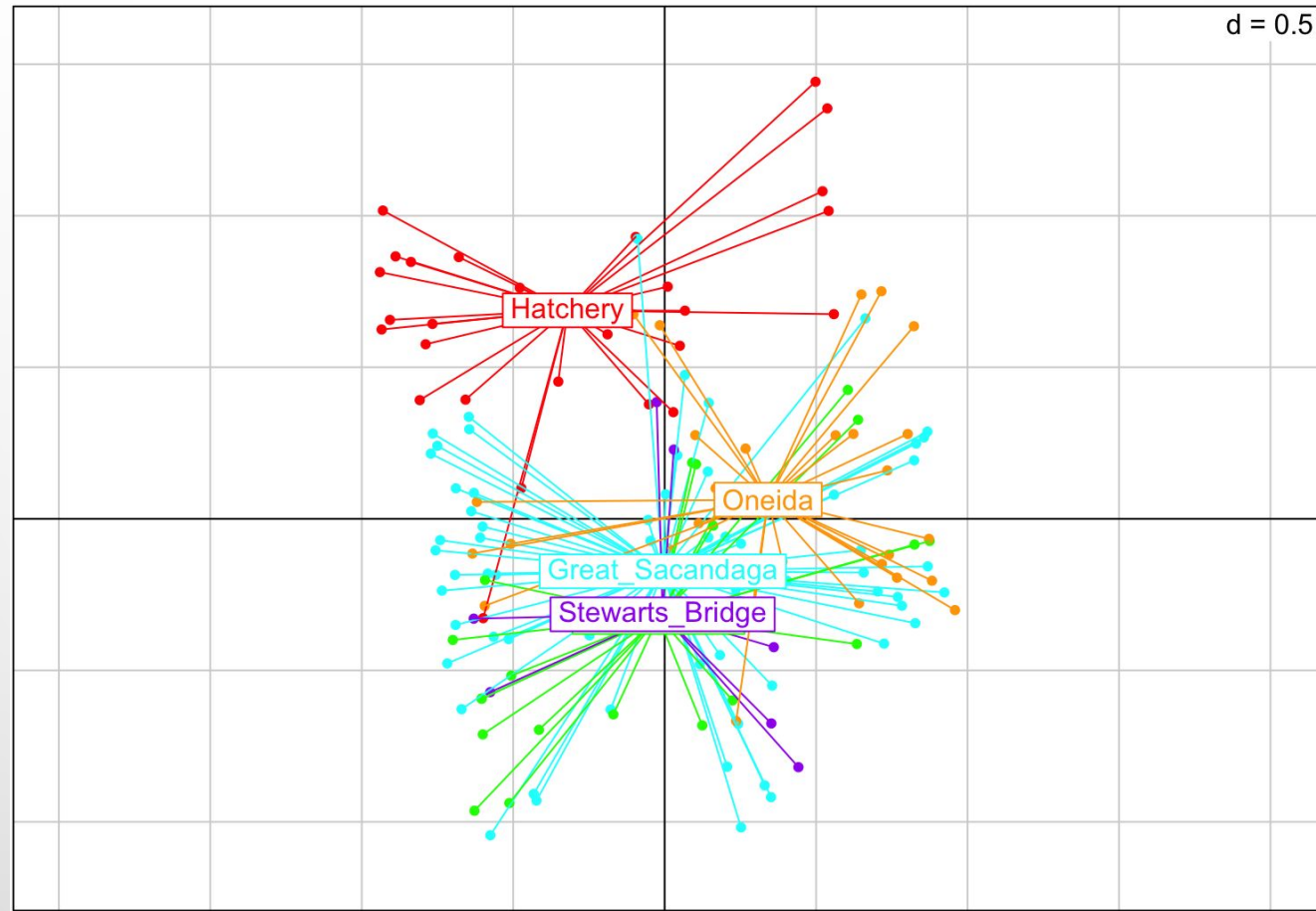


The background of the entire image is a light gray gradient. It is decorated with numerous realistic water droplets of various sizes. Some droplets are large and prominent, while others are small and subtle. They are scattered across the frame, with a higher concentration in the top-left and bottom-right corners. The droplets have highlights and shadows, giving them a three-dimensional appearance.

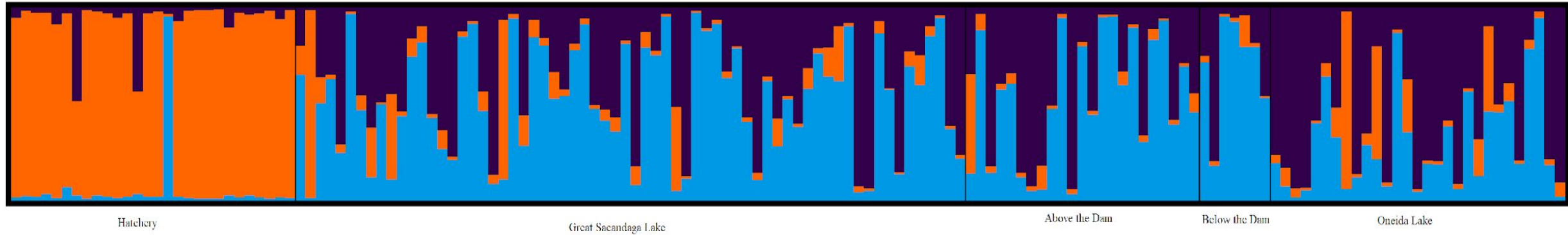
NEW YORK WALLEYE

Population	Hatchery	Great Sacandaga	Above Dam	Below Dam
Great Sacandaga	0.076 (0.05-0.10)			
Above Dam	0.097 (0.05-0.15)	-0.0005 (0-0.006)		
Below Dam	0.093 (0.06-0.13)	-0.003 (-0.01-0.01)	-0.002 (-0.02-0.01)	
Oneida	0.088 (0.06-0.11)	0.030 (0.02-0.04)	0.037 (0.02-0.05)	0.029 (0.01-0.05)

These values represent the F_{ST} between each population (a measurement of genetic differentiation of two populations'). The greater the F_{ST} value, the more distinct the two populations are. Since the F_{ST} values of the hatchery population compared to all other populations are the highest, we can conclude that the Hatchery population is the most genetically distinct of the populations. Within Great Sacandaga, F_{ST} values are all close to zero, indicating that there is no difference between the different segments of the system and that the dam does not impede gene flow. The values in the parentheses represent the range of F_{ST} values that produce a 95% confidence interval.



This PCA graph maps the raw data collected and plots the samples based on how different they are. While no actionable conclusions can be drawn using PCA data, it provides a baseline as to what you expect to see after analyzing the data. In this case, the PCA differentiated the Hatchery population from the rest from the populations. We also see that there is a split within the 4 wild sampled populations along the y-axis (left to right).



Our model found that there was the most likely of 3 distinct genetic ancestries, indicated by the 3 different colors. The Hatchery population is dominated by the orange color, with this ancestry being found in all other systems, with Oneida and Great Sacandaga Lake having the highest. This is an artifact of the stocking, and the hatchery being originated from Oneida. This shows that genetics from the hatchery are being found in Great Sacandaga Lake. The reason the hatchery is different from Oneida is likely due to the methods of propagation that the farm uses, as we would expect the hatchery to be the most similar to Oneida.

	Hatchery	Great Sacanaga	Above The Dam	Below The Dam	Oneida
N	28	66	23	7	29
A	63	80	58	36	68
%	62.39	80.01	57.52	35.58	67.45
Ar	4.98	5.33	5.26	4.25	5.27
Ho	0.55	0.65	0.66	0.65	0.63
He	0.71	0.77	0.76	0.71	0.76
HWE	0	0	0	0.309	0
Fis	0.2238	0.1634	0.125	0.0744	0.1791
Fis_Low	0.1441	0.1196	0.06	-0.1713	0.1072
Fis_High	0.303	0.207	0.1957	0.2614	0.2462

The table above provides the number of individuals from the population (N), number of alleles (A), percentage of total alleles observed per population (%), allelic richness (Ar), the observed heterozygosity (Ho), the expected heterozygosity (He), p-value for Hardy-Weinberg equilibrium (HWE), the inbreeding coefficient (Fis), the lower bound for the 95% interval for Fis, and the higher bound for the 95% confidence interval for the Fis.

The Hatchery population has the lowest diversity from allelic richness as well as the highest Fis compared to all other populations except for Below the Dam with is an artifact of sample size.