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Do sea trout migrations promote interbasin connectivity between populations?

J. Chat*, S. Masson, A. Manicki, F. Gueraud, J. Rives, F. Lange, E. Huchet,
P. Coste, J-C Aymes & O Lepais.

INRA, Saint Pee Sur Nivelle, France.

ABSTRACT

Gene flow is one of the most important factors driving evolution in structured populations. Effective dispersal (i.e. movement followed by reproduction) affects patterns of neutral genetic diversity and influence metapopulation dynamics. Understanding factors shaping gene flow and population connectivity is vital to improve management and conservation practices. Facultative anadromy in brown trout offers a good opportunity to assess the impact of sea trout migration on inter-basin gene flow and population structure.

We genotyped 11 microsatellite loci from 900 juveniles and 700 sea trout collected, respectively, by electrofishing and trapping, across >70 rivers located in south-western France. Using juvenile genotypes as a reference for the background population genetic structure, we were able to quantify and dissociate sea trout movement from effective dispersal. We found that homing and straying behaviours of sea trout vary greatly depending on the source population. We observed a source-sink dynamics of migratory sea trout with asymmetric movements from south to north; which does not necessarily translate into effective dispersal and gene flow.

These findings have important implications for regional management practice and our broader understanding of brown trout population functioning

*Lead Contact: chat@st-pee.inra.fr



Iascach Intíre Éireann
Inland Fisheries Ireland



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BOOK OF ABSTRACTS

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