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Education

- 1981 B.Sc. Animal Science, Huazhong Agricultural University, Wuhan, China
1986 Ph.D. Genetics, University of Edinburgh, Edinburgh, Scotland, UK, Advisor: Prof. W. G. Hill

Positions

- 1982.2—1983.9 Department of Animal Science, Huazhong Agricultural University, Wuhan, China,
Assistant Lecturer
1986.10— Department of Statistics (1986.10—present), Department of Genetics (2001.6—2013.6),
Department of Biological Sciences (2013.7—present), Bioinformatics Research Center
(2001.6—present), North Carolina State University
Postdoctoral Research Associate (1986.10-1990.11) (with the late Prof. C. Clark Cockerham)
Visiting Assistant Professor (1990.12-1991.12)
Research Assistant Professor (1992.1-1994.6) (tenure-track)
Research Associate Professor (1994.7-1999.6) (tenured in 1994)
Research Professor (1999.7-2001.6)
Professor (2001.7—2005.6)
William Neal Reynolds Distinguished Professor (2005.7—)
2006.1—2011.6 Director, Bioinformatics Research Center
2006.1—2011.6 Co-Director, Genomics Science Graduate Programs;
Director, Bioinformatics Graduate Program
2006.1— Director, NIH/NIEHS Bioinformatics Graduate Training Program
2004.2—2004.8 Academic sabbatical in Institute of Cell, Animal and Population Biology, The University of
Edinburgh, UK
2007.8—2008.7 Academic sabbatical in National Institute of Biological Sciences, Beijing, China &
Peking University, College of Life Science, Beijing, China.

Honors and Awards

- 1998 China Bridge International Fellow
2001 [D. D. Mason Faculty Award](#), Department of Statistics, North Carolina State University
2005 [William Neal Reynolds Distinguished Professorship](#)
2008 Fellow of the American Statistics Association

Professional Activities

- 1994—2002 Associate Editor, [GENETICS](#)
1995—2000 Associate Editor, [THEORETICAL POPULATION BIOLOGY](#)

- 2001— Editorial Board, [JOURNAL OF ZHEJIANG UNIVERSITY](#) (Agri. & Life Sci.)
 2004—2010 Editorial Board, Genetics and Genomics
 2005—2012 Associate Editor, [BMC GENETICS](#)
 2006— Editorial Board, ACTA AGRONOMICA SINICA
 2012— Editorial Board, The Crop Journal
- 1996-1997 NSF Computational Biology Activities Review Committee
 1996, 1997 NIH/NHLBI Special Emphasis Review Committee
 1997 USDA/ARS Animal Genome and Genetic Mechanisms Review Committee
 2000 NIH/NHGRI Genome Research Review Committee
 2002 NIH Genome Study Section
 2002-2006 NIH/NIGMS Biomedical Research and Research Training Committee
 2005, 2009 NIH Genomics, Computational Biology and Technology Study Section
 2005 Joint NSF-NIGMS Mathematical Biology Review Committee
 2006 NIEHS Director's Challenge Initiatives Program Review
 2007 NIH Behavioral Genetics and Epidemiology Study Section
 2007-2009 NIEHS Environmental Health Sciences Review Committee
 2013 NIH Centers of Biomedical Research Excellence (COBRE) [P20] Special Emphasis Panel
 2015 NIH Genes, Genome and Genetics F08 Fellowship Review Committee (ZRG1 F08 B(20))
- 1995 Organizer of invited symposium on “Mapping Quantitative Trait Loci”,
 Annual Meeting of the Society for the Study of Evolution, Montreal, Canada
 1998 Organizer of invited symposium on “Mapping and Characterizing Genes Affecting Quantitative
 Traits”, The XVIIIth International Congress of Genetics, Beijing, China
 2001 Vice Chairman of “International Symposium on Mapping and Identification of Genes for
 Complex Polygenic Traits and Diseases”, Changsha, Human, China
 2002-2005 Representative of the Eastern and Western North American Regions of the International
 Biometric Society (ENAR/WNAR) to Section G: Biological Sciences of the
 American Association for the Advancement of Science (AAAS)
 2004 Organizer of invited session on “Gene Expression QTL Analysis”, The Joint Statistics Meetings,
 Toronto
 2006-2007 Co-Chair of the Organizing Committee of “The Third International Conference on Quantitative
 Genetics”, August 18-24, 2007, Hangzhou, China
 2013 Organizing Committee of “Impact of Large-Scale Genomic Data on Statistical and quantitative
 Genomics Conference”, November 24-26, 2013, University of Washington, Seattle, USA
- 1993-1995 Consultant to Pioneer Hi-Bred International Inc.
 1994-1996 Consultant to Ciba Geigy
 2000-2002 Consultant to Monsanto/Cereon Genomics
 2005 Consultant to BASF Plant Science
 2013-2015 Consultant to Syngenta Biotechnology
- 2010 The LeClerc Rotary Lecture, Biometrics Program, University of Maryland

Publications [citation number by Google Scholar as 12/13/2013]

1. **Zeng, Z.-B.** (1986) Theoretical studies on genetic limits to natural and artificial selection with mutation. Ph.D Thesis, Department of Genetics, The University of Edinburgh. [1]
2. **Zeng, Z.-B.** and W.G. Hill (1986) [The selection limit due to the conflict between truncation and stabilizing selection with mutation](#). *Genetics* **114**:1313-1328. [23]
3. **Zeng, Z.-B.** (1987) Genotypic distribution at the limit to natural and artificial selection with mutation. *Theoretical Population Biology* **32**:90-113. [10]

4. **Zeng, Z.-B.** (1988) [Long-term correlated response, interpopulation covariation and interspecific allometry.](#) *Evolution* **42**: 363-374. [[136](#)]
5. **Zeng, Z.-B.**, H. Tachida and C.C. Cockerham (1989) [Effects of mutation on selection limits in finite populations with multiple alleles.](#) *Genetics* **122**:977-984. [[16](#)]
6. **Zeng, Z.-B.** (1989) A genetic model of interpopulation variation and covariation of quantitative characters. *Genetical Research* **53**:215-221. [[3](#)]
7. **Zeng, Z.-B.**, D. Houle and C.C. Cockerham (1990) [How informative is Wright's estimator of the number of genes affecting a quantitative character?](#) *Genetics* **126**:235-247. [[92](#)]
8. **Zeng, Z.-B.** and C.C. Cockerham (1990) Long-term response to artificial selection with multiple alleles--- Study by simulations. *Theoretical Population Biology* **37**: 254-272. [[11](#)]
9. **Zeng, Z.-B.** and H. Tachida (1990) How important is mutation for selection responses? In Proceedings of the 4th World Congress on Genetics Applied to Livestock Production **13**: 301-305. [1]
10. **Zeng, Z.-B.** and C.C. Cockerham (1991) [Variance of neutral genetic variances within and between populations for a quantitative character.](#) *Genetics* **129**:535-553. [[18](#)]
11. **Zeng, Z.-B.** (1992) [Correcting the bias of Wright's estimates of the number of genes affecting a quantitative character---A further improved method.](#) *Genetics* **131**: 987-1001. [[74](#)]
12. **Zeng, Z.-B.** and C.C. Cockerham (1993) [Mutation models and quantitative genetic variation.](#) *Genetics* **133**: 729-736. [[24](#)]
13. **Zeng, Z.-B.** (1993) [Theoretical basis of separation of multiple linked gene effects on mapping quantitative trait loci.](#) *Proceedings of the National Academy of Science USA* **90**:10972-10976. [[1010](#)]
14. **Zeng, Z.-B.** (1994) [Precision mapping of quantitative trait loci.](#) *Genetics* **136**: 1457-1468. [[2629](#)]
15. **Zeng, Z.-B.** (1994) A composite interval mapping method for locating multiple QTLs. *Proceedings of the 5th World Congress on Genetics Applied to Livestock Production* **21**: 37-40.
16. Basten, C.J., B.S. Weir and **Z.-B. Zeng** (1994) ZMAP---A QTL Cartographer. *Proceedings of the 5th World Congress on Genetics Applied to Livestock Production* **22**:65-66. [[365](#)]
17. Jiang, C. and **Z.-B. Zeng** (1995) [Multiple trait analysis of genetic mapping for quantitative trait loci.](#) *Genetics* **140**: 1111-1127. [[671](#)]
18. Dragani, T. A., **Z.-B. Zeng**, F. Canzian, M. Gariboldi, G. Manenti and M. A. Pierotti (1995) Molecular mapping of body weight loci on mouse chromosome X. *Mammalian Genome* **6**: 778-781. [[59](#)]
19. Liu, J. J. M. Mercer, L. F. Stam, G. C. Gibson, **Z.-B. Zeng** and C.C. Laurie (1996) [Genetic analysis of a morphological shape difference in the male genitalia of *Drosophila simulans* and *D. mauritiana*.](#) *Genetics* **142**:1129-1145. [[168](#)]
20. Cockerham, C. C. and **Z.-B. Zeng** (1996) [Design III with marker loci.](#) *Genetics* **143**:1437-1456. [[171](#)]
21. **Zeng, Z.-B.** and B. S. Weir (1996) Statistical methods for mapping quantitative trait loci. *Acta Agronomica Sinica* **22**: 535-549. [[33](#)]
22. **Zeng, Z.-B.** (1997) Combining information from data in mapping analysis: use of multiple markers and multiple traits. *Animal Biotechnology* **8**:145-150. [[4](#)]
23. Kao, C.-H. and **Z.-B. Zeng** (1997) [General formulae for obtaining the MLEs and the asymptotic variance-covariance matrix in mapping quantitative trait loci when using the EM algorithm.](#) *Biometrics* **53**: 653-665. [[152](#)]
24. True, J. R., J. Liu, L. F. Stam, **Z.-B. Zeng** and C. C. Laurie, (1997) [Quantitative genetic analysis of divergence in male secondary sexual traits between *Drosophila simulans* and *Drosophila mauritiana*.](#) *Evolution* **51**:816-832. [[94](#)]
25. Nuzhdin, S. V., E. G. Pasyukova, C. L. Dilda, **Z.-B. Zeng** and T. F. C. Mackay (1997) [Sex-specific quantitative trait loci affecting longevity in *Drosophila melanogaster*.](#) *Proceedings of the National Academy of Science USA* **94**: 9734-9739. [[Data](#)] [[241](#)]
26. Doerge, R. W., **Z.-B. Zeng** and B. S. Weir (1997) [Statistical issues in the search for genes affecting quantitative traits in experimental populations.](#) *Statistical Science* **12**: 195-219. [[119](#)]
27. Jiang, C. and **Z.-B. Zeng** (1997) [Mapping quantitative trait loci with dominant and missing markers in various crosses from two inbred lines.](#) *Genetica* **101**:47-58. [[145](#)]
28. Basten, C. J., B.S. Weir and Z.-B. Zeng (1997) QTL Cartographer: a reference manual and tutorial for QTL mapping. Department of Statistics, NC State University. [[417](#)]

29. Kao, C.-H., **Z.-B. Zeng** and R. D. Teasdale (1999) [Multiple interval mapping for quantitative trait loci](#). *Genetics* **152**:1203-1216. [[778](#)]
30. Weber, K., R. Eisman, S. Higgins, L. Kuhl, A. Patty, J. Sparks and **Z.-B. Zeng** (1999) [An analysis of polygenes affecting wing shape on chromosome three in *Drosophila melanogaster*](#). *Genetics* **153**: 773-786. [[Data](#)] [[96](#)]
31. **Zeng, Z.-B.**, C.-H. Kao, and C. J. Basten (1999) [Estimating the genetic architecture of quantitative traits](#). *Genetical Research* **74**:279-289. [[244](#)]
32. Vieira, C., E. G. Pasyukova, **Z.-B. Zeng**, J. B. Hackett, R. F. Lymanand, T. F. C. Mackay (2000) [Genotype-environment interaction for quantitative trait loci affecting lifespan in *Drosophila melanogaster*](#). *Genetics* **154**:213-227. [[Data](#)] [[266](#)]
33. **Zeng, Z.-B.**, J. Liu, L. F. Stam, C.-H. Kao, J. M. Mercer and C.C. Laurie (2000) [Genetic architecture of a morphological shape difference between two *Drosophila* species](#). *Genetics* **154**: 299-310. [[Data](#)] [[145](#)]
34. Wu, R., B. Li and **Z.-B. Zeng** (2000) Molecular dissection of quantitative traits: new perspectives from *Populus*. pp. 475-490 in ``Molecular Biology of Woody Plants" edited by S. M. Jian and S. C. Minocha, Kluwer Academic Publishers, The Netherlands. [[2](#)]
35. Wu, R.L., **Z.-B. Zeng**, D. M. O'Malley, S. E. McKeand and R. R. Sederoff (2000) The case for molecular mapping in forest tree breeding. *Plant Breeding Reviews* **19**: 41-68. [[25](#)]
36. Liu, Y. and **Z.-B. Zeng** (2000) [A general mixture model approach for mapping quantitative trait loci from diverse cross experimental designs involving multiple inbred lines](#) . *Genetical Research* **75**: 345-355. [[46](#)]
37. Wu, R.L., Y.F. Han, J.J. Hu, J.J. Fang, L. Li, M.L. Li. and **Z.-B. Zeng** (2000) [An integrated genetic map of *Populus deltoides* based on amplified fragment length polymorphisms](#). *Theoretical and Applied Genetics* **100**: 1249-1256. [[83](#)]
38. Luo, Z.L., S. H. Tao and **Z.-B. Zeng** (2000) [Inferring linkage disequilibrium between a polymorphic marker locus and a trait locus in natural populations](#). *Genetics* **156**: 457-467. [[29](#)]
39. Wu, R.L., and **Z.-B. Zeng** (2001) [Joint linkage and linkage disequilibrium mapping in natural populations](#). *Genetics* **157**:899-909. [[72](#)]
40. Yin, T.M., M.R. Huang, M.X. Wang, L.H. Zhu, **Z.-B. Zeng** and R.L. Wu (2001) Preliminary interspecific genetic maps of the *Populus* genome constructed from RAPD markers. *Genome* **44** (4): 602-609. [[44](#)]
41. Wu, R.L., M. Gallo-Meagher, R. C. Littell, and **Z.-B. Zeng** (2001) [A General Polyploid Model for Analyzing Gene Segregation in Outcrossing Tetraploid Species](#). *Genetics* **159**: 869-882. [[63](#)]
42. Weber, K., R. Eisman, S. Higgins, L. Morey, A. Patty, M. Tausek and **Z.-B. Zeng** (2001) [An analysis of polygenes affecting wing shape on chromosome 2 in *Drosophila melanogaster*](#). *Genetics* **159**: 1045-1057. [[Data](#)] [[54](#)]
43. Wu, S. S., R. Wu, C.-X. Ma, **Z.-B. Zeng**, M. C. K. Yang and G. Casella (2001) [A multivalent pairing model of linkage analysis in autotetraploids](#). *Genetics* **159**: 1339-1350. [[29](#)]
44. **Z.-B. Zeng** (2001) Quantitative trait loci: statistical methods for mapping their positions. *Encyclopedia of Genetics* (edited by Eric. C. R. Reeve) Fitzroy Dearborn Publishers, London.
45. Kao, C.-H. and **Z.-B. Zeng** (2002) [Modeling epistasis of quantitative trait loci using Cockerham's model](#). *Genetics* **160**: 1243-1261. [[162](#)]
46. Wu, R., C.-X. Ma, S. S. Wu and **Z.-B. Zeng** (2002) [Linkage mapping of sex-specific differences](#). *Genetical Research* **79**: 85-96. [[29](#)]
47. Wu, R.L., C.-X. Ma, I. Painter and **Z.-B. Zeng** (2002) [Simultaneous maximum likelihood estimation of linkage and linkage-phases in outcrossing species](#). *Theoretical Population Biology* **61**: 349-363. [[60](#)]
48. **Z.-B. Zeng** (2002) QTL Mapping. *Encyclopedia of Genetics* (edited by S. Brenner and J. H. Miller) Vol 3:1587-1593, Academic Press, San Diego.
49. Tao, Y., **Z.-B. Zeng**, J. Li, D. L. Hartl and C. C. Laurie (2003) [Genetic dissection of hybrid incompatibilities between *Drosophila simulans* and *Drosophila mauritiana*, II. Mapping hybrid male sterility loci on the third chromosome](#). *Genetics* **164**:1399-1418 [[61](#)]
50. **Z.-B. Zeng** (2003) Quantitative Trait Loci Mapping. *Encyclopedia of the Human Genome* (edited by David Cooper). Macmillan Publishers Ltd, Nature Publishing Group.
51. Balding DJ, Carothers AD, Marchini JL, Cardon LR, Vetta A, Griffiths B, Weir BS, Hill WG, Goldstein D, Strimmer K, Myers S, Beaumont MA, Glasbey CA, Mayer CD, Richardson S, Marshall C, Durrett R, Nielsen R, Visscher PM, Knott SA, Haley CS, Ball RD, Hackett CA, Holmes S, Husmeier D, Jansen RC,

- ter Braak CJF, Maliepaard CA, Boer MP, Joyce P, Li N, Stephens M, Marcoulides GA, Drezner Z, Mardia K, McVean G, Meng XL, Ochs MF, Pagel M, Sha N, Vannucci M, Sillanpaa MJ, Sisson S, Yandell BS, Jin CF, Satagopan JM, Gaffney PJ, **Zeng ZB**, Broman KW, Speed TP, Fearnhead P, Donnelly P, Larget B, Simon DL, Kadane JB, Nicholson G, Smith AV, Jonsson F, Gustafsson O, Stefansson K, Donnelly P, Parmigiani G, Garrett ES, Anbazhagan R, Gabrielson E (2002) [Discussion on the meeting on 'Statistical modelling and analysis of genetic data'](#), *Journal of the Royal Statistical Society, Series B-Statistical Methodology* 64: 737-775 Part 4. [\[22\]](#)
52. **Zeng, Z.-B.** (2005) [QTL mapping and the genetic basis of adaptation: recent developments](#). *Genetica* 123: 25-37. [Also published in *Georgia Genetics Review III: Genetics of Adaptation*. Edited by Rodney Mauricio (2005) pp.25-37. Springer] [\[28\]](#)
53. **Zeng, Z.-B.**, T. Wang and W. Zou (2005) [Modeling quantitative trait loci and interpretation of models](#). *Genetics* 169:1711-1725. [\[110\]](#)
54. Kirst, M., C. J. Basten, A. A. Myburg, **Z.-B. Zeng** and R. R. Sederoff (2005) [Genetic architecture of transcript level variation in differentiating xylem of an Eucalyptus hybrid](#). *Genetics* 169:2295-2303. [\[100\]](#)
55. Liu, Y. and **Z.-B. Zeng** (2005) [Mixture model equations for marker-assisted genetic evaluation](#). *J. Anim. Breed. Genet.* 122: 229-239. [\[4\]](#)
56. Wang, T., and **Z.-B. Zeng** (2006) Models and partition of variance for quantitative trait loci with epistasis and linkage disequilibrium. *BMC Genetics* 7:9. (Highly Accessed) [\[29\]](#)
57. Wang, T., B.S. Weir and **Z.-B. Zeng** (2006) [A population-based latent variable approach for association mapping of quantitative trait loci](#). *Annals of Human Genetics* 70: 506-523. [\[6\]](#)
58. Li, J., S. Wang and **Z.-B. Zeng** (2006) Multiple interval mapping for ordinal traits. *Genetics* 173: 1649-1663. [\[29\]](#)
59. Zou, W., D.L. Aylor and **Z.-B. Zeng** (2007) [eQTL Viewer: Visualizing how sequence variation affects genome-wide transcription](#). *BMC Bioinformatics* 8:7 [\[17\]](#)
60. Melchinger, A.E., H.F. Utz, H.P. Piepho, **Z.-B. Zeng**, and C.C. Schon (2007) Quantitative genetic theory to elucidate the role of epistasis in the manifestation of heterosis. *Genetics* 177: 1815-1825. [\[58\]](#)
61. Lai, C.-Q., J. Leips, W. Zou, J. M. Roberts, K. R. Wollenberg, L. D. Parnell, **Z.-B. Zeng**, J. M. Ordovas and T. F. C. Mackay (2007) Speed-mapping quantitative trait loci using microarrays. *Nature Methods* 4(10):839-841. [\[30\]](#)
62. Yang, R., H. Gao, X. Wang, J. Zhang, **Z.-B. Zeng** and R. Wu (2007) A semiparametric approach for composite functional mapping of dynamic quantitative traits. *Genetics* 177: 1859-1870. [\[13\]](#)
63. Kim, Y., S. Feng and **Z.-B. Zeng** (2008) Measuring and partitioning the high order linkage disequilibrium by multiple order Markov chains. *Genetic Epidemiology* 32:301-312. [\[9\]](#)
64. Aylor, D.L. and **Z.-B. Zeng** (2008) From classic genetics to quantitative genetics to systems biology: modeling epistasis. *PLoS Genetics* 4(3). [\[26\]](#)
65. Garcia, A. A. F., S. Wang, A. E. Melchinger and **Z.-B. Zeng** (2008) Quantitative trait loci mapping and the genetic basis of heterosis in maize and rice. *Genetics* 180:1707-1724. [\[43\]](#)
66. Huang, L., A. S. Heinloth, **Z.-B. Zeng**, R. S. Paules and P.R. Bushel (2008) Genes related to apoptosis predict necrosis of the liver as a phenotype observed in rats exposed to a compendium of hepatotoxicants. *BMC Genomics* 9:288. [\[22\]](#)
67. Zou, W. and **Z.-B. Zeng** (2008) Statistical methods for mapping multiple QTL. *International Journal of Plant Genomics* (article ID 286561). [\[8\]](#)
68. **Zeng, Z.-B.** (2008) The Hill-Robertson effect is a consequence of interplay between linkage, selection and drift: a commentary on the paper 'The effect of linkage on limits to artificial selection' by W.G. Hill and A. Robertson. *Genetics Research* 89: 333-334
69. Wang T., H. Jacob, S. Ghosh, X.J. Wang and **Z.-B. Zeng** (2009) A joint association test for multiple SNPs in genetic case-control studies. *Genetic epidemiology* 33: 151-163. [\[4\]](#)
70. Weir BS, Hill WG, Zhu J, **Zeng Z.-B.** (2009) The Third International Conference of Quantitative Genetics. *Genetica*. 136(2):211-2. [\[1\]](#)
71. Zou, W. and **Z.-B. Zeng** (2009) Multiple interval mapping for gene expression QTL analysis. *Genetica* 137: 125-134. [\[20\]](#)
72. Wang, T. and **Z.-B. Zeng** (2009) Contribution of genetic effects to genetic variance components with epistasis and linkage disequilibrium. *BMC Genetics* 10:52 [\[6\]](#)

73. E Silva, L.D.C, and **Z.-B. Zeng** (2010) Current progress on statistical methods for mapping quantitative trait loci from inbred line crosses. *Journal of Biopharmaceutical Statistics*, 20: 2, 454-481. [[4](#)]
74. Kaddurah-Daouk, R., R.A. Baillie, H. Zhu, **Z.-B. Zeng**, M.M. Wiest, U.T. Nguyen, S.M. Watkins, R.M. Krauss (2010) Lipidomic analysis of variation in response to simvastatin in the cholesterol and pharmacogenetics trial. *Metabolomics* 6(2):191-201. [[29](#)]
75. E Silva, L.D.C, S.-M. Chang and **Z.-B. Zeng** (2010) Power, sample size and confidence interval for quantitative trait loci mapping on multiple traits. (manuscript).
76. Hu F., J.F. Liu, **Z.-B. Zeng**, X.D. Ding, C.C. Yin and Y.N. Gong and Q. Zhang (2010) QTL identification using combined linkage and linkage disequilibrium mapping for milk production traits on BTA6 in Chinese Holsterin population. *Asian-Austrasian Journal of Animal Sciences* 23(10):1261-1267. [[1](#)]
77. Ji, Y, S Hebbring, H Zhu, GD Jenkins, J Biernacka, K Snyder, M Drews, O Fiehn, **ZB Zeng**, D Schaid, DA Mrazek, R Kaddurah-Daouk and RM Weinshilboum (2011) Glycine and a Glycine Dehydrogenase (GLDC) SNP as Citalopram/Escitalopram Response Biomarkers in Depression: Pharmacometabolomics-Informed Pharmacogenomics. *Clinical pharmacology & Therapeutics* 89:1 (doi:10.1038/clpt.2010.250).
78. Chakraborty, S; **Zeng, ZB** (2011) QTL Mapping for Days to Flowering under Drought Condition in Rice (*Oryza sativa*L.) Genome. *NOTULAE BOTANICAE HORTI AGROBOTANICI CLUJ-NAPOCA* 39(1):58-63
79. Duarte-Woods, CW and **Z.-B. Zeng** (2011) High-confidence discovery of genetic network regulators in expression quantitative trait loci. *Genetics* 187:955-964. [[5](#)]
80. Kaddurah-Daouk, R., RA Baillie, HJ Zhu, **Z-B Zeng**, NM Wiest, UT Nguyen, SM Wojnoonski, SM Watkins, M Trupp, RM Krauss (2011) Enteric Microbiome Metabolites Correlate with Response to Simvastatin Treatment, *PLOS ONE* 6:10 (e25482. DOI: 10.1371/journal.pone.0025482). [[25](#)]
81. Abo, R; Hebbring, S; Ji, Y; Zhu, HJ; **Zeng, ZB**; Batzler, A; Jenkins, GD; Biernacka, J; Snyder, K; Drews, M; Fiehn, O; Fridley, B; Schaid, D; Kamatani, N; Nakamura, Y; Kubo, M; Mushiroda, T; Kaddurah-Daouk, R; Mrazek, DA; Weinshilboum, RM (2012) Merging pharmacometabolomics with pharmacogenomics using '1000 Genomes' single-nucleotide polymorphism imputation: selective serotonin reuptake inhibitor response pharmacogenomics. *PHARMACOGENETICS AND GENOMICS* 22(4):247-253 (DOI: 10.1097/FPC.0b013e32835001c9). [[10](#)]
82. E Silva, L.D.S., S.C. Wang and **Z.-B. Zeng** (2012) Composite interval mapping and multiple interval mapping: procedures and guidelines for using Windows QTL Cartographer. In: "Quantitative Trait Loci (QTL): Methods and Protocols" Scott A. Rifkin (Ed). *Methods in Molecular Biology Series*, Vol. 871, Springer Protocols, Humana Press, New York, p. 75-119. [[3](#)]
83. Silva, L.D.E.; S.C. Wang and **Z.-B. Zeng** (2012) Multiple trait multiple interval mapping of quantitative trait loci from inbred line crosses. *BMC GENETICS* 13:67 (DOI: 10.1186/1471-2156-13-67). [[1](#)]
84. Trupp, M; Zhu, HJ; Wikoff, WR; Baillie, RA; **Zeng, ZB**; Karp, PD; Fiehn, O; Krauss, RM; Kaddurah-Daouk, R (2012) Metabolomics Reveals Amino Acids Contribute to Variation in Response to Simvastatin Treatment. *PLOS ONE* 7: 7 (Article Number: e38386 DOI: 10.1371/journal.pone.0038386). [[11](#)]
85. Kaddurah-Daouk, R; Yuan, PX; Boyle, SH; Matson, W; Wang, Z; **Zeng, ZB**; Zhu, HJ; Dougherty, GG; Yao, JK; Chen, G; Guitart, X; Carlson, PJ; Neumeister, A; Zarate, C; Krishnan, RR; Manji, HK; Drevets, W (2012) Cerebrospinal Fluid Metabolome in Mood Disorders-Remission State has a Unique Metabolic Profile. *SCIENTIFIC REPORTS* 2: 667 (DOI: 10.1038/srep00667). [[4](#)]
86. Huang, L., H.H. Zhang, **Z.-B. Zeng** and P.R. Bushel (2013) Improved sparse multi-class sVM and its applications for gene selection in cancer classification. *Cancer informatics* 12, 143.
87. Laurie, C., S. Wang, L.A. Carlini-Garcia and **Z.-B. Zeng** (2014) Mapping epistatic quantitative trait loci. *BMC Genetics* 15(1), 112 (Highly Accessed)

Software

1. Basten, C., B. S. Weir and **Z.-B. Zeng** (1995-2005) [QTL Cartographer](#). Department of Statistics, North Carolina State University, Raleigh, NC [[1786](#)]
2. Wang, S., C. Basten and **Z.-B. Zeng** (2001-2010) [WINDOWS QTL Cartographer](#). Department of Statistics, North Carolina State University, Raleigh, NC [[1196](#)]

3. Zou, W., D.L. Aylor and **Z.-B. Zeng** (2006) [eQTL Viewer](#). Bioinformatics Research Center, North Carolina State University, Raleigh, NC

Past Ph.D. Students

- 1995 Chen Hung Kao, PhD in Statistics, NC State Univ. "[Statistical methods for locating positions and analyzing epistasis of multiple quantitative trait genes using molecular marker information](#)"
- 2000 Shengchu Wang, PhD in Genetics and Plant Breeding, Zhejiang Univ. China, "Simulation study on the methods for mapping quantitative trait loci in inbred line crosses" (co-chair with Jun Zhu of Zhejiang Univeristy, China)
- 2000 Wen Zeng, PhD in Forestry and Statistics, NC State Univ. "Statistical methods for detecting major genes of quantitative trait loci using phenotypic data of a diallel mating" (co-chair with Bailian Li)
- 2001 Tao Wang, PhD in Biomathematics, NC State Univ. "[Modeling and inferring quantitative trait loci C:\zeng\www\Tao-Wang-Thesis.pdfusing linkage disequilibrium in natural populations](#)"
- 2005 Jian Li, PhD in Genetics, NC State Univ. "[Implementation of multiple interval mapping for ordinal data](#)"
- 2005 Sheng Feng, PhD in Statistics, NC State Univ. "[Statistical studies of genomics data](#)"
- 2006 Wei Zou, PhD in Bioinformatics, NC State Univ. "Transcriptional regulatory patterns in yeast revealed through expression quantitative trait locus mapping"
- 2007 Jessica Maia, PhD in Bioinformatics, NC State Univ. "Joint analysis of multiple gene expression traits to map expression quantitative trait loci"
- 2007 Hao Mei, PhD in Bioinformatics, NC State Univ. "Novel methods for mapping complex disease" (co-chair with Eden Martin of Duke University)
- 2008 Linggang Huang, PhD in Bioinformatics and Statistics, NC State Univ. "Variable selection in multi-class support vector machine and applications in genomics data analysis"
- 2008 David L. Aylor, PhD in Bioinformatics, NC State Univ. "Not just another trait: methods for the genetic analysis of gene expression"
- 2008 Xuemei Lou, PhD in Bioinformatics, NC State Univ. "Methods evaluation and application in complex human genetic diseases" (co-chair with Elizabeth Hauser of Duke University)
- 2008 Yunjung Kim, PhD in Bioinformatics, NC State Univ. "Analysis of multilocus linkage disequilibrium structure in the human genome"
- 2008 Youfang Liu, PhD in Bioinformatics, NC State Univ. "Analytic tool for population-based association studies" (co-chair with Jung-Ying Tzeng)
- 2009 Xiaohua Gong, PhD in Bioinformatics and Statistics, NC State Univ. "Mapping Quantitative Trait Loci in Outbred Half-sib Populations"
- 2009 Sihui Zhao, PhD in Bioinformatics, NC State Univ. "Analysis of Cis-acting regulatory motifs involved in alternative splicing: (co-chair with Steffen Heber)
- 2009 Christine W. Duarte, PhD in Bioinformatics and Statistics, NC State Univ. "A new method for genetic network reconstruction in expression QTL data sets"
- 2010 Luciano Da Costa E Silva, PhD in Statistics, NC State University. "Multiple trait multiple interval mapping of quantitative trait loci from inbred line crosses"
- 2011 Hongjie Zhu, PhD in Bioinformatics and Statistics, NC State University. "Pharmacometabolomics data analysis and nonlinear sufficient dimension reduction for genome-scale studies"

Past Postdoctoral Research Associates

- 1996 Chen Hung Kao, Currently Research Fellow in Institute of Statistical Science, Academia Sinica, Taiwan, ROC.
- 1996-2000 Yue-Fu Liu, Currently Geneticist in Canadian Centre for Swine Improvement, Inc.
- 1996-2000 Rongling Wu, Currently Professor in Department of Public Health Sciences and Statistics, Pennsylvania State University.
- 2000-2002 Shengchu Wang, Currently Senior Research Scientist in Syngenta, RTP, NC
- 2001-2003 Xuejun Qin, Currently Research Scientist in Center for Human Genetics, Duke University.
- 2004-2006 Antonio Augusto Franco Garcia, Currently Professor, Department of Genetics,

- Agricultural College, University of Sao Paulo, Brasil.
- 2004-2006 Luciana Ap. Carlini-Garcia, Currently Research Scientist, Agronomic Institute of Campina, IAC, Brazil.
- 2006 Lisa Denogean,
- 2013-2014 Hailong Ning, Professor, Department of Crop Science, Northeastern Agricultural Univ. China

Teaching

- ST 372 “Introduction of Statistical Inference and Regression”
- ST 370 “Probability and Statistics for Engineers”
- ST/GN 790 “Statistical Methods of Mapping Quantitative Trait Loci”
- ST/GN 770 “Statistical Concepts in Genetics”
- ST/GN 757 “Statistics for Molecular Quantitative Genetics”
- ST 610E “QTL Mapping” (Web-based Distance Learning course)
- “Human Molecular Genetics” (offered as a series of lectures in Peking University, China in 2011-2012)
- “Genetics of Complex Traits” (offered as a series of lectures in Shanghai Jiaotong University, Shanghai, China, 2011, 2012)

Short Courses

- Offered various short courses on “Mapping Quantitative Trait Loci” in
- 1996-2005 Summer Institute in Statistical Genetics at North Carolina State University
- 2006-2009 Summer Institute in Statistical Genetics at University of Washington
- 1995 China Agriculture University, Beijing, China
- 1998 Bloemfontein, South Africa
- 2001 46^a Reunião Anual da Região Brasileira da Sociedade Internacional de Biometria e 9^o Simpósio de Estatística Aplicada à Experimentação Agronômica, Departamento de Ciências Exatas, ESALQ / USP, Piracicaba, SP, Brazil
- 2001 Southern Summer Institute in Statistical Genetics, Christchurch, New Zealand
- 2002 Smurfit Institute of Genetics, Trinity College, Dublin, Ireland
- 2003 Institute in Statistical Genetics, La Trobe University, Melbourne, Australia
- 2003 National Taiwan University, Taipei, Taiwan
- 2004 European Institute in Statistical Genetics, University of Algarve, Faro, Portugal
- 2005 Asia Institute in Statistical Genetics, Yonsei University, Seoul, Korea
- 2006 Scandinavian Institute in Statistical Genetics, Aarhus University, Aarhus, Denmark
- 2007 Zhongshan University, Guangzhou, China
- 2007 Asia Institute in Statistical Genetics, Seoul National University, Seoul, Korea
- 2007,2009,2011,2013 European Institute in Statistical Genetics, Liege University, Belgium
- 2008 Southern Summer Institute in Statistical Genetics, Auckland University, Auckland, New Zealand
- 2010 Peking University, Beijing, China
- 2014 University of Sao Paulo, Piracicaba, SP, Brazil
- 2015 National Taiwan University and Institute of Statistics, Academia Sinica, Taiwan

Grants and Contracts

- 1990-1995 NIH GM 45344: Project 3 “Theoretical Quantitative Genetics” (P.I.: C. C. Cockerham) of the program project “Statistical and Quantitative Genetics” (Director: Bruce S. Weir), Investigator, \$436,834
- 1993-1995 NSF DEB-9220856: “Theoretical Study of Quantitative Variation”, Principal Investigator, \$85,000
- 1993-1995 Pioneer Hi-Bred International Inc. Competitive Research Award: “Software Development of Mapping Quantitative Trait Loci Based on a New Statistical Method”, Principal Investigator, \$60,000.
- 1994-1996 Ciba Geigy: “Software Development of Mapping Quantitative Trait Loci Based on a New Statistical Method”, Principal Investigator, \$20,000.
- 1994-1996 USDA Plant Genome 94-37300-0407: “Algorithms and programs for mapping quantitative trait loci” Principal Investigator, \$141,904.
- 1996-1998 USDA Plant Genome 96-35300-3652: “Algorithms and programs for mapping quantitative trait

loci" Principal Investigator, \$125,000.

1998-2001 USDA Plant Genome 98-35300-6191: "Algorithms and programs for mapping quantitative trait loci" Principal Investigator, \$285,000.

1995-2000 NIH GM 45344: Project 3 "Statistical Quantitative Genetics" of the program project "Statistical and Quantitative Genetics" (Director: Bruce S. Weir), Principal Investigator, \$490,000.

2000 Pharmacia Corporation: "QTL mapping data analysis in diallel cross populations", Principal Investigator, \$20,000.

2000-2005 NIH GM 45344: Project 2 "Statistical Quantitative Genetics" of the program project "Statistical and Quantitative Genetics" (Director: Bruce S. Weir), Principal Investigator, \$552,880

2003-2005 USDA Plant Genome 2003-35300-13170: "Algorithms and programs for mapping quantitative trait loci" Principal Investigator, \$175,000

2005-2007 USDA Plant Genome 2005-00754: "Algorithms and programs for mapping quantitative trait loci" Principal Investigator, \$130,000

2006-2009 Oak Ridge National Laboratories: "Assistance in identifying, documenting, managing, and archiving microarray data. PI, \$57,638

2006-2010 NIEHS 2 T32 ES007329: "Graduate Training in Bioinformatics", Director, \$1,954,757

2008-2011 NIH R24GM078233 "Metabolomics Network for Drug Response Phenotype", PI for subcontract from Duke U. \$150,000

2009-2012 NIH RC2GM092729 "Metabolomics Network for Drug Phenotypes", PI for subcontract from Duke U. \$200,000

2009-2011 NSF "Acquisition of Massively Deep-read Sequencing Technology at NCSU", Co-PI. \$452,500

2010-2015 NIEHS 5 T32 ES007329: "Graduate Training in Bioinformatics", Director, \$2,189,496

2012-2015 North Carolina Biotechnology Center "Multiple interval mapping with epistasis and marker-assisted predictive breeding", \$200,000

2014-2018 Bill & Melinda Gates Foundation "Genomic Tools for Sweet potato Improvement", \$800,000 (my project, with total project funding \$12,000,000).

And various supports from industry and research institutes on research, consulting and graduate internships

1994-1996 Ciba Geigy, \$20,000

2000-2002 Monsanto/Cereon Genomics, \$10,000

2003-2007 Hamner Institutes, \$128,811

2003-2007 National Institute of Environmental Health Sciences, \$172,508

2004-2007 Duke University, \$102,000

2004-2006 Duke University, \$84,198

2004-2006 GlaxoSmithKline, \$66,533

2005-2007 Duke University, \$85,663

2005-2007 University of Miami, \$37,215

2006-2010 Research Triangle Institute, \$197,138

2006-2009 GlaxoSmithKline, \$153,946

2007 University of Miami, \$27,489

2007 Food & Drug Administration, \$2,000

2008-2009 Duke University, \$19,182

2008 Duke University, \$5,768

Invited Presentations

1. "Genotypic distribution at the limit to natural and artificial selection" Department of Genetics, The University of Edinburgh, Edinburgh, Scotland, November 1985
British Population Genetics Group Meeting, Exter, England, December, 1985
2. "Long-term correlated response and interpopulation covariation" Annual Meeting of the Society for the Study of Evolution, Bozeman, Montana, June 1987
3. "Interaction of selection, mutation and drift on evolution of quantitative characters" Department of Statistics, North Carolina State University, Raleigh, February 1991

4. "Statistical issues on estimating the number of genes contributing to quantitative trait variation within and between populations" Department of Statistics, North Carolina State University, Raleigh, May 1991
5. "Precision mapping of quantitative trait loci" Department of Genetics, North Carolina State University, Raleigh, January 1993; The Workshop of Quantitative Genetics in the XVIIth International Congress of Genetics, Birmingham, England, August 1993
6. "Mutation models and quantitative genetic variation" Institute of Cell, Animal and Population Biology, The University of Edinburgh, Edinburgh, Scotland, August 1993
7. "Precision mapping of quantitative trait loci Applications" Plant Breeding and Genetics Seminars, North Carolina State University, Raleigh, November 1993
8. Symposium in Quantitative Genetics, Raleigh NC, May 1994
9. Workshop in Quantitative Genetics (Chair), The Annual Meeting of the Society for the Study of Evolution, Athens, Georgia, June 1994
10. The 5th World Congress of Genetics Applied to Livestock Production, Guelph, Canada, August 1994
11. Gordon Research Conference on Quantitative Genetics and Biotechnology, Ventura, California, February 1995
12. Symposium on Mapping Quantitative Trait Loci (Organizer and Speaker) in the Annual Meeting of the Society for the Study of Evolution, Montreal, Canada, July 1995
13. A short course in China Agricultural University, Beijing, China, Sept. 16 - Sept. 30, 1995
14. Institute of Genetics, Chinese Academy of Science, Beijing, China, Sept. 27, 1995
15. Series lectures in Huazhong Agricultural University, Wuhan, China, Oct. 4 - 6, 1995
16. Plenary lecture in the 5th Congress of the Genetics Society of China, Taian, China, Oct. 13, 1995
17. International Symposium on the Mechanisms of Evolution, Taian, China, Oct. 15, 1995
18. International Symposium on Molecular Evolution and Population Genetics, Shanghai, China, Oct. 22, 1995
19. Two lectures in Zhejiang Agricultural University, Hangzhou, China, Oct. 24 - 25, 1995
20. Workshop of Mapping Quantitative Trait Genes, Annual Meeting of American College of Neuropsychopharmacology, San Juan, Puerto Rico, December 13, 1995
21. University of Chicago, February 5, 1996 University of Oregon, April 21, 1996
22. "The Genetic and Physiological Bases of Heterosis", Bodega Marine Laboratory, University of California, Davis, September 12-14, 1996
23. Allerton II: Genetic Analysis of Economically Important Traits in Livestock Conference, University of Illinois at Urbana-Champaign, November 6-9, 1996
24. Symposium "Statistical genetic tools for analyzing genetic marker data", Annual meeting of American Society of Agronomy, Crop Science Society of America, and Soil Science Society of America, October 26-31, 1997
25. Department of Dairy Science, Virginia Polytechnic Institute and State University, November 4, 1997
26. Genomic Computing Techniques and Applications Workshop, Plant and Animal Genome VI, San Diego, January 18-22, 1998
27. Department of Animal Science, University of Illinois at Urbana-Champaign, May 20, 1998
28. (Four lectures) Department of Animal Science, Huazhong Agricultural University, Wuhan, China, August 1-3, 1998
29. Symposium "Mapping and characterizing genes affecting quantitative traits" (Chair and Speaker), The XVIIIth International Congress of Genetics, August 10-15, 1998, Beijing, China
30. Institute of Cell, Animal and Population Biology, Edinburgh University, March 18, 1998
31. European HSSS Workshop on "Bayesian and MCMC Methods in Gene Mapping", Lammi, Finland, March 24-27, 1999
32. Cereon Genomics, Cambridge, MA, June 25, 1999
33. Human Genetics Center, The University of Texas Houston Health Science Center, June 30, 1999
34. NSF Workshop on Biotechnology and Integration of Behavioral Science, NSF, Washington, DC, July 6-8, 1999
35. Nanjing Forestry University, Nanjing, China, October 6-7, 1999
36. Zhejiang University, Hangzhou, China, July 5, 2000
37. Second NSF Workshop on Biotechnology and Integration of Behavioral Science, NSF, Washington, DC, August 14-15, 2000
38. Plant Genetics and Breeding Program, University of Wisconsin at Madison, November 15, 2000

39. Triangle Bioinformatics Seminars, Triangle Research Institute, NC, February 16, 2001
40. Quantitative Genetics and Plant Breeding in the 21st Century: An International Symposium, The Louisiana State University Chapter of Sigma Xi, The Scientific Research Society, March 26-28, 2001
41. Huazhong Agricultural University, Wuhan, China, May 20-21, 2001
42. International Symposium on Mapping and Identification of Genes for Complex Polygenic Traits and Diseases, Changsha, Hunan, China, May 23-26, 2001
43. Jackson Laboratory, Bar Harbor, Maine, June 19, 2001
44. The 46 Annual Brazil Regional Meeting of International Society of Biometrics, Agronomy Department, ESALQ /USP, Piracicaba, Brazil, Sept 9-13, 2001
45. Biomathematics Graduate Program, North Carolina State University, September 5, 2001
46. Workshop on Mathematical Approaches to the Analysis of Complex Phenotypes, Jackson Laboratory, Bar Harbor, Maine, September 30 October 7, 2001
47. Georgia Genetics Symposium on The Genetics of Adaptation, University of Georgia, Athens, Georgia, November 24, 2001
48. Department of Biostatistics, University of North Carolina at Chapel Hill, November 14, 2001
49. Australasian Biometrics and New Zealand Statistical Association Joint Conference and the Southern Summer Institute in Statistical Genetics, Christchurch, New Zealand, December 13-18, 2001
50. Applied Mathematics Colloquium, University of Arizona, Tucson, Arizona, April 4-5, 2002
51. Department of Statistics, Ohio State University, Columbus, Ohio, May 7, 2002
52. Workshop on Mathematical Approaches to the Analysis of Complex Phenotypes, Jackson Laboratory, Bar Harbor, Maine, October 4, 2002
53. Experimental designs and sample size requirement for QTL mapping, Plant and Animal Genome XI, San Diego, CA, January 11-15, 2003
54. Capabilities and Limitations of QTL Mapping, Symposium on Quantitative and Statistical Genetics in honor of William George Hill, North Carolina State University, May 16, 2003
55. QTL analysis and genetic architecture of complex traits: where have we been and where are we going? Department of Statistics, George Washington University, September 5, 2003
56. College of Science, Donghua University, Hualien, Taiwan, October 9, 2003
57. Institute of Statistical Sciences, Academia Sinica, Taipei, Taiwan, October 13, 2003
58. College of Life Science, Tsinghua University, Hsinchu, Taiwan, October 14, 2003
59. College of Medicine (October 23) and College of Life Science (October 24), National Taiwan University, Taipei, Taiwan.
60. Xiangshan Conference in Genomics and Evolution, Beijing, China, October 28-30, 2003
61. Institute of Genetics and Development, Chinese Academy of Science, Beijing, China, October 31, 2003
62. Huazhong Agriculture University, Wuhan, China, November 6, 2003
63. How to estimate and interpret QTL effects and epistasis in a disequilibrium population, Institute of Cell, Animal and Population Biology, Edinburgh University, UK, March 3, 2004
64. QTL, epistasis, genetic correlation and beyond, ACTA Genetica Sinica Editorial Meeting and Genetics Symposium, Xiameng, China, May 17, 2004
65. Hualang Agricultural University, Guanzhou, China, May 20, 2004
66. Zhejiang University, Hangzhou, China, May 21, 2004
67. Bruce Weirs contributions to statistical and population genetics, Symposium in Statistical Genetics in Honor of Prof. Bruce Weir, NC State University, June 15, 2004
68. Using QTL analysis to study epistasis and genetic correlation, School of Biosciences, The University of Birmingham, UK, August 5, 2004
69. Statistical methods for constructing genetic effect network between QTL, gene expression and phenotypes, Symposium on Gene Expression QTL Analysis, The Joint Statistics Meetings, Toronto, August 8, 2004
70. Gene expression QTL analysis: from sequence variation to gene expression variation and to quantitative trait variation, CSIRO Emerging Science Workshop, Coffs Harbour, Australia, March 15-17, 2005
71. QTL, epistasis, genetic correlation and beyond, CSIRO Forestry and Forest Products, Canberra, Australia, March 23, 2005
72. Gene expression QTL analysis: From QTL to genes to genetic networks, Huazhong Agricultural University, Wuhan, China, August 8, 2005

73. Gene expression QTL analysis: From QTL to genes to genetic networks, The 13th Meeting of Chinese Animal Genetics and Breeding, Harbin, China, August 19, 2005
74. Department of Biostatistics, University of Washington, September 13, 2005
75. Rosetta Inpharmatics, Seattle, WA, September 14, 2005
76. Department of Statistics, North Carolina State University, September, 23, 2005
77. Department of Statistics, Cornell University, October 12, 2005
78. Department of Animal Science, NC State University, November 15, 2005
79. Keystone Symposia on Genome Sequence Variation and the Inherited Basis of Common Disease and Complex Traits, Big Sky, Montana, Jan 8-13, 2006
80. Zhejiang University, Hangzhou, China, April 28, 2006
81. International Symposium on Genomics and Evolution, Zhongshan University, Guangzhou, China, January 3, 2007
82. Department of Statistics, University of Florida at Gainesville, April 5, 2007
83. The Third International Conference on Quantitative Genetics, Hangzhou, China, August 19-24, 2007
84. Department of Statistics, Michigan State University, Lance, Michigan, October 9, 2007
85. Department of Biostatistics, University of Washington, Seattle, Feb 28, 2008
86. Indo-Chinese Bilateral Workshop on “Plant Genomics and Quantitative Genetics”, Meerut, India, February 14-16, 2009
87. Department of Statistics, Texas A&M University, April 8, 2009
88. Department of Ecology and Evolution, Chicago University, April 14, 2009
89. College of Life Science, Peking University, Beijing, China, August 6, 2009
90. College of Life Science, Huazhong Agricultural University, Wuhan, China, August 9, 2009
91. International Conference of Heterosis in Plants, Hohenheim University, Stuttgart, Germany, September 7-11, 2009
92. Department of Plant Breeding, China Agricultural University, Beijing, China, Oct. 13, 2009
93. Darwin-China 200, Peking University, Beijing, China, Oct. 14-16, 2009.
94. LeClerc Rotary Lecture, Biometrics Program, University of Maryland, March 15-19, 2010
95. CAS-MPG Partner Institute for Computational Biology, Shanghai, China, March 30, 2010
96. Three lectures (“Genetics of Complex Traits: Linkage Analysis”, “Genetics of Complex Traits: Association Analysis”, “Genetics of Complex Traits: Systems Genetic Analysis”), Shanghai Jiao Tong University, Shanghai, China, April 18-28, 2011
97. “Study genetic basis and pathway of complex traits”, National Center for Gene Research, Shanghai, China, April 20, 2011
98. “Study genetic basis and pathway of complex traits”, School of Agriculture and Biology, Shanghai Jiao Tong University, Shanghai, China, April 26, 2011
99. “Mapping epistatic QTL”, College of Life Science, Peking University, Beijing, China, April 29, 2011
100. “Study genetic basis and pathway of complex traits”, National Institute of Biological Sciences Annual Meeting, August 15, 2011, Beijing, China
101. “Understanding gene interactions”, September 13, 2011, Huazhong Agricultural University, Wuhan, China
102. “Study genetic basis and pathway of complex traits”, Evolutionary Biology Forum, Institute of Botany, The Chinese Academy of Sciences, Beijing, China, Oct 20, 2011.
103. “Study genetic basis and pathway of complex traits”, Symposium in Computational Biology and Bioinformatics, Beijing Institute of Genomics, The Chinese Academy of Sciences, Beijing, China, Oct 27-28, 2011.
104. “Statistical issues in studying genetics of complex traits”, Academy of Mathematics and Systems Sciences, The Chinese Academy of Sciences, Beijing, China, Nov 4, 2011.
105. “Study genetic basis and pathway of complex traits”, Annual meeting of China-US joint laboratory in tobacco molecular breeding, Yunnan Academy of Tobacco Agriculture Science, Jinhong, Yunnan, China, Dec 6, 2011.
106. “Analysis of genomics, transcriptomics and metabolomics data for the study of complex traits”, Zhengzhou Tobacco Research Institute, Zhengzhou, China, Dec 9, 2011.
107. “Study genetic basis and pathway of complex traits”, Joint Meeting of the 2011 Taipei International Statistical Symposium, Institute of Statistical Science, Academia Sinica, Taipei, Taiwan, Dec 16-19, 2011.

108. Six lectures (“Genetics of Complex Traits: Linkage Analysis I & II”, “Genetics of Complex Traits: Association Analysis I & II”, “Systems Biology Analysis”, “Systems Genetics Analysis”), Shanghai Jiao Tong University, Shanghai, China, March 5-22, 2012.
109. “Study genetic basis and pathway of complex traits”, Center for Systems Biology, Soochow University, Soochow, China, March 16, 2012.
110. The 10th international bioinformatics workshop, Changchun, China, July 7-8, 2012.
111. “Study QTL epistasis and marker-assisted selection strategy”, Syngenta, Inc, RTP, NC, November 20, 2012.
112. “Statistics for mapping epistatic QTL”, Department of Ecology and Evolution, University of Chicago, April 29, 2013.
113. “Statistical issue in studying QTL epistasis”, Triangle Statistical Genetics Conference, Duke University, October 7, 2013.
114. “Mapping epistatic QTL”, Impact of Large-Scale Genomic Data on Statistical and Quantitative Genetics Conference, Department of Biostatistics, University of Washington, November 24-26, 2013.
115. “Mapping epistatic QTL”, Genetics Program Seminar, Department of Biological Sciences, NC State University, April 7, 2014.
116. “How much genetics epistasis in plant populations”, Plant Breeding, Genetics and Biotechnology Program, Michigan State University, April 2, 2015
117. “How much genetics epistasis in plant populations”, Agronomy Department, Iowa State University, April 24, 2015