Unidirectional Diversity hypothesis in two Salix(willow) species along riparian corridors

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During of the summer of 2014, I continued an investigation of the genetic hypothesis known as the unidirectional diversity hypothesis by using microsatellite assays.

Kermit Ritland’s unidirectional diversity hypothesis is a hypothesis concerning genetic flow relative to the unidirectional flow of abiotic environmental influences, particularly stream flow (Markwith, 2007). Although several potential flow patterns were created, Ritland sought to linearly correlate genetic flow parallel to abiotic environmental force in a “stepping stone” manner in populations down a geographic gradient. According to Markwith and Scanlon, Ritland’s data was not conclusive, and he could not decisively connect genetic flow to unidirectional abiotic flow. As of the Markwith and Scanlon paper, there was a “dearth” of research on the evolutionary processes of riparian macrophytes. Consequently, this study provides an important contribution to the burgeoning wealth of knowledge regarding the unidirectional diversity hypothesis, helping compare Ritland’s hypothesis to other genetic hypotheses and theories such as Richard Levin’s metapopulation theory.¹

This investigation into the unidirectional diversity hypothesis employs microsatellite analysis. Leaf tissue compromises the samples in this study, which come from approximately fourteen sites on the Mokelumne and Cosumnes rivers in California. From each site, there are 40 samples of two species, Red Willow (Salix laevigata) and Sandbar Willow (Salix exigua). Microsatellite analysis analyzes genetic variation of particular genetic loci called microsatellites, or short tandem repeats. Unique genetic markers surround the microsatellites in the subject organism’s genome, which are used to cut out the microsatellites via chemical tools called primers. These excised sections of DNA are then amplified using polymerase chain reaction, which greatly increases the amounts of the DNA fragments to render perceivable and differentiable results during analysis. This study currently involves the amplification of ten genetic loci on the sample organisms’ genomes. Amplification can be unsuccessful for a variety of reasons, so amplifications are tested via gel electrophoresis. Successful amplifications are sent to an outside lab for more advanced chemical analysis that yields more precise data on the location and presence of microsatellites at particular loci. The data from the outside lab is then entered into a genetic analysis software for scoring, which is the process of analyzing the data and entering the results into an excel spreadsheet. The correlation, or lack thereof, to aspects of Ritland’s unidirectional diversity hypothesis will be the main subject of this investigation. This research and subsequent discussion will benefit scientific understanding of microevolution and the anthropogenic effects on microevolution of activities such as dam building (Liu, 2006) and stream restoration (Markwith, 2007). Initial results suggest that Ritland’s hypothesis may be supported, and analysis is being continued. This project may see the addition of an epigenetic aspect in the future.

Faculty Mentor: Vladimir Douhovnikoff
Funded by the Bowdoin College Fellowship in the Life Sciences

References


¹ Hastings, Alan and Harrison, Susan. 1994. Metapopulation Dynamics and Genetics. Annual Review of Ecology and Systematics. 25: 167-188. Levin’s Metapopulation theory concerns the dynamic of populations as they colonize, perish, and recolonize an environment and the effects of these phenomena on the populations, such as populational genetic variation.