

マイクロサテライト DNA マーカーによる
サクラマス^aの遺伝的多様性と集団の遺伝的分化

**Studies on the Genetic Diversity of Wild Populations of Masu Salmon,
Oncorhynchus masou masou, by Microsatellite DNA Markers**

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野口大毅^{a,b}・谷口順彦^{a,b}
Daiki Noguchi^{a,b} and Nobuhiko Taniguchi^{a,b}

^a 東北大学大学院農学研究科 *Graduate School of Agricultural Science, Tohoku University,
Sendai, Miyagi 981-8555, Japan*

^b 現所属：福山大学内海生物資源研究所 *The Research Institute of Marine Bioresources,
Fukuyama University, Onomichi, Hiroshima 722-2101, Japan*

A large number of hatchery masu salmon, *Oncorhynchus masou masou*, have been released into the rivers in Japan in order to enhance the fisheries resources of this species. Unconscious genetic changes that may occur during artificial seed production should be prevented if we are to perform effective and responsible resource enhancement. In this paper, the genetic variability and population structure of masu salmon were estimated using five microsatellite DNA markers (msDNA). Masu salmon showed a high level of genetic variability at the msDNA loci. Average allele numbers ranged between 10.40 and 15.00, average numbers of allele richness between 9.74 and 11.72, and expected heterozygosities between 0.824 and 0.874. Genetic differentiation was not observed between different year classes. Meanwhile, genetic differentiation was detected among captured locations, but distinct correlation between genetic distance and geographic distance was not observed. Finally, methods of brood stock management in artificial propagation to prevent genetic change and loss of variation for conservation of genetic diversity in wild populations are discussed.