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PS-26 Genetics and morphology of two gizzard shads, *Nematalosa japonica* and *N. come*, in a hybrid zone of Okinawa Island (Clupeiformes: Clupeidae).

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Two species of gizzard shad, *Nematalosa japonica* Regan and *N. come* (Richardson), are distributed in Okinawa Island, Japan. This study purposes to identify those morphologically similar two species. This study used allozyme locus (*SOD*) and two nuclear PCR-based DNA markers (*ITS-1* and *CaM*) which diagnostically identify these species and examined species composition of the sympatric and allopatric population samples from Tungkang in southern Taiwan to Okinawa Island and Shikoku Island, Japan. In addition, a PCR-based mtDNA marker (*16S*) was used to characterize the distribution of mtDNA haplotypes among them. Gizzard shads with hybrid genotypes were detected in only three population samples of Okinawa Island. The frequency of hybrid ranged from 1.2 to 67.0%. In the dominant hybrid frequencies of one population sample, backcross was 1.8% but not detected in other sites. Morphological examinations showed intermediacy of the hybrids. Hybrid indices of three meristic characters of the hybrids fell between those of parental species, ranging from 38.3 to 54.5, with a mean of 49.4. Principal-components analysis showed the difference between *N. japonica* and *N. come* based on the first principal-component scores, while hybrids is difficult to be identified. Thus, it is necessary to identify those species and hybrids by genetic tool. Okinawa Island is the only place where two species are sympatrically distributed. Close spawning season and decreased spawning grounds due to recent reclamation may have contributed to producing hybrid zone.