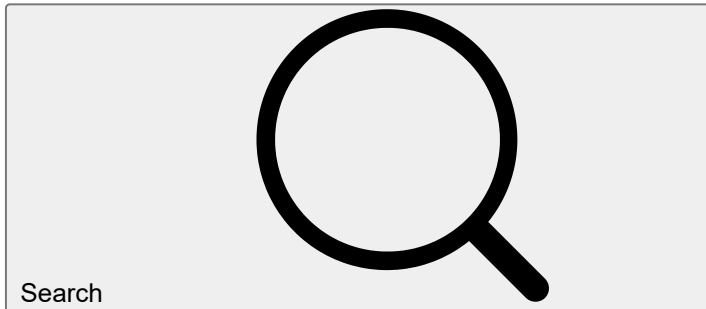


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Genetic differentiation of Japanese sardinella (*Sardinella zunasi*) populations in the Northwest Pacific revealed by ISSR analysis

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Abstract

Knowledge of population genetic structure plays an important role in fisheries management. In this research, Inter-Simple-Sequence-Repeat (ISSR) markers were employed to evaluate the genetic structure of Japanese sardinella (*Sardinella zunasi*) populations in the Northwest Pacific. Eighty seven individuals from 5 locations were screened using 4 highly polymorphic primers. A total of 173 polymorphic loci were detected out of 191 loci amplified. Small but significant genetic differentiation was detected between the Chinese and Japanese populations by both AMOVA and pairwise F_{ST} analyses, which was further supported by cluster analysis. We consider that climate change during glaciations should be responsible for the genetic differentiation. Isolation by geographic distance among populations was observed, indicating that the distance might also lead to the genetic differentiation. However, no genetic structure was found within the populations off both the Chinese and Japanese coasts, indicating a high-level along-coast gene flow, which might result from ocean current transport and common ground for over-wintering.

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