

# Population structuring of chum salmon, *Oncorhynchus keta*, populations in the Far East Asia



Moongeun Yoon, Syuiti Abe<sup>1</sup>, Ju Kyoung Kim, and Kwan Eui Hong

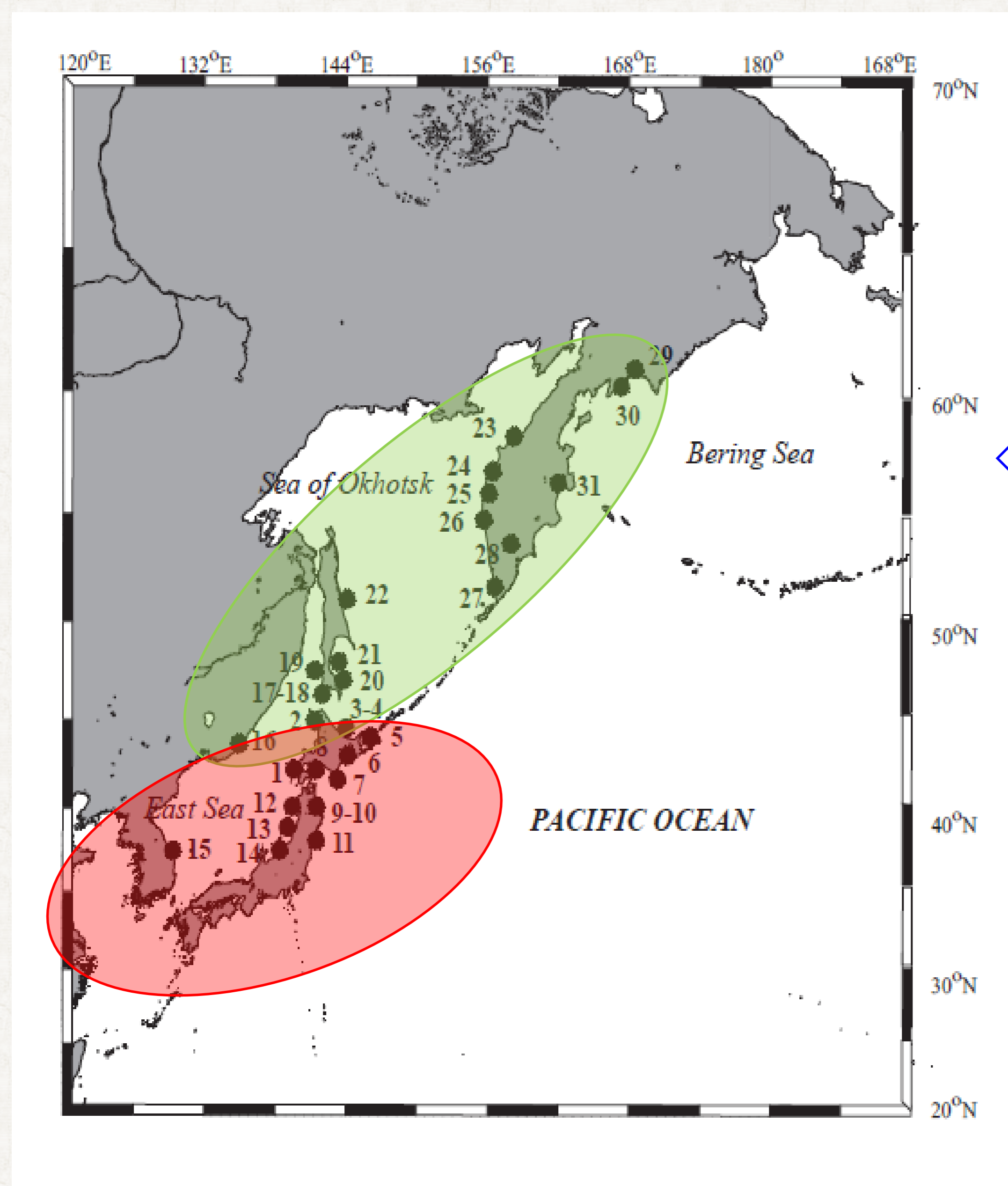
Yangyang Salmon Station, Korea Fisheries Resources Agency, Yangyang, 215-821, Korea

<sup>1</sup>. Division of Biological Sciences, Graduate School of Science, Hokkaido University, Hakodate, 041-8611, Japan

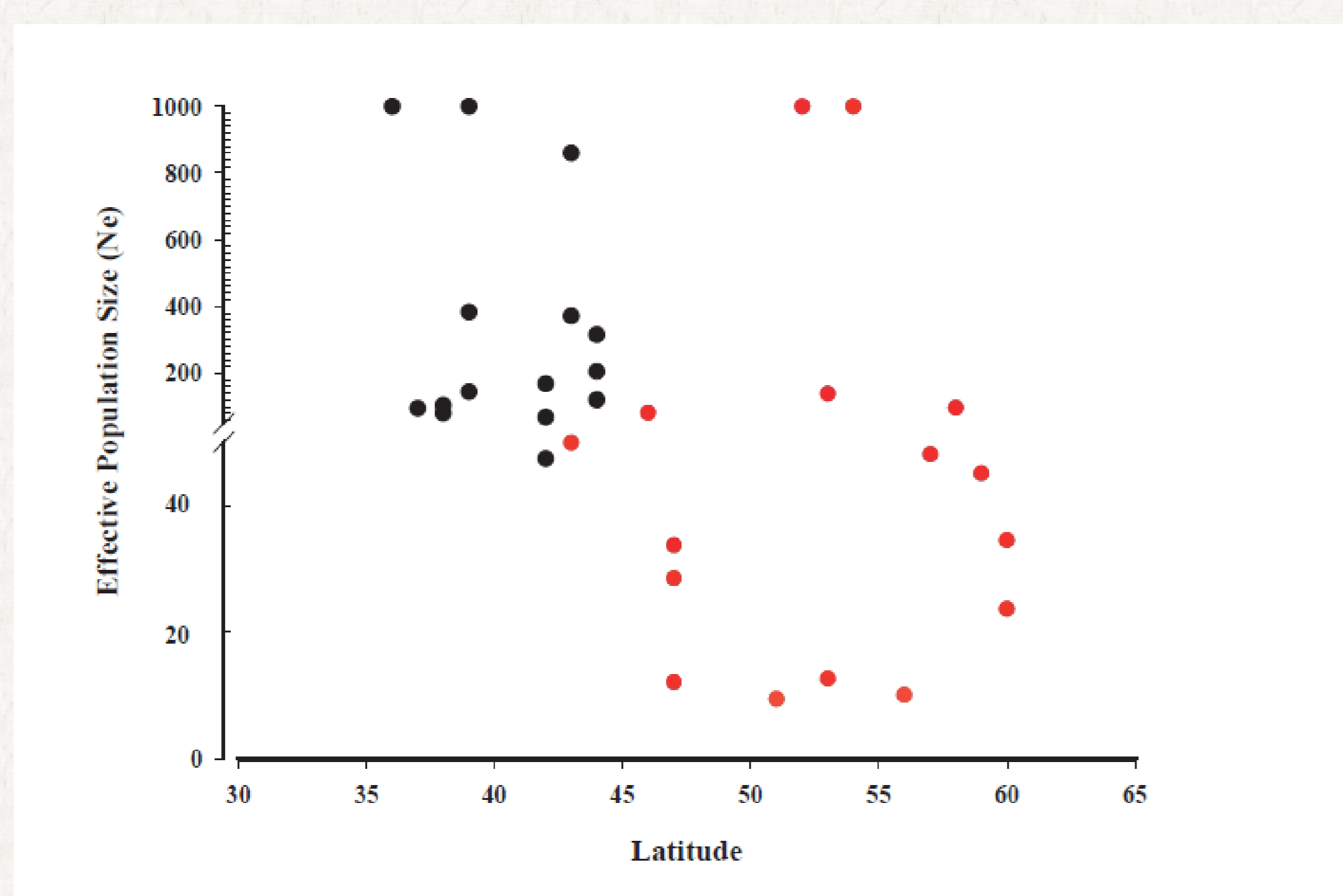
Previously discussed the significant differentiation among regions in Pacific Rim for chum salmon reflects contemporary restrictions on gene flow.

Concerning the historical events and processing of their genetic structure in the Northwest Pacific still remain unclear.

In the present study, microsatellite DNA analyses were used to estimate the genetic structure of chum salmon populations in the Far East Asia.

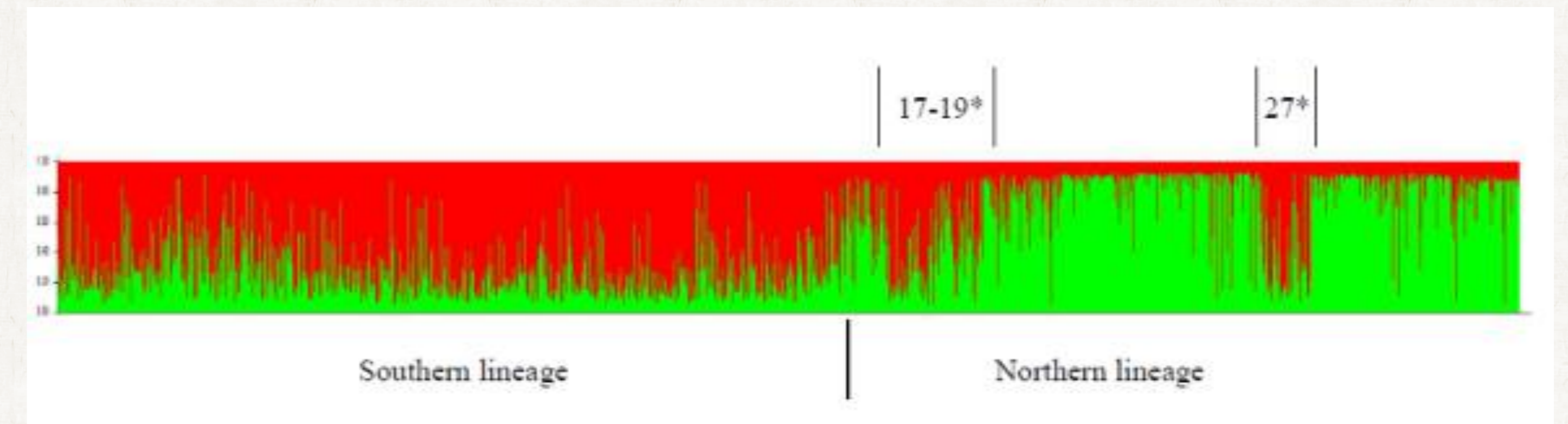


Geographical position of chum salmon sampling site

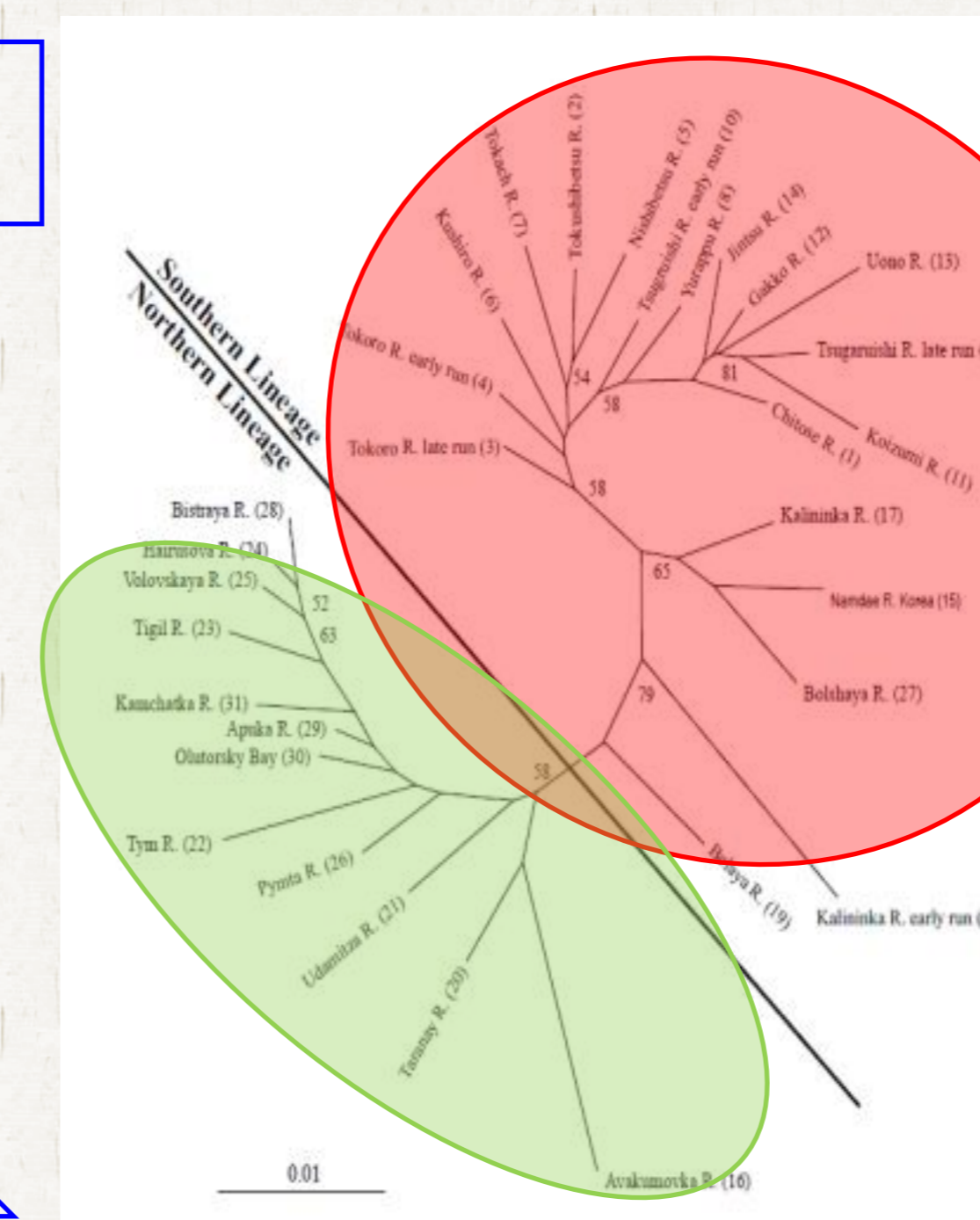


Effective population size ( $N_e$ ) estimated by NeEstimator 1.3

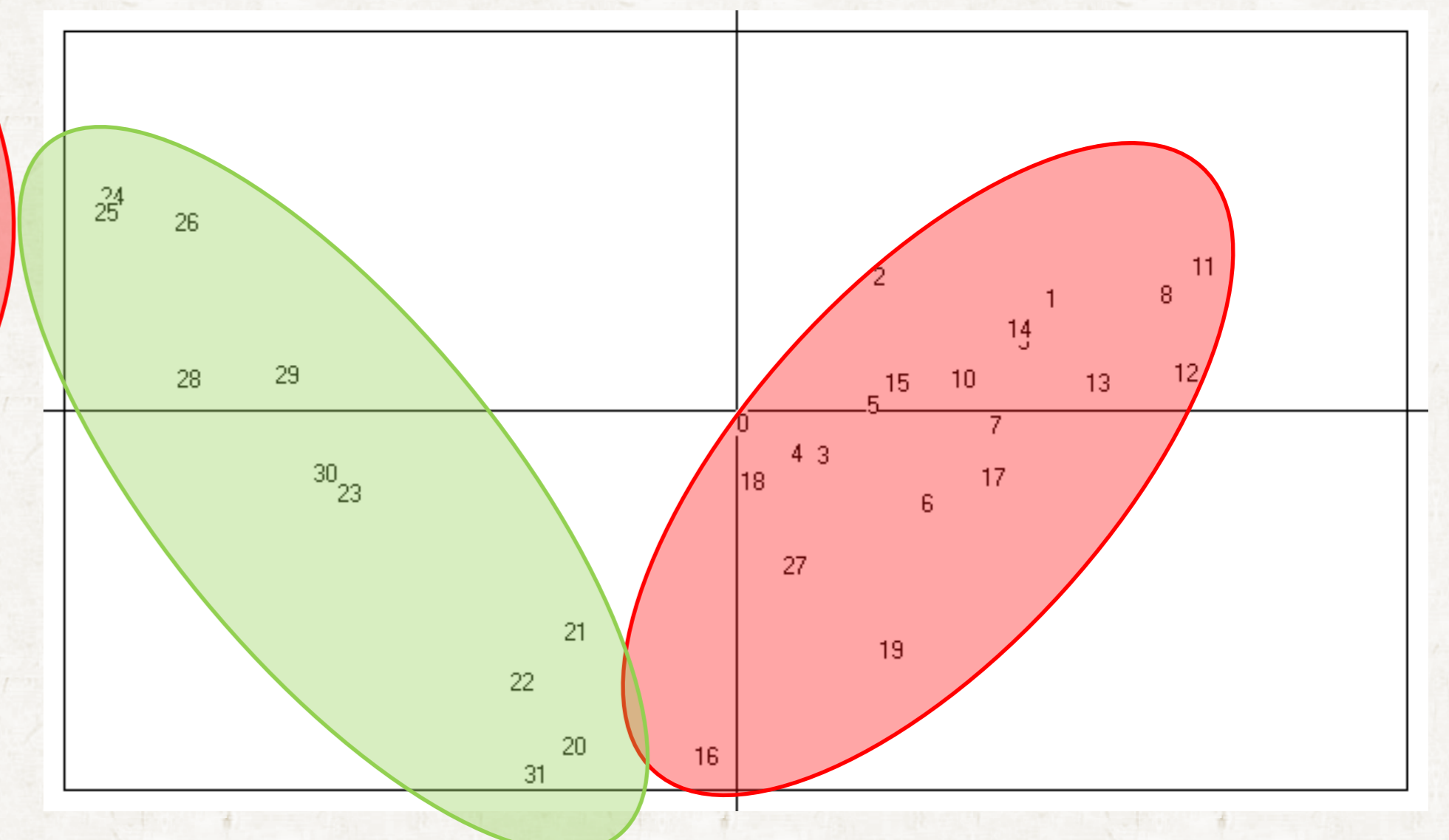
## Structure analysis



Structuring

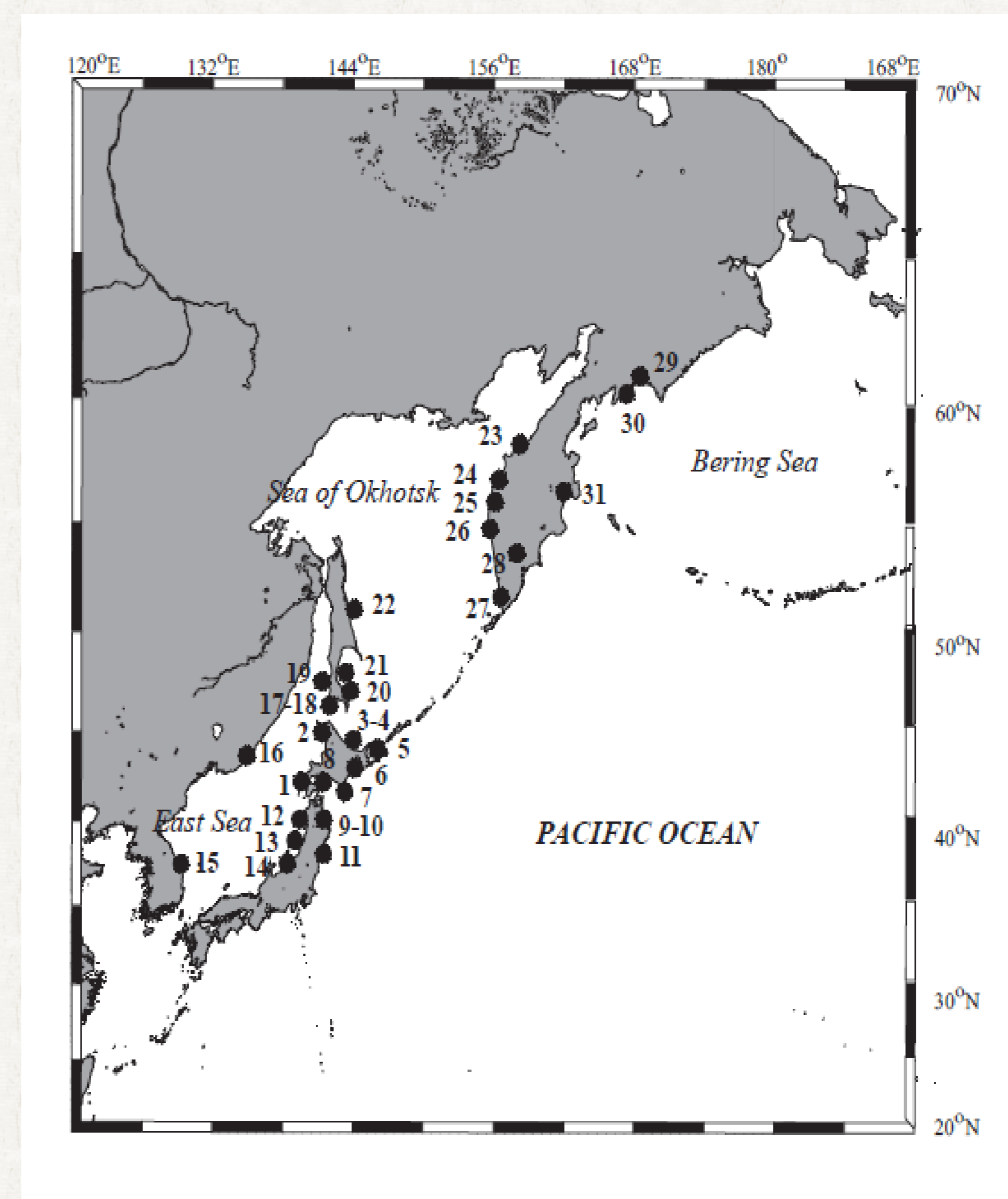


N-J analysis



PCA

Phylogeographic



Wilcoxon Signed Rank Test using  $P$ -values under three mutation model

● Mutation-drift equilibrium

Our analyses give differentiation between two regions for effective population size, genetic bottleneck signature and gene flow. This finding carefully suggests that Long-term historical events, such as postglacial recolonization from different glacial refuges may influence genetic population structure. It may glacial population extinctions and interglacial colonization in the contemporary populations of chum salmon along the Far East Asia.