United States Department of Agriculture
National Institute of Food and Agriculture

UMassAmherst | College of Natural Sciences
Center for Agriculture, Food, and the Environment

MHC Class IIβ Exon 2 Diversity in Fragmented Brook Trout *(Salvelinus fontinalis)* Populations

By: Jessalyn Kaur

Objective:

The goal of this study is to understand how habitat fragmentation and changing environmental conditions impact disease resistence.

Image (1): Map of study cite (Teffer, A, [image]) Image (2): Image of Brook Trout (Salvelinus fontinalis. *Learning*. North Carolina Wildlife Resources Commission. (n.d.). Retrieved September 13, 2021, from https://www.ncwildlife.org/Learning/Species/Fish/Brook-Trout.

Introduction

- Brook trout are an ideal model system to observe the impact of fragmentation as many populations are already spatially constrained due to restrictive habitat configurations
- One way to examine disease resistance is by characterizing an organism's functional diversity by looking at variation in the Major Histocompatibility Complex (MHC) genes.
- Different populations experience varying environmental factors according to their location, including pathogen types and loads, which can lead to variation in their MHC genes.
- **The level of diversity among fragmented populations in MHC Class IIβ exon 2 region will give vital information regarding the ability of Brook Trout to combat shifts in pathogen exposure due to changing environmental conditions and fragmentation.**

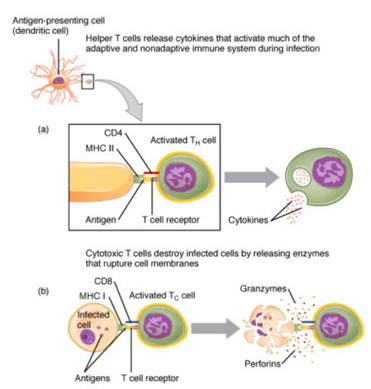

Image (3): MHC Class II mechanism. Betts, J et al., (2019) [image]. Open Stax. https://opentextbc.ca/anatomyandphysiologyopenstax/

Hypotheses:

1. Because certain populations have been isolated from one another due to habitat fragmentation, **I hypothesize that isolated populations will have different MHC diversity relative to connected metapopulations as the environmental factors will differ between populations.**

2. I hypothesize that fragmented populations will have lower functional versus neutral diversity when compared to non-fragmented populations as fragmented populations will have smaller range environmental stressors and therefore not undergo rapid selection.

Methods:

1. DNA extraction

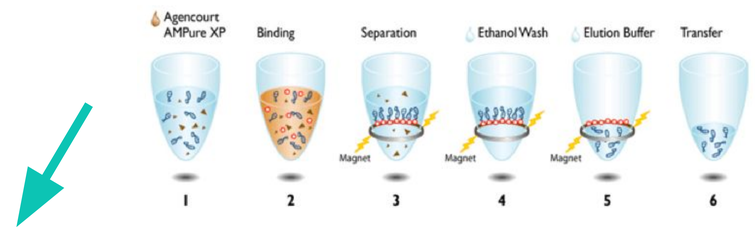

Image (4): Ampure DNA extraction diagram. Beckma Coulter. (2013). Agencourt AMPure XP Protocol, PN B37419AA. *Economic Studies, 63(2): 97-109*, *August*, 1–86. www.beckmancoulter.com

2. Amplicon Workflow

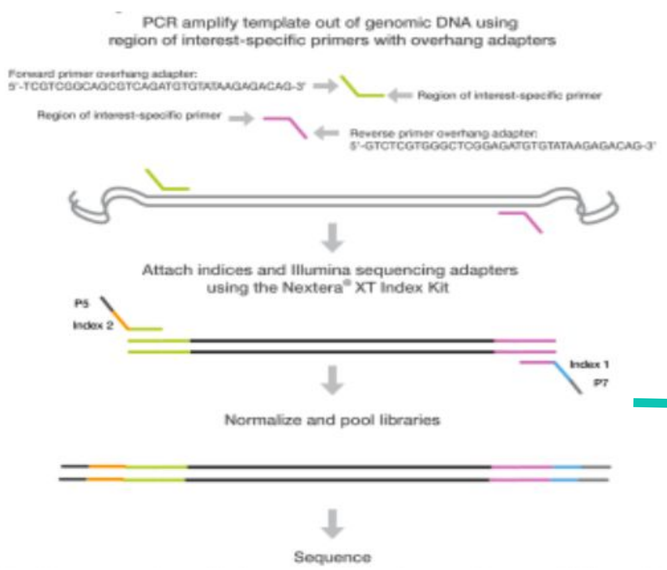

Image (5): 16S two step PCR workflow. Illumina. (2013). 16S Metagenomic Sequencing Library. *Illumina.Com*, *B*, 1–28. http://support.illumina.com/content/dam/illumina-support/documents/documentation/chemistry_documentation/16s/16s-metagenomic-library-prep-guide-15044223-b.pdf

3) Bioinformatics analysis using R to quantify the allelic diversity within and among locations

Image (6) R logo. R®

Future Steps:

- **Complete second round of PCR on all samples followed by normalization and a pooling step before gene sequencing**
- **Data will then be analyzed using R studio and Genious**

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