

QUEEN'S UNIVERSITY HAIDA GWAI AVIAN GENETICS PROJECT - ABSTRACTS OF PAPERS PUBLISHED IN
PEER-REVIEWED JOURNALS AND THESES

Bull, Roger D. 2005. **Patterns of genetic differentiation in Orange-crowned Warbler *Vermivora celata* populations across their breeding range.** M. Sc. Thesis, Queen's University, Kingston, Ontario.

The Orange-crowned Warbler *Vermivora celata* is a Neotropical migrant passerine broadly distributed across North America. The breeding range of this species would have been subject to a cycle of contractions and expansions during the Pleistocene glaciations. This may have isolated populations in different glacial refugia resulting in allopatric differentiation. This scenario has been invoked to explain concordant biogeographic patterns seen in many North American taxa. The Orange-crowned Warbler breeds on Haida Gwaii, British Columbia (formerly known as the Queen Charlotte Islands). Largely due to a pattern of morphological endemism in diverse taxa, a glacial refugium is thought to have persisted in the area of this archipelago during the Pleistocene glaciation. To investigate intra-specific genetic structure in the Orange-crowned Warbler on continental and regional scales, I analysed patterns of microsatellite variability among seven breeding localities, encompassing two of the four described subspecies. I found low genetic differentiation among populations ($F_{ST} = 0.022$), with significant continental-scale structuring and weak differentiation within western populations. Weak population genetic structure in the Orange-crowned Warbler is consistent with results for species with similar life-histories and distributions. I did not find evidence of a genetically endemic population of Orange-crowned Warblers in Haida Gwaii. Microsatellite differentiation supports the classification of two of the four currently recognised subspecies (*V. c. celata* and *V. c. lutescens*). Evidence of equilibrium between gene flow and drift supports a hypothesis of restricted contemporary gene flow between *V. c. lutescens* and *V. c. celata*. Further genetic research, including analysis of *V. c. orestera* and *V. c. sordida*, is required to fully elucidate the taxonomy and conservation priorities of this species.

Burg, Theresa M., Anthony J. Gaston, Kevin Winker and Vicki L. Friesen. 2005. **Rapid divergence and postglacial colonization in western North American American Steller's jays (*Cyanocitta stelleri*).** *Molecular Ecology* 14: 3745-3755.

Post-Pleistocene avian colonization of deglaciated North America occurred from multiple refugia, including a coastal refugium in the northwest. The location of a Pacific Coastal refugium is controversial; however, multiple lines of evidence suggest that it was located near the Queen Charlotte Islands (also known as Haida Gwaii). The Queen Charlotte Islands contain a disproportionately large number of endemic plants and animals including the Steller's jay *Cyanocitta stelleri carlottae*. Using five highly variable microsatellite markers, we studied population structure among eight populations of Steller's jay ($N = 150$) from geographical areas representing three subspecies in western North America: *C. s. carlottae*, *C. s. stelleri* and *C. s. annectens*. Microsatellite analyses revealed genetic differentiation between each of the three subspecies, although more extensive sampling of additional *C. s. annectens* populations is needed to clarify the level of subspecies differentiation. High levels of population structure were found among *C. s. stelleri* populations with significant differences in all but two pairwise comparisons. A significant isolation by distance pattern was observed amongst populations in the Pacific Northwest and Alaska. In the *C. s. carlottae* population, there was evidence of reduced genetic variation, higher number of private alleles than northern *C. s. stelleri* populations and higher levels of divergence between Queen Charlotte Island and other populations. We were unable to reject the hypothesis that the Queen Charlotte Islands served as a refugium during the Pleistocene. Steller's jay may have colonized the Queen Charlotte Islands near the end of the last glaciation or persisted throughout the Pleistocene, and this subspecies may thus represent a glacial relic. The larger number of private alleles, despite reduced genetic variation, morphological distinctiveness and high divergence from other populations suggests that the Queen Charlotte Island colonization pre-dates that of the mainland. Furthermore, our results show rapid divergence in Steller's jay populations on the mainland following the retreat of the ice sheets.

Burg, Theresa M., Anthony J. Gaston, Kevin Winker and Vicki L. Friesen. 2006. **Effects of Pleistocene glaciations on population structure of North American chestnut-backed chickadees.** *Molecular Ecology* in press

The postglacial recolonization of northern North America was heavily influenced by the Pleistocene glaciation. In the Pacific Northwest, there are two disjunct regions of mesic temperate forest, one coastal and the other interior. The chestnut-backed chickadee is one of the species associated with this distinctive ecosystem. Using seven microsatellite markers we found evidence of population structure among nine populations of chestnut-backed chickadees. High levels of allelic variation were found in each of the populations. Northern British Columbia and central Alaska populations contained a large number of private alleles compared to other populations, including those from unglaciated regions. The disjunct population in the interior was genetically distinct from the coastal population. Genetic and historical records indicate that the interior population originated from postglacial inland dispersal. Population structuring was found within the continuous coastal population, among which the peripheral populations, specifically those on the Queen Charlotte Islands and the central Alaska mainland, were genetically distinct. The pattern of population structure among contemporary chickadee populations is consistent with a pioneer model of recolonization. The persistence of genetic structure in western North American chestnut-backed chickadees may be aided by their sedentary behaviour, linear distribution, and dependence on cedar–hemlock forests