



2014 Summer Research Experiences (SRE) for Undergraduates and Teachers

Abstract

BORIBONG, B., CRUZ, M., HONG, F., EARL, J. and S. HOBAN. A meta-analysis of coastal populations' genetic diversity of species throughout their range. National Institute for Mathematical and Biological Synthesis, Knoxville, TN; University of Scranton, Scranton, PA; California State University, San Marcos, CA; Mount Holyoke College, South Hadley, MA.

Higher genetic diversity in the centers of many species' ranges have been thought to account for the abundant-center hypothesis, which states that populations found in the center of their natural distribution are more abundant than those found at the edges. Despite the prevalence of the abundant-center hypothesis in population studies, the assumption of differential genetic diversity throughout ranges has rarely been tested in a rigorous way across many taxa. On the other hand, studies that have tested the genetic variation in plants and animals along their species' ranges did not account for variation in sample sizes among studies. To better test the validity of the abundant center hypothesis, this study investigated how genetic diversity of populations distributing along world's coastlines is affected by location within the species' range using a meta-analysis. As an explanatory factor of genetic diversity among populations, populations' distance to the center of a range is hypothesized to be positively correlated with the genetic diversity. An effect size of correlation coefficient (Pearson's r) for each genetic measurement of each species versus relative distance to center was calculated from the meta-analysis. Results showed positive correlations for most taxa and insignificant correlations for others. Independence tests using correlation matrix, pivot tables and two-way ANOVAs eliminated variables that might produce similar results, showing that the remaining ones would explain a wide range of variations. Factors like range dimension, relative direction of sample sites and taxa showed significant associations with how genetic variables respond to populations' distance to range centers, which is represented by r values. By determining if there is a difference in genetic diversity among populations throughout their ranges, conservation efforts can target individual populations, as opposed to protecting the entire species as one entity. This study can potentially give insights and directions for developing more effective and feasible coastal conservation practices.