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PS- 7 Phylogeography of *Cynops ensicauda* (Amphibia: Caudata) as revealed by nucleotide sequences of mitochondrial DNA

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Recent progress in molecular techniques has been improving our knowledge of the genetic and taxonomic relationships among organismal populations from different islands. For many terrestrial organisms, however, little studies have been made on the geographic patterns or degrees of genetic variation within an island, making it difficult to estimate temporal changes in their distributions at the intra-island level. We surveyed genetic variation of the endemic newt of the Central Ryukyus (*Cynops ensicauda*), and conducted phylogenetic and phylogeographic analyses to infer processes of genetic differentiations and distributional changes including those at within-island level in this species. We obtained complete DNA sequences of cytochrome *b* gene for 270 individuals from 45 sampling sites representing whole distributional range of this species. The result of phylogenetic analyses supported the presence of remarkable differentiation between the Amami and Okinawa Group populations, as was proposed by foregoing allozyme and morphological studies. Also, the result showed that populations from each of these two island groups compose two mitochondrial sub-groups. The degree of genetic differentiation between the sub-groups is greater in the Okinawa Group than in the Amami Group. In each island group, geographic ranges of the two mitochondrial sub-groups overlapped to some extent. Phylogeographic analysis (NCPA), while failing to estimate the process of formation of the two sub-groups within each island group, showed the absence of intermediate haplotypes between the two sub-groups. The foregoing allozyme study did not recognize such substantial genetic divergence of the newt assemblage in either of the two island groups, rejecting the possibility of the presence of one or more cryptic biological species. Such phylogeographic mitochondrial pattern as shown by the newt in each island group is likely to have been formed through its initial geographic division into two isolated assemblages and their attainment of subsequent sympatry before acquisition of reproductive isolation mechanisms. NCPA further indicates that the current geographic patterns of divergence within each sub-group have been formed under the effects of repetitive restricted gene flow with isolation by distance, continuous range expansion, fragmentation, and long distance movement.