

# Comparison of lake trout (*Salvelinus namaycush*) fatty acid signatures in the Finger Lakes

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## INTRODUCTION

Fatty acid signatures (FAS) are biochemical tracers used to study predator-prey relationships in aquatic food-webs.

FAS estimate foraging patterns that can reflect predator diet composition of over a period of weeks to months based on the principle “you are what you eat”, where fatty acids are conservatively transferred from prey to predator.

Lake trout *Salvelinus namaycush* is a native species in the Great Lakes region that relies on different prey throughout the Finger Lakes. Therefore, we predict that lake trout will present different FAS among lakes.

The objective of this study was to identify differences in the lake trout diet estimates among six Finger Lakes. Ultimately, these results will be compared with FAS of prey species to evaluate lake trout diet composition in each Finger Lake.

## MATERIALS AND METHODS

Lake trout were collected from Canadice, Canandaigua, Cayuga, Keuka, Seneca, and Skaneateles lakes between 2016 and 2020 by the New York State Department of Environmental Conservation (Figure 1, Table 1).

Lipids were extracted from lake trout belly flap (Folch et al. 1957) and fatty acids were transmethylated (Metcalf and Schmitz 1961) for quantification with gas chromatography/mass spectrometry.

Multivariate statistics were used to compare FAS among the Finger Lakes using Primer V6.

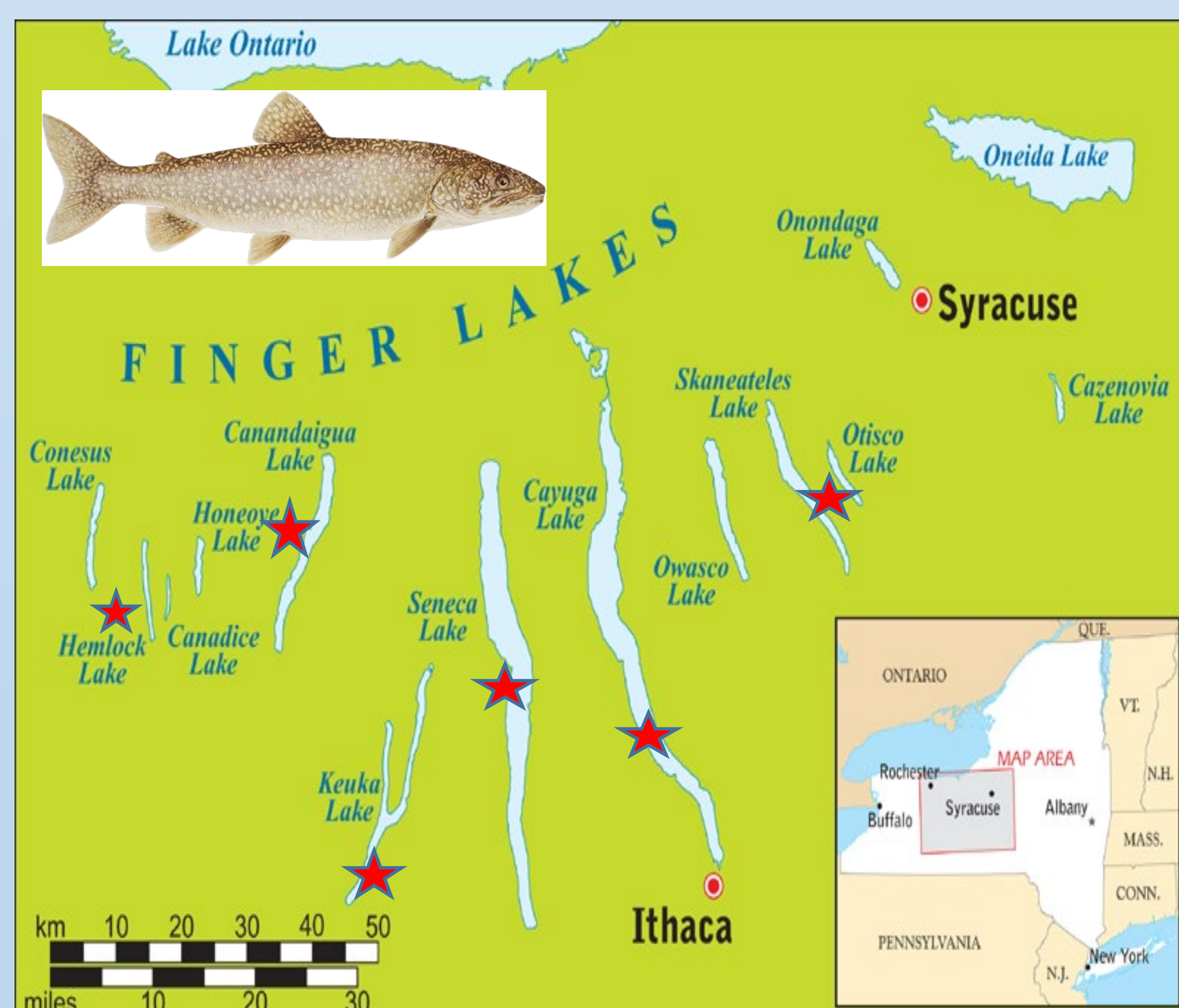


Figure 1. Lake trout sampling locations in the Finger Lakes.

Table 1. Yearly number of lake trout collected from six Finger Lakes between 2016 and 2020.

	2016	2017	2018	2019	2020
Canadice	-	-	-	17	-
Canandaigua	-	-	32	-	-
Cayuga	-	15	-	18	-
Keuka	23	-	-	-	-
Seneca	-	19	-	-	7
Skaneateles	-	11	-	-	-

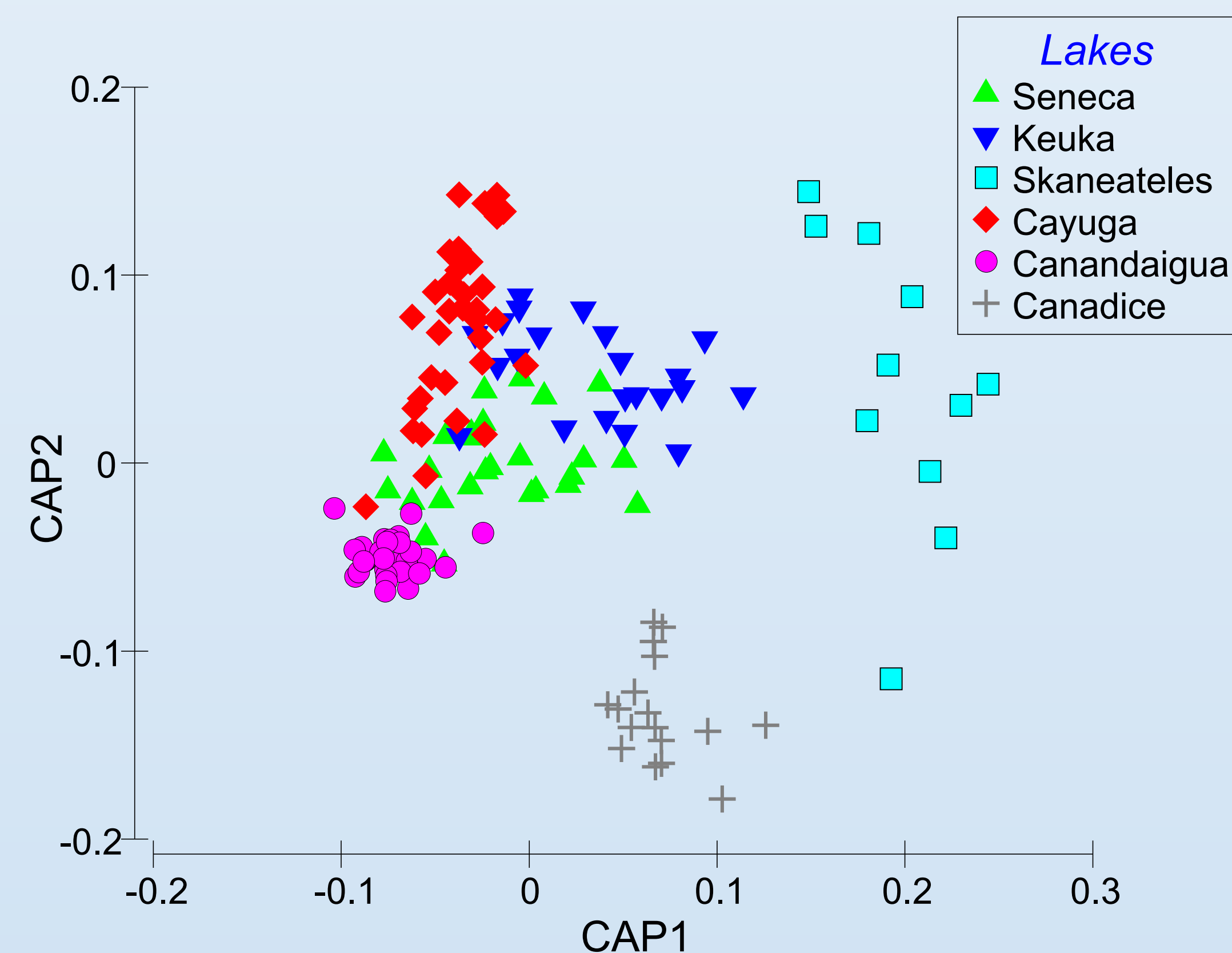


Figure 2. Canonical analysis of principle coordinates of lake trout FAS from six Finger Lakes.

Table 2. ANOSIM R values and FAS dissimilarities (%) between lakes.

Lakes	R	Dis.
Seneca - Keuka	0.510	8.24
Seneca - Skaneateles	0.932	14.86
Seneca - Cayuga	0.330	7.86
Seneca - Canandaigua	0.831	7.87
Seneca - Canadice	0.866	8.96
Keuka - Skaneateles	0.862	14.81
Keuka - Cayuga	0.573	10.47
Keuka - Canandaigua	0.748	8.09
Keuka - Canadice	0.691	9.26
Skaneateles - Cayuga	0.876	14.49
Skaneateles - Canandaigua	0.983	17.7
Skaneateles - Canadice	0.868	14.56
Cayuga - Canandaigua	0.790	10.78
Cayuga - Canadice	0.779	11.52
Canandaigua - Canadice	1	9.15

## RESULTS AND CONCLUSIONS

Lake trout FAS significantly differed among the six Finger Lakes (ANOSIM, global R = 0.709, P < 0.001) (Figure 2, Table 2).

FAS of Seneca lake trout and Cayuga lake trout were the least dissimilar while Skaneateles Lake trout and Canandaigua Lake trout were the most dissimilar (Table 2).

Fatty acids with the most variation among lakes were 18:1n-9, 22:6n-3, 20:5n-3, 16:1n-7, and 16:0 (Figure 3).

Lake trout from Seneca and Cayuga were characterized by higher concentrations of fatty acids associated with pelagic foraging (e.g., 18:1n-9), in contrast to Canandaigua, Keuka, and Skaneateles lakes (e.g., 20:5n-3, characteristic of benthic foraging) (Figures 2 and 3).

Differences observed within and among lake trout FAS allow for future comparisons with FAS of prey fish from the Finger Lakes.

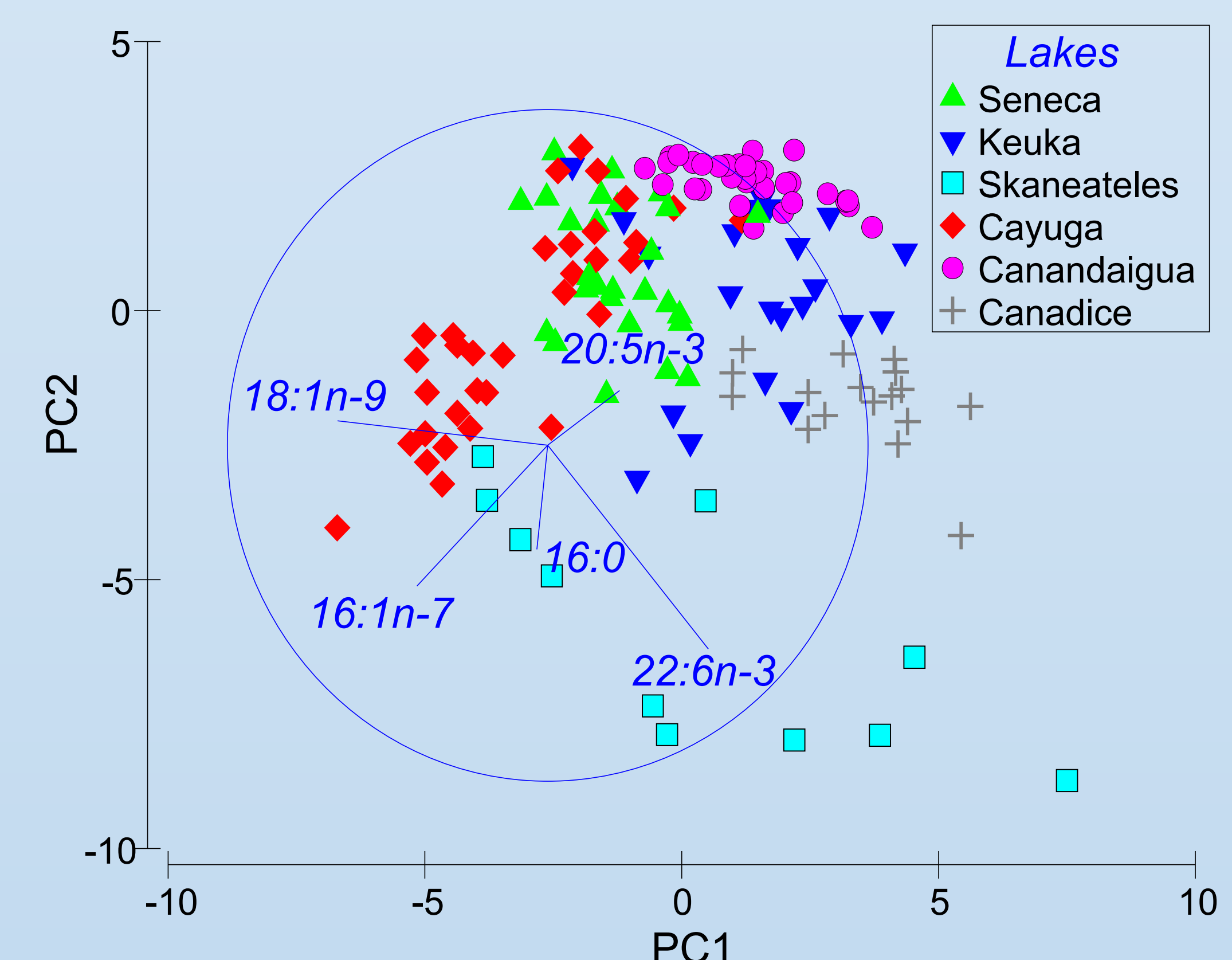


Figure 3. Principal component analysis for lake trout FAS among six Finger Lakes. Vectors are shown for fatty acids with the greatest differences among lakes.

## REFERENCES

- Folch, J., M. Lees, and G.H. Sloane-Stanley. 1957. J. Biol. Chem. 226: 497-509.  
 Metcalfe, L.D. and A.A. Schmitz. 1961. Anal. Chem. 33: 363-364.