

Producing F2 by a crossing experiment of Japanese pure line and alien species of genus *Neocaridina* and analysis of rostrum of a pure line.

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Abstract

Two traditional systems for *Neocaridina denticulata denticulata* had already been suggested before an invasion of an alien species to Japan due to live bait importation from China after 1970 as shown by DNA analysis from a study in 2017 (Niwa *et al.*). In Hyogo Sugo River we found 10 male *N. palmata*, 7 male *N. d. davidi* but none of the native species was detected. One male replaced with a middle character of *koriana* and *denticulata* was found (Shih, Cai, Niwa, Yoshigou & Nakahara, 2016 unpublished). Related species within the *Neocaridina* genus from China and Korea, have reportedly been found in the northeast of eastern Japan where they were found as well as western Japan and Hokkaido. There is concern for the effects of genetic permeation due to hybridization between the native and alien species. The rostrum of species found in Okayama were regarded as belonging to that of a pure native species in a preceding study, the rostrum sizes were short, but we found that short, long and medium sized mutations exist. We considered whether the DNA analysis results were related to the form of the rostrum. By crossing the *N.d.d.* native with the foreign population to produce an F1 generation. F1×F1 was made to produce F2 on January 7th, 2019. The DNA data was analyzed from 6 territories in total: 2 areas within mitochondrially encoded 16SRNA, 3 areas within 28SRNA, and Toripisin, H3 in nuclear DNA, in addition to CO I territory of mitochondrial DNA.