Improved breeding of fugu following whole genome sequencing.

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[Outline of survey]

Following the release of the draft human genome sequence, it was decided that the next vertebrate genome to be sequenced was tora-fugu (*Takifugu rubripes*). Until now, fugu is only commercially valuable fish species to undergo genome sequencing. Here, we report the potential application of the fugu genome database to help improve breeding efficiency in this species. The technical merit of our study lies in the use of inter-species hybridization. Individuals belonging to the second generation (F2) of progeny bred via interbreeding between tora-fugu and kusa-fugu (*Takifugu niphobles*) independently exhibit significant diversity in many phenotypes. In this study, we plan to analyze both the genomic loci and the genes responsible for each phenotype, using fine genetic linkage mapping strategies which we already established. In particular, we will focus on the genes resistance, and manageability for the commercial fish farmer.

[Expected results]

The purpose of this study is to establish strategies and methods for improved breeding in fugu by exploitation of genomic sequence database available for this species. By the end of this project, we will be able to identify several genomic loci that are responsible for beneficial phenotypes, which characterize the species differences between tora- and kusa-fugu. Among the loci studied, we will determine a number of key genes. We will then survey the individual fugu possessing superior genes with the aim of selecting desirable traits. Interbreeding of fugu species may offer the additional possibility of studying the process of evolution that results in the production of key inter-species differences.

[References by the principal researcher]

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【Term of project】	FY2008- 2012	[Budget allocation] 146,600,000 yen (direct cost)	
【Homepage address】	http://www.se.a.u-tokyo.ac.jp/		