

Inferring the Geographic Mode of Speciation by Contrasting Autosomal and Sex-Linked Genetic Diversity

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Abstract

When geographic isolation drives speciation, concurrent termination of gene flow among genomic regions will occur immediately after the formation of the barrier between diverging populations. Alternatively, if speciation is driven by ecologically divergent selection, gene flow of selectively neutral genomic regions may go on between diverging populations until the completion of reproductive isolation. It may also lead to an unsynchronized termination of gene flow between genomic regions with different roles in the speciation process. Here, we developed a novel Approximate Bayesian Computation pipeline to infer the geographic mode of speciation by testing for a lack of postdivergence gene flow and a concurrent termination of gene flow in autosomal and sex-linked markers jointly. We applied this approach to infer the geographic mode of speciation for two allopatric highland rosefinches, the vinaceous rosefinch *Carpodacus vinaceus* and the Taiwan rosefinch *C. formosanus* from DNA polymorphisms of both autosomal and Z-linked loci. Our results suggest that the two rosefinch species diverged allopatrically approximately 0.5 Ma. Our approach allowed us further to infer that female effective population sizes are about five times larger than those of males, an estimate potentially useful when comparing the intensity of sexual selection across species.

Key words: allopatric speciation, *Carpodacus vinaceus*, *Carpodacus formosanus*, Approximate Bayesian Computation.

Drastic post-LGM expansion and lack of historical genetic structure of a subtropical fig-pollinating wasp (*Ceratosolen* sp. 1) of *Ficus septica* in Taiwan

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Abstract

The climatic oscillations of the last glacial period have had profound influences on the demography and levels of genetic diversity of extant species. Molecular evidence of glacial effects on temperate species has been well documented, whereas little is known regarding that on subtropical species. Here we present analyses based on partial sequences of the mitochondrial cytochrome *c* oxidase subunit I (*COI*) gene (1052 bp) and genotypes at 15 microsatellite loci to investigate the historical demography, population structure and ongoing gene flow of an undescribed fig-pollinating wasp (*Ceratosolen* sp. 1) of *Ficus septica* in subtropical Taiwan. Reconstructed historical demography based on the coalescent tree of *COI* sequences suggests that *C. sp. 1* has undergone a drastic population expansion which was tightly coupled with climatic changes since the last glacial maximum (LGM). The magnitude of the population size change was approximately 500-fold, indicating that the population of this wasp and its host was likely highly compressed during the last glacial period. The lack of significant population differentiation ($F_{ST} < 0.02$, for all pairwise F_{ST} values) may be due to rapid postglacial expansion facilitated by long-distance dispersal, although a low frequency of first-generation migrants was detected. Our results clearly demonstrate how recent climatic changes since the LGM and dispersal ability have jointly shaped the genetic composition of a subtropical fig-pollinating wasp.

Keywords: *Ceratosolen*, demography, fig wasp, gene flow, population expansion, last glacial maximum

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Drastic population fluctuations explain the rapid extinction of the passenger pigeon

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To assess the role of human disturbances in species' extinction requires an understanding of the species population history before human impact. The passenger pigeon was once the most abundant bird in the world, with a population size estimated at 3–5 billion in the 1800s; its abrupt extinction in 1914 raises the question of how such an abundant bird could have been driven to extinction in mere decades. Although human exploitation is often blamed, the role of natural population dynamics in the passenger pigeon's extinction remains unexplored. Applying high-throughput sequencing technologies to obtain sequences from most of the genome, we calculated that the passenger pigeon's effective population size throughout the last million years was persistently about 1/10,000 of the 1800's estimated number of individuals, a ratio 1,000-times lower than typically found. This result suggests that the passenger pigeon was not always super abundant but experienced dramatic population fluctuations, re-

went extinct 100 y ago. These sequences allowed us to estimate the long-term population history in unprecedented detail and to provide a novel hypothesis as to why the most abundant bird the world had known became extinct so rapidly.

Migratory flocks of the passenger pigeon were once so immense that they were said to have blanketed the skies of eastern North America (8). In one of many illustrative descriptions, John James Audubon recounted a mile-wide flock of migrating passenger pigeons that passed overhead, blocking the sun for 3 consecutive days (9). The vast numbers of passenger pigeons have led ecologists to suggest that this bird was a keystone species in North American ecosystems (10, 11). This pigeon is believed to have influenced forest composition by consuming and dispersing acorns, beechnuts, and other mast crops on which it fed (10, 11), disrupted local communities, out-competed other mast-eating species, damaged trees by the weight of large flocks