

Fish populations revealed through seawater analysis

March 7 2016



A group of Japanese jack mackerel in Maizuru bay. Credit: MASUDA Reiji (Kyoto University)

A research group led by YAMAMOTO Satoshi, a research fellow at the Kobe University Graduate School of Human Development and Environment, has shown that measuring quantities of fish DNA in seawater can reveal how many fish inhabit that environment. This discovery could enable quicker and more effective surveys of fish

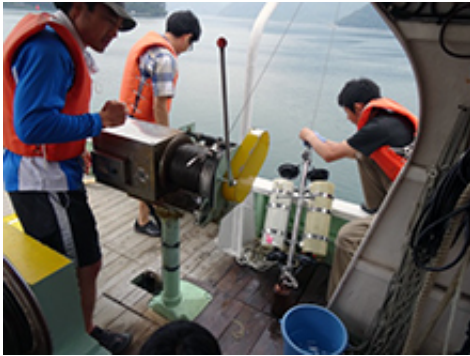
distribution, and has potential applications in long-term monitoring. The findings will be published on March 3 in the online science journal *PLOS ONE*.

Until now, the distribution of marine species was calculated using two main methods: fish capture and fish finder equipment. However, these survey methods involve heavy costs in time and manpower, and specialist knowledge is required to use the measuring apparatus. On the other hand, a method was already available for determining whether the target fish inhabit a certain area of [water](#): analysis of the fish DNA released into the water. Doctor YAMAMOTO's research group took this a step further, testing whether it was possible to discover the location of fish and size of their schools by measuring the amounts of DNA released into the environment (known as environmental DNA, or eDNA).

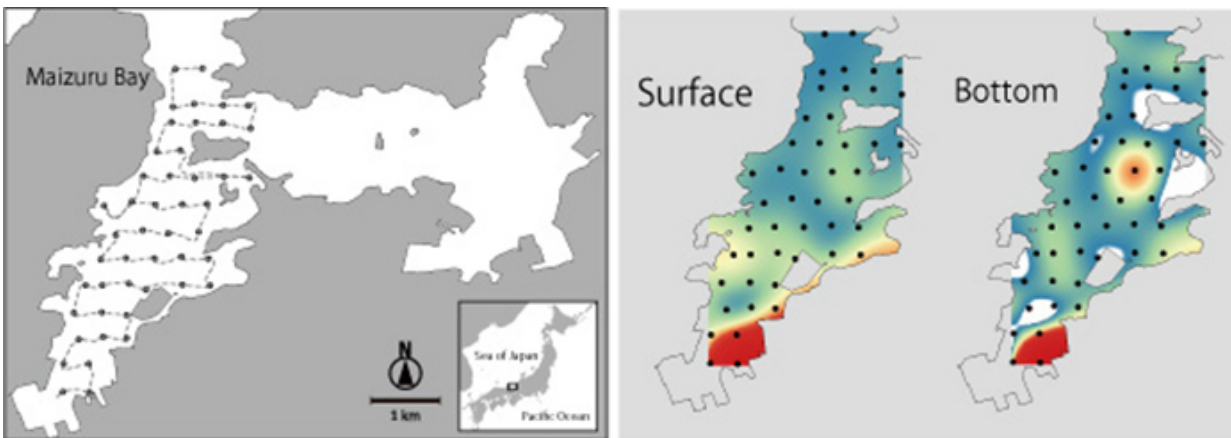
In June 2014, a research group led by YAMAMOTO Satoshi (Kobe University research fellow), MINAMI Kenji (Specially Appointed Assistant Professor at Hokkaido University), and FUKAYA Keiichi (Project Assistant Professor at the Institute of Statistical Mathematics) collected 1-liter samples of surface water and bottom water from 47 locations in Maizuru bay, and estimated the concentration of eDNA of Japanese jack mackerel using real-time PCR. As a result of comparison between the eDNA concentration in the 47 locations and the biomass of Japanese jack mackerel that was simultaneously measured during water collection using fish finder equipment, they discovered that the eDNA concentration of a location reflected the biomass within 10-150 meters of the location. This proves that environmental DNA reflects the biomass of the target fish species, and environmental DNA analysis methods can be used to quantitatively measure the distribution and school size of saltwater [fish](#).

This method is simple, requires no specialist knowledge, and can be used for large-scale surveys over a short period of time. These features also

make it suitable for long-term monitoring. The method has the potential to drastically improve efficiency for surveys of the amount and distribution of marine resources.



The researchers collect seawater samples. Credit: Kobe University



The researchers collected 1-liter samples of surface water and bottom water from 47 locations in Maizuru bay, and analyzed the environmental DNA of Japanese jack mackerel using real-time PCR. The red parts of the image show the highest concentrations of DNA. When they compared the distribution of DNA to the results for fish distribution calculated using fish finders, their findings proved that environmental DNA can be used to quantitatively estimate the distribution of Japanese jack mackerel. Credit: Kobe University

More information: Satoshi Yamamoto et al. Environmental DNA as a 'Snapshot' of Fish Distribution: A Case Study of Japanese Jack Mackerel in Maizuru Bay, Sea of Japan, *PLOS ONE* (2016). DOI: 10.1371/journal.pone.0149786

Provided by Kobe University

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