



## Prof. Takashi Gojobori 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.

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### 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). Functional annotation of a full-length mouse cDNA collection, *Nature* 409(6821): 685-90; International Human Genome sequencing Consortium (DNA sequence databases: DNA Data Bank of Japan *et al.*) (2001). Initial sequencing and analysis of the human genome, *Nature*, 409(6822): 860-921; Gaudieri, S., Dawkins, R.L., Habara, K., Kulski, J.K., and Gojobori, T. (2000), SNP profile within the human major histocompatibility complex reveals an extreme and interrupted level of nucleotide diversity, *Genome Res.* 10(10): 1579-86; Yamaguchi-Kabata, Y. and Gojobori, T. (2000), Reevaluation of amino acid variability of the human immunodeficiency virus type 1 gp120 envelope glycoprotein and prediction of new discontinuous epitopes, *J. Virology* 74(9):4335-50; Gaudieri, S., Kulski, J., Dawkins, R., and Gojobori, T. (1999), Different evolutionary histories in two subgenomic regions of the major histocompatibility complex, *Genome Res.* 9(6): 541-9; Bellgard, M. and Gojobori, T. (1999), Inferring the direction of evolutionary changes of genomic base composition, *Trends in Genetics* 15(7): 254-6; Itoh, T., Takemoto, K., Mori, H., and Gojobori, T. (1999), Evolutionary instability of operon structures disclosed by sequence comparisons of complete microbial genomes, *Mol. Biol. Evol.* 16(3): 332-46; Yamaguchi, Y. and Gojobori, T. (1997), Evolutionary mechanisms and population dynamics of the third variable envelope region of HIV within single hosts, *Proc. Natl. Acad. Sci. USA.* 94(4): 1264-9; Gojobori, T., Tateno, Y., and Ohta, T., ed. (1997), Special Issue: Networks and Evolution of Molecular Information, *J. Mol. Evol.*, Vol. 44. S1-S180; Endo, T., Ikeo, K., and Gojobori, T. (1996), Large-scale search for genes on which positive selection may operate, *Mol. Biol. Evol.* 13(5): 685-90; Miura, T., Fukunaga, T., Igarashi, T., Yamashita, M., Ido, E., Funahashi, S.-I., Ishida, T., Washio, K., Ueda, S., Hashimoto, K.-I., Yoshida, M., Osame, M., Singhal, B.S., Zaninovic, V., Cartier, L., Sonoda, S., Tajima, K., Ina, Y., Gojobori, T., and Hayami, M. (1994), Phylogenetic subtypes of human T-lymphotropic virus type I and their relations to the anthropological background, *Proc. Natl. Acad. Sci. USA.* 91: 1124-7; Gojobori, T. and Ikeo, K. (1994), Molecular evolution of serine protease and its inhibitor with special reference to domain evolution, *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 344(1310): 411-5; Gojobori, T., Moriyama, E.N., Ina, Y., Ikeo, K., Miura, T., Tsujimoto, H., Hayami, M., and Yokoyama, S. (1990), Evolutionary origin of human and simian immunodeficiency viruses, *Proc. Natl. Acad. Sci. USA.* 87(11): 4108-11; Orito, E., Mizokami, M., Ina, Y., Moriyama, E.N., Kameshima, N., Yamamoto, M., and Gojobori, T. (1989), Host-independent evolution and a genetic classification of the hepadnavirus family based on nucleotide sequences, *Proc. Natl. Acad. Sci. USA.* 86(18): 7059-62; Tsujimoto, H., Hasegawa, A., Maki, N., Fukasawa, M., Miura, T., Speidel, S., Cooper, R.W., Moriyama, E.N., Gojobori, T., and Hayami, M. (1989), Sequence of a novel simian immunodeficiency virus from a wild-caught African mandrill, *Nature* 341(6242): 539-41; Gojobori, T. and Yokoyama, S. (1985), Rates of evolution of the retroviral oncogene of Moloney murine sarcoma virus and of its cellular homologues, *Proc. Natl. Acad. Sci. USA.* 82(12): 4198-201; Shimotohno, K., Takahashi, Y., Shimizu, N., Gojobori, T., Golde, D.W., Chen, I.S.Y.,

Miwa, M., and Sugimura, T. (1985), Complete nucleotide sequence of an infectious clone of human T-cell leukemia virus type II: An open reading frame for the protease gene, *Proc. Natl. Acad. Sci. USA*. 82(10): 3101-5; Gojobori, T. (1983), Codon substitution in evolution and the 'saturation' of synonymous changes, *Genetics* 105(4): 1011-27; Li, W.-H., Gojobori, T., and Nei, M. (1982), Reply on Goodman's comment 'Positive selection causes purifying selection', *Nature* 295: 630; Gojobori, T., Li, W.-H., and Graur, D. (1982). Patterns of nucleotide substitution in pseudo-genes and functional genes, *J. Mol. Evol.* 18(5): 360-9; Gojobori, T., Ishii, K., and Nei, M. (1982), Estimation of average number of nucleotide substitutions when the rate of substitution varies with nucleotide, *J. Mol. Evol.* 18(6): 414-23; Li, W.-H., Gojobori, T., and Nei, M. (1981), Pseudogenes as a paradigm of neutral evolution, *Nature* 292(5820): 237-9.