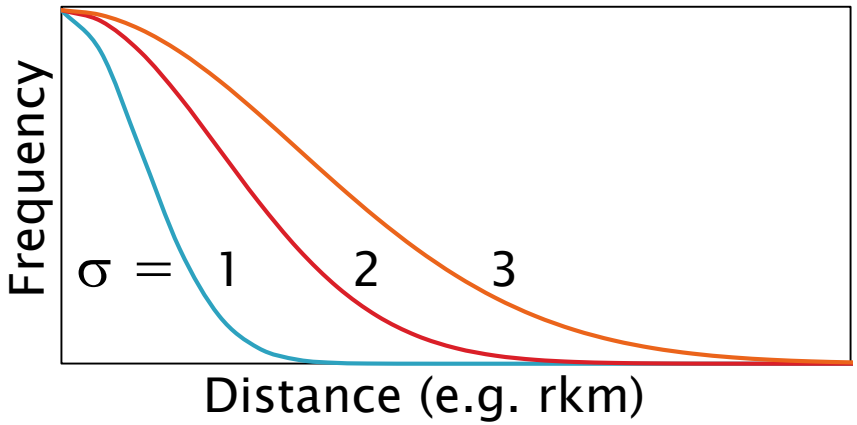
Mantel test: P = 0.048

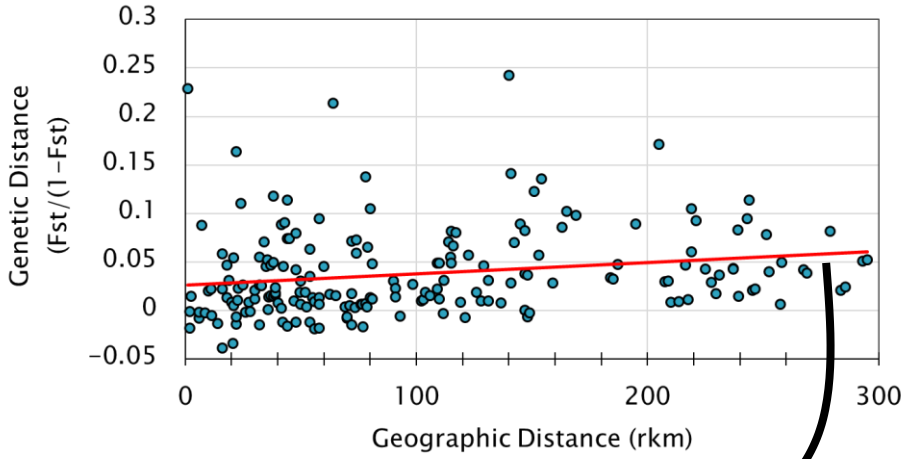
Regression: P = 0.005, Slope = 1.2×10^{-4}



Parent-Offspring dispersal distance

- "Average dispersal distance" of offspring can be estimated from IBD slope (Rousset 1997)





$$f(x) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{x^2}{2\sigma^2}}$$

Gaussian dispersal kernel

Slope of regression line

Parent-Offspring dispersal distance

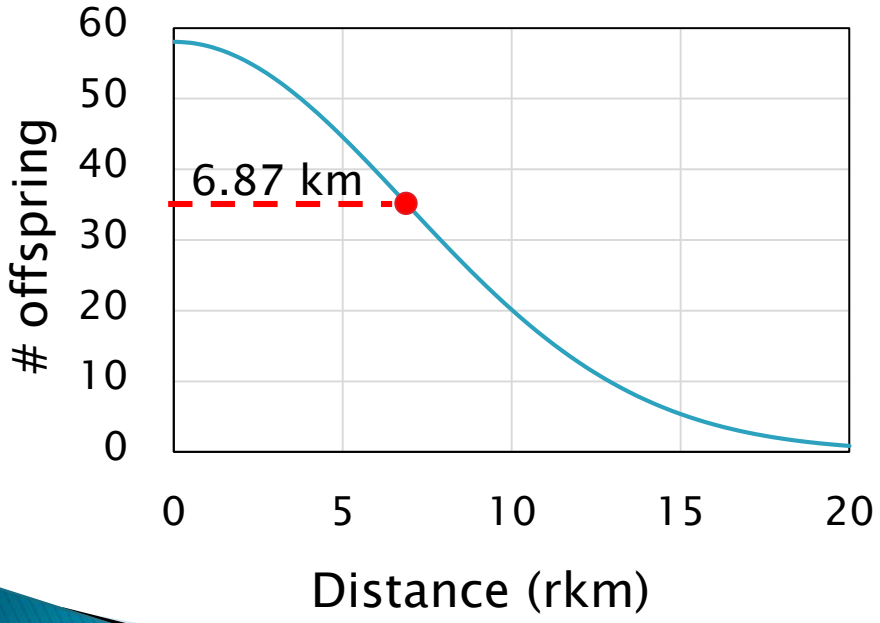
- Requires estimate of mating adult density
  - From DGIF population monitoring:
    - **Avg. ~295 mature SMB/ rkm**
  - From Rafetto et al (1990) multiyear study on adult breeding success in SMB:
    - Avg. proportion of adults breeding per year: **0.42**
    - Avg. proportion of males breeding per year: **0.26**
  - From Cooke et al (2003):
    - Average nest success in lotic environments: **0.52**

Parent-Offspring dispersal distance

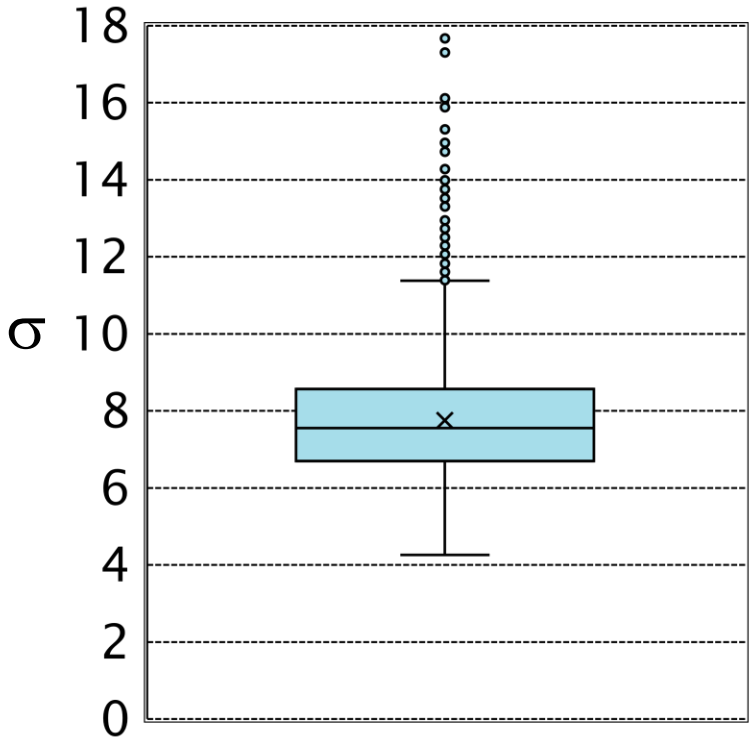
Based on available data:

$\sigma = 6.87$ km

Predicted distribution of 100 offspring



Bootstrapped estimates of σ with parameter uncertainty

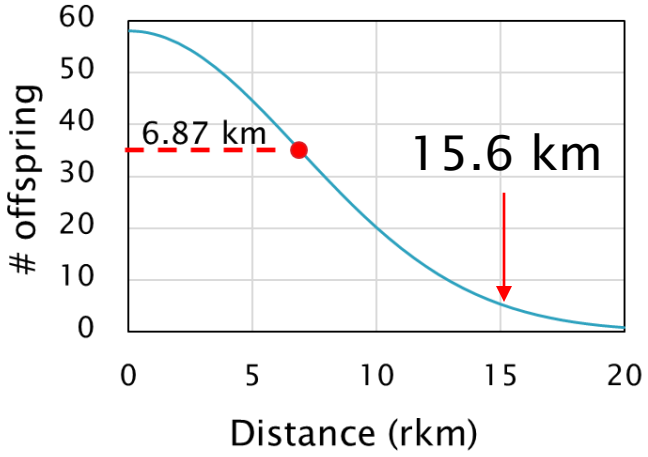


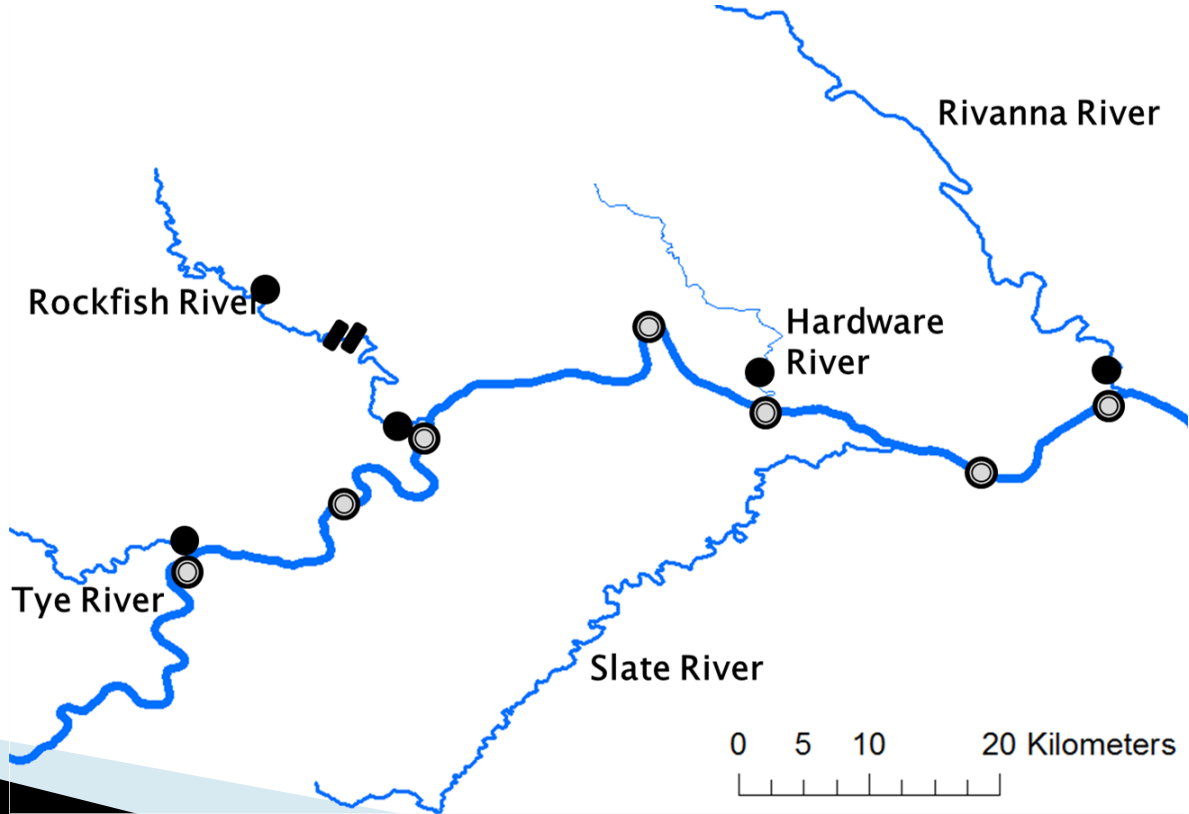
Timescale of Dispersal

- Generation Time: 3.4 yrs
  - Following Caughley (1977), “average age of the parents of all offspring produced by a single cohort.”
  - Calculated from life table assembled from survival and male spawning success.

Otolith Results: Dispersal distance

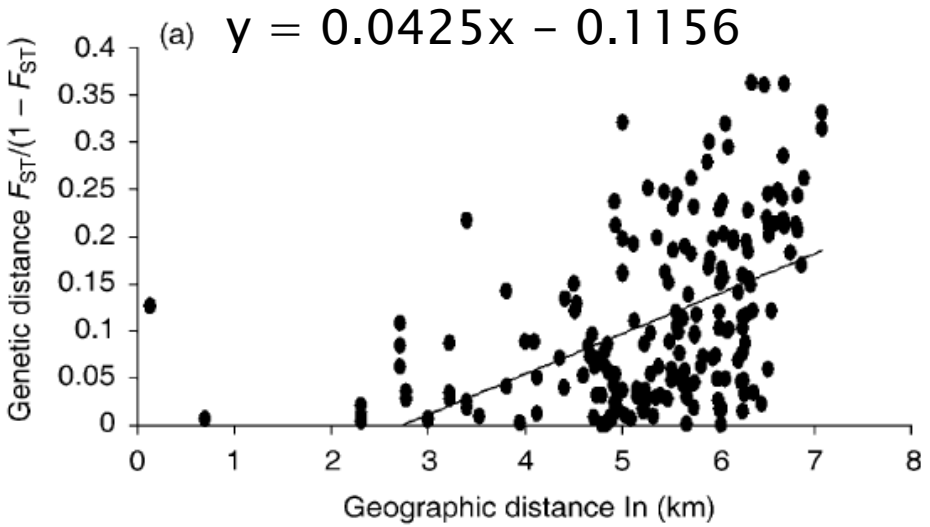
- For fish where a “minimum dispersal distance” could be estimated:
  - Mean distance from natal river = 15.6 km



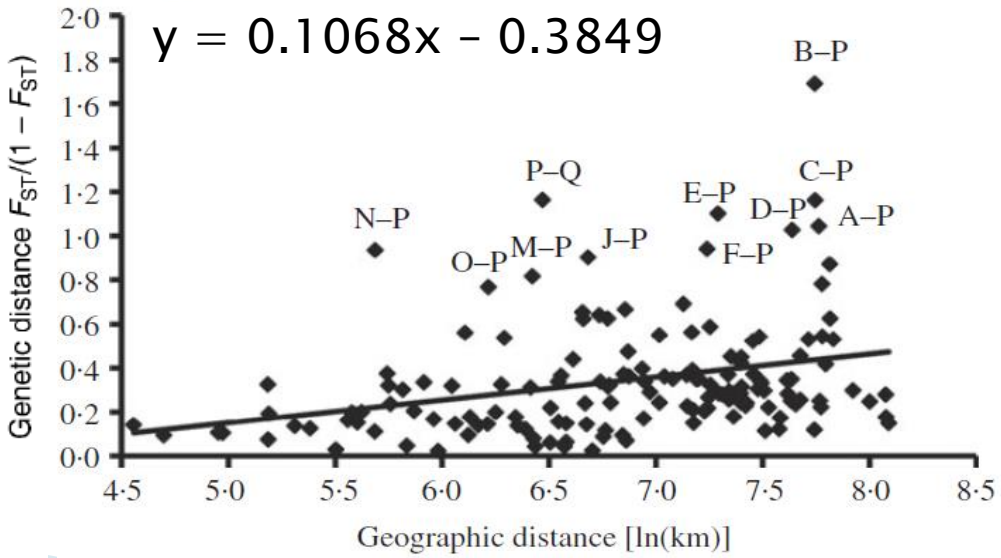


Other estimates: Genetic

- Stepien et al. (2007)
  - $\sigma = 0.13$ km



- Stepien et al. (2017)
  - $\sigma = 0.09$ km



Other estimates: direct methods

- Literature review of SMB tag / telemetry:
  - "Mean movement distance"
    - Mean = 8.8 km
    - Max = 77.3 km
  - Maximum observed movement:
    - Mean = 28.5 km
    - Max = 118 km

Conclusions

- IBD provides strong inference on scale of movement if coupled with good estimate of adult density.
- Smallmouth bass dispersal in rivers is substantial
- Rivers ≠ Lakes

Acknowledgements

- Paul Cabe, Kelly Bezold (W&L)
- Johnathon Harris (DGIF) for support in planning collections and study design
- Many students (W&L) who contributed assistance with lab work and collections
- Mellon Foundation, Jeffress Memorial Trust