

X-G Collaborative Research with FANTOM Consortium

The collaboration with Okazaki Institute for Integrative Bioscience has focused with the interaction of the Fantom Consortium. In this context, the group of Dr. Seto has focused on the analysis of the Ubiquitin protein within the Fantom-3 dataset, and to analyze the function.

X-G-1 The international Consortium, FANTOM*, Discovered UBL Domains Interspersed over Mammalian Genomes

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Ubiquitin is a protein that has been well investigated in the fields of protein degradation and transport systems. Several proteins are reported that they have ubiquitin-like sequence, UBL domains. These proteins were named UBL-containing proteins, and comparative analyses of all UBL-containing proteins were performed among various species, including humans, mice, flies, worms, and yeast in this report.

We compared human UBL-containing proteins with mouse UBL-containing proteins, and found 43 orthologous pairs (74% in human UBL-containing proteins). The UBL-containing proteins were divergent protein family. We found two human UBL-containing proteins whose mouse orthologs did not possess a UBL domain. We also found three mouse UBL-containing proteins whose human orthologs did not possess a UBL domain. Moreover, 12 human UBL-containing proteins had no orthologs in the mouse genome, and 8 mouse UBL-containing proteins had no human orthologs. About 60% of the conserved UBL-containing proteins between human and mouse were expressed in the nervous system in FANTOM3 dataset. By using the phylogenic analysis of all UBL domains in humans, mice, flies, worms, and yeast, we found that 33% of UBL domains were species-specific, and that 40% of UBL domains were found in the human/mouse conserved group. Therefore, this study on the UBL-containing proteins show a tendency to diversify their amino acid sequences during the evolution.

* FANTOM: Functional Annotation Of Mouse