Curriculum Vitae

Name	Gene Kurosawa
Date of Birth	June 9, 1974
Place of Birth	Nagoya, Aichi Prefecture, Japan

Education

1998	Graduated from Mie University Faculty of Bioresources (Advisor: Prof. Kunio Imai)
2003	Graduated from Nagoya Graduate School Department of Biological Science (Adviser: Prof. Hiroshi Hori)
2003	Obtained the degree of PhD from Nagoya University

Research

2000-2003	Special graduate student supported by a grant from Japan Society for the Promotion of Science (JSPS)
2003-2006	Post doctoral fellow at Fujita Health University supported by a grant from the Ministry of Education, Culture, Sports, Science and Technology (MEXT)
2006-2008	Research Fellow at Fujita Health University supported by a grant from New Energy and Industrial Technology Development Organization (NEDO)
2008-2009	Visiting Researcher at MedImmune Cambridge UK

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List of Publication

Gene Kurosawa

1. A. Koga, Y. Wakamatsu, G. Kurosawa, H. Hori:
Oculocutaneous albinism in the i6 mutant of the medaka fish is associated with a deletion in the tyrosinase gene. ***Pigment Cell Res.*** 12: 252-258 (1999)

2. G. Kurosawa, K. Yamada, H. Ishiguro and H. Hori:
Hox gene complexity in medaka fish may be similar to that in puffer fish rather than zebrafish. ***Biochem. Biophys. Res. Commun.*** 260: 66-70 (1999)

3. G. Kurosawa, N. Takamatsu, M. Takahashi, M. Sumitomo, E.Sanaka, K. Yamada, K. Nishi, M. Matsuda, S. Asakawa, H. Ishiguro, K. Miura, Y. Kurosawa, N. Shimizu, Y. Kohara and H. Hori:
Organization and structure of hox gene loci in medaka fish genome and comparison with those of pufferfish and zebrafish genomes. ***Gene*** 370:75-82 (2006)

4. N. Takamatsu, G. Kurosawa, M. Takahashi, R. Inokuma, A. Kanamori and H. Hori: Duplicated Abd-B class genes in medaka hoxAa and hoxAb clusters exhibit novel expression patterns in pectoral fin buds. ***Dev. Gene. Evol.*** 217: 263-73 (2007)

5. G. Kurosawa, Y. Akahori, M. Morita, M. Sumitomo, N. Sato, C. Muramatsu, K. Eguchi, K. Matsuda, A. Takasaki, M. Tanaka, Y. Iba, S. Hamada-Tsutsumi, Y. Ukai, M. Shiraishi, K. Suzuki, M. Kurosawa, S. Fujiyama, N. Takahashi, R. Kato, Y. Mizoguchi, M. Shamoto, H. Tsuda, M. Sugiura, Y. Hattori, S. Miyakawa, R. Shiroki, K. Hoshinaga, N. Hayashi, A. Sugioka, and Y. Kurosawa:
Comprehensive screening for antigens overexpressed on carcinomas via isolation of human mAbs that may be therapeutic. ***Proc. Natl. Acad. Sci. USA*** 105: 7287-7292 (2008)

6. Yasushi Akahori, **Gene Kurosawa**, Mariko Sumitomo, Miwa Morita, Chiho Muramatsu, Keiko Eguchi, Miho Tanaka, Kazuhiro Suzuki, Mototaka Sugiura, Yoshitaka Iba, Atsushi Sugioka, Yoshikazu Kurosawa
Isolation of antigen/antibody complexes through organic solvent (ICOS) method
Biochem Biophys Res Commun. 378 (2009) 832-835.

7. Yuka Kitamura, **Gene Kurosawa**, Miho Tanaka, Mariko Sumitomo, Chiho Muramatsu, Keiko Eguchi, Yasushi Akahori, Yoshitaka Iba, Hiroyuki Tsuda, Mototaka Sugiura, Yoshinobu Hattori, Yoshikazu Kurosawa
Frequent overexpression of CADM1/IGSF4 in lung adenocarcinoma
Biochem Biophys Res Commun. in press

Research Resume

Gene Kurosawa

Undergraduate (April 1997 - March 1998)

I joined to Professor Imai's group which had been working on dispause hormone （Biosci. Biotechnol。 Biochem. 62: 1875-1879, 1998). I chemically synthesized various kinds of oligopeptides to know minimum structure for biological activity. Owing to this experience, I studied how to purify the peptides by HPLC and how to use MS and NMR equipments for examining the purity of peptides.

Graduate course (April 1998 - March 2003)

When I was a graduate student in Nagoya University, I revealed organization of *Hox* gene loci in medaka fish. The change in number and the genomic organization of *Hox* genes seemed to play an important role in metazoan body-plan evolution. They make cluster(s) and in vertebrates each cluster contains different number of *Hox* genes that have been classified into 13 groups. Before I started this project, *Hox* gene loci of zebrafish and those of pufferfish had been analyzed. In order to estimate the evolutionary origin of *Hox* organization in rayfinned fishes, we searched for *Hox* genes in the medaka fish *Oryzias latipes*, with a taxon thought to be widely separated from those of pufferfish and zebrafish. We synthesized various mixed oligonucleotides that can work as group-specific primers for PCR, then cloned and sequenced amplified fragments. Numbers of *Hox* genes identified in the present study were 2 for group 1, 2 for group 2, 1 for group 3, 3 for group 4, 6 for groups 5-7, 2 for group 8, 4 for group 9, 3 for group 10, 1 for group 12, and 3 for group 13. The primers specific for group 11 did not function in this study. Thus, at least 27 *Hox* genes are present in medaka genome, suggesting that the *Hox* gene complexity of the medaka genome is similar to that of the pufferfish rather than the zebrafish (Kurosawa *et al.* BBRC, 1999).

Using the *Hox* gene probes I isolated BAC clones that cover the entire *hox* gene loci in the medaka fish *Oryzias latipes*. The BAC clones were characterized by the Southern hybridization with many *hox* gene probes isolated in my previous study and by PCR using primers designed for selective amplification of respective *hox* genes. Then, the BAC clones have been subjected to shotgun sequencing. Results showed the

organization of the entire hox gene loci. Forty-six *hox* genes in total are encoded in seven clusters as follows: 10 *hox* genes in *Aa* cluster; 5 in *Ab*; 9 in *Ba*; 4 in *Bb*; 10 in *Ca*; 6 in *Da*; and 2 in *Db*. Together with the information on the hox gene loci registered in the Fugu genome database and in the Danio genome database, the physical maps of three fish genomes were constructed and compared one another. Results showed the not only numbers of *hox* genes but also the distances between the neighboring *hox* genes are highly similar between medaka and fugu. As for six clusters, *Aa, Ab, Ba, Bb, Ca* and *Da* that are commonly present in the three fishes, only few or no differences were found in each cluster. Thus, the *hox* gene sets should have been well conserved once they had been established in respective species (Kurosawa et al. Gene, 2006).

Postdoctoral fellow and research fellow (April 2003- present)

The project published in PNAS has been performed by many researchers as co-laboratory work. When I joined this project, the Ab library had been constructed and the screening method had also been established. First, I contributed to improvement of the screening method (ICOS method). Since so many clones have been isolated and so many data including a lot of immuno histochemical analyses have been accumulated, I noticed that we should make our own data base. Otherwise, we could not even compare the data of all clones. After I constructed the system for data base, all the data and information about all the clones could have been easily compared among them. Essentially, I have had a responsibility for identification of antigens recognized by respective antibodies that showed cancer cell-specific staining patterns by the immunohistochemical analysis. We isolated 2,114 mAbs that bind to the surface of cancer cells. I devised two methods for comprehensive identification of TAAs. The first method is "GFC (grouping by flow cytometry) method". The essence of this method was described in session "Identification of 21 TAAs" in the paper. The second method is " SITE (simultaneous identification by three dimensional ELISA) method". This methods was described only briefly. By development of these methods, we succeeded not only to identify TAAs but also to isolate so many clones. If we tried to identify the antigens recognized by respective mAbs one-by-one, it seemed to have been an endless work. After we published papers, four more TAAs have been identified by these methods to date.