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Proposal Review 1 : 2127466

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Agency Name: National Science Foundation

Agency Tracking Number: **2127466**

Organization:

NSF Program: OCE Postdoctoral Fellowships

PI/PD: Gatins, Remy

Application Title: OCE-PRF-Deleterious mutational load in climate driven marine range expansions

Rating: Excellent

Review

Summary

In the context of the five review elements, please evaluate the strengths and weaknesses of the proposal with respect to intellectual merit.

Strengths

EecSeq represents a cost-effective approach to subsample genomes for coding regions, without previously developed genomic resources for the species, making it suitable for non-model species such as the Black Sea Bass. EecSeq synthesizes probes in situ from expressed mRNA sequences, and it does not require having a draft genome in hand.

Sponsoring scientist Dr. Lotterhos developed EecSeq and so is an appropriate choice.

The experimental design, and outline of hypotheses is logical and robust, not withstanding minor comments below.

Weaknesses

The study might benefit from expanded sampling, for multiple reasons.

Selection of what geography constitutes the edge of the species' range (between Long Island and the historical range end at Cape Cod) is selected by the researcher is arbitrary; a sensitivity analysis to different locations for the range center-edge boundary would help determine the robustness of the results. It is unclear if the proposed sample size (450 individuals, 150 from each region) is adaptable to changing the center-edge border for a sensitivity analysis.

The study focuses on juveniles to avoid individuals that may have immigrated to the sampling area. Expanding the sampling to cover recruits (also unlikely to have swam into the sampling area) could enable comparison between recruits and juveniles, which could reveal selection against deleterious

alleles that are weeded out by the juvenile stage.

The samples to be analyzed represent a combination of archived samples and to-be-collected samples, all spanning at least 3 years. Is there a concern for confounding effect of sampling year, and could this be controlled for (e.g., via larger to-be-collected sample size, all in one year, so that it could be analyzed independently)?

For the phenotypic analysis, controlling for sex could be important and does not seem to be included in the proposed analysis.

The phenotypic analysis covers three conditions (body length-weight ratio, % protein, and C:N ratio). It is unclear how interpretation will proceed if the conditions disagree in their correlation with deleterious mutation load.

EecSeq is limited in the sense that the probes are designed from expressed RNA, and so investigators should be careful to choose which tissues and life stages would be relevant. The study mentions muscle, fin and gill tissue, but does not specify if/what tissues will be the focus of the research.

In the context of the five review elements, please evaluate the strengths and weaknesses of the proposal with respect to broader impacts.

Strengths

Broader Impacts effect students at university and K-12 levels, and community members (the public, fishers).

Weaknesses

Nothing to report

Please evaluate the strengths and weaknesses of the proposal with respect to any additional solicitation-specific review criteria, if applicable

Summary Statement

The proposal is to test for increased presence of deleterious mutations and their effect on fitness at the range end of a range-expanding species, using Black Sea Bass (*Centropristis striata*) along the US East coast as a case study and expressed exome capture sequencing (EecSeq) and PROVEAN molecular and bioinformatic methods for identifying genomic loci under selection and with deleterious allele changes, and measurement of morphometric and physiological proxies of phenotypic fitness in individuals collected in the species' historical and expanded range. The study will further test for the effect of fishing (harvest of the model species) on accumulation of deleterious alleles in the expanded range using a simulation model.

The theme of the research on accumulation of deleterious alleles and loss of fitness in marine species exhibiting range shifts due to climate change, and exacerbating effects of fisheries on deleterious allele accumulation and fitness loss, is highly timely and of great intellectual and practical interest. Background understanding of the topic is robust, and the experimental design and hypotheses are, for the most part, logical and compelling. The host organization and sponsoring scientists will provide valuable support for the project's success.

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