

From: molec@wiley.com

Subject: Request to Review 'Adaptive genomic divergence under high gene flow between freshwater and brackish-water ecotypes of prickly sculpin (*Cottus asper*) revealed by Pool-Seq' for Molecular Ecology

Date: 26 January 2016 at 18:01

To: baochengguo@gmail.com

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26-Jan-2016

Dear Dr. Guo:

A manuscript titled "Adaptive genomic divergence under high gene flow between freshwater and brackish-water ecotypes of prickly sculpin (*Cottus asper*) revealed by Pool-Seq" has been submitted to Molecular Ecology (Manuscript ID MEC-16-0059). We would appreciate your expert opinion on this manuscript. The author names and abstract appear at the end of this letter.

If you are able to review, please click the "Agreed" link below, which will automatically register your reply with our online manuscript system, Manuscript Central. You'll also be sent an e-mail containing reviewer instructions, access information for your online Reviewer Centre, and a direct link to the manuscript under review.

To ensure an efficient review process, we ask that you return your review within two weeks. If you need an extension to this deadline, please contact our editorial office (molec@wiley.com). Please note that there may be a delay with registering your reply in our system if you respond via email. We ask for your patience with any automatic reminders that you may receive in the interim.

If you are unable to review at this time, we would appreciate suggestions for other suitable reviewers; these can be entered after you click the "Declined" link below.

Policy on Conflicts of Interest: Please consider whether you have any conflict(s) of interest that may have an impact on the impartiality of your review (including in relation to any Company and/or commercial product mentioned in the article). If your conflict is serious enough to preclude your participation, you should decline this invitation to review. For example, if you are currently collaborating with the author(s) or contributed substantially to the manuscript, then you should decline this request. More diffuse connections (such as past or future collaborations, or sample donations) may be fine, but please describe these in the 'confidential comments' section of your review. Please contact the Editorial Office prior to accepting this invitation if you'd like to discuss what constitutes a serious conflict.

Molecular Ecology may refer good quality papers that we are unable to accept to the open access journal Ecology and Evolution. If the authors choose to transfer their manuscript, any peer reviewer reports will be transferred as well. A primary objective of this collaboration is to efficiently channel papers to an appropriate journal without the need for additional rounds of peer review.

Papers published in Molecular Ecology should use multi-locus molecular genetic techniques to address consequential questions in ecology, evolution, behaviour and conservation. We discourage papers that are primarily descriptive and relevant only to the taxon being studied. Our expert reviewers greatly contribute to maintaining these high standards, and we thank you for your participation.

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Best regards,
Shuqing Xu
Editor, Molecular Ecology

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MANUSCRIPT DETAILS

TITLE: Adaptive genomic divergence under high gene flow between freshwater and brackish-water ecotypes of prickly sculpin (*Cottus asper*) revealed by Pool-Seq

AUTHORS: Dennemoser, Stefan; Vamosi, Steven; Nolte, Arne; Rogers, Sean

SUBJECT EDITOR: Dr. Shuqing Xu

ABSTRACT: Understanding the genomic basis of adaptive divergence in the presence of gene flow remains a major challenge in evolutionary biology. In prickly sculpin (*Cottus asper*), an abundant euryhaline fish in northwestern North America, high genetic connectivity among brackish-water (estuarine) and freshwater (tributary) habitats of coastal rivers does not preclude the build-up of neutral genetic differentiation and emergence of different life history strategies. Because these two habitats present different osmotic niches, we predicted high genetic differentiation at known teleost candidate genes underlying salinity tolerance and osmoregulation. We applied whole genome sequencing of pooled DNA samples (Pool-Seq) to explore adaptive divergence between two estuarine and two tributary habitats. Paired-end sequence reads were mapped against the similar genomes of threespine stickleback and European Cottus to characterize the gene content of candidate regions. Sodium/potassium ATPase (*atp1a1a*) and Na⁺/Cl⁻ co-transporter (NCC) genes showed strong signals of repeated differentiation among brackishwater-freshwater comparisons, indicating their potential role in local adaptation to different osmotic niches. Overall, the presence of both repeated and unique signatures of differentiation across many loci scattered throughout the genome demonstrates a role for polygenic adaptation from standing genetic variation and locally variable selection pressures in the early stages of life history divergence.

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