Effects of mountain elevation on the genetic diversity of Blue Mountains Water Skink *(Eulamprus leuraensis)*

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Abstract

Species can respond to global climate change in several different ways, either by persisting in their current environment, migrating, or going extinct. However, with species such as the Blue Mountains Water Skink *(Eulamprus leuraensis)* that are habitat specialists and restricted to montane habitats, migrating, or persisting in new environments may prove difficult. Using the dataset from Dubey and Shine (2010) consisting of 241 individuals and 13 populations, I investigate the effects of mountain elevation on the genetic diversity of *Eulamprus leuraensis* species. I find a significant relationship between allelic richness (AR) and mountain elevation (P=0.0022), with allelic richness increasing with higher elevation. I also find a significant relationship between expected heterozygosity (Hs) and elevation (P=0.0038), with expected heterozygosity increasing with higher elevation. These findings suggest restricted gene flow caused by genetic drift among populations, explaining higher genetic diversity at higher elevation sites than lower elevation sites. The significance of these findings can predict current and potential future trends to a population's gene flow and spatial genetic structure under changing landscape and environmental variables. Knowledge of such trends can guide conservation managers in facilitating appropriate strategies in preventing climate-induced extinction of these endangered populations.

Introduction

Global climate change is ranked as the most significant threat to biodiversity (Radchuk et al. 2019). Such impacts may well initiate fragmentation, resulting in reduced population size and limited dispersal, and thereby leading to a loss of genetic diversity and gene flow (Radchuk et al. 2019). However, accurately predicting how species and populations respond to climate change remains a difficult task as they can respond in several different ways, either by persisting in their current environment, migrating, or going extinct (Coretes 2016). But considering species that are already restricted to montane habitats, migrating may not be an

option (Razgour 2015). Consistent with that prediction, persistence in new environments may prove difficult for species such as reptiles and amphibians that have low thermal tolerances making them sensitive to climate change (Razgour 2015).

The Blue Mountains water skink *(Eulamprus leuraensis)* is one example of such a taxa that exhibits low thermal tolerances and is restricted to montane habitats (Dubey et al. 2013; Gorisen et al. 2016). *E. leuraensis* is a medium-sized (up to 20cm in length) skink found in the family Scincidae (Dubey et al. 2013). The species are found only in 30 isolated swamps at 560-1060m elevations across the Newnes Plateau and the Blue Mountains of New South Wales Australia. Because the species is restricted to montane areas of high elevations, it may put them at greater risk from global climate change (Dubey et al. 2013). Lower rainfall and higher temperatures are predicted at higher elevations, which can have negative consequences on the lizard's habitat as reduced rainfall and higher temperatures can dry out the hanging swamps (Dubey and Shine, 2010). Because of the species restricted distribution and ongoing threats, they are classified as endangered under the *Environmental Protection and Biodiversity Conservation Act 1999* and the *Threatened Species Conservation Act 1995* (Dubey and Shine, 2010).

Using the dataset from Dubey and Shine (2010) consisting of 241 individuals and 13 populations, I aim to investigate the effects of mountain elevation on the genetic diversity of *E. leuraensis* species. Based on the information from the literature, I hypothesise that there will be a difference in the genetic diversity of *E. leuraensis* populations between mountain elevations. I predict that allelic richness will be lower in higher elevations than lower elevations. I also predict that expected heterozygosity will be lower in higher elevations than lower elevations.

Methods

Data

In this study, I used the data obtained from Dubey and Shine (2010) study comprising of *Eulamprus leuraensis* individuals provided to me by Associate Professor Adam Stow. The data set consists of 241 individuals and 13 populations across the Blue Mountains and Newnes Plateau of New South Wales, Australia.

Statistical Analyses

All statistical analyses were performed using the software package R version (3.1.0) (R Development Core Team 2015). Linear regression was used to assess the relationship between the independent variables (elevation: levels 500, 600, 700, 800, 900, 1000, 1100 metres) and the dependent variables (genetic diversity: levels allelic richness and expected heterozygosity). The statistical null hypothesis for linear regression is that the linear relationship between Y (allelic richness and expected heterozygosity) and X (elevation) is equal to 0. The alternative hypothesis is that the linear relationship between Y (allelic richness and expected heterozygosity) and X (elevation) is not equal to 0.

Assumptions of linear regression are independence of data within and among samples, X variable is measured without error, normality of the residuals about the fitted line, m X + b, homogeneity of variances for residuals about the fitted line m X + b, and a linear relationship. To ensure that this study includes an adequate number of replicates given logical constraints a post-hoc priori power analyses were undertaken on both measurement variables (allelic richness and expected heterozygosity). An arcsin square root-transformation was conducted on allelic richness (dependent) and elevation (independent) variables, to ensure the log-transformed data follow a log-normal distribution. However, expected heterozygosity (dependent) and elevation (independent) did not need to be log-transformed as they followed a normal distribution.

Results

There is a significant relationship between allelic richness (AR) and mountain elevation (Linear regression: Df=1,11, R^2=0.59, P=0.0022), with allelic richness increasing with higher elevation (Figure 1). Therefore, I reject the null hypothesis that the linear relationship between allelic richness and elevation is equal to 0. A 95% confidence interval for the slope is (+/- 0.111, 0.074). A post hoc priori power analysis on allelic richness (Power=0.90), showed that an adequate number of replicates were used in this experiment.
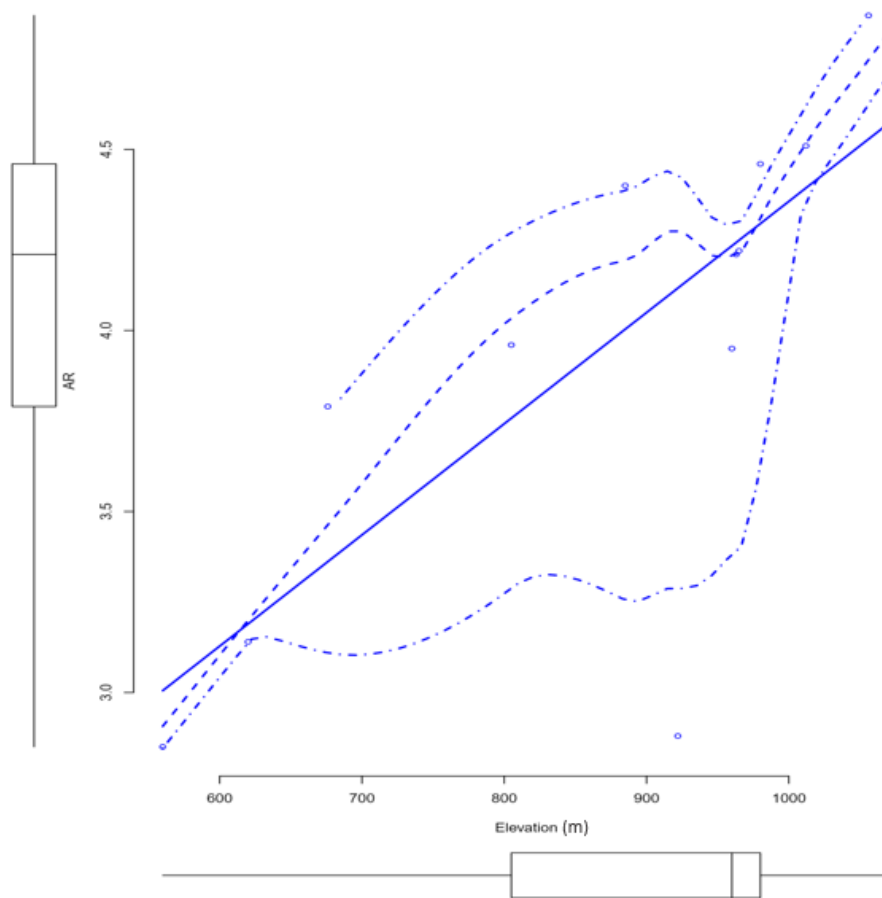
Figure 1: Relationship between elevation (m) and allelic richness (AR) across 13 populations of *E. leuraensis* individuals in the Newnes Plateau and Blue Mountains of New South Wales, Australia.

There is also a significant relationship between expected heterozygosity (Hs) and elevation (Linear regression: Df=1,11, R^2=0.54, P=0.0038) (Figure 2), with expected heterozygosity increasing with higher elevation. Therefore, I reject the null hypothesis that the linear relationship between expected heterozygosity (Hs) and elevation is equal to 0. A 95% confidence interval for the slope is (+/- 1174.62, 322.69). A post hoc priori power analysis on expected heterozygosity (Power=0.90), showed that an adequate number of replicates were used in this experiment.
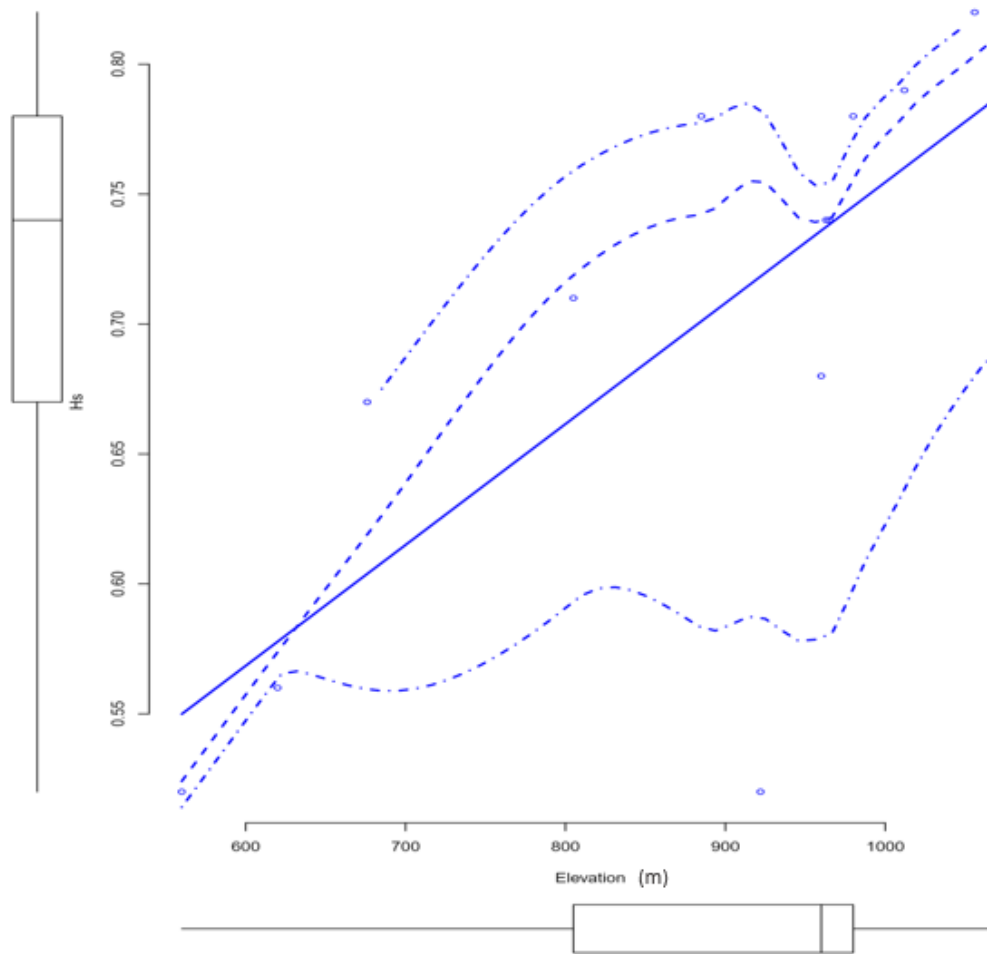
Figure 2: Relationship between elevation (m) and expected heterozygosity (Hs) across 13 populations of *E. leuraensis* individuals in the Newnes Plateau and Blue Mountains of New South Wales, Australia.

Both plots illustrate an approximately linear relationship between allelic richness and elevation and expected heterozygosity and elevation, even though one outlier was detected in each dataset (Figure 3 and 4). This suggests that the assumption the relationship is linear is reasonable. It also illustrates that the variation around the estimated regression line is constant suggesting that the assumption of equal variances is reasonable. The assumption of normality also seems reasonable as values follow a reasonably straight line.
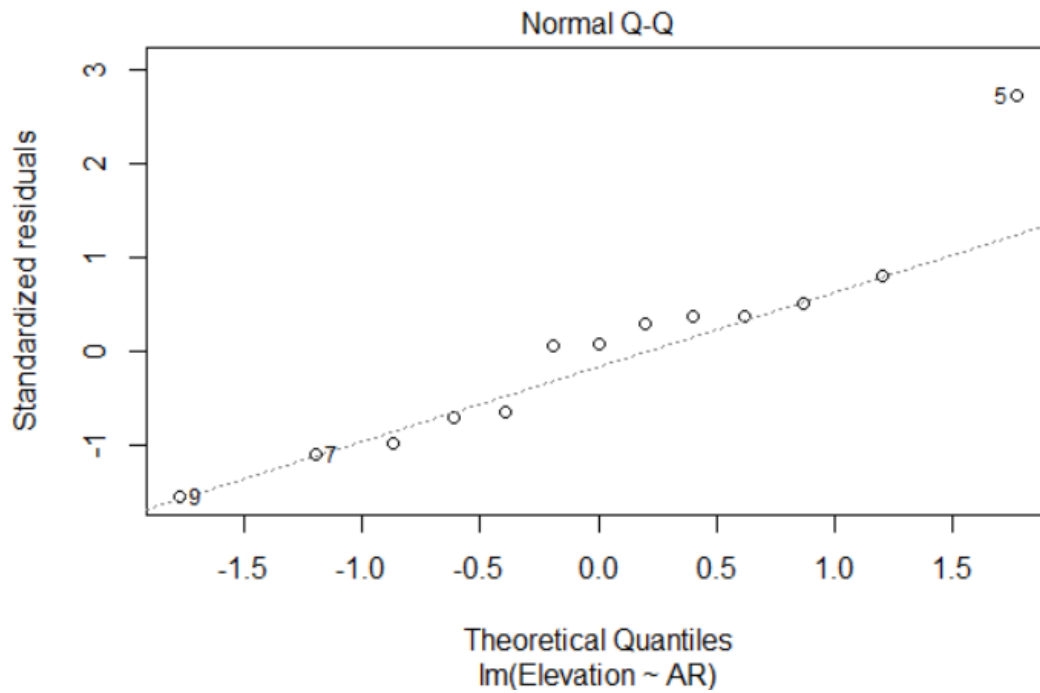
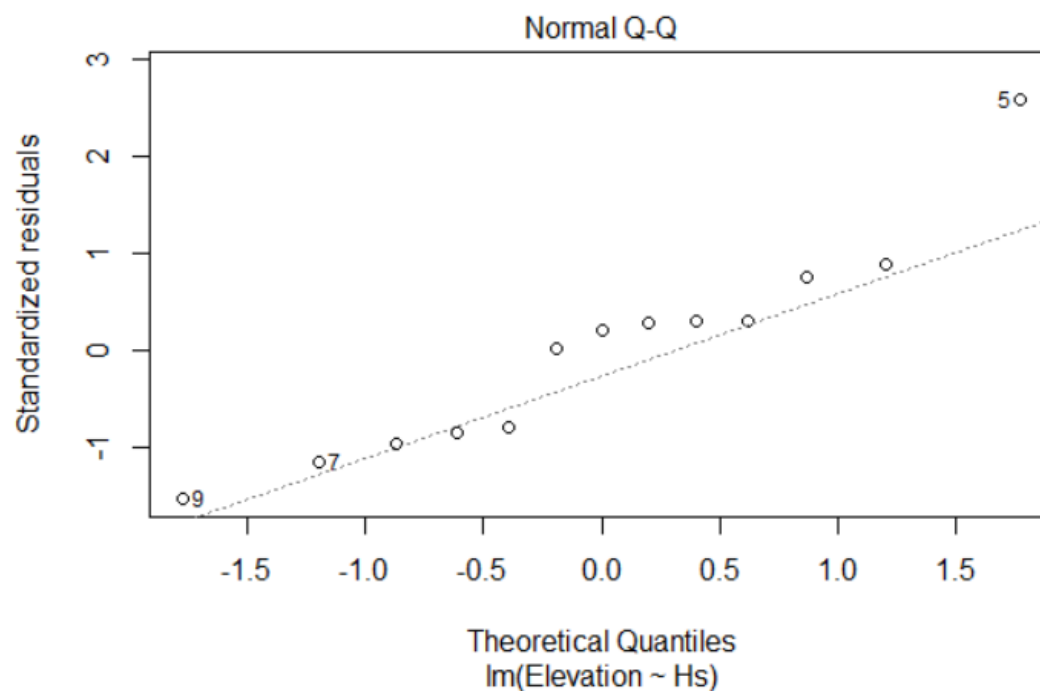Figure 3: Normal qqplot illustrating the relationship between elevation and allelic richness (AR).

Figure 4: Normal qqplot illustrating the relationship between elevation and expected heterozygosity (Hs)

Discussion

Previously, I hypothesized that there will be a difference in genetic diversity of *E. leuraensis* populations between elevations. I predicted that both allelic richness (AR) and expected heterozygosity (Hs) will be lower in higher elevations than lower elevations. However, my results did not support my predictions and revealed that both allelic richness (AR) and expected heterozygosity (Hs) was higher in higher elevations than lower elevations across the 13 populations. My results are consistent with the findings of Polato et al. (2017) in their study of montane mayflies revealing higher genetic diversity at higher elevations than lower elevations. The findings from Polato et al. (2017) study, as well as the findings from my research, suggests reduced gene flow separated by either genetic drift or topographical barriers amongst population sites. Indeed, *E. leuraensis* populations are restricted to 30 isolated swamps separated by about 20km in two distinct patches (in the Newnes Plateau and the Blue Mountains) resulting in population fragmentation and thereby leading to reduced gene flow and genetic differentiation (Dubey and Shine, 2010).

The reduced gene flow of remnant populations of *E. leuraensis* has considerable consequences for the conservation of this endangered species (Coretest 2016; Cushman and Landguth, 2010). Because my study showed higher genetic diversity at high-elevation sites, *E. leuraensis* populations are expected to be at higher risk of climate-induced extinction due to limited amounts of genetic variation and lower effective population size (Radchuk et al. 2019). Climate variation models predict that *E. leuranesis* habitats will become drier (by up to 40%) and warmer (by up to 5 degrees C) within the next century (Razgour 2015). Such changes can have cascading consequences on the lizards and their montane habitats, via an increase in bushfire intensity and frequency, and their swamps drying out (Dubey and Shine, 2010; Gorisen et al. 2016). Furthermore, *E. leuranesis* are also specialist species, making them more sensitive to environmental changes, thus their conservation remains an urgent priority (Dubey and Shine, 2010).

As *E. leuraensis* are an endangered species, previous research has suggested habitat colonization as a potential conservation strategy (Gorisen et al. 2016). However, this method may not be possible as *E. leuraensis* populations inhabit high elevations, hence future work should consider habitat corridors as a potential alternative (Ramiadantsoa et al. 2015). The success of habitat corridors has been demonstrated in Ramiadantsoa et al. (2015) study revealing increased viability and landscape connectivity of fragmented populations in

Madagascar. Future work should also consider the effects of elevation on the genetic diversity of different species and taxa, including their physiological responses to different elevations (Segelbacher et al. 2010). One of the limitations of this study was that it only focused on the effects of mountain elevation on the genetic diversity of one species. Addressing the effects of elevational gradients in different species and taxa will be an important next step in further research into species vulnerability to elevational range shifts and climate change (Polato et al. 2017).

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