Correlation of Protacanthopterygii

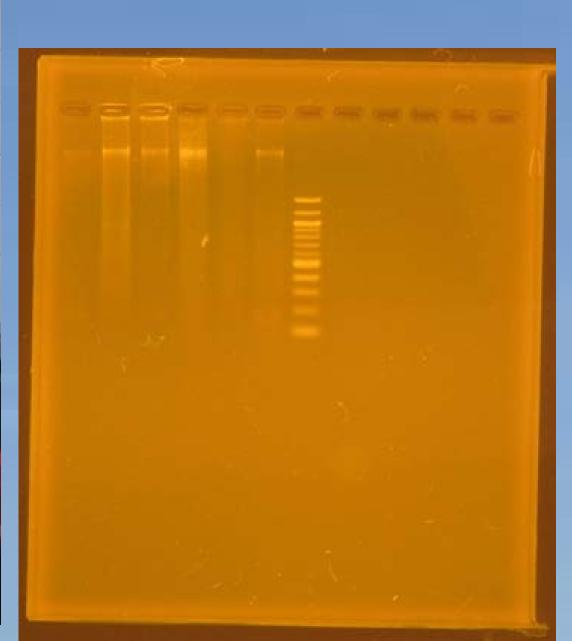
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Introduction

Understanding the Evolutionary history of the Protacanthopterygii Superorder. Includes: pike, salmon, and the smelt species. Reviewing the SVEP gene locating the different sequences in each species to see how diverse they became over time.





between the salmon and smelt were far more related then the salmon and pike. Using the SVEP1 Gene (Sushi, Von willebrand factor type A, EGF and Pentraxin domain-containing protein 1-like) to track the differences in each species locating the mutations and determining the changes over time. Concluded that the Pike species were more closely related to the Salmon species.

Methods

DNA extraction is a routine procedure in order to examine the close relation between the species. We extracted DNA from the following Specie groups of Salmonids, Escocids, Osmerids and an out group species. Followed by extraction is PCR creating a large amount of copies of the desired gene. Running Electrophoresis is to analyzing how many base pairs are found of the gene. Doing its yet another time being sure to use high quality DNA for sequencing. In sequencing DNA florescent is use to examine the base pares of each species. Analyzing the sequenced DNA from the species to determine the correlation of the superorder of Protacanthopterygii.

Results

Traditional

Smelt Salmon

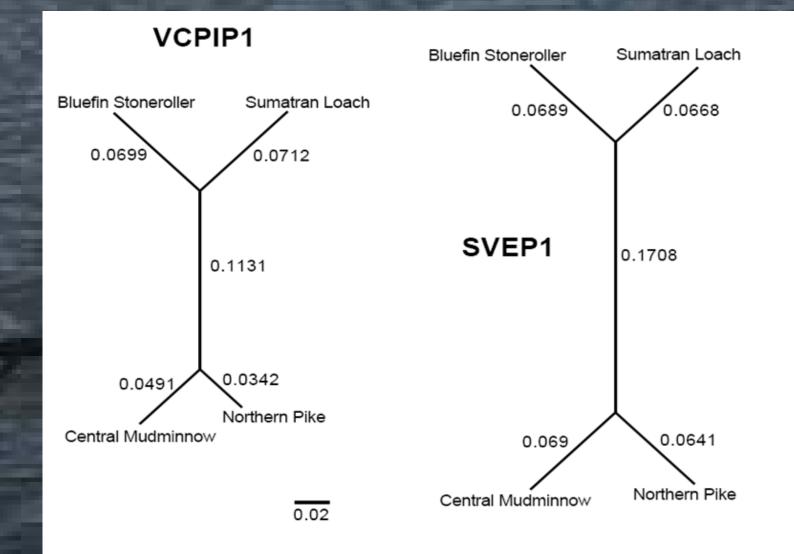
Our research found that the relation

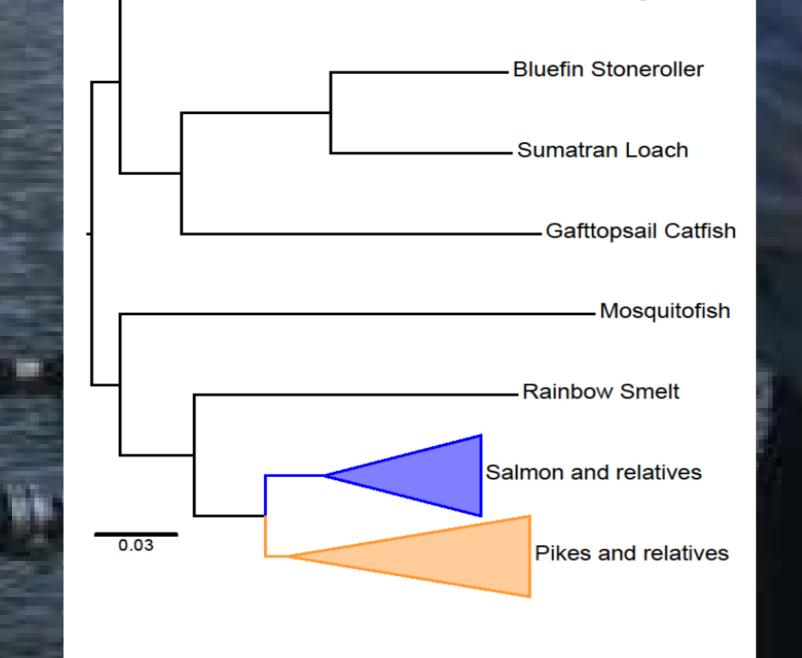
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Modern

Smelt

Salmon





Specimens **Salmonids**

- Arctic Char (Salvelinus alpinus)
- Chinook Salmon (Oncorhynchus tshawytscha)
- **Arctic Grayling (Thymallus arcticus)**
- White Fish (Coregonus)

Osmerids

- Rainbow Smelt (Osmerus Mordax)
- Capelin (Mallotus Villosus)

Escocids

- Amur Pike (Esox reichertii)
- Alaska Blackfish (Dallia pectoralis)
- Olympic Mudminnow (Novumbra Hubbsi)
- Central Mudminnow (Umbra Limi)





