PhD Samuel 17 January 2018

(Roger, Anja and Samuel)

1. CZDoff and CZoff experiment

Swedish populations (CZDoff):

Wave-like tanks have been cleaned and all individuals phenotyped and dissected before the Christmas break. These populations contained already the second-generation offspring.

Tanks without any evident presence of offspring were left untouched.

<u>Next:</u>

Week 6 (12 Feb 2018) Samuel will check again the status of the individuals and plan the next sampling accordingly.

Analysis of CZoff

Aim: Evaluate whether phenotypic clines observed in the wild are replicated in the lab

Expectation #1: Plastic effect, shallow clines and decrease in variance particularly at the hybrid zones where the natural environment is more heterogeneous

Expectation #2: Relaxed Selection effect, cline shifts and increase in variance due to the standardised environment of the lab

Expectation #3: Relaxed Selection and Plastic effect, shallow and shifted clines

The change in the variance is stronger at the centre rather than at the ends of the transect because of the limited amount of variance presence in the pure crab and pure wave habitats.

Method #1: cline fitting for the wild individuals and cline fitting for the lab individuals using mean and variance for each population according to the parental shore position

Method #2: cline fitting for the wild and separate cline fitting for the lab using the population or deme information

Spanish populations:

Snails seems to cope well with the lab environment (closed system) with the exceptions of the individuals in two aquaria.

The water is changed once a week.

<u>Next:</u>

Week 6 (12 Feb 2018) Samuel and Kerstin will remove the adult females from the tanks.

Morphometrics of CZoff

Jenny has developed a friendly Matlab script that allows the position of any points along the shell aperture. These points are then used to fit a cubic spline and thus construct new equidistant data points or coordinates on the aperture. Each snail picture can contain 100-150 x-y coordinates that can be exported for the outline analysis using the R package Momocs.

Next:

Figure out the minimum number of harmonics suitable for the identification of crab and wave ecotypes and deformed and non-deformed apertures.

> Approach: examine the scree plot from a PCA based on the harmonics. Also consider whether a landmark can be included in this analysis.

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2. Mating experiment

The best model for all the contact zones or the best models for each contact zone will be selected after an exhaustive search of all possible subsets or combination of additive and 2-way interaction effects between candidate variables (i.e., female size, size ratio, size ratio squared, size ratio cube, shape, reference ecotype and shore).

Next:

Compare log-likelihoods of 4-shore models with the sum of the 1-shore models

Apply the same strategy to the copulation time

Add the estimates of sexual isolation to Marina's model

Compare standard logistic regression with the Gaussian formulation implemented into a Bayesian framework

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3. INDELs and local adaptation

Variant calling using GATK HaplotypeCaller detects both SNPs and INDELs and the report contains the necessary information for the successive cline analysis step.

Next:

Filter raw variants using the same approach as ANG and CZs. Add specific filters for INDELs, if any.

Distinguish between variants occurring inside and outside the rearrangements using information contained in the linkage map.

First, polarise and look at the unfolded Site Frequency Spectrum of variants outside CRs and compare spectra btw SNPs and INDELs

Expectation #1:

Balancing selection (high number of variants with intermediate frequency, allele frequency distribution shows a bump in the middle) or purifying selection (high number of singletons and very common variants, allele frequency distribution show a valley in the middle)

Expectation #2:

Fewer non-neutral INDELs than non-neutral SNPs because INDELs are longer and thus more likely to be deleterious.