## **Genomic Identification of Anisakis Simplex Larvae by PCR-RAPD**

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**Abstract :** Anisakiasis is a disease caused by infection with an anisakid larvae, mostly Anisakis simplex. The larvae commonly infect in marine fish and the disease is frequently reported in areas of the world where fish is consumed raw, lightly pickled or salted. In Japan, people have the habit of eating raw fish such as 'sushi' or 'sashimi', so they have more chance of infection with larvae of anisakid nematodes. There are three sibling species in A. simplex larvae, namely, A. simplex sensu stricto (Asss), A. pegreffii (Ap) and A. simplex C. It was revealed that Ap is dominant among the larvae from fish (Scomber japonics) in the Japan Sea side and Asss is dominant among those of the Pacific Ocean side conversely. Although anisakiasis has happened in Japan among both the Japan Sea side area and the Pacific Ocean side area. The aim of this study was to investigate genetic variations between the siblings (Asss and Ap) and within the same sibling species by random amplified polymorphic DNA (RAPD) technique. In order to investigate the genetic difference among the each A. simplex larvae, we used RAPD technique to differentiate individuals of A. simplex obtained from Scomber japonics fish those were caught in the Japan sea (Goto Islands in Nagasaki Prefecture) and the cost of Pacific Ocean (Kanagawa Prefecture). The RAPD patterns of the control DNA (Genus Raphidascaris) were markedly different from those of the A. simplex. There were differences in amplification patterns between Asss and Ap. The RAPD patterns for larvae obtained from fish of the same sea were somewhat different and variations were detected even among larvae from the same fish. These results suggest the considerable high genetic variability between Asss and Ap and the possible existence of genetic variation within the sibling species.

Keywords : Anisakiasis in Japan, Anisakis simplex, genomic identification, PCR-RAPD

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