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- Svenning M.-A., Falkegård M., Niemelä E., Vähä J.-P., Wennevik V., Ozerov M., Prusov S., Dempson J. B., Power M., Fauchald P. (2019) Coastal migration patterns of the four largest Barents Sea Atlantic salmon stocks inferred using genetic stock identification methods. (2019) **ICES Journal of Marine Science** 76: 1379–1389
- Mobley K., Granroth-Wilding H., Ellmen M., Vähä J.-P., Aykanat T., Johnston S., Orell P., Erkinaro J., Primmer C. (2019) Home ground advantage: Local Atlantic salmon have higher reproductive fitness than dispersers in the wild. **Science Advances** 5:
- Aykanat T., Ozerov M., Vähä J.-P., Orell P., Niemelä E., Erkinaro J., Primmer C. (2019) Co-inheritance of sea age at maturity and iteroparity in the Atlantic salmon vglI3 genomic region. **Journal of Evolutionary Biology** 32: 343-355
- Pritchard V., Mäkinen H., Vähä J.-P., Erkinaro J., Orell P., ja Primmer C., (2018) Genomic signatures of fine-scale local adaptation in Atlantic salmon suggest involvement of sexual maturation, energy homeostasis, behaviour, and immune defence-related genes. **Molecular Ecology** 27: 2560-2575.
- Gilbey J., Coughlan J., Wennevik V., Prodöhl P., Cauwelier E., Cherbonnel C., Coulson M. W., Cross T., Crozier W., Dillane E., Ellis J., Ensing D., Garcíá-Vázquez E., Griffiths A. M., Gudjonsson S., Hindar K., Karlsson S., Knox D., Machado-Schiaffino G., Meldrup D., Nielsen E. E., Ólafsson K., Primmer C., Prusov S., Stradmeyer L., Stevens J. R., Vähä J.-P., Veselov A., Webster L. M. I., McGinnity P. and Verspoor E. (2017) A microsatellite baseline for genetic stock identification of European Atlantic salmon (*Salmo salar* L.). **ICES Journal of Marine Science in press**
- Vasemägi A., Nousiainen I., Saura A., Vähä J.-P., Valjus J., Huusko A. (2017) First record of proliferative kidney disease agent *Tetracapsuloides bryosalmonae* in wild brown trout and European grayling in Finland. **Diseases of Aquatic Organisms**, 125:73-78.
- Ozerov M., Vähä J.-P., Wennevik V., Niemelä E., Svenning M.-A., Prusov S., Diaz Fernandez R., Unneland L., Vasemägi A., Falkegård M., Kalske T., and Christiansen B. (2017) Comprehensive microsatellite baseline for genetic stock identification of Atlantic salmon (*Salmo salar* L.) in northernmost Europe. **ICES Journal of Marine Science** 74: 2159-2169.
- Vähä J.-P., Erkinaro J., Niemelä E., Falkegård M. (2016) Genetic stock identification of Atlantic salmon and its evaluation in a large population complex. **Canadian Journal of Fisheries and Aquatic Sciences** 74: 327–338
- Kahar S., Debes P.V., Vuori K.A.M., Vähä J.-P., and Vasemägi A., (2016) Heritability, Environmental Effects, and Genetic and Phenotypic Correlations of Oxidative Stress Resistance-Related Enzyme Activities During Early Life Stages in Atlantic Salmon. **Evolutionary Biology** 43:215-226
- Kjærner-Semb E., Ayllon F., Furmanek T., Wennevik V., Dahle G., Niemelä E., Ozerov M., Vähä J.-P., Glover K.A., Rubin C.J., Wargelius A., and Edvardsen R.B. 2016. Atlantic salmon populations reveal adaptive divergence of immune related genes - A duplicated genome under selection. **BMC Genomics** 17: 610-622.
- Ozerov M.Y., Gross R., Bruneaux M., Vähä J.-P., Burimski O., Pukk L., Vasemägi A. 2016. Genomewide introgressive hybridization patterns in wild Atlantic salmon influenced by inadvertent gene flow from hatchery releases. **Molecular Ecology** 6: 1275-1293.

- Jensen A., Gilbey J., Friedland K., McGinnity P., Mork K. J., Coughlan J., Cross T., Einarsson S., Ensing D., Erkinaro J., Fiske P., Garcia de Leaniz C., Hansen L.P., Haugland M., Holm M., Holst J.C., Jacobsen J.A., Karlsson S., Ó Maoléidigh N., Nielsen E., Primmer C., Prodohl P., Stevens J., Thomas K., Vähä J.-P., Verspoor E., Wennevik V., Whelan K. 2014. Increased understanding of the marine life of a migratory fish gained by combining data on an individual's ecology and genetic assignment. Submitted to **Proceedings of the Royal Society B**
- Ozerov M., Vasemägi A., Wennevik V., Diaz-Fernandez R. Niemelä E., Prusov S., Kent M.P., and Vähä J.-P. 2013 Finding markers that make a difference: DNA pooling and SNP-arrays identify population informative markers for genetic stock identification. **PLOS One** 8(12): e82434. doi:10.1371/journal.pone.0082434
- Johnston S.E., Lindqvist M., Niemelä E., Orell P., Erkinaro J., Kent M.P., Lien S., Vähä J.-P., Vasemägi A., and Primmer C. 2013. Fish scales and SNP chips: SNP genotyping and allele frequency estimation in individual and pooled DNA from historical samples of Atlantic salmon (*Salmo salar*). **BMC Genomics** 14: 439-447
- Ozerov M., Vasemägi A., Wennevik V., Niemelä E., Prusov S., Kent M.P., and Vähä J.-P. 2013 Cost-effective genome-wide estimation of allele frequencies from pooled DNA in Atlantic salmon (*Salmo salar* L.). **BMC Genomics** 14: 12-21
- Papakostas, S., Vasemägi A., Vähä, J.-P., Himberg, M., Peil, L., Primmer, C. 2012. A proteomics approach reveals divergent molecular responses to salinity in populations of European whitefish (*Coregonus lavaretus*). **Molecular Ecology** 21: 3516-3530
- Ellis J.S., Gilbey J., Armstrong A., Balstad T., Cauwelier E., Cherbonnel C., Consuegra S., Coughlan J., Cross T.F., Crozier W., Dillane E., Ensing D., García de Leániz C., García-Vázquez E., Griffiths A.M., Hindar K., Hjørleifsdottir S., Knox D., Machado-Schiaffino G., McGinnity P., Meldrup D., Nielsen E.E., Olafsson K., Primmer C.R., Prodohl P., Stradmeyer L., Vähä J.P., Verspoor E., Wennevik V., Stevens J.R. 2011. Microsatellite standardization and evaluation of genotyping error in a large multi-partner research programme for conservation of Atlantic salmon (*Salmo salar* L.). **Genetica** 3: 353-67
- Vähä J.-P., Erkinaro J., Niemelä E., Saloniemi I., Primmer C.R., Johansen M., Svenning M. and Brørs S. 2011. Temporally stable population-specific differences in run timing of one-sea-winter Atlantic salmon returning to a large river system. **Evolutionary Applications** 4: 39–53.
- Erkinaro J, Niemelä E, Vähä J-PK, Primmer CR, Brørs S, Hassinen E, Orell P & Länsman M. 2010. Distribution and biological characteristics of escaped farmed salmon in a major subarctic salmon river, River Teno, Finland/Norway). **Canadian Journal of Fisheries and Aquatic Sciences** 67:130–142
- Vähä, J.-P., J. Erkinaro, E. Neimelä, and C. R. Primmer. 2008. Temporally stable genetic structure and low migration in an Atlantic salmon population complex: implications for conservation and management. **Evolutionary Applications** 1:137–154.
- Vähä, J.-P., J. Erkinaro, E. Niemelä, and C.R. Primmer. 2007. Life–history and habitat features influence the within–river genetic structure of Atlantic salmon. **Molecular Ecology** 16:2638–2654.
- Vähä, J.-P. ja Primmer, C.R. 2006. The efficiency of model-based Bayesian methods for detecting hybrid individuals under different hybridization scenarios and with different numbers of loci. **Molecular Ecology** , 15: 63–72