

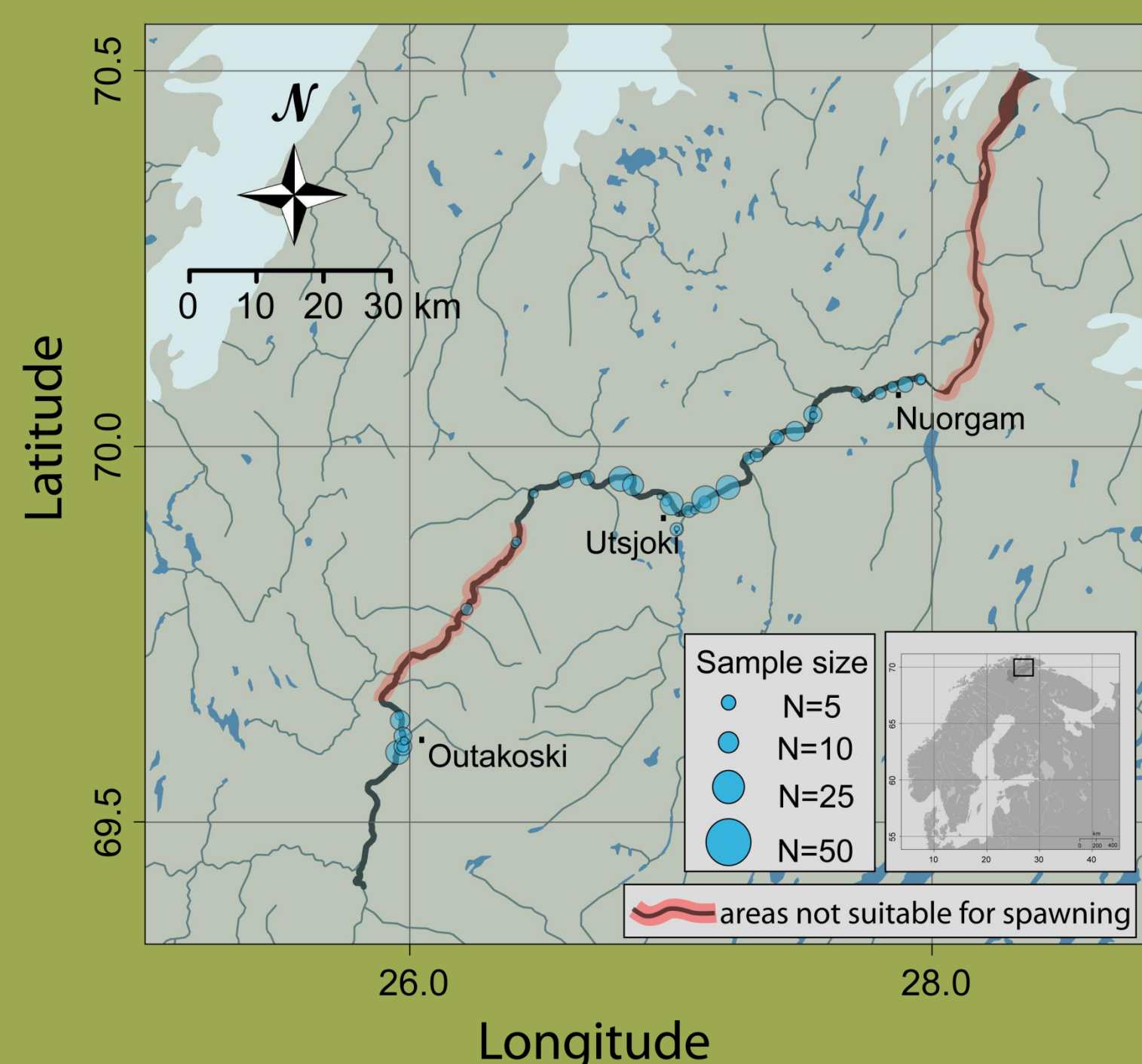
# Cryptic population structure: two phenotypically diverged Atlantic salmon populations discovered in the Teno River mainstream.

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Defining populations and ecological differences affecting genetic structure is important for efficient management and conservation practices.

We combined genetic and phenotypic information to assess fine-scale population structure of Atlantic salmon that spawn in Teno River mainstream, Finland.

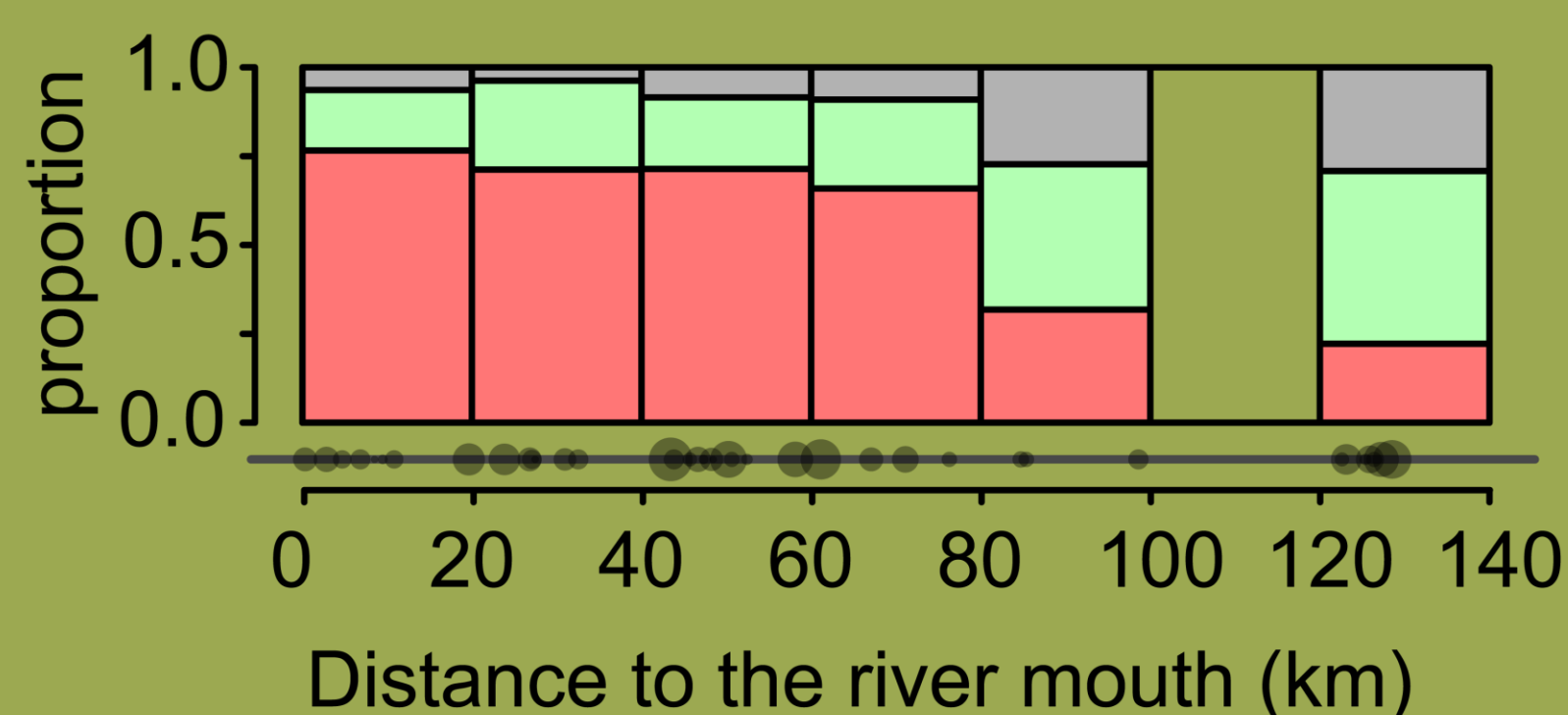


662 adult salmon were collected along the Teno mainstream by co-operating local fishermen.

Scales were used to extract DNA, and infer age and growth rate. Length and weight were also measured.

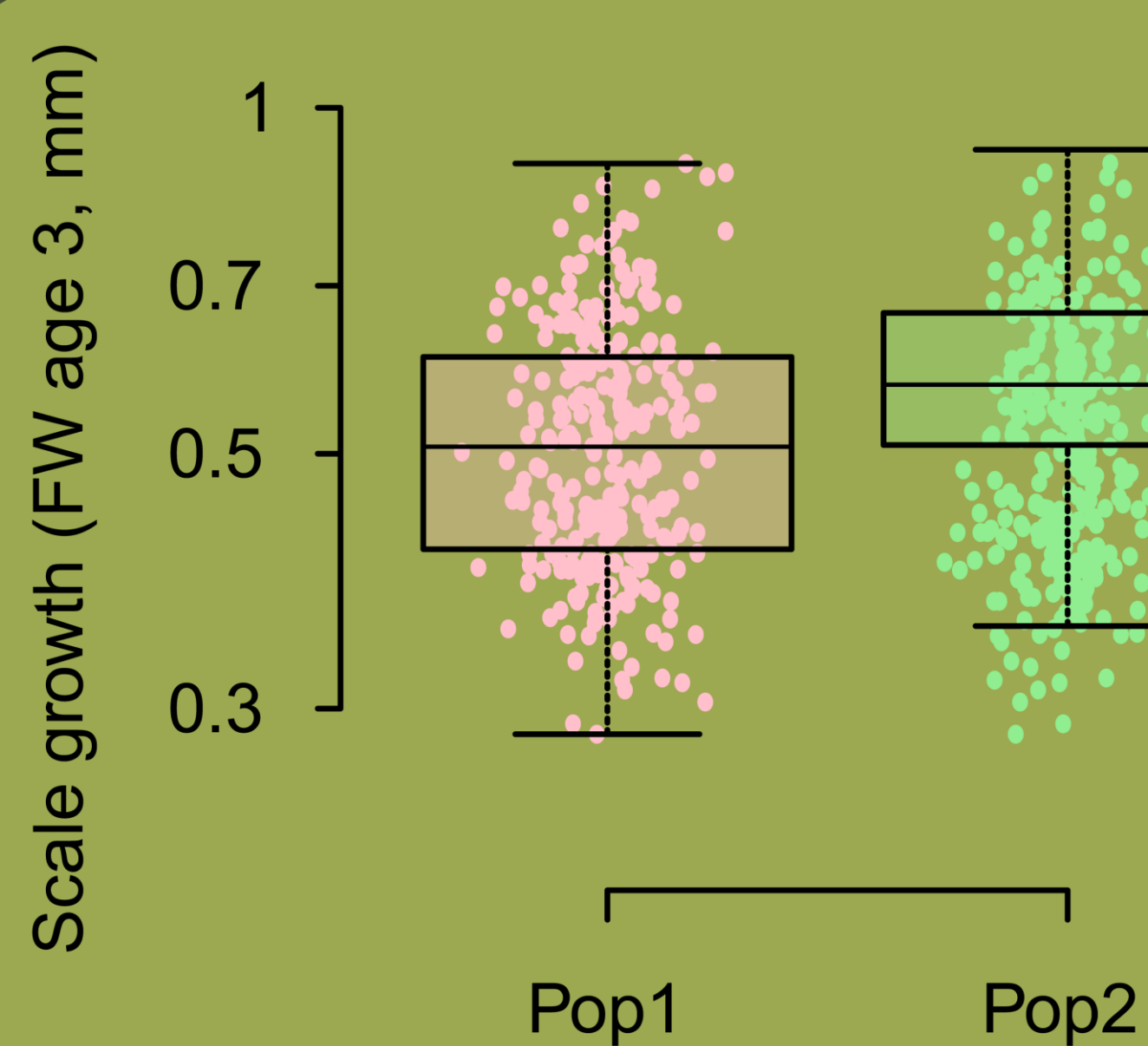
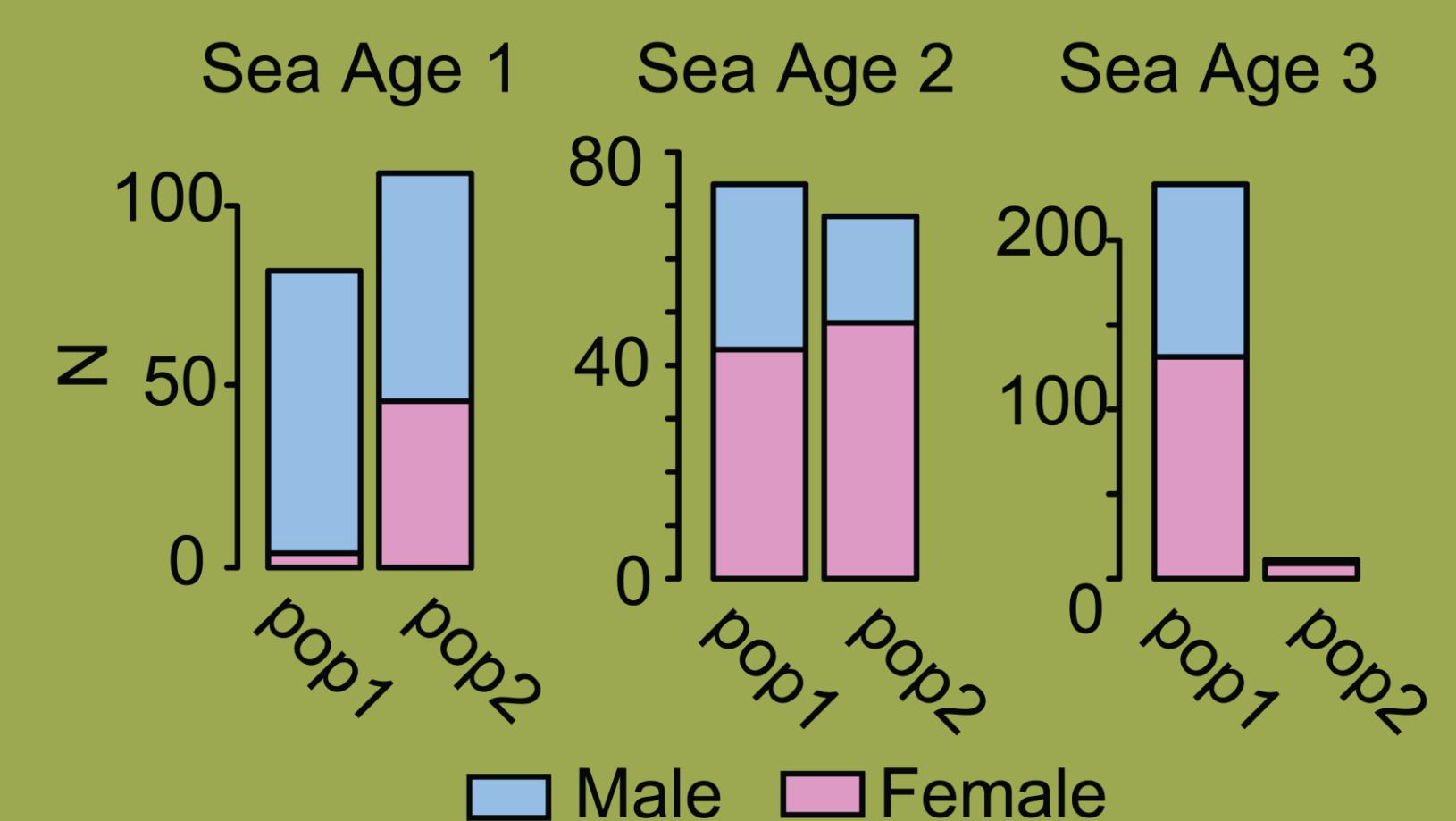


Scale growth rings can be used for age determination and measuring annual growth.



Distribution of populations along the mainstream. (Population 1, population 2, and admixed)

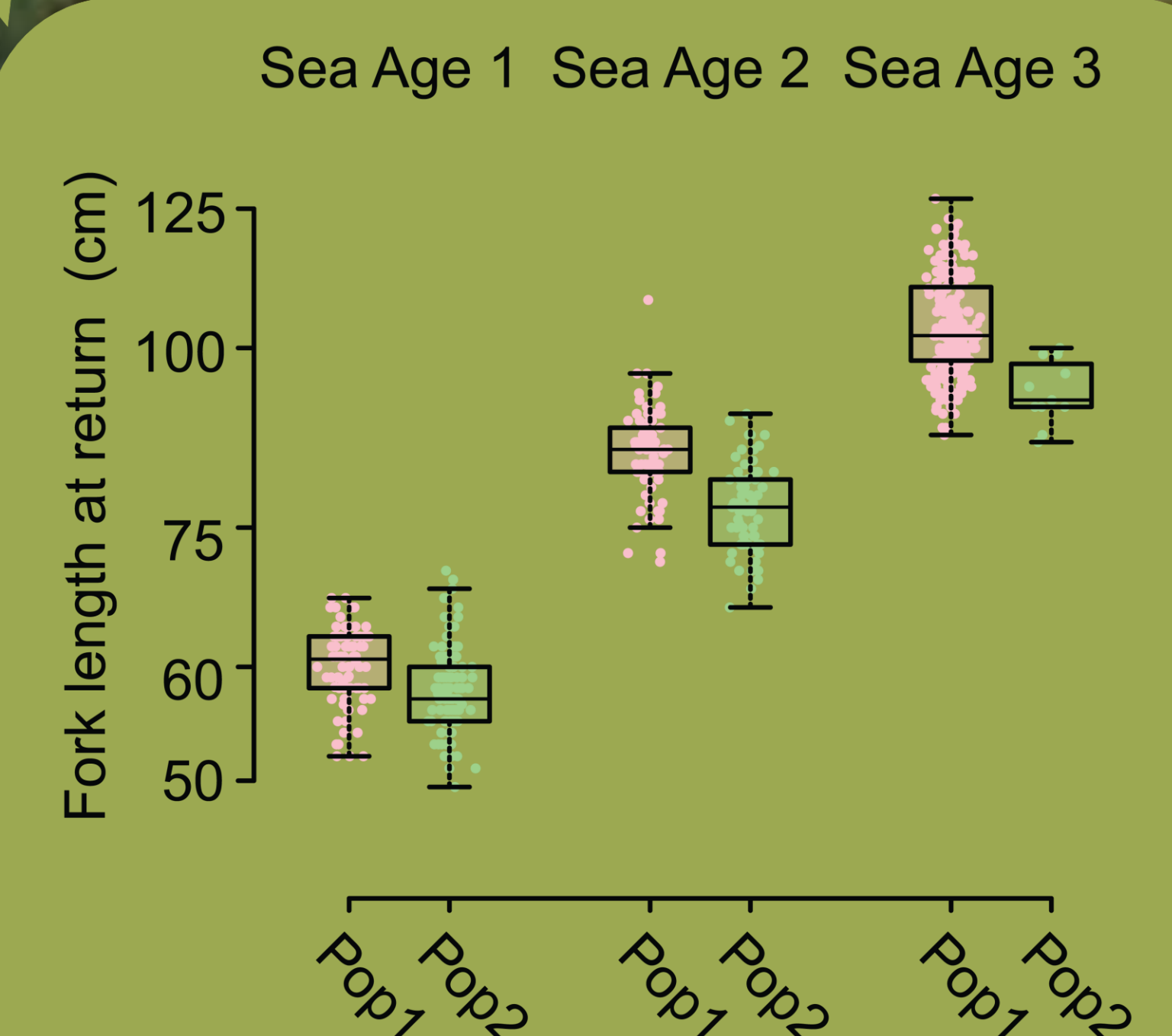
Genetic analyses revealed two distinct spawning populations occurring sympatrically in the mainstream. Genetic divergence was low ( $F_{ST} = 0.018$ ), but phenotypic differences were large.



Fish from Population 2 grow faster in freshwater ( $P < 0.001$ ).

Sea-age composition differs between populations and sexes.

Populations have contrasting growth patterns: fast growth in fresh water and slow growth in the sea, or vice versa.



Fish from Population 1 grow faster in the ocean ( $P < 0.001$ ).

**Conclusion:** Seemingly one stock is composed of two populations with very different phenotypic properties.

**What we don't yet know, but are curious to find out:**

What is the: physiological / behavioral / ecological basis of this differentiation?  
expected stock composition under different climate and fisheries scenarios?