



Takashi Gojobori



Date of Birth 24 October 1951

Place Fukuoka (Japan)

Nomination 5 September 2007

Field Evolutionary Genomics

Title Professor

Most important awards, prizes and academies

Society Prize (Kihara Medal), The Genetic Society of Japan (2005); Society Prize (Motoo Kimura Medal), The Society of Evolutionary Studies, Japan (2004); The Gaetano Salvatore Gold Medal, Stazione Zoologica, Anton Dohrn, Italy (2004); Science Award from Japan Science and Technology Corporation (JST) (1997); Science Award from Hitoshi Kihara Memorial Foundation, Japan (1995); Promotion Award from Japanese Society of Genetics (1987). *Fellowships*: Visiting Research Fellow at Imperial Cancer Research Fund (ICRF) in London (1989); Fellow of American Association for the Advancement of Science (AAAS) (2006). *Academies and Professional organisations*: Foreign Honorary Member of the American Academy of Arts and Sciences (2006); Member of the Pontifical Academy of Sciences (2007); Vice-Chairman, The International Society of Molecular Evolution; Member, The American Society of Genetics; Member, The Society of Molecular Biology and Evolution; Member, The Japanese Society of Genetics; Member, The Japanese Society of Evolutionary Studies.

Summary of scientific research

He has worked extensively on the rates of synonymous and nonsynonymous substitutions, positive selection, horizontal gene transfer, viral evolution, genomic evolution, and comparative gene expression. In recent years he has focused on the evolution of the brain and of the Central Nervous System. He has contributed to the DDBJ/GenBank/EMBL international nucleotide sequence database construction as well as the H-Invitational human gene database.

Main publications

Jung Shan, H., Ohyanagi, H., Hayakawa, S., Osato, N., Nishimiya-Fujisawa, C., Ikeo, K., David, C., Fujisawa, T. and Gojobori, T. (2007), The evolutionary emergence of cell type specific genes inferred from the gene expression analysis of hydra, *Proc. Natl. Acad. Sci. USA*. 104(37), 14735-40; The Rice Annotation Project: Ito, T. and Gojobori, T., *et al.* (2007), Curated Genome Annotation of *Oryza sativa ssp. Japonica* and Comparative Genome Analysis with *Arabidopsis thaliana*, *Genome Res.* 17(2), 175-83; Iwama, H., Gojobori, T., Itoh, T., Niimura, Y., Fujii, Y., Habara, T., Sakai, H., Sato, Y., Wilson, G., Kumar, K., McCouch, S., Juretic, N., Hoen, D., Wright, S., Bruskiwich, R., Bureau, T., Miyao, A., Hirochika, H., Nishikawa, T., Kadowaki, K. and Sugiura, M. (2005), The map-based sequence of the rice genome, *Nature* 436: 793-800; Nakamura, Y., Itoh, T., Matsuda, H. and Gojobori, T. (2004), Biased biological functions of horizontally transferred genes on 324,653 open reading frames of 116 prokaryotic complete genomes, *Nature Genetics* 36(7): 760-6; Iwama, H. and Gojobori, T. (2004), Highly conserved upstream sequences for transcription factor genes and implications for the regulatory network, *Proc. Natl. Acad. Sci. USA*. 101, 17156-61; Imanishi, T., other 152 authors, Gojobori, T., and Sugano S. (2004), Integrative annotation of 21,037 human genes validated by full-length cDNA clones, *PLoS Biol.* 2, 1-21; Andrews, T.D. and Gojobori, T. (2004), Strong positive selection and recombination drive the antigenic variation of the Pile protein of the human pathogen neisseria meningitidis, *Genetics* 166, 25-32; Anzai, T., Shiina, T., Kimura, N., Yanagiya, K., Kohara, S., Shigenari, A., Yamagata, T., Kulski, J.K., Naruse, T.K., Fujimori, Y., Fukuzumi, Y., Yamazaki, M., Tashiro, H., Iwamoto, C., Umehara, Y., Imanishi, T., Meyer, A., Ikeo, K., Gojobori, T., Bahram, S. and Inoko, H. (2003), Comparative sequencing

of human and chimpanzee MHC class I regions unveils insertions/deletions as the major path to genomic divergence, *Proc. Natl. Acad. Sci. USA.* 100(13):7708-13; Nakazawa, M., Cebria, F., Mineta, K., Ikeo, K., Agata, K. and Gojobori, T. (2003), Search for the evolutionary origin of a brain. Planarian brain characterized by microarray, *Mol. Biol. Evol.* 20(5): 784-91; Mineta, K., Nakazawa, M., Cebria, F., Ikeo, K., Agata, K. and Gojobori, T. (2003), Origin and evolutionary process of CNS elucidated by comparative genomics analysis of planarian ESTs, *Proc. Natl. Acad. Sci. USA.* 100(13): 7666-71; Niimura, Y. and Gojobori, T. (2002), In silico chromosome staining: Reconstruction of Giemsa bands from the whole human genome sequence, *Proc. Natl. Acad. Sci. USA.* 99(2): 797-802; Tanaka, Y., Hanada, K., Mizokami, M., Yeo, A.E.T., Shih, J.W.-K., Gojobori, T. and Alter, H.J. (2002), A Comparison of the molecular clock of hepatitis c virus in the United States and Japan predicts that hepatocellular carcinoma incidence in the United States will increase over the next two decades, *Proc. Natl. Acad. Sci. USA.* 99, 15584-9; Sasaki, T., Yamamoto, K., Sakata, K., Baba, T., Katayose, Y., Wu, J., Niimura Y., Cheng Z., Nagamura Y., Kanamori, H., Hosokawa, S., Masukawa, M., Arikawa, Antonio, B.A. and Gojobori, T. (2002), The genome sequence and structure of rice chromosome 1., *Nature* 420: 312-6; Fantom Consortium (Okazaki, Y., Gojobori, T., *et al.*), Riken Genome Exploration Research Group Phase I & II Team, Mouse Genome Sequencing Consortium, Scientific management: Y. Hayashizaki (2002). Analysis of the Mouse Transcriptome based on Functional Annotation of 60,770 full-length cDNAs, *Nature* 420: 563-73; RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium (Okazaki, Y., Gojobori, T., *et al.*), General organizer: Y. Hayashizaki (2001). 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