

Curriculum Vitae
Yun-Xin Fu

Address

Yun-Xin Fu, Ph.D.
Betty Wheless Trotter Professor
Director, Computational Genomics Section
Human Genetics Center and Division of Biostatistics
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Education

INSTITUTION AND LOCATION	DEGREE	YEAR CONFERRED	FIELD OF STUDY
Zhongshan University, China	BS.C.	1978-82	Mathematics and statistics
University of Reading, England	Ph.D.	1984-88	Statistics
Nat. Inst. for Med. Res. London	Postdoc.	1988-89	Sequence alignment
University of Georgia, Athens	Postdoc.	1989-90	Population genetics
University of Texas, Houston	Postdoc.	1990	Molecular evolution

PhD thesis

Change point theory and its application to the prediction of protein secondary structure,
Department of Applied Statistics, University of Reading, England.

PhD supervisor

Robert N. Curnow, Ph.D.

Postdoctoral supervisors

Tom Kirkwood, Ph.D. (London)
Jonathan Arnold, Ph.D. (Georgia)
Wen-Hsiung Li, Ph.D. (Houston)

Professional Appointments

Guest Professor, Yunnan University, China, Sept. 2003-present

Guest Professor, University of Sun Yet-sen, China, Sept. 2003- present

Betty Wheless Trotter professorship, School of Public Health (SPH), Jan. 2002-present

Director, Computational Genomics Section, Human Genetics Center, Oct. 2001- present

Full Professor with tenure, Human Genetics Center, SPH, University of Texas at Houston, Sept. 2001 – present

Associate Professor with tenure, Human Genetics Center, SPH, University of Texas at Houston, Sept. 1996 – Aug. 2001

Assistant Professor (tenure-track), Human Genetics Center,SPH, University of Texas at Houston, Oct. 1994 – Aug. 1996

Assistant Professor (tenure-track), Center for Demographic and Population Genetics, Graduate School of Biomedical Sciences(GSBS), University of Texas at Houston, Oct. 1991– Aug. 1994

Research Assistant Professor, Center for Demographic and Population Genetics, GSBS, University of Texas at Houston, Jan. 1991 - Sept. 1991

Faculty Associate, Center for Demographic and Population Genetics, GSBS, University of Texas at Houston, Sept.1990 - Dec. 1990

Assistant Lecturer, Department of Basic sciences, South China College of Tropical Crops, China. Mar. 1982- Aug. 1984

Research Area and Interests

Human population history and human genome diversity

Population and quantitative genetics, conservation biology

Coalescent theory and its applications

Statistics/Mathematics

Evolution of infectious disease

Phylogenetic reconstruction and molecular evolution

Computational biology, comparative genomics and functional genomics

Honors

Overseas Research Student Award (by British Council of Education). 1985 - 1988

Outstanding Research Student Award (Reading University, England). 1986 - 1988

Short-term visiting Professorship (Japan Society for Promotion of Science (JSPS)) (1998)

Memberships and Service

The Society for the Study of Evolution

The Society for Molecular Biology and Evolution

Webmaster for the *Society of Molecular Biology (1995-1999) and Evolution*, and for the

journal *Molecular Biology and Evolution*

Associate Editor for *Molecular Biology and Evolution*, Oct. 1998 -Oct. 2001

Associate Editor for *Genetics*, Dec. 1998 - present

Ad-hoc member of the NIH Study Section, Oct. 1998, Oct. 2004, Feb. 2006, Mar. 2005

Panel member of the NIEHS site visit to University of Southern California, Dec. 2001

Ad-hoc member of the NIH Genetics Study Section, Feb. 1998

Member of the NIH Genetics Study Section, Oct. 1999 - 2004

Member, Membership committee of the Society of Chinese Bioscientists in America, 1999-present

Teaching Experience

2000 - 2006: Lecturer of GSBS and SPH course “Introduction to Genomics and Bioinformatics”(two credit hours)

2001 - 2006: Lecturer of GSBS and SPH course “Evolution of Protein and DNA sequences”(two credit hours)

1991 - 2006: Lecturer (sole lecturer in most years) of GSBS and SPH course “Population Genetics” (two credit hours)

2002-2006 : Lecturer of GSBS and SPH course “Statistical Genetics”

2006 fall: Lecturer for SPH course ”Monte Carlo Approach in Statistics and Genetics”(two credit hours)

Note: GSBS – Graduate School of Biomedical Sciences, SPH – School of Public Health

Postdoctoral Fellows trained

Hongwen Deng, 1995–1996, supported by grant R29 GM50428

Daniel C. Vasco, 1997– 1998, supported by grant R29 GM50428

Haiying Huai, 1998 - 2004, supported by grant R29 GM50428

David de Lorenzo, 1998 - 2001, supported by grant DEB-9707567

Yuande Tan, 2000 - 2001, supported by grant HL51021

Haipeng Li, 2000 - 2004, supported by grant GM50428

Visiting Scholar

Dr. Long-Zhen Tong, 1994 – 1995

Graduated Students

Li Jin, Ph.D. student, graduated in 1994. Served on Supervisory Committee. Currently Professor in Fudan University, China

Benny Chang, Ph.D. student, graduated in 1995. Served on both Examining and Supervisory Committees. Currently Assistant Professor, Baylor College of Medicine

Xun Gu, Ph.D. student, graduated in 1996. Served on Advisory, Examining and Supervi-

sory Committees. Currently Associate Professor, University of Iowa

Julia Krushkal, Ph.D. student, graduated in 1996. Served on Advisory, Examining and Supervisory Committees. Currently Assistant Professor, University of Tennessee

George Li, Ph.D. student, graduated in 1996. Served on Supervisory Committee. Current a senior statistician in a biotechnology company, California

Grier Page, MSc. student, graduate in 1997. Served on Examining Committee. Currently Associate Professor, University of Alabama at Birmingham

Andrew Rodin, Ph.D. student, graduated in 1999. Served as on-site Supervisory Professor. Currently Assistant Professor, University of Texas at Houston

Zhongming Zhao, Ph.D. student, graduated in 2000. Served as on-site Supervisory Professor. Currently Assistant Professor, Virginia Tech.

Qiqing, Huang, Ph.D. student graduated in(2002). Served as supervisor. Currently a Research Scientist in Johnson & Johnson, Virginia

Hongyan, Xu, Ph.D. (2003), Served as supervisor. Currently Assistant Professor, University of Georgia at Augusta

Haipeng, Li, Ph.D. (2002) and postdoc. Served as Supervisor. Currently postdoctoral fellow, University of Munich, Germany

Feng Zhan Ph.D. (2004), Served as thesis advisor. Currently a Research Statistician, US oncology, Houston

Liu, Xiaoming Ph.D. (2006) Served as Supervisor

Huang, Jin, MSc. Thesis Advisor. Current Ph.D. student

Zhao, Hui, MSc. current Ph.D. student. Served as Supervisor

Rafael Gonzalez, (2005) Visiting Ph.D. student from Mexico

University or School Committees Served

Academic Computing Committee of the Health Science Center at Houston (1993-1996)

Admission Committee of Genetics Program, GSBS. (1992-1996)

Admission Committee, Disease Control module, SPH (1999-2003)

Scientific Review Committee, UT Health Science Center (2001-2005)

Faculty Council, Member, SPH (2006-2008)

Completed Grants

NIH FIRST AWARD (R29 GM50428)

Title: “*Coalescent theory and analysis of DNA polymorphisms*”

Total Cost: \$499,000

Period: August,1994 — July 2000

Position: Principle Investigator

NIH Supplement grant (R29 GM50428)

Title: “*Coalescent theory and analysis of DNA polymorphisms*”

Total Cost: \$24,000

Period: Sept,1998 — July 2000
Position: Principle Investigator

NSF Grant (DEB-9707567)

Title: “*Estimating the age of the common ancestor of a population*”

Total Cost: \$120,000

Period: Sept 15,1997 — Sept 14, 2000 (no-cost extension to August 31,2001)

Position: Principle Investigator

NIH grant (R01 HG01708)

Title: “*Statistical methods for studying disease gene history*”

Total Cost: \$377,074

Period: Sept 30, 1997 — Sept 29, 2000 (no cost extension to August 31,2001)

Position: Principle Investigator

NIH grant (R01 GM55759 subcontract)

Title: “*Human DNA polymorphism and evolution*”

Total Cost: \$189,855

Period: Jan. 1, 1998 – 12/30/2001

Position: Principle Investigator

NIH grant (HL51021)

Title: “*Molecular epidemiology of essential hypertension*”

Total Cost: \$5,297,411

Period: June. 1999 — May 2004

Position: co-investigator (5%) (PI: Eric Boerwinkle)

NIH grant (R25 CA57730 subcontract)

Title: “*Supplement in genetic epidemiology education*”

Total Cost: \$505,967

Period: Sept. 1999 – Aug. 2004

Position: : co-investigator (10%) (PI: Eric Boerwinkle)

NIH grant R01 GM50428-06A1

Title: “*Coalescent theory and analysis of DNA polymorphism*”

Period: August 1, 2000 - July 31, 2005

Total Cost: \$737,479

Position: Principle Investigator

Chinese NSF grant

Title: “*Award for outstanding Chinese scientist abroad*”

Period: Jan. 1, 2001 - Dec 31, 2003

Total Cost: 400,000 yen (about \$50,000)

Position: Principle Investigator(Dr. Yaping Zhang as host)

Active Grants

NIH “*Statistical methods for studying infectious disease*”

Total Cost: \$250,000 + indirect cost

Period: Sept. 1, 2001 - Aug. 31, 2006

Position: Principle Investigator

NIH “*Molecular epidemiology of essential hypertension*”

Total Cost: \$922,000 + indirect cost

Period: Aug. 15, 2004 - June 30, 2009

Position: : Co-investigator (5%) (PI: Eric Boerwinkle)

NIH “*Molecular epidemiology of CA-MRSA*”

Total Cost: \$25,000 + indirect cost

Period: Jan 1, 2006 - Dec. 30, 2008

Position: : PI of subcontract

NIH “*Training program in biostatistics at UTHSC-SPH*”

Total Cost: \$106,550 Year One for student expenses only. No funds for faculty/administrative salaries or faculty/administrative expenses

Period: July 14, 2006 - June 30, 2011

Position: : Investigator (PI Robert Hardy)

Publications:

1. **Fu, Y. X.** and Curnow, R. N. (1990) Locating a changed segment in a sequence of Bernoulli variables. *Biometrika*, 77:295–304.
2. **Fu, Y. X.** and Curnow, R. N. (1990) Maximum likelihood estimate of multiple change points. *Biometrika*, 77:563–573.
3. **Fu, Y. X.** and Arnold, J. (1991) On the association of restriction fragment length polymorphisms across species boundaries. *Proc. Natl. Acad. Sci.*, 88:3967–3971.
4. **Fu, Y. X.** and Li, W. H. (1991) Necessary and sufficient conditions for the existence of certain quadratic invariants under a phylogenetic tree. *Math. Biosci.*, 105:229–238.
5. **Fu, Y. X.** and Arnold, J. (1992) Dynamics of cytonuclear disequilibria in finite populations and comparison with a two-locus nuclear system. *Theor. Popul. Biol.*, 41:1–25.
6. **Fu, Y. X.** and Li, W. H. (1992) Necessary and sufficient conditions for the existence of linear invariants in phylogenetic inference. *Math. Biosci.*, 108:203–218.
7. **Fu, Y. X.** and Li, W. H. (1992) Construction of linear invariants in phylogenetic inference. *Math. Biosci.*, 109:201–228.
8. **Fu, Y. X.** , Timberlake, W.E. and Arnold, J. (1992) On the design of genome mapping experiments using short synthetic oligonucleotides. *Biometrics*, 48:337-359.
9. **Fu, Y. X.** and Arnold, J. (1992) A table of exact sample sizes for the use with Fisher's exact test for 2X2 tables. *Biometrics*, 48:1103–1112.
10. Li, W. H. and **Fu, Y. X.** (1992) Method of linear invariants for phylogenetic reconstruction. In the Proc. Int. Conf. on “ Modeling and Computer Methods in Molecular Biology and Genetics”. Nova Science Publishers, Inc.
11. **Fu, Y. X.** and Li, W. H. (1993) Statistical tests of neutrality of mutations. *Genetics*, 133:693–709.
12. **Fu, Y. X.** and Li, W. H. (1993) Maximum likelihood estimate of population parameters. *Genetics*, 134:1261-1270.
13. **Fu, Y. X.** (1994) An phylogenetic estimator of effective population size or mutation rate. *Genetics*, 136:685–692.
14. Li, W. H. and **Fu, Y. X.** (1994) Estimation of population parameters and detection of natural selection from DNA sequences. In “Non-neutral evolution: Theories and Molecula Data”. Golding, B.(ed.). NY: Chapman and Hall, pp. 112–125.
15. **Fu, Y. X.** (1994) Estimating effective population size or mutation rate using the frequencies of mutations of various classes in a sample of DNA sequences. *Genetics*, 138:1375–1386.
16. **Fu, Y. X.** (1995) Linear invariants with Jukes' and Cantor's one-parameter model, *J. Theor. Biol.*, 173:339–352.

17. Steel, M. and **Fu, Y. X.** (1995) Classifying and counting linear phylogenetic invariants for Jukes-Cantor model. *J. Computational Biol.*, **2**:39–47.
18. **Fu, Y. X.** (1995) Statistical properties of segregating sites. *Theor. Popul. Biol.*, **48**: 172-197.
19. Gu, X., **Fu, Y. X.** and Li, W. H. (1995) Maximum likelihood estimation of heterogeneity of substitution rate among nucleotide sites. *Mol. Biol. Evol.*, **12**:546–557.
20. **Fu, Y. X.** (1996) New statistical tests of neutrality for DNA samples from a population. *Genetics*, **143**:557–570.
21. **Fu, Y. X.** and Li, W. H. (1996) Estimating the age of the common ancestor of men from the *ZFY* intron. *Science*, **272**:1356–1357.
22. Datta, S., **Fu, Y. X.** and Arnold, J. (1996) Dynamics and equilibrium behavior of cytonuclear disequilibrium under genetic drift, mutation and migration. *Theor. Popul. Biol.*, **50**:298-824.
23. **Fu, Y. X.** (1996) Estimating the age of the common ancestor of a DNA sample using the number of segregating sites. *Genetics*, **144**:829–838.
24. Deng, H. W. and **Fu, Y. X.** (1996) The effects of variable mutation rates across sites on the phylogenetic estimation of effective population size or mutation rate of DNA sequences. *Genetics*, **144**:1271–1281.
25. **Fu, Y. X.** and Li, W. H. (1997) Estimating the age of the common ancestor of a sample of DNA sequences. *Mol. Biol. Evol.*, **14**:195–199.
26. **Fu, Y. X.** (1997) Coalescent theory for a partially selfing population. *Genetics*, **146**:1489–1499.
27. **Fu, Y. X.** (1997) Statistical tests of neutrality of mutations against population growth, hitchhiking and background selection. *Genetics*, **147**:915–925.
28. Huang, W., **Fu, Y. X.** , Chang, B. H. J., Gu, X., Jorde, L. B. and Li, W. H. (1998) Sequence variation in ZFX introns in human populations. *Mol. Biol. Evol.* **15**:138-142.
29. Deng, H. W. and **Fu, Y. X.** (1998) Conditions for positive and negative correlations between fitness and heterozygosity in equilibrium populations. *Genetics*, **148**:1333-1340.
30. Stockbauer, K. E., Grigsby, D. Pan, X., **Fu, Y. X.** , Perea-Mejia L. M., Cravioto, A. and Musser, J. M. (1998) Hypervariability generated by natural selection in an extracellular complement inhibiting protein of serotype M1 strains of group A *streptococcus*. *Proc. Natl. Acad. Sci.* **95**:3128-3133.
31. **Fu, Y. X.** (1998) Probability of a segregating pattern in a sample of DNA sequences. *Theor. Popul. Biol.*, **54**:1-10.
32. Deng, H. W. and **Fu, Y. X.** (1998) Estimating the gamma rate of variation based on parsimony analysis. Proceeding of the Trinational Workshop on Human Evolution.
33. Deng, H. W. and **Fu, Y. X.** (1998) On the three methods for estimating deleterious genomic mutation parameters. *Genet. Res.*, **71**:223-236.

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34. Deng, H. W., **Fu, Y. X.** and Lynch, M. (1998) Inferring the major genomic mode of dominance and overdominance. *Genetica*, 102/103:559-567.
 35. **Fu, Y. X.** and Chakraborty, R. (1998) Simultaneous estimation of all the parameters in a step-wise mutation model. *Genetics*, 150:487-497.
 36. Li, W. H. and **Fu, Y. X.** (1998) Coalescent theory and its applications in population genetics. In “*Statistics in Genetics*”, Halloran, M.E., and Geisser, S. (eds.). NY:Springer-Verlag, pp. 45-79.
 37. **Fu, Y. X.** and Li, W. H. (1999) Coalescing into the 21st century: an overview and prospects of coalescent theory. *Theor. Popul. Biol.* 56:1-10.
 38. Hoe, N. P., Nakashima, K., Lukomski, S., Grigsby, D., Liu, M., Kordari, P., Dou, S. J., Pan, X., Vuopio-Varkila, J., Salmelina, S., McGeer, A., Low, D.E., Schwartz, B., Schuchat, A., Naidich, S., De Lorenzo, D., **Fu, Y. X.** and Musser, J. M. (1999) Rapid selection of complement-inhibiting protein variants of Group A *Streptococcus* epidemic waves. *Nature Med.*, 5:924-929.
 39. **Fu, Y. X.** (2000) Measures of genetic variation. In *Encyclopedia of Life Sciences*, Stockton Press.
 40. Deng, H.-W. and **Fu, Y. X.** (2000) Counting mutations by parsimony and estimation of mutation rate variation across nucleotide sites. *Math. Comput. Modeling*, 32:83-95.
 41. Vasco, D. A., Crandle, K. A. and **Fu, Y. X.** (2000) Molecular population genetics: coalescent methods using summary statistics. In “Computational and Evolutionary Analysis of HIV Molecular Sequences”. Rodrigo, A.G. and Learn, G.H. (eds.). Boston, MA: Kluwer Academic Publishers, pp. 175-218.
 42. **Fu, Y. X.** (2000) Neutrality and selection in molecular evolution: Statistical tests. In “*Encyclopedia of Life Sciences*”. Stockton Press.
 43. **Fu, Y. X.** (2000) Interpreting DNA evidence. *Theor. Popul. Biol.*, 57:399-400.
 44. Zhao, Z., L. Jin, **Y. X. Fu**, M. Ramsay, T. Jenkins, E. Leskinen, P. Pamilo, M. Trexler, L. Patthy, L. B. Jorde, S. Ramos-Onsins, N. Yu, and W.-H. Li. (2000) Worldwide DNA sequence variation in a 10 kb noncoding region on human chromosome 22. *Proc. Natl. Acad. Sci. USA*, 97:11354-11358.
 45. Ding, Y. C., S. Wooding, H. Harpending, H.C. Chi, H. P. Li, **Y. X. Fu**, J. F. Pang, Y. G. Yao, J.G. Xiang-Yu, R. Moyzis, and Y. P. Zhang (2000) Population structure and history in East Asia. *Proc. Natl. Acad. Sci. USA*, 97:14003-14006.
 46. **Fu, Y. X.** (2001) Estimating mutation rate and generation time from longitudinal samples of DNA sequences. *Mol. Biol. Evol.*, 18:620-626.
 47. Yu, N., Z. Zhao, **Y. X. Fu**, N. Sambuughin, M. Ramsay, T. Jenkins, E. Leskinen, L. Patthy, L.B. Jorde, T. Kuromori and W.-H. Li (2001) Global patterns of human DNA sequence variation in a 10-kb region on chromosome 1. *Mol. Biol. Evol.*, 18:214-222.
 48. Hoe N. P., J. Vuopio-Varkila, M. Vaara, D. Grigsby, D. De Lorenzo, **Y. X. Fu**, S.-J. Dou, X. Pan, K. Nakashima and J. M. Musser (2001) Distribution of streptococcal
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- inhibitor of complement variants in pharyngitis and invasive isolates in an epidemic of serotype M1 group A Streptococcus infection. *J. Infect. Dis.*, 183:633-639.
49. Su, B., **Y. X. Fu**, Y. Wang, L. Jin and R. Chakraborty (2001) Genetic diversity and population history in Red Pandas (*Ailurus fulgens*) as inferred from mitochondrial DNA sequence variation. *Mol. Biol. Evol.*, 18:1070-1076.
 50. Yao Y. G., L. Nie, H. Harpending, **Y. X. Fu**, Z.G. Yuan and Y.P. Zhang (2002) Genetic relationship of Chinese ethnic populations revealed by mtDNA sequence diversity. *Am. J. Phy. Anthropol.*, 118:63-76.
 51. Yu, N., **Y. X. Fu**, and W.-H. Li (2002) DNA polymorphism in a world-wide sample of human X chromosomes. *Mol. Biol. Evol.*, 19:2131-2141.
 52. Lu, X. M., **Y. X. Fu** and Y. -P. Zhang (2002) Evolution of mitochondrial cytochrome b pseudogene in genus *Nycticebus*. *Mol. Biol. Evol.*, 19:2237-2341.
 53. Li, H. P. Y. -W. Zhang, Y. -P. Zhang and **Y. X. Fu** (2003) Neutrality tests using DNA polymorphism from multiple samples. *Genetics*, 163:1147-1151.
 54. Li, H. P., S.-J. Meng, Z. M. Meng, **Y. X. Fu** and Y. P. Zhang (2003) Genetic diversity and population history of golden monkeys (*Rhinopithecus roxellana*). *Genetics*, 164:269-275.
 55. **Fu, Y. X.** and H. Y. Huai (2003) Estimating mutation rate: how to count mutations. *Genetics*, 164:797-805.
 56. Zhao, Z., **Y. X. Fu**, D. Hewett-Emmett and E. Boerwinkle (2003) Investigating single nucleotide polymorphism (SNP) density in the human genome and its implications for molecular evolution. *Gene*, 312:207-213.
 57. Huang, Q., **Y. X. Fu** and E. Boerwinkle (2003) Comparison of strategies for selecting single nucleotide polymorphisms for case/control association studies. *Hum. Genet.*, 113:253-357.
 58. Xu, H. Y. and **Y. X. Fu** (2004) Estimating effective population size or mutation rate with microsatellites. *Genetics*, 166:555-563.
 59. Choudhary, M., **Y. X. Fu**, C. Mackenzie, and S. Kaplan (2004) DNA sequence duplication in *Rhodobacter sphaeroides* 2.4.1: Evidence of an ancient partnership between chromosomes I and II. *J. Bacteriol.*, 186:2019-2027.
 60. Zhao, Z., H. Li, X. Wu, Y. Zhong, K. Zhang, Y. Zhang, E. Boerwinkle, and **Y. X. Fu** (2004) Moderate mutation rate in the SARS coronavirus genome and its implications. *BMC Evol. Biol.*, 4:21.
 61. Graviss, E., X. Ma, and **Y. X. Fu** (2004) IL-8 Polymorphism is not associated with pulmonary tuberculosis in the Gambia and to original article: association between interleukin-8 gene alleles and human susceptibility to tuberculosis disease. A rebuttal. *J. Infect. Dis.*, 189:1545-1546.
 62. Shi, S., Y. Huang, K. Zeng, F. Tan, H. He, and **Y. X. Fu** (2005) Molecular phylogenetic analysis of mangroves: independent evolutionary origins of vivipary and salt secretion.

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- Mol. Phylogenet. Evol. 34:159-166.
63. Xu, H., R. Chakraborty and **Y. X. Fu** (2005) Mutation rate variation at human dinucleotide microsatellites. *Genetics*, 170:305-312.
 64. **Fu, Y. X.** (2006) Exact coalescent for the Wright-Fisher model. *Theor. Pop. Biol.*, 69(4):385-394.
 65. Lynch, H.T., A. de la Chapelle, H. Hampel, A. Wagner, R. Fodde, J.F. Lynch, R. Okimoto, M.B. Clark, S. Coronel, A. Trowonou, **Y. X. Fu** , G.R. Haynatzki and G. Gong (2005) American founder mutation for Lynch syndrome: prevalence estimates and implications. *Cancer* 106(2):448-452.
 66. Chen, J.H., D. Pan, C. Groves, Y.X. Wang, E. Narushima, H. Fitch-Snyder, P. Crow, V.N. NgocThanh, O. Ryder, H. W. Zhang, **Y. X. Fu** , and Y.P. Zhang (2006) Molecular phylogeny of *Nycticebus* inferred from mitochondrial genes. *Int. J. Primatol.* 27:1187-1200.
 67. Pan, D., **Y. X. Fu** , and Y.P. Zhang (2006) Population genetics of *Rhinopithecus bieti*: A study of the mitochondrial control region. *Yi Chuan* 28(4):432-436 (in Chinese).
 68. Gong, G., G. Haynatzki, V. Haynatzka, S. Kosoko-Lasaki, R. Howell, **Y. X. Fu** , J.C. Gallaher and M.R. Wilson (2006) Bone mineral density of recent African immigrants in the United States. *J. Natl. Med. Assoc.* 98(5):746-752.
 69. Gong, G., G. Haynatzki, V. Haynatzka, R. Howell, S. Kosoko-Lasaki, **Y. X. Fu** , F. Yu, J.C. Gallaher and M.R. Wilson (2006) Bone mineral density-affecting genes of Africans. *J. Natl. Med. Assoc.* 98(7):1102-1108.
 70. Tan, Y.D. and **Y. X. Fu** (2006) A novel method for estimating linkage maps. *Genetics* 173(4):2383-2390.
 71. Shi, P., L. Yu, **Y. X. Fu** , J.-F. Huang, K.-W. Zhang and Y.-P. Zhang (2006) Evolutionary implications of Avian Infectious Bronchitis Virus (AIBV) analysis *Cell Res.* 16(3):323-327.
 72. Zhao, Z., N. Yu, **Y. X. Fu** , and W.H. Li (2006) Nucleotide variation and haplotype diversity in a 10-kb noncoding region in three continental human populations. *Genetics* 174:399-409.
 73. Gonzalez, R., A. Revol de Mendoza, D. Esquivel, G. Corrales, R. Rodriguez, V. Gonzalez, G. Davila, Q. Cao, P. de Jong, **Y. X. Fu** and H.A. Barrera (2006) Growth hormone locus expands and diverges after the separation of New and Old World monkeys. *Gene* 380:38-45.
 74. Tan, Y. and **Y. X. Fu** (2006) A new strategy for estimating recombination fractions between dominant markers from F2 population. *Genetics* 2006 Oct 22 Epub ahead of print.
 75. Zeng, K., S. Shi, **Y. X. Fu** , and C.-I. Wu (2006) Statistical tests for detecting positive selection by utilizing high frequency variants. *Genetics* 2006 Sept 1 Epub ahead of print.
 76. Tan, Y.D., M. Fornage and **Y. X. Fu** (2006) Ranking analysis of microarray data: A
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- powerful method for identifying differentially expressed genes. Genomics 2006 Sept 14 Epub ahead of print.
77. Liu, X., M. Gutacker, J. M. Musser and **Y. X. Fu** (2006) Evidence for recombination in mycobacterium tuberculosis. J. Bactiol. 2006 Sept 22 Epub ahead of print.
 78. Xu, H., **Y. X. Fu** , M. Kimmel and R. Chakraborty (2006) Detecting selection using microsatellite loci data. Genetics (submitted).
 79. **Fu, Y. X.** (2006) Variance and covariance of linear functions of segregating sites of various types. J. Math. Biol. (submitted).
 80. **Fu, Y. X.** (2006) Shift of the most recent common ancestor of a population and its effect on genealogy. Genetics (submitted).
 81. **Fu, Y. X.** and C. Xue (2006) The probability of preservation of duplicate genes by subfunctionalization. Genetics (submitted).
 82. Zhan, F. and **Y. X. Fu** (2006) An improved BLUE estimator of mutation parameter from samples of DNA sequences. Mol. Biol. Evol. (submitted).
 83. Xue, C. and **Y. X. Fu** (2006) Mean time to resolution of gene duplication. Genetics (submitted).
 84. Liu, X. and **Y. X. Fu** (2006) Test of genetical isochronism for longitudinal samples of DNA sequences. Genetics (submitted).
 85. Liu, S. and **Y. X. Fu** (2006) Dynamic domains and geometrical properties of HIV-1 gp 120 during conformational changes induced by CD4 binding. J. Mol. Med. (submitted).
 86. Liu, X. and **Y. X. Fu** (2006) Improvements and extensions for recombination lower bounds. Genetics (submitted).