CURRICULUM VITAE

Jun Wang Birth date: June 4, 1976 Citizenship: P.R.China

BIOGRAPHY

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WANG Jun (WJ), who was born on June 4 1976, graduated Ph.D. from the Peking University in 2002, the same year as he received the national excellent Ph.D. thesis for highest academic standing from the Ministry of Education, China.

The Bioinformatics Department of Beijing Genomics Institute (BGI) was founded by his efforts in 1999. It has been moved to Shenzhen, and has been referred as BGI Shenzhen since 2007. It is now widely recognized as one of China's premier research facilities, committed to excellence in genome sciences. WJ has been leading the scientific direction and daily operation of BGI genomics and its informatics part since 2002. In 2003, WJ was appointed as associate director and professor at BGI. During 2004-06 he was for 24 months invited guest professor at the University of Aarhus, Denmark. WJ was then appointed as Ole Rømer professor of University of Southern Denmark from September 2006 to July 2009, the professorship has been transferred to University of Copenhagen since October 2009. In 2005, he was appointed professor of genomics (personal chair) at the life science college, Peking University and since 2007 he has been chairing the same position at the University of Aarhus.

For the last 8 years WJ has been leading a research group of 100+ people engaged in studies of genomics and its informatics. In 1999, WJ finished the analysis of a 1% region of human genome, which is sequenced by BGI. Then he devoted himself to genomics and its analysis, including genome assembly, annotation, expression, genome duplication, comparative genomics, molecular evolution, transcriptional regulation, genome variation analysis, database construction as well as related methodology development such as the sequence assembler and alignment tools. He also focuses on interpretation of the definition of "gene" by expression and conservation study. In 2003, Jun Wang was also been involved in the SARS genome analysis and the silkworm genome assembly and analysis in cooperation with Chinese Southeast Agricultural University. The Pig Genome Survey Project was also completed with his leading effort at BGI. He has led a group finishing the chicken genome variation map and the TreeFam in collaboration with the Sanger Institute. Recently, he and his group have finished the first Asian diploid genome, and was published as cover story at Nature. Now, he is working on the population genomics and medical genomics, such as the 1000 genome project, YanHuang Project, large genome association study of Diabetes; metagenomics project of gut microbita. He is also leading genome variation projects of rice, silkworm, and pig genome project, as well as the molecular mechanisms of the domestication process.

WJ has been mentor for 6 academics who have defended their Ph.D. degrees, and is supervising 25 Ph.D. students. He has three years of bioinformatics teaching at the graduate school of CAS and Peking University, and has been awarded the "CAS Excellent Course and Teaching" award 2004. He has authored 90+ peer-reviewed original papers – of which many are published in high impact journals as *Nature, Nature Genetics, Nature Biotechnology, Nature Review Genetics, Science, PloS Biology, Genome Research, Proceedings of National Academy of Science* and Plant Cell.

For the scientific achievements, WJ has been recognized with Award from His Royal Highness Prince Foundation, Young Elite Scientist from the Danish Research Council, Lundbeck Talent Price, Outstanding Science and Technology Achievement from the Chinese Academy of Sciences, Top 10 Scientific Achievements In China, The first "TopSUN" Scientific Paper Award from Peking University, Tan Jiazhen Life Science Award from Fudan University, and Prize for Important Innovation and Contribution from Chinese Academy of Sciences.

Title

Professor of Genomics and Bioinformatics

Education/training	
1997.9 - 2002.7	College of Life Sciences, Peking University, Beijing, China
	Ph.D. in life science
1992.9 - 1997.7	College of Life Sciences, Peking University, Beijing, China
	B.Sc. in life science

Positions	
2009 -	Ole Rømer Professor, University of Copenhagen, Denmark
2009 -	Professor of genomics (personal chair), The Chinese University of Hongkong, Hongkong, China
2008 -	Executive Director, BGI, China
2007 -	Associate Director, BGI-Shenzhen, China
2006 -	Professor of genomics (personal chair), Aarhus University
2006 - 2009	Ole Rømer Professor, University of Southern Denmark, Denmark
2004 - 2006	Visiting Professor, University of Southern Denmark/Aarhus University, Denmark
2004 -	Visiting Professor, Peking University, Beijing, China.
2003 - 2007	Professor and Director of Beijing Campus, BGI, China
2001	Director of Hangzhou Campus, BGI, China
1999 - 2007	Head of Bioinformatics Department, BGI, China

Honours, grants, and awards

"Top 10 Scientific Achievements In China" (for BGI's first Asian genome sequence) (2008)

"Award for Science and Sino-Danish Collaboration" (by His Royal Highness Prince Foundation, Denmark) (2007)

"National New Century BaiQianWan talents" (by the China National Authorities) (2006)

"Young Elite Scientist" (by the Danish Research Council) (2006)

"Talent Price" (by the Lundbeck Foundation) (2005)

"Excellent Course and Teaching" (by Graduate School of Chinese Academy of Sciences) (2004)

"Outstanding Science and Technology Achievement" (by Chinese Academy of Sciences) (2003)

"The Excellent Youth in China" (2003)

"Top 10 Scientific Achievements In China" (for BGI's Research on SARS) (2003)

"Award for Excellent Scientific Team Achievements" (by Hong Kong "QiuShi" Foundation) (2002)

The first "TopSUN" Scientific Paper Award (by Peking University) (2002)

"Top 10 Elitist in Academia" (by Peking University) (2002)

"Tan Jiazhen Life Science Award" (by Fudan University) (2002)

"Prize for Important Innovation and Contribution" (by Chinese Academy of Sciences) (2002)

"The Excellent Ph.D. Thesis in China" (by Ministry of Education) (2002)

"Top 10 Scientific Achievements In China" (for BGI's rice fine genome sequence) (2002)

"Top 10 Scientific Achievements In China" (for BGI's rice draft genome sequence) (2001)

"Top 10 Scientific Achievements In China" (for BGI's "Chinese Chapter" of Human Genome Sequence) (2000)

Educational activities

Supervised 6 Ph.D., 2 Master Students. Presently, 38 graduate students are training in the laboratory.

Presentations

Numerous pre- and postgraduate educational activities at the University of Copenhagen, the University of Southern Denmark, the University of Aarhus, the Peking University, Chinese Academy of Sciences, the Zhejiang University, and the Zhongshan University. More than 100 invited lectures at international and national scientific meetings.

Publications

Presently 90+ peer-reviewed original scientific papers, of which several are published in high-impact journal including *Nature, Nature Genetics, Nature Review Genetics, Science, PloS Biology, Genome Research, Proceedings of National Academy of Science* and *Plant Cell.* Expert reviewer for 5 international journals in genomics and bioinformatics.

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X. Yi , ... J. Wang[‡]. 2010. Sequencing of Fifty Human Exomes Reveals Adaptation to High Altitude. *Science*. [Accepted on 21 May 2010]

H. Xiang, ... J. Wang[‡]. 2010. Single base-resolution methylome of the silkworm reveals a sparse epigenomic map. *Nature Biotechnology* May 02. [Epub ahead of print]

N. Li, ... J. Wang[‡]. 2010. Whole genome DNA Methylation analysis based on high throughput sequencing technology. *Methods*. Apr 26. [Epub ahead of print]

G. Zhang, ... J. Wang[‡]. 2010. Deep RNA sequencing at single base-pair resolution reveals high complexity of the rice transcriptome. *Genome Research* Mar 19. [Epub ahead of print]

D. Li, ... J. Wang, et al. 2010. Genetic diversity, molecular phylogeny and selection evidence of the silkworm mitochondria implicated by complete resequencing of 41 genomes. BMC Evolutionary Biology 10:81

J. Qin, ... J. Wang[‡]. 2010. A human gut microbial gene catalog established by deep metagenomic sequencing. [Cover Story]. *Nature* 464:59-65.

M. Rasmussen, ... J. Wang[‡], E. Willerslev. 2010. Ancient human genome sequence of an extinct Palaeo-Eskimo. [Cover Story]. *Nature* 463:757-62.

R. Li, ... J. Wang[‡]. 2010. De novo assembly of the human genomes with massively parallel short read sequencing. *Genome Research* 20:265-72.

R. Li, ... J. Wang[‡]. 2010. The sequence and de novo assembly of the giant panda genome. [Cover Story]. *Nature* 463:311-7.

R. Li, ... J. Wang[‡], J. Wang. 2010. Building the sequence map of the human pan-genome. *Nature Biotechnology* 28:57-63.

J. Duan, ... J. Wang, et al. 2010. SilkDB v2.0: a platform for silkworm (Bombyx mori) genome biology. *Nucleic Acids Res.* 38:D453-6.

Q. Hao, ... J. Wang, et al. 2009. ADD1/SREBP1c activates the PGC1-alpha promoter in brown adipocytes. *Biochim Biophys Acta*. Dec 2. [Epub ahead of print]

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Q. Xia, ... J. Wang[‡]. 2009. Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm (Bombyx). *Science* 326: 433-6.

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R. Li, ... J. Wang[‡]. 2009. SOAP2: an improved ultrafast tool for short read alignment. *Bioinformatics* 25:1966-7.

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Y. Zhou, ... J. Wang, et al. 2009. The Schistosoma japonicum genome reveals features of host-parasite interplay. [Cover Story]. *Nature* 460: 345-51.

R. Li, ... J. Wang[‡]. 2009. SNP detection for massively parallel whole genome resequencing. *Genome Research* 19:1124-32.

J. Li, ... <u>J. Wang[‡]</u>. 2009. Correlation between Ka/Ks and Ks is related to substitution model and evolutionary lineage. *J Mol Evol*. 68:414-23.

M. Schierup, ... J. Wang, et al. 2009. Haplotype frequencies in a sub-region of chromosome 19q13.3, related to risk and prognosis of cancer, differ dramatically between ethnic groups. BMC Med Genet. 3:10-20

L. Ma, ... J. Wang[‡], et al. 2009. The YH database: the first Asian diploid genome database. *Nucleic Acids Res.* 37:D1025-8.

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S. Xu, ... J. Wang[‡], X. Zheng. 2008. Gene conversion in the rice genome. *BMC Genomics* 9:93.

L. Fang, ... J. Wang[‡]. 2008. Positive correlation between recombination rate and nucleotide diversity is shown under domestication selection in the chicken genome. *Chin. Sci. Bull.* 53: 746-50.

J. Ruan, ... J. Wang[‡], R. Durbin. 2008. TreeFam: 2008 Update. Nucleic Acids Res. 36:D735-40.

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Q. Xia, ... J. Wang*, et al. 2004. A draft sequence for the genome of the domesticated silkworm (Bombyx mori). Science 306: 1937-1940.

G.K. Wong, B. Liu, <u>J. Wang*</u>, *et al.* 2004. A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. *Nature* 432: 717-722.

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J. Hu, ... J. Wang, et al. 2003. Evolution and variation of the SARS-CoV genome. *Genomics Proteomics Bioinformatics* 1: 216-25.

S. Bi, ... J. Wang, et al. 2003. Complete genome sequences of the SARS-CoV: the BJ Group (Isolates BJ01-BJ04). *Genomics Proteomics Bioinformatics* 1: 180-92.

Z. Xu, ... J. Wang, et al. 2003. The R protein of SARS-CoV: analyses of structure and function based on four complete genome sequences of isolates BJ01-BJ04. *Genomics Proteomics Bioinformatics* 1: 155-65.

Q. Wu, ... J. Wang, et al. 2003. The E protein is a multifunctional membrane protein of SARS-CoV. Genomics Proteomics Bioinformatics 1: 131-44.

E. Qin, ... J. Wang, et al. 2003. A genome sequence of novel SARS-CoV isolates: the genotype, GD-Ins29, leads to a hypothesis of viral transmission in South China. *Genomics Proteomics Bioinformatics* 1: 101-7.

E. Qin,... J. Wang, et al. 2003. A complete sequence and comparative analysis of a SARS-associated virus(Isolate BJ01). *Chin. Sci. Bull.* 48: 941-948.

L. Zhong,... J. Wang, et al. 2003. A statistical approach designed for finding mathematically defined repeats in shotgun data and determining the Length distribution of clone-inserts. *Genomics Proteomics Bioinformatics* 1: 43-57.

Y. Zhou, ... J. Wang, et al. 2003. Gene identification and expression analysis of 86,136 Expressed Sequence Tags (EST) from the rice genome. *Genomics Proteomics Bioinformatics* 1: 26-42.

G.K. Wong, J. Wang, et al. 2002. Compositional gradients in *Gramineae* genes. [Cover Story]. *Genome Res.* 12: 851-856.

<u>J. Wang[‡]</u>, *et al.* 2002. RePS: a sequence assembler that masks exact repeats identified from the shotgun data. *Genome Res.* 12: 824-831.

X. Zhang, ... J. Wang, et al. 2002. Genomic organization, transcript variants and comparative analysis of the human nucleoporin 155 (NUP155) gene. *Gene* 288: 9-18.

J. Yu, S. Hu, <u>J. Wang</u>*, *et al.* 2002. A draft sequence of the rice genome (*Oryza sativa* L. ssp. *indica*) [Cover Story]. *Science* 296: 79-92.

J. Yu, S. Hu, <u>J. Wang*</u>, *et al.* 2001. A draft sequence of the rice (Oryza sativa ssp. indica) genome. *Chin. Sci. Bull.* 46: 1937-1942.

J. Wang, as one of the authors in the International Human Genome Sequencing Consortium. 2001. Initial sequencing and analysis of the human genome. *Nature* 409: 860-921.

<u>J. Wang</u>, S. Li. 2001. Artificial intelligent work for imitating the evolution of lady beetle's searching behavior, *Chinese Journal of Ecology* 20: 65-69.

REFERENCES

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