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## Population structure of *Coilia nasus* in the Yangtze River revealed by insertion of short interspersed elements<sup>☆</sup>

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### ABSTRACT

*Coilia nasus* is found in the Yangtze River and the coastal waters of China, Korea, and Japan. Two ecotypes (anadromous and freshwater-resident populations) are distributed throughout the Yangtze River basin based on their ecology and behavior, but relatively little is known about the population structure of this species. Analysis of short interspersed element (SINE) insertions, which vary among individuals, has been acknowledged to provide a unique way to study population divergence. SINEs isolated from *C. nasus* were characterized, and this enabled analysis of the SINE insertion pattern in six populations distributed throughout the Yangtze River basin. In all populations, four SINE loci displayed individual polymorphism, and two SINE loci showed a stochastic loss in all individuals of two resident populations. The correlation between genetic and geographic populations indicated a degree of genetic isolation in this species. In contrast with *Coilia grayii* and *Coilia mystus*, two SINE loci appeared only in *C. nasus*. Sequencing analysis indicated that the high insertion variability of SINEs was attributed mainly to the tails, which contained various repeat copies. The results in this study will be useful for sustainable management of fishery resources and conservation of this species.

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## 1. Introduction

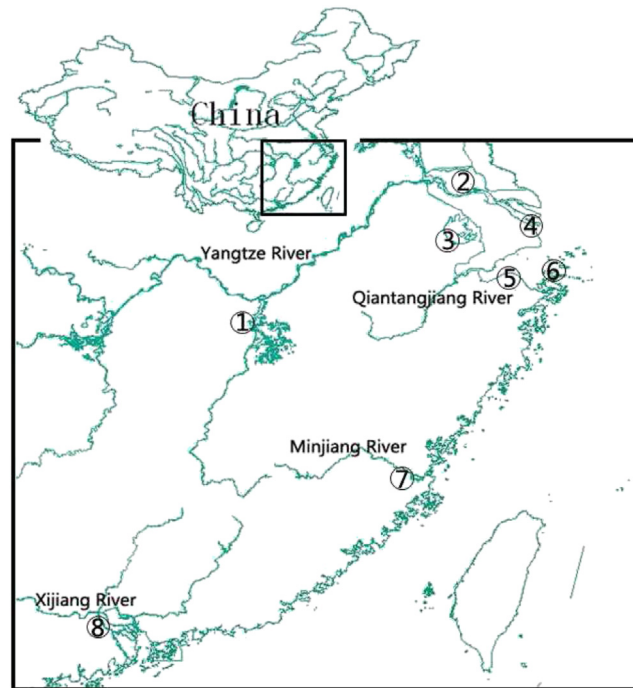
The grenadier anchovy *Coilia nasus* in the family Engraulidae is a coastal, estuarine, and freshwater species. This species is distributed widely throughout the western coastal waters of Korea and the Ariake Sound of southwestern Japan, as well as the middle and lower reaches of the Yangtze River, the East Sea, and the Yellow Sea of China (Whitehead et al., 1988). Within its distribution, *C. nasus* exhibits remarkable diversity in terms of morphology, ecology, and behavior. Two ecotypes of *C. nasus* have been found in the middle and lower reaches of the Yangtze River basin: a resident population and an anadromous population (Zhang, 2001). The former population is composed of a freshwater-resident population, *Coilia brachygnathus*, and a landlocked population, *C. nasus taihuensis*. The various geographic populations are formed through species expansion and adaptive radiation, with an estimated age of 0.17–0.13 Myr (Yang et al., 2008).

The freshwater-resident population inhabits only fresh water and spawns and lives in the middle and lower reaches of the Yangtze River basin. The landlocked population is found only in Taihu Lake, a short distance from the Yangtze River. Taihu Lake

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**Fig. 1.** The eight sampling sites for *C. nasus*, *C. mystus*, and *C. grayii*. The collection sites (circles) correspond to locations given in the text: ① Poyang Lake, ② Jingjiang, ③ Taihu Lake, ④ Jiu Duan Sha, ⑤ Qiantang Jiang, ⑥ Zhoushan, ⑦ Mingjiang, and ⑧ Xijiang.

is the third largest freshwater lake in China, with an area of 2250 square kilometers (Chang, 1996). The anadromous population migrates for spawning from its oceanic habitat to the Yangtze River during its reproductive season from March to August, swimming 1400 km up the Yangtze River. From September to November, after reproduction, these fish and their progeny migrate back to the ocean (Zhang, 2001). Otolith strontium-to-calcium ratios in the anadromous population have confirmed their life history pattern (Dou et al., 2012). This home-migrating fish is one of the most important fish in China, with high economic value owing to its delicacy and nutritional value, whereas the freshwater-resident fish is of less economic value. However, the anadromous population has significantly decreased as a resource during the past decade due to overfishing, pollution, coastal construction, and other factors (Zhang et al., 2005). Interestingly, catches of the landlocked population continued to increase from 1952 to 2004, and the species is now the dominant fish in Taihu Lake (Liu et al., 2005). Therefore, it is important to understand the population structure of *C. nasus* in the Yangtze River basin to ensure better management and conservation of this species' fishery resources.

Significant genetic diversity, based on mitochondrial DNA control region sequences, has been reported among geographical populations of *C. nasus* in the Yangtze River, the Yalu Jiang River, and the Minjiang River (e.g., Ma et al., 2012). Various geographic populations collected from the Yangtze River basin have also shown genetic differences that were not correlated with geographical locations (Yang et al., 2008), despite prodigious morphological differences (e.g., jaw length, number of vertebrae, and anal fin rays). In previous studies, populations of *C. nasus* distributed in the Yangtze River and Taihu Lake were each treated as closely related to the species *C. brachygnathus* (which has a shorter jaw length than *C. nasus*) and the subspecies *C. nasus taihuensis* (which has fewer vertebrae than *C. nasus*), based on morphometric characteristics and ecological and physiological attributes (Yuan et al., 1980). Species identification of *C. nasus* distributed in the Yangtze River was resolved by exploring various markers such as allozymes and mitochondrial DNA (Liu, 1995; Tang et al., 2007; Yang et al., 2008; Zhou et al., 2010). Closely related species of *C. brachygnathus* and subspecies of *C. nasus taihuensis* regarded as synonymous to *C. nasus* should be geographical/ecological populations of this species (Tang et al., 2007; Zhou et al., 2010). No geographical differentiations have been observed in these populations based on genetic data, although significant morphological differences have been found (Xie, 2012). It is not known whether these population-specific morphometric characters are influenced by environmental or genetic factors. The genetic diversity of *C. nasus* is thought to be closely related to its adaptability, variability, and evolutionary potential, prerequisites for living organisms to cope with uncertainty in the environment (Ma et al., 2012). Some populations have discrete geographic distributions, such as the Taihu Lake population, which, based on mitochondrial data, is not genetically different from other populations (Yang et al., 2008; Ma et al., 2012). Perhaps because the mitochondrial genome is maternally inherited, using it as a genetic marker does not permit the detection of species undergoing population expansion events during short periods. A sensible molecular marker should be identified to detect such events.

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