



Genome Wide Divergence Among population pairs of parasitic and non-parasitic lampreys (*Lampetra fluviatilis* and *L. planeri*)

Quentin Rougemont, Sophie Launey, Arnaud Gaigher, Anne-Laure Besnard, Emilien Lasne, Guillaume Evanno

► To cite this version:

Quentin Rougemont, Sophie Launey, Arnaud Gaigher, Anne-Laure Besnard, Emilien Lasne, et al.. Genome Wide Divergence Among population pairs of parasitic and non-parasitic lampreys (*Lampetra fluviatilis* and *L. planeri*). 144. Annual Meeting of the American Fisheries Society, Aug 2014, Québec, Canada. , 2014. hal-01210215

HAL Id: hal-01210215

<https://hal.science/hal-01210215>

Submitted on 2 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

hypothesis of eastern Atlantic affinities of salmon in southeastern Newfoundland This work highlights the utility of RAD-seq based approaches for the resolution of complex spatial patterns, further resolves a region of trans-Atlantic secondary contact in Atlantic salmon, and reinforces the difficulty in identifying loci associated with adaptive divergence under complex demographic scenarios

T-205A-13 Detecting Genotypic Changes Associated with Selective Mortality at Sea in Atlantic Salmon: Polygenic Multilocus Analysis Surpasses Genome Scan

Vincent Bourret*, Université Laval, Melanie Dionne, Ministère du Développement Durable, de l'Environnement, de la Faune et des Parcs and Louis Bernatchez, IBIS, Université Laval

Here, we genotyped 5568 SNPs in Atlantic salmon populations across two cohorts to test for differential allelic and genotypic frequencies between juveniles (smolts) migrating to sea and adults (grilses) returning to freshwater after one year at sea Given the complexity of the traits potentially associated with sea mortality, we contrasted the outcomes of a single-locus F_{ST} based genome scan method with a new multi-locus framework to test for genetically-based differential mortality at sea While numerous outliers were identified by the single-locus analysis, no evidence for parallel, temporally repeated selection was found In contrast, the multi-locus approach detected repeated patterns of selection for a multi-locus group of 34 SNPs in one of the two populations No significant pattern of selective mortality was detected in the other population, suggesting different causes of mortality among populations Overall, these results support the hypothesis that selection mainly causes small changes in allele frequencies among many co-varying loci rather than a small number of changes in loci with large effects Consequently, moving away from the “selective sweep paradigm” and towards a multi-locus genetics framework may be a more useful approach for studying the genomic signatures of natural selection on complex traits in wild populations

T-205A-14 Genome-Wide Divergence Among Population Pairs of Parasitic and Non-Parasitic Lampreys (*Lampetra fluviatilis* and *L. planeri*)

Quentin Rougemont*, INRA UMR Ecologie et Santé des Ecosystèmes, Sophie Launey, INRA UMR Ecologie et Santé des Ecosystèmes, Arnaud Gaigher, Université de Lausanne, Anne-Laure Besnard, INRA UMR Ecologie et Santé des Ecosystèmes, Emilien Lasne, INRA UMR CARRTEL and Guillaume Evanno, INRA UMR Ecologie et Santé des Ecosystèmes

The degree of speciation between the European ‘paired’ species *Lampetra planeri* (Lp) and *Lampetra fluviatilis* (Lf) is unclear as these taxa are morphologically and phylogenetically very similar and may represent two ecotypes of a single species We investigated the level of gene flow between Lf and Lp populations in France using population genetics (13 microsatellites loci) and genomics (RAD sequencing) approaches We aimed at *i*) comparing the estimates of gene flow between sympatric Lf and Lp populations obtained with microsatellite and RAD markers and *ii*) identifying RAD loci putatively involved in the adaptive divergence between species Results based on the microsatellite genotyping of 665 individuals from six river systems revealed moderate to strong levels of gene flow between Lf and Lp populations sampled in the same rivers Estimates of genetic differentiation were much higher among Lp than Lf populations with the latter displaying higher levels of genetic diversity Overall, these results support the hypothesis that Lf and Lp are two ecotypes of a single species but common garden experiments are required to validate this hypothesis These results also suggest that the connectivity between Lp and Lf populations should be restored to maintain high levels of genetic diversity in Lp populations