

The common raven (*Corvus corax*) is a morphologically uniform species with a distribution that expands across the entire Northern Hemisphere. Recently, analysis of mtDNA and nuclear introns have revealed a deep genetic break that separates the common raven into two clades dubbed as the 'Holarctic Clade' and 'California Clade'. Despite the distinct genetic variation found, several ravens within the species remain unclassified including those found in the Revillagigedo Islands. We compared mitochondrial DNA obtained from common raven found across Clarion, which is one of these islands. Specifically, we examined control region in each individual to detect differences. We hypothesized that both continent and island populations would be most similar to populations in the California Clade. Using a phenol/chloroform protocol, we extracted DNA from toepads obtained from ancient specimens collected several years ago (as early as the 1800s). Using PCR, we amplified the control region in each sample and analyzed each fragment using Sequencher to see if there were genetic differences among these populations. Samples collected included ravens expanding Mexico, however due to the difficulty of extracting and sequencing, we started by using island samples, as well as samples gathered from a few states. Fragments were obtained from 14 individuals in the sample, 11 from continental Mexico and 3 from Revillagigedo Islands. Using AMOVA we found that there was no differentiation between the island and continent populations. These findings reveal there is some gene flow between continent and island populations. Obtaining more samples will help us figure out if the gene flow is recent or historic. We also found that ravens from Clarion are genetically more similar to the California clade.