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Visioconférence Jitsi

DEMOGRAPHIC HISTORY SHAPED WITHIN SPECIES VARIATION IN THE DELETERIOUS MUTATION LOAD IN A BROADLY DISTRIBUTED PACIFIC SALMON

par

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📍 A thorough reconstruction of historical processes is necessary to understand the genomic and geographical distribution of nucleotide diversity. Past and current conditions influencing effective population size have important evolutionary implications for the efficacy of selection, increased accumulation of deleterious mutations, and loss of adaptive potential. Here, we gather extensive genome-wide data that represent the extant diversity of the Coho salmon (*Oncorhynchus kisutch*) to address two objectives.

📍 First, we demonstrate that a single glacial refugium is the source of most of the present-day genetic diversity, with detectable inputs from a putative secondary micro-refugia. We found statistical support for a scenario whereby ancestral populations located south of the ice sheets expanded in postglacial time, swamping out most of the diversity from other putative micro-refugia. Our demographic inferences further accounted for linked selection revealing that large parts of the genome were affected by this process.

📍 Second, we demonstrate that the recent demographic history of this species generated differences in the load of deleterious mutations among populations, a finding that mirrors recent results from human populations and provides increased support for models of expansion load. Taken together, we found considerable support for the joint contribution of demographic history and linked selection to the load of deleterious mutations. We suggest that insights from these inferences should be better integrated in conservation planning of wild organisms which currently focuses largely on neutral genetic diversity and local adaptation.

📍 Cet exposé sera donné en français.