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Sent: 04 January 2017 11:43

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Subject: Royal Society Open Science - Decision on Manuscript ID RSOS-160548.R1

04-Jan-2017

Dear Mr Vendrami,

I am pleased to inform you that your manuscript entitled "ddRAD sequencing resolves fine-scale population structure in a benthic invertebrate with implications for understanding phenotypic plasticity" is now accepted for publication in Royal Society Open Science.

You can expect to receive a proof of your article in the near future. Please contact the editorial office (openscience_proofs@royalsociety.org and openscience@royalsociety.org) to let us know if you are likely to be away from e-mail contact. Due to rapid publication and an extremely tight schedule, if comments are not received, your paper may experience a delay in publication.

Royal Society Open Science operates under a continuous publication model (<http://bit.ly/cpFAQ>). Your article will be published straight into the next open issue and this will be the final version of the paper. As such, it can be cited immediately by other researchers. As the issue version of your paper will be the only version to be published I would advise you to check your proofs thoroughly as changes cannot be made once the paper is published.

In order to raise the profile of your paper once it is published, we can send through a PDF of your paper to selected colleagues. If you wish to take advantage of this, please reply to this email with the name and email addresses of up to 10 people who you feel would wish to read your article.

On behalf of the Editors of Royal Society Open Science, we look forward to your continued contributions to the Journal.

Kind regards,
Alice Power
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Reviewer(s)' Comments to Author:

Reviewer: 1

Comments to the Author(s)

Authors have thoroughly addressed comments from both referees. I am glad the authors have found the contribution of both reviewers valuable, leading to a significantly improved manuscript. I do not have any objections to recommend acceptance (as is).

Journal Name: Royal Society Open Science Journal Code: RSOS Online ISSN: 2054-5703 Journal Admin Email: openscience@royalsociety.org Journal Editor: Emilie Aime Journal Editor Email: emilie.aime@royalsociety.org MS Reference Number: RSOS-160548.R1 Article Status: ACCEPTED MS Dryad ID: RSOS-160548.R1 MS Title: ddRAD sequencing resolves fine-scale population structure in a benthic invertebrate with implications for understanding phenotypic plasticity MS Authors: Vendrami, David; Telesca, Luca; Weigand, Hannah; Weiss, Martina; Fawcett, Katie; Lehman, Katrin; Clark, Melody; Leese, Florian; McMinn, Carrie; Moore, Heather; Hoffman, Joseph Contact Author: David Vendrami Contact Author Email: david.vendrami@student.unife.it Contact Author Address 1: University of Bielefeld Contact Author Address 2: Postfach 100131 Contact Author Address 3: 33501 Bielefeld Contact Author City: Bielefeld Contact Author State:

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Keywords: Pecten maximus, phenotypic plasticity, microsatellite, single nucleotide polymorphism, morphometrics, great scallop

Abstract: The field of molecular ecology is transitioning from the use of small panels of classical genetic markers such as microsatellites to much larger panels of SNPs generated by approaches like RAD sequencing. However, few empirical studies have directly compared the ability of these methods to resolve population structure. This could have implications for understanding phenotypic plasticity, as many previous studies of natural populations may have lacked the power to detect genetic differences, especially over micro-geographic scales. We therefore compared the ability of microsatellites and RAD sequencing to resolve fine-scale population structure in a commercially important benthic invertebrate by genotyping great scallops (*Pecten maximus*) from nine populations around Northern Ireland at 13 microsatellites and 10,539 SNPs. The shells were then subjected to morphometric and colour analysis in order to compare patterns of phenotypic and genetic variation. We found that RAD sequencing was superior at resolving population structure, yielding higher F_{st} values and support for two distinct genetic clusters whereas only one cluster could be detected in a Bayesian analysis of the microsatellite dataset. Furthermore, appreciable phenotypic variation was observed in size-independent shell shape and colouration, including among localities that could not be distinguished from one another genetically, providing support for the notion that these traits are phenotypically plastic. Taken together, our results suggest that RAD sequencing is a powerful approach for studying both population structure and phenotypic plasticity in natural populations.

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