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## Genetic and morphological analyses of a putative hybrid population of native and exotic freshwater turtles in Honshu, Japan

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There has recently been an increasing notion that artificially introduced organisms deliver various unfavorable effects to the native biodiversity. Such effects include one in the form of genetic introgression to indigenous species from their exotic relatives through hybridization. This type of effect is theoretically relatively well discussed, but suffers paucity in actual examples detected especially in terrestrial vertebrates. Turtles are frequently transported artificially for various purposes, and intentional and accidental releases resulting from such activities often lead to formation of feral populations. Moreover, turtles are known to easily hybridize between different species and sometimes even between different genera, chiefly on the basis of captive observations. Nevertheless, little is known of frequencies and consequences of such hybridization events in the wild. I studied one freshwater turtle assemblage in Honshu, Japan, which includes individuals characterized by unique combinations of morphological character states. In the preliminary analysis of a partial sequence of mitochondrial genome from three specimens of the assemblage with such unique character state combinations, two were shown to have a haplotype identical to that of *Chinemys reevesii* (a species native to Honshu), whereas the other had a haplotype of *Mauremys mutica* (a species not naturally occurring there). I thus assessed hybridity of this freshwater turtle assemblage in detail. For the genetic analysis, I examined ten nuclear markers, i. e., four allozyme loci and six SINE loci, and a partial sequence of mitochondrial genome. Most individuals had diagnostic alleles only of *C. reevesii*, but a few individuals also had alleles characteristic of *M. mutica* heterozygously. The exact probability test revealed no statistically significant deviation of the observed genotypic frequency from the frequency expected on the basis of Hardy-Weinberg equilibrium at any of the polymorphic allozyme loci investigated. In the mitochondrial genome sequence, a few individuals that had alleles characteristic of *M. mutica*, also had a haplotype of *M. mutica*. The other individuals had a haplotype of *C. reevesii*. In the morphological analysis, nearly half of the individuals examined had various combinations of diagnostic character states of both *C. reevesii* and *M. mutica*, whereas the remainder exhibited character states invariably diagnostic of *C. reevesii*. These results indicate that the assemblage represents a random mating population, and consists primarily of *C. reevesii*, but with descendants of its hybridization with *M. mutica* and subsequent backcrosses. The results also suggest that indications of such past hybridization may remain more explicitly in morphological characters than in some genetic markers.