Genome-wide study on the regulation of fish muscle differentiation

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## **Outline of survey**

Myosin is the major contractile protein in muscle tissues, the molecule of which consists of two heavy chains (MYH) and four light chains. An active site of the myosin molecule for muscular contraction is located in MYH through which myosin hydrolyzes ATP by interacting with actin. Many MYHs with different primary structures have been identified in vertebrate muscles. Various physiological factors affect MYH expression. Difference in MYH expression leads to the formation of different muscle-fiber types such as fast and slow muscle ones, and their spatial arrangements define muscle physiological functions. However, the details of the molecular mechanisms involved in a complex expression pattern of MYHs are still unknown. Meanwhile, fish is an attractive model for study on the muscle differentiation, because genome databases are available for several fish species. While fish change MYH isoforms in association with temperature acclimation and show indeterminate growth by hyperplasia even in an adult stage, fast and slow muscles are anatomically separated, which is not observed in mammalian muscular tissues.

In this study, we propose to employ torafugu having the smallest genome size and small fish including medaka and zebrafish as well where various transgenic approaches are possible. We will analyze the differences in the expression pattern and physiological functions of their MYHs. Subsequently, we will produce transgenic medaka and zebrafish which would express a fluorescent protein under the control of the regulatory region of the torafugu MYH genes. Based on such strategies, we will reveal the molecular mechanisms underlying muscular differentiation during embryonic and larval development, and growth and wound healing in an adult stage.

## [Expected results]

Torafugu has been proven to be an excellent genome model animal, because its genome size is the smallest among vertebrates. On the other hand, small fish such as medaka and zebrafish have been recognized as excellent models for development. Our study takes such advantages of these fish and the results to be achieved will clarify the molecular mechanisms involved in muscle differentiation not only for fish but also for higher vertebrates such as mammals where many ambiguities have still remained. Moreover, it is expected that our study will contribute in practical aspects: for example, the improvement of fish meat quality by producing advantageous muscle-fiber types. The application of indeterminate growth for selective breeding may be also possible.

## [References by the principal investigator]

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【Term of project】 FY20	07-2011	[Budget allocation] 25,400,000 yen
		(2007 direct cost)
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