A large salmon population genetically differentiated within, but not between rivers

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Introduction

There is potential for strong local adaptation within and among salmonid populations ⇨ Populations must be managed sustainably to maintain their genetic resilience

Question

Is there genetic structure in the largest remaining wild 'Baltic salmon' (*Salmo salar*) population, in the interconnected Tornio and Kalix rivers?

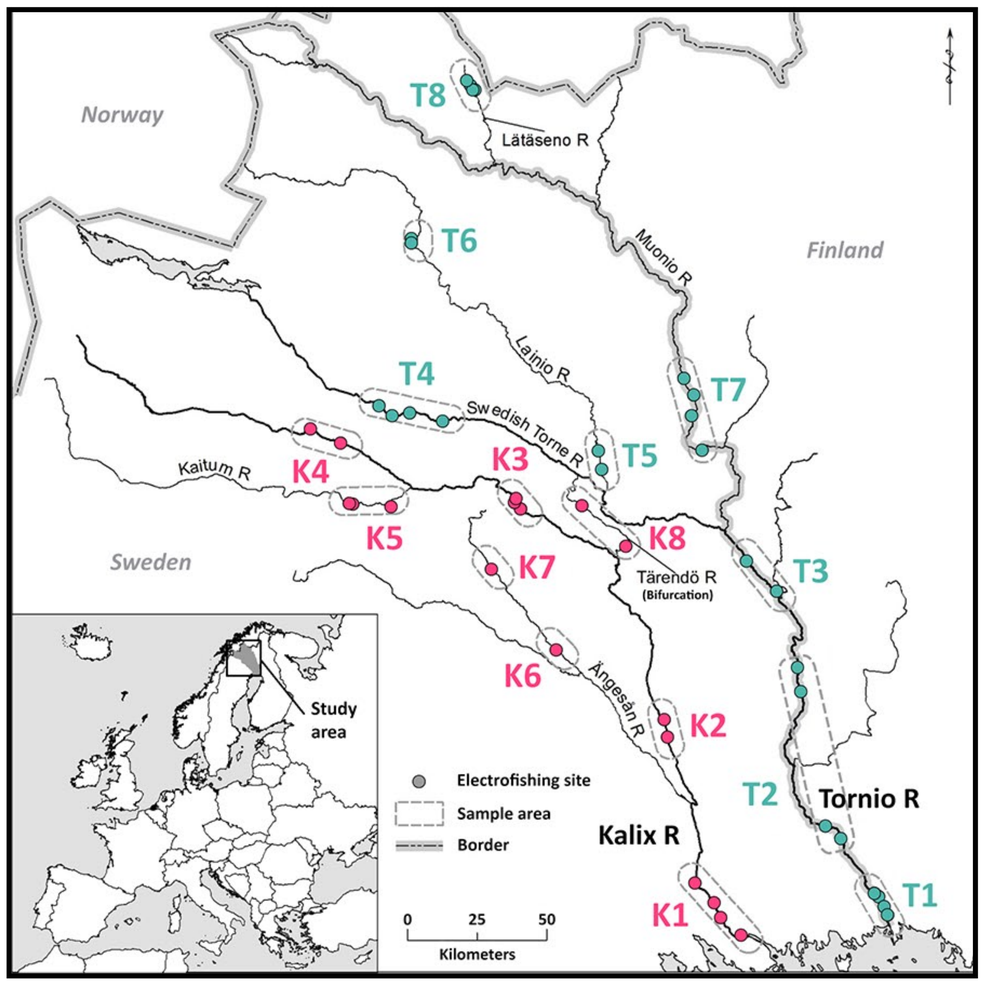
Results

No genetic difference between the Tornio and Kalix rivers (F_{ST} = -0.0004, P = 0.411), but differences between sites within the rivers (F_{ST} = 0.015, P < 0.001)

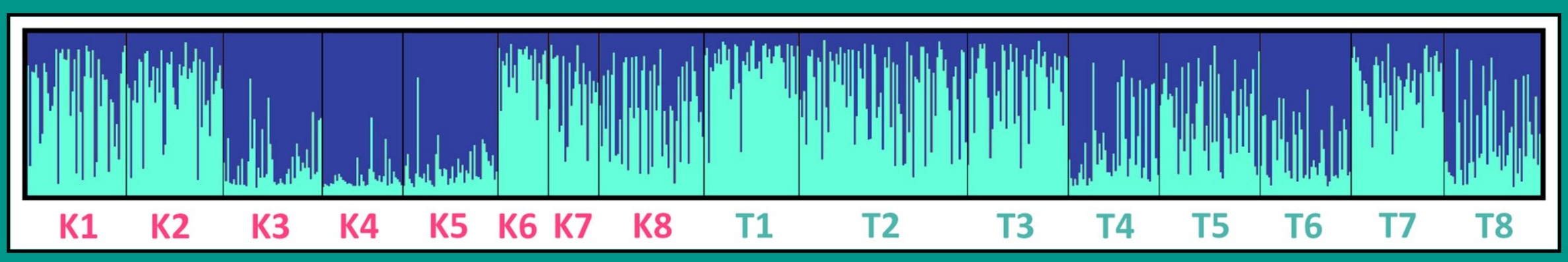
Isolation by distance across the rivers (r = 0.49, P < 0.001) and within them (Tornio: r = 0.49, P = 0.046; Kalix: r = 0.71, P = 0.002)

Within each river, downstream and upstream populations appear genetically differentiated

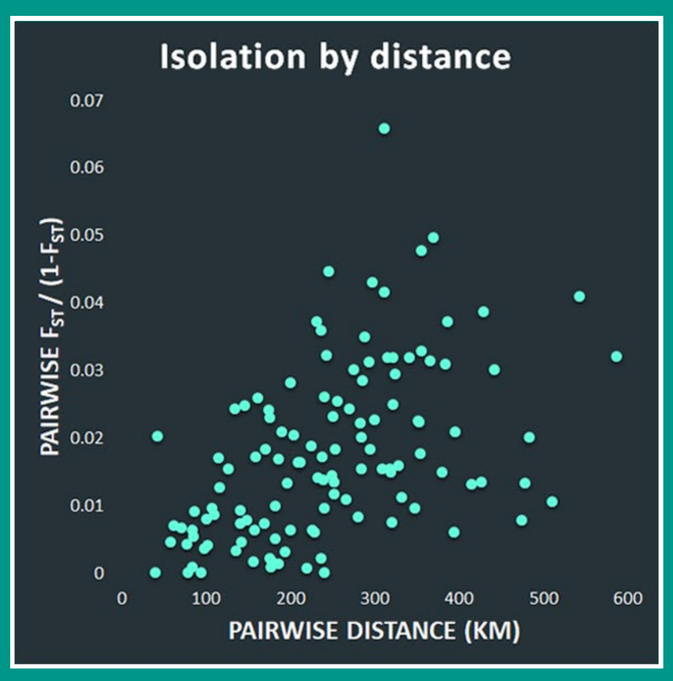
TORNIO-KALIX RIVER SYSTEM

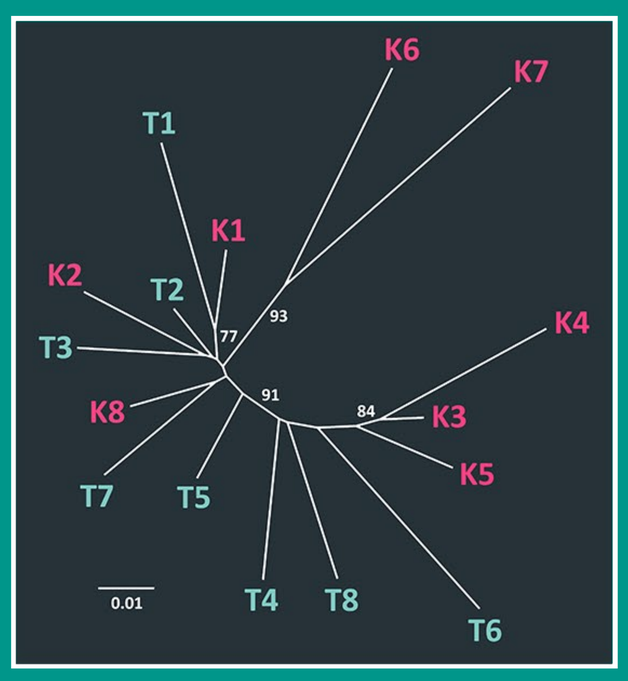


Material & methods: 749 juvenile salmon sampled from marked locations (K1-K8 & T1-T8) were analyzed with 18 microsatellite markers



Genetic structure in the river system based on Bayesian clustering by the STRUCTURE software





Neighbour-joining tree based on Nei's D_A, with support values (%) based on 5,000 bootstraps

Discussion

Relatively weak population structure compared to other large salmon rivers in the region

No separate stocks in the Tornio and Kalix rivers
⇨ Significance for management?

Future

Genomic analyses of contemporary and historic samples to study adaptive variation and human impact on the populations

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