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CURRICULUM VITAE

Shizhong Xu
Professor of Genetics and Statistics

Department of Botany and Plant Sciences
University of California Riverside
Riverside, CA 92521
Tel: (951)-827-5898
Fax: (951)-827-4437
E-mail: shizhong.xu@ucr.edu

Education

B.S.	Animal Sciences	Shenyang Agricultural University, P.R. China, 1981
M.S.	Genetics	Northeast Agricultural University, P.R. China, 1984
Ph.D.	Genetics	Purdue University, 1989

Professional Experiences

Lecturer, Northeast Agricultural University, 1/1985-12/1986.
Teaching Assistant, Purdue University, 1/1988-12/1989.
Statistical and Computer Software Consultant, Purdue University, 5/1988-12/1989.
Assistant Research Scientist, Purdue University, 1/1990-9/1991.
Postdoctoral Fellow, Rutgers University, 10/1991-11/1992.
Postdoctoral Research Associate, North Carolina State University, 12/1992-6/1995.
Assistant Professor, University of California, Riverside, 7/1995-6/1999.
Associate Professor, University of California, Riverside, 7/1999-6/2001.
Professor, University of California, Riverside, 7/2001-present.
Director of Genetics, Genomics and Bioinformatics (GGB) Program, UCR, 9/2011-8/2014.

Professional Societies

American Association for the Advancement of Science (AAAS), 2004 – present.
Genetics Society of America, 1995-present.

Awards

Presidential Chair of the University of California, awarded in 2001.
Fellow of the American Association for the Advancement of Science (AAAS), elected in 2006.

Teaching at UC Riverside

STAT231B – Statistics for Biological Sciences (Graduate)
BPSC148 – Quantitative Genetics (Undergraduate)
GEN240B – Advances in Bioinformatics & Genomics (Graduate)
BPSC234 – Statistical Genomics (Graduate)
STAT288 – Lecture Seminar in Statistics (Graduate)
STAT183 – Statistical Consulting (Undergraduate Senior)

Extramural Grant Activities

PI, United States Department of Agriculture (USDA CSREES 9503837), “Multistage Selection for Multiple Trait Genetic Improvement," $80,000, 10/1995 – 10/1997.

PI, United States Department of Agriculture (USDA CSREES 95-37205-2313), “Multipoint Mapping of QTL and Marker-Assisted Selection in Outbred Populations," $140,000, 11/1997 – 10/2000.

PI, National Institutes of Health (NIH R01 GM55321-01-05), “Random Model Methodology for Genetic Mapping," $556,259, 1/1997 – 12/2001.

Co-PI (PI, Hans Cheng at Michigan State University), United States Department of Agriculture (USDA CSREES 58-3635-9131), “Identification of Quantitative Trait Loci for Production Traits in Poultry," $215,000, 10/1998 – 9/2001.

PI, United States Department of Agriculture (USDA CSREES 00-35300-9245), “Bayesian Analysis of Quantitative Traits Under the Plant Model,” $150,000, 9/2000-9/2003.

PI, National Institutes of Health (NIH R01 GM55321-06-09), “Mixed Model Approach to Genetic Mapping for Complex Traits,” $503,365, 1/2002 – 12/2006.

PI, National Science Foundation (NSF DBI-0345205), "Optimal Utilization of Genomic Information for Dissecting Complex Traits," $126,843, 9/1/2005 – 8/31/2007.

PI, United States Department of Agriculture (USDA CSREES 2007-35300-18285), “Mapping QTL for Multiple Traits Using Bayesian Statistics,” $394,500, 7/15/2007-7/14/2012.

PI, International Rice Research Institute (IRRI, A-2015-50. DRPC2015-49), “Green Super Rice for the Resource-Poor of Africa and Asia Phase III,” $130,000, 9/1/2016 – 8/31/2018.

PI, National Science Foundation (NSF DBI - 1458515), "Collaborative Research: ABI Innovation: Plant Genotype-Phenotype (G2P) Association Discovery via Integrative Genome-scale Biological Network & Genome-wide Association Analysis," $246,123, 7/1/2015 – 6/30/2020.

Editorial Board Service

Section Editor of “National Science Review”, 2022 – Present
Associate Editor of “Frontiers in Genetics, Statistical Genetics Section” 2021 - Present
Associated Editor of “Forestry Research”, 2021 – Present
Associate Editor of “The Crop Journal”, 2013 – Present
Associate Editor of "Heredity", 2005 – 2016
Associate Editor of "International Journal of Plant Genomics", 2006 – 2017
Associate Editor of "Molecular Biology and Evolution", 2012 – 2015
Executive Editor of “Genetics Research”, 2008 ー 2012

Publications

A Technical Journal Articles

1. Xu, S. 1986. Studies on combined selection. *Acta Genetica Sinica.* 13:221-226 (in Chinese with English abstract).
2. Xu, S. 1986. Application of computer simulation to artificial selection. *Journal of Northeast Agricultural College.* 17:429-434 (in Chinese with English abstract).
3. Xu, S. and W. M. Muir. 1990. The application of ridge regression to multiple trait selection indices. *Journal of Animal Breeding and Genetics.* 107:81-88.
4. Xu, S. and W. M. Muir. 1991. Multistage selection for genetic gain by orthogonal transformation. *Genetics.* 129:963-974.
5. Muir, W. M. and S. Xu. 1991. An approximate method for optimal independent culling level selection for *N* traits with explicit solutions. *Theoretical and Applied Genetics.* 82:450-459.
6. Xu, S. and W. M. Muir. 1992. Selection index updating. *Theoretical and Applied Genetics.* 83: 451-458.
7. Muir, W. M., W. E. Nyquist and S. Xu. 1992. Alternative partitioning of the genotype by environment interaction. *Theoretical and Applied Genetics.* 84:193-200.
8. Levy, M., F. J. Correa-Victoria, R. S. Zeigler, S. Xu and J. E. Hamer. 1993. Genetic diversity of the rice blast fungus in a disease nursery in Colombia. *Phytopathology.* 83:1427-1433.
9. Atchley, W. R., S. Xu and C. Vogl. 1994. Developmental quantitative genetic models of evolutionary change. *Developmental Genetics.* 15:92-103.
10. Xu, S. 1994. Weighted least squares estimation of DNA fragment lengths. *The Journal of Heredity.* 85:151-152.
11. Xu, S., C.J. Kobak and P.E. Smouse. 1994. Constrained least squares estimation of mixed population stock composition from mtDNA haplotype frequency data. *Canadian Journal of Fisheries and Aquatic Sciences.* 51:417-425.
12. Vogl, C., W. R. Atchley and S. Xu. 1994. The ontogeny of morphological differences in the mandible in two inbred strains of mice. *Journal of Craniofacial Genetics and Developmental Biology.* 14:97-110.
13. Xu, S., W. R. Atchley and W. M. Muir. 1994. Partial and conditional maximum likelihood for variance component estimation. *Journal of Animal Breeding and Genetics.* 111:178-188.
14. Xu, S., W. R. Atchley and W. Fitch. 1994. Phylogenetic inference under the pure drift model. *Molecular Biology and Evolution*. 11:949-960.
15. Xu, S., T. G. Martin and W.M. Muir. 1995. Multistage selection for maximum economic return with an application to beef cattle breeding. *Journal of Animal Science.* 73:699-710.
16. Xu, S. and W. R. Atchley. 1995. A random model approach to interval mapping of quantitative trait loci. *Genetics.* 141:1189-1197.
17. Xu, S. and W. R. Atchley. 1995. Heterozygosity of F_2 from two segregating populations. *The Journal of Heredity.* 86:477-480.
18. Xu, S. 1995. A comment on the simple regression method for interval mapping. *Genetics*. 141:1657-1659.

19. Xu, S. and W. R. Atchley. 1996. Mapping quantitative trait loci for complex binary diseases using line crosses. *Genetics*. 143:1417-1424.
20. Xu, S. 1996. Mapping quantitative trait loci using four-way crosses*. Genetical Research.* 68:175-181
21. Xu, S. and W. R. Atchley. 1996. A Monte Carlo algorithm for maximum likelihood estimation of variance components. *Genetics, Selection and Evolution.* 28:329-343.
22. Xu, S. 1996. Computation of the full likelihood function for estimating variance at a quantitative trait locus. *Genetics.* 144:1951-1960.
23. Gessler, D. D. G. and S. Xu. 1996. Using the expectation or the distribution of identical-by-descent for mapping quantitative trait loci under the random model. *American Journal of Human Genetics.* 59:1382-1390.
24. Xie, C. and S. Xu. 1996. Best linear unbiased prediction under selection. *Journal of Genetics and Breeding.* 50:287-294.
25. Atchley, W. R., S. Xu and D. E. Cowley. 1997. Altering developmental trajectories in mice by restricted index selection. *Genetics.* 146:629-640.
26. Xie, C. and S. Xu. 1997. Restricted multistage selection indices. *Genetics, Selection and Evolution.* 29:193-203.
27. Xie, C., S. Xu and J. A. Mosjidis. 1997. Multistage selection indices for maximum genetic gain and economic efficiency in red clover. *Euphytica.* 98:75-82.
28. Xu, S. 1998. Further investigation on the regression method of mapping quantitative trait loci. *Heredity.* 80:364-373.
29. Xie, C. and S. Xu. 1998. Efficiency of marker-assisted multistage selection in the improvement of multiple quantitative traits. *Heredity.* 80:489-498.
30. Xu, S. 1998. Mapping quantitative trait loci using multiple families of line crosses. *Genetics.* 148:517-524.
31. Xu, S. and D. D. G. Gessler. 1998. Multipoint genetic mapping of quantitative trait loci using a variable number of sibs per family. *Genetical Research.* 71:73-83.
32. Xie, C., D. D. G. Gessler and S. Xu. 1998. Combining different line crosses for mapping quantitative trait loci using the identical by descent based variance component method. *Genetics.* 149:1139-1146.
33. Gessler, D. D. G. and S. Xu. 1998. An embarrassment of riches: the stochastic generation of beneficial mutations. *Genetica.* 102/103:145-155.
34. Rao, S. Q. and S. Xu. 1998. Mapping quantitative trait loci for categorical traits in four-way crosses. *Heredity.* 81:214-224.
35. Xie, C, D. Gessler and S. Xu. 1998. Sib mating designs for mapping quantitative trait loci. *Genetica.* 104:9-19.
36. Xie, C. and S. Xu. 1998. Strategies of marker-aided recurrent selection. *Crop Science.* 38:1526-1535.
37. Xu, S. 1998. Iteratively reweighted least squares mapping of quantitative trait loci. *Behavior Genetics.* 28:341-355.
38. Xu, S., N. Yonash, R. L. Vallejo and H. H. Cheng. 1998. Mapping quantitative trait loci for binary traits using a heterogeneous residual variance model: An application to Marek's disease susceptibility in chickens. *Genetica.* 104:171-178.
39. Gessler, D. D. G. and S. Xu. 1999. On the evolution of recombination and meiosis. *Genetical Research.* 73:119-131.

40. Xie, C. and S. Xu. 1999. Mapping quantitative trait loci with dominant and missing markers in four-way crosses. *Theoretical and Applied Genetics.* 98:1014-1021.
41. Yi, N. and S. Xu. 1999. Mapping quantitative trait loci for complex binary traits in outbred populations. *Heredity.* 82:668-676.
42. Yi, N. and S. Xu. 1999. A random model approach to mapping quantitative trait loci for complex binary traits in outbred populations. *Genetics.* 153:1029-1040.
43. Gessler, D. D. G. and S. Xu. 1999. Multipoint genetic mapping of quantitative trait loci with dominant markers in outbred populations. *Genetica.* 105:281-291.
44. Xu, S. 2000. Phylogenetic analysis under reticulate evolution. *Molecular Biology and Evolution.* 17:897-907.
45. Xu, S. and C. Vogl. 2000. Maximum likelihood analysis of quantitative trait loci under selective genotyping. *Heredity.* 84:525-537.
46. Yi, N. and S. Xu. 2000. Bayesian mapping of quantitative trait loci for complex binary traits. *Genetics.* 155:1391-1403
47. Vogl, C. and S. Xu. 2000. Multipoint mapping of segregation distorting loci using molecular markers. *Genetics.* 155:1439-1447
48. Xie, C. and S. Xu. 2000. Mapping quantitative trait loci in tetraploid populations. *Genetical Reseach.* 76:105-115
49. Yi, N. and S. Xu. 2000. Bayesian mapping of quantitative trait loci under the IBD-based variance component model. *Genetics.* 156:411-422
50. Gessler, D. D. G. and S. Xu. 2000. Meiosis and recombination at low mutation rates. *Genetics.* 156:449-456.
51. Xu, S. and N. Yi. 2000. Mixed model analysis of quantitative trait loci. *Proc. Natl. Acad. Sci. USA.* 97:14542-14547.
52. Yi, N. and S. Xu. 2001. Bayesian mapping of quantitative trait loci under complicated mating designs. *Genetics.* 157:1759-1771.
53. Li, X., W. Gu, G. Masinde, M. Hamilton-Ulland, S. Xu, S. Mohan and D. J. Baylink. 2001. Genetic control of the rate of wound healing in mice. *Heredity.* 86: 668-674.
54. Li, X., G. Masinde, W. Gu, J. Wergedal, M. Hamilton-Ulland, S. Xu, S. Mohan and D. J. Baylink. 2002. Chromosomal regions harboring genes for the work to femur failure in mice. *Functional and Integrative Genomics.* 1:367-374.
55. Yi, N. and S. Xu. 2002. Mapping quantitative trait loci with epistatic effects. *Genetical Research.* 79:185-198
56. Yi, N. and S. Xu. 2002. Linkage analysis of quantitative trait loci in multiple line crosses. *Genetica.* 114:217-230.
57. Vogl, C. and S. Xu. 2002. QTL analysis in arbitrary pedigrees with incomplete marker information. *Heredity.* 89:339-345.
58. Kopp, A., R. M. Graze, S. Xu, S. B. Carroll and S. V. Nuzhdin. 2003. Quantitative trait loci responsible for variation in sexually dimorphic traits in Drosophila melanogaster. *Genetics.* 163:771-787.
59. Xu, S. 2003. Estimating polygenic effects using markers of the entire genome. *Genetics* 163:789-801.
60. Xu, C., X. He and S. Xu. 2003. Mapping quantitative trait loci underlying triploid endosperm traits in cereals. *Heredity.* 90:228-235.

61. Luo, L., Y. Mao and S. Xu. 2003. Correcting the bias in estimation of genetic variances contributed by individual QTL. *Genetica.* 119:107-113.
62. Luo, L. and S. Xu. 2003. Mapping viability loci using molecular markers. *Heredity.* 90:459-467.
63. Yi, N., S. Xu and D. B. Allison. 2003. Bayesian model choice and search strategies for mapping interacting quantitative trait loci. *Genetics.* 165:867-883.
64. Xu, S., N. Yi, D. Burke, A. Galecki, and R. A. Miller. 2003. An EM algorithm for mapping binary disease loci: application to fibrosarcoma in a four-way cross mouse family. *Genetical Research.* 82:127-138.
65. Xu, S. 2003. Theoretical basis of the Beavis effect. *Genetics.* 165:2259-2268.
66. Yi, N., S. Xu, V. George and D. B. Allison. 2004. Mapping multiple quantitative trait loci for ordinal traits. *Behavior Genetics.* 34:3-14.
67. Qu, Y. and S. Xu. 2004. Supervised cluster analysis for microarray data based on multivariate Gaussian mixture. *Bioinformatics.* 20:1905-1913.
68. Zhang, Y. –M. and S. Xu. 2004. Mapping quantitative trait loci in F_2 incorporating phenotypes of F_3 progeny. *Genetics.* 166:1981-1993.
69. Mao, Y. and S. Xu. 2004. Mapping QTL for traits measured as percentage. *Genetical Research.* 83:159-168.
70. Beasley, T. M., D. Yang, N. Yi, D. C. Bullard, C. I. Amos, S. Xu and D. B. Allison. 2004. Joint tests for quantitative trait loci in experimental crosses. *Genetics, Selection & Evolution.* 36:601-619.
71. Xu, C., Y. –M. Zhang and S. Xu. 2005. An EM algorithm for mapping quantitative resistance loci. *Heredity.* 94:119-128.
72. Mao, Y. and S. Xu. 2005. A Monte Carlo algorithm for computing the IBD matrices using incomplete marker information. *Heredity*. 94:305-315.
73. Luo, L, Y. –M. Zhang and S. Xu. 2005. A quantitative genetics model for viability selection. *Heredity.* 94:347-355.
74. Xu, C., Z. Li and S. Xu. 2005. Joint mapping of quantitative trait loci for multiple binary characters. *Genetics.* 169:1045-1059.
75. Zhang, Y. –M., Y. Mao, C. Xie, H. Smith, L. Luo and S. Xu. 2005. Mapping quantitative trait loci using naturally occurring genetic variance among commercial inbred lines of maize (*Zea mays* L.). *Genetics*. 169:2267-2275.
76. Wang, H., Y. –M. Zhang, X. Li, G. L. Masinde, S. Mohan, D. J. Baylink and S. Xu. 2005. Bayesian shrinkage estimation of quantitative trait locus parameters. *Genetics.* 170:465-480.
77. Zhang, Y. –M. and S. Xu. 2005. A penalized maximum likelihood method for estimating epistatic effects of QTL. *Heredity.* 95:96-104.
78. Hansen, C., N. Yi, Y. –M. Zhang, S. Xu, J. Gavora and H. H. Cheng. 2005. Identification of QTL for production traits in chickens. *Animal Biotechnology.* 16:67-79.
79. Jia, Z. and S. Xu. 2005. Clustering expressed genes based on their association with a quantitative phenotype. *Genetical Research*. 86:193-207.
80. Li, X., R. J. Quigg, J. Zhou, S. Xu, G. Masinde, S. Mohan and D. J. Baylink. 2006. A critical evaluation of the effect of population size and phenotypic measurement on QTL detection and localization using a large F_2 murine mapping population. *Genetics and Molecular Biology*. 29:166-173.

81. Qu, Y. and S. Xu. 2006. Quantitative trait associated microarray gene expression data analysis. *Molecular Biology and Evolution.* 23:1558-1573.
82. Yang, R., Q. Tian and S. Xu. 2006. Mapping QTL for longitudinal traits in line crosses. *Genetics*. 173:2339-2356.
83. Yang, R., N. Yi and S. Xu. 2006. Box-Cox transformation for QTL mapping, *Genetica.* 128:133-143.
84. Xu, S. and C. Xu. 2006. A multivariate model for ordinal trait analysis. *Heredity.* 97:409-417.
85. Xu, S. 2007. An empirical Bayes method for estimating epistatic effects of quantitative trait loci. *Biometrics.* 63:513-521.
86. Xu, S. and Z. Jia. 2007. Genomewide analysis of epistatic effects for quantitative traits in barley. *Genetics.* 175:1955-1963.
87. Jia, Z. and S. Xu. 2007. Mapping quantitative trait loci for expression abundance. *Genetics.* 176:611-623.
88. Yang, R. and S. Xu. 2007. Bayesian shrinkage analysis of quantitative trait loci for dynamic traits. *Genetics.* 176:1169-1185.
89. Chen, H., V. E. T. M. Ashworth, S. Xu and M. T. Clegg. 2007. Quantitative genetic analysis of growth rate in avocado. *Journal of American Society of Horticultural Science.* 132:691-696.
90. Xu, S. 2007. Derivation of the shrinkage estimates of quantitative trait locus effects. *Genetics.* 177:1255-1259.
91. Yu, H., D. J. Baylink, G. L. Masinde, R. Li, B. Nguyen, H. M. Davidson, S. Xu and S. Mohan. 2007. Mouse chromosome 9 quantitative trait loci for soft tissue regeneration: Congenic analysis and fine mapping. *Wound Repair and Regeneration.* 15:922–927.
92. Yang, R., J. Li and S. Xu. 2008. Mapping quantitative trait loci for traits defined as ratios. *Genetica.* 132: 323-329.
93. Hu, Z. and S. Xu. 2008. A simple method for calculating the statistical power for detecting a QTL located in a marker interval. *Heredity.* 101:48-52.
94. Yi, N. and S. Xu. 2008. Bayesian LASSO for quantitative trait locus mapping. *Genetics.* 179: 1045–1055.
95. Jia, Z. and S. Xu. 2008. Bayesian mixture model analysis for detecting differentially expressed genes. *International Journal of Plant Genomics*. Volume 2008, Article ID 892927, 12 pages. doi:10.1155/2008/892927.
96. Han, L and S. Xu. 2008. A Fisher scoring algorithm for the weighted regression method of QTL mapping. *Heredity.* 101:453-464.
97. Xu, S. 2008. Quantitative trait locus mapping can benefit from segregation distortion. *Genetics.* 180: 2201-2208.
98. Muir, W. M, G.J.M. Rosa, B.R. Pittendrigh, S. Xu, S.D. Rider, M. Fountain and J. Ogas 2009. A mixture model approach for the analysis of small exploratory microarray experiments. *Computational Statistics and Data Analysis.* 53: 1566-1576.
99. Xu, C., X. Wang, Z. Li and S. Xu. 2009. Mapping QTL for multiple traits using Bayesian statistics. *Genetics Research.* 91:23-37.
100. Xu, N. W., S. Xu and J. Ehlers. 2009. Estimating the broad-sense heritability of early growth of cowpea. *International Journal of Plant Genomics*. Vol. 2009, Article ID 984521. doi:10.1155/2009/984521.

101. Xu, S. 2010. An expectation-maximization algorithm for the Lasso estimation of quantitative trait locus effects. *Heredity.* 105: 483-494, doi:10.1038/hdy.2009.180.
102. Xu, S. and Z. Hu. 2010. Mapping quantitative trait loci using distorted markers. *International Journal of Plant Genomics.* Vol 2009, Article ID 410825, 11 pages, doi:10.1155/2009/410825.
103. Xu, S. and Z. Hu. 2010. Generalized linear model for interval mapping of quantitative trait loci. *Theoretical and Applied Genetics.* 121: 47-63. doi: 10.1007/s00122-1290-0.
104. Che, X. and S. Xu. 2010. Significance test and genomic selection in Bayesian shrinkage analysis. *International Journal of Plant Genomics.* Volume 2010, Article ID 893206, 11 pages, doi:10.1155/2010/893206.
105. Chen, X., F. Zhao and S. Xu. 2010. Mapping environment-specific quantitative trait loci. *Genetics.* 186: 1053-1066, doi: 10.1534/genetics.110.120311.
106. Han, L. and S. Xu. 2010. Genome-wide evaluation for quantitative trait loci under the variance component model. *Genetica.* 138:1099-1109, doi 10.1007/s10709-010-9497-1.
107. Xu, S. and Z. Hu. 2011. Mapping quantitative trait loci using the MCMC procedure in SAS. *Heredity.* 106:357-369, doi:10.1038/hdy.2010.77.
108. Zhan, H., X. Chen and S. Xu. 2011. A stochastic expectation and maximization (SEM) algorithm for detecting quantitative trait associated genes. *Bioinformatics.* 27: 63-69, doi:10.1093/bioinformatics/btq558.
109. Sharma, S., S. Xu, B. Ehdaie, A. Hoops, T. Close, A. Lukaszewski and J. Waines. 2011. Dissection of QTL effects for root traits using a chromosome arm-specific mapping population in bread wheat. *Theoretical and Applied Genetics.* 122: 759–769, doi 10.1007/s00122-010-1484-5.
110. Hu, Z., Y. Li, X. Song, Y. Han, X. Cai, S. Xu and W. Li. 2011. Genomic value prediction for quantitative traits under the epistatic model. *BMC Genetics*. 12:15 (11 pages), doi:10.1186/1471-2156-12-15.
111. Cai, X., A. Huang and S. Xu. 2011. Fast empirical Bayesian Lasso for multiple quantitative trait locus mapping. *BMC Bioinformatics.* 12: 211, doi:10.1186/1471-2105-12-211.
112. Zhan, H. and S. Xu. 2011. Generalized linear mixed model for segregation distortion analysis. *BMC Genetics.* 12:97, http://www.biomedcentral.com/1471-2156/12/97.
113. Zhao, F. and S. Xu. 2012. An expectation and maximization algorithm for estimating Q×E interaction effects. *Theoretical and Applied Genetics*. 124(8):1375-1387. doi:10.1007/s00122-012-1794-x.
114. Xing, J., J. Li, R. Yang, X. Zhou and S. Xu. 2012. Bayesian B-spline mapping for dynamic quantitative traits. *Genetics Research, Cambridge*. 94: 85-95. doi:10.1017/S0016672312000249.
115. Che, X. and S. Xu. 2012. Generalized linear mixed models for mapping multiple quantitative trait loci. *Heredity.* 109:41-49. doi:10.1038/hdy.2012.10.
116. Zhao, F. and S. Xu. 2012. Genotype by environment interaction of quantitative traits – A case study in barley. *G3: Genes|Genomes|Genetics.* 2:779-788. doi: 10.1534/g3.112.002980

117. Hu, Z., Z. Wang and S. Xu. 2012. An infinitesimal model for quantitative trait genomic value prediction. *PLoS One.* 7(7): e41336. doi:10.1371/journal.pone.0041336.
118. Zhan, H. and S. Xu. 2012. Adaptive ridge regression for rare variant detection. *PLoS One.* 7(8): e44173. doi:10.1371/journal.pone.0044173.
119. Chen X, Xu S, McClelland M, Rahmatpanah F, Sawyers A, Z. Jia and D. Mercola. 2012. An accurate prostate cancer prognosticator using a seven-gene signature plus gleason score and taking cell type heterogeneity into account. *PLoS One.* 7(9):e45178.doi:10.1371/journal.pone.0045178.
120. Xu, S. 2012. Testing Hardy-Weinberg disequilibrium using the generalized linear model. *Genetics Research, Cambridge*. 94: 319-330, doi:10.1017/S0016672312000511.
121. Huang, A., S. Xu and X. Cai. 2013. Empirical Bayesian LASSO-logistic regression for multiple binary trait locus mapping. *BMC Genetics.* 14:5, http://www.biomedcentral.com/1471-2156/14/5.
122. Xu, S. 2013. Genetic mapping and genomic selection using recombination breakpoint data. *Genetics.* 195:1103-1115, doi: 10.1534/genetics.113.155309.
123. Xu, S. 2013. Mapping quantitative trait loci by controlling polygenic background effects. *Genetics.* 195:1209-1222, doi:10.1534/genetics.113.157032/-/DC1.
124. Yi, N., S. Xu, H. Mallick and X. –Y. Lou. 2014. Multiple comparisons in genetic association studies: a hierarchical modeling approach. *Statistical Applications in Genetics and Molecular Biology (SAGMB).* 13(1) 35-48. doi: 10.1515/sagmb-2012-0040.
125. Xu, P., S. Xu, X. Wu, Y. Tao, B. Wang, S. Wang, D. Qin, Z. Lu and G. Li. 2014. Population genomic analyses from low-coverage RAD-Seq data: A case study on the non-model cucurbit gourd. *The Plant Journal.* 77:430-442. doi: 10.1111/tpj.12370.
126. Huang, A., S. Xu and X. Cai. 2014. Whole-genome quantitative trait locus mapping reveals major role of epistasis on yield of rice. *PLoS One.* 9(1): e87330. doi: 10.1371/journal.pone.0087330.
127. Xu, Shizhong, Dan Zhu and Qifa Zhang. 2014. Predicting hybrid performance in rice using genomic best linear unbiased prediction. *Proc. Natl. Acad. Sci. USA.* 111: 12456-12461.
128. Huang, Anhui, Shizhong Xu and Xiaodong Cai. 2015. Empirical Bayesian elastic net for multiple quantitative trait locus mapping. *Heredity.* 114:107-115.
129. Ma, Shujie and Shizhong Xu. 2015. Semiparametric nonlinear regression for detecting gene and environment interactions. *Journal of Statistical Planning and Inference.* 156:31-47.
130. Ma,Shujie, Raymond J. Carroll, Hua Liang and Shizhong Xu. 2015. Estimation and inference in generalized additive coefficient models for nonlinear interactions with high-dimensional covariates. *The Annals of Statistics.* 43(5): 2102-2131.
131. Cui, Yanru, Fan Zhang, Zhikang Li and Shizhong Xu. 2015. Mapping quantitative trait loci in selected breeding populations: A segregation distortion approach. *Heredity.* 115:538-546, doi:10.1038/hdy.2015.56.
132. Xiao, Yingjie, Hao Tong, Xiaohong Yang, Shizhong Xu, Qingchun Pan, Feng Qiao, Mohammad Sharif Raihan, Yun Luo , Haijun Liu, Xuehai Zhang, Ning Yang , Xiaqing Wang, Min Deng, Minliang Jin, Lijun Zhao, Xin Luo , Yang Zhou, Xiang Li, Jie Liu,Wei

Zhan, Nannan Liu, Hong Wang, Gengshen Chen, Ye Cai, Gen Xu, Weidong Wang, Debo Zheng and. 2016. Genome-wide dissection of the maize ear genetic architecture using multiple populations. *New Phytologist*. 210(3):1095-106, doi: 10.1111/nph.13814.

133. Wang, Qishan, Julong Wei, Yuchun Pan and Shizhong Xu. 2016. An efficient empirical Bayes method for genome-wide association studies. *Journal of Animal Breeding and Genetics.* 133: 253–263, doi:10.1111/jbg.12191.
134. Wei, Julong and Shizhong Xu. 2016. A random model approach to QTL mapping in multi-parent advanced generation inter-cross (MAGIC) populations. *Genetics.* 202: 471-486 doi:10.1534/genetics.115.179945.
135. Wang, Shi-Bo, Jian-Ying Feng, Wen-Long Ren, Bo Huang, Ling Zhou, Yang-Jun Wen, Jin Zhang, Jim M. Dunwell, Shizhong Xu and Yuan-Ming Zhang, 2016. Improving power and accuracy of genome-wide association studies via a multi-locus mixed linear model methodology. *Scientific Reports.* 6:19444 doi:10.1038/srep19444.
136. Zhang W, Dai X, Wang Q, Xu S, Zhao PX, 2016. PEPIS: A pipeline for estimating epistatic effects in quantitative trait locus mapping and genome-wide association studies. *PLoS Computational Biology.* 12(5): e1004925. doi: 10.1371/journal.pcbi.1004925.
137. Zhao, Fangming, Haitao Zhu, Ruizhen Zeng, Guiquan Zhang and Shizhong Xu. 2016. Detection of additive and additive×environment interaction effects of QTLs for yield component traits of rice using single segment substitution lines (SSSL). *Plant Breeding.* 135: 452-458, doi:10.1111/pbr.12385.
138. Xu, Shizhong, Yang Xu, Liang Gong and Qifa Zhang. 2016. Metabolomic prediction of yield in hybrid rice. *The Plant Journal.* 88(2): 219-227, doi: 10.1111/tpj.13242.
139. Zhao, Fangming, Yu Tan, Liyuan Zheng, Ke Zhou, Guanghua He, Yinghua Ling, Lihua Zhang and Shizhong Xu. 2016. Identification of rice chromosome segment substitution line Z322-1-10 and mapping QTLs for agronomic traits from the F_3 population. *Cereal Research Communication.* 44(3): 370-380, doi:*10.1556/0806.44.2016.022.*
140. Xu, Shizhong, 2017. Predicted residual error sum of squares of mixed models – An application for genomic prediction. *G3: Genes|Genomes|Genetics.* 7: 895-909, doi:10.1534/g3.116.038059.
141. Xavier, Alencar, Shizhong Xu, William Muir and Katy Martin Rainey. 2017. Genomic prediction using subsampling. *BMC Bioinformatics.* 18:191, doi: 10.1186/s12859-017-1582-3.
142. Su, Chengfu, Wei Wang, Shunliang Gong, Jinghui Zuo, Shujiang Li and Shizhong Xu. 2017. High density linkage map construction and mapping of yield trait QTLs in maize (Zea mays) using the genotyping-by-sequencing (GBS) technology. *Frontiers in Plant Science (Crop Science and Horticulture Section).* 8: 706. doi: 10.3389/fpls.2017.00706.
143. Xu, Yang, Chenwu Xu and Shizhong Xu. 2017. Prediction and association mapping of agronomic traits in maize using multiple omic data. *Heredity.* 119: 174–184. doi:10.1038/hdy.2017.27.
144. Xu, Shizhong and Theodore Garland. 2017. A mixed model approach to genome-wide association studies for selection signatures. *Genetics.* 207: 785-799, doi: https://doi.org/10.1534/genetics.117.300102.

145. Ithnin, Maizura, Yang Xu, Marhalil Marjuni, Norhalida Mohamed Serdari, Mohd Din Amiruddin, Leslie Low Eng Ti, Yung-Chie Tan, Soon-Joo Yap, Leslie Ooi Cheng-Li, Rajanaidu Nookiah, Rajinder Singh and Shizhong Xu. 2017. Multiple locus genome-wide association studies for important economic traits of oil palm. *Tree Genetics & Genomes*. 13:103, doi: 10.1007/s11295-017-1185-1
146. Howard, Reka, Alencar Xavier, Diego Jarquin, Vishnu Ramasubramanian, James Specht, George Graef, William Beavis, Brian Diers, Qijian Song, Perry Cregan, Randall Nelson, Rouf Mian, J Shannon, Leah McHale, Dechun Wang, William Schapaugh, Aaron Lorenz, Shizhong Xu, William Muir, Katy Rainey. 2017. Genome-wide analysis of grain yield stability and environmental interactions in a multi-parental soybean population. *G3: Genes|Genomes|Genetics.* 8 (2): 519-529, https://doi.org/10.1534/g3.117.300300.
147. Huynh, Bao-Lam; Ehlers, Jeffrey; Huang, Bevan Emma; Muñoz-Amatriaín, María; Lonardi, Stefano; Santos, Jansen; Ndeve, Arsenio; Batieno, Benoit; Boukar, Ousmane; Cisse, Ndiaga; Drabo, Issa; Fatokun, Christian; Kusi, Francis; Agyare, Richard; Guo, Yi-Ning; Herniter, Ira; Lo, Sassoum; Wanamaker, Steve; Xu, Shizhong; Close, Timothy; Roberts, Philip. 2018. A multi-parent advanced generation inter-cross (MAGIC) population for genetic analysis and improvement of cowpea (Vigna unguiculata L. Walp.). *The Plant Journal.* 93, 1129–1142. doi: 10.1111/tpj.13827.
148. Ning, Chao, Dan Wang, Huimin Kang, Raphael Mrode, Lei Zhou, Shizhong Xu and Jian-Feng Liu. 2018. A rapid epistatic mixed-model association analysis by linear retransformations of genomic estimated values. *Bioinformatics.* 34 (11): 817–1825, https://doi.org/10.1093/bioinformatics/bty017.
149. Cui Y, Zhang W, Lin X, Xu S, Xu J and Li Z. 2018. Simultaneous improvement and genetic dissection of drought tolerance using selected breeding populations of rice. *Frontiers in Plant Science.* 9:320. doi: 10.3389/fpls.2018.00320.
150. Quan, Yuan, Meng-Yuan Liu, Ye-Mao Liu, Li-Da Zhu, Yu-Shan Wu, Zhi-Hui Luo, Xiu-Zhen Zhang, Shi-Zhong Xu, Qing-Yong Yang and Hong-Yu Zhang. 2018 Facilitating anti-cancer combinatorial drug discovery by targeting epistatic disease genes. *Molecules.* 23, 736; doi:10.3390/molecules23040736.
151. Lo, Sassoum, María Muñoz-Amatriaín1, Ousmane Boukar, Ira Herniter, Ndiaga Cisse, Yi-Ning Guo, Philip A. Roberts, Shizhong Xu, Christian Fatokun and Timothy J. Close. 2018. Identification of QTL controlling domestication-related traits in cowpea (*Vigna unguiculata L. Walp*). *Scientific Reports.* 8:6261 doi:10.1038/s41598-018-24349-4.
152. Deng, Wenping, Kui Zhang, Sanzhen Liu, Patrick Zhao, Shizhong Xu and Hairong Wei 2018. JRmGRN: Joint reconstruction of multiple gene regulatory networks with common hub genes. *Bioinformatics.* 34(20):3470-3478. doi: 10.1093/bioinformatics/bty354.
153. Zhang, Wenchao, Xinbin Dai, Shizhong Xu and Patrick X. Zhao. 2018. 2D association and integrative omic analysis in rice provides systems biology view in trait analysis. *Communications Biology.* 1:153, DOI: 10.1038/s42003-018-0159-7, www.nature.com/commsbio

154. Xu, Shizhong. 2019. An alternative derivation of Harville's restricted log likelihood function for variance component estimation. *Biometrical Journal*. 61:157-161, DOI: 10.1002/bimj.201800319.
155. Kim, Bongsong, Xinbin Dai, Wenchao Zhang, Darlene L. Sanchez, Thomas Lübberstedt, Yun Kang, Michael Udvardi, William D. Beavis, Shizhong Xu, Patrick X. Zhao 2019. GWASpro: A high-performance genome-wide association analysis server. *Bioinformatics*. doi: 10.1093/bioinformatics/bty989.
156. Wang, Meiyue and Shizhong Xu. 2019. Statistical power in genome-wide association studies and quantitative trait locus mapping. *Heredity*. 123(3): 278-306.
157. Wang, Meiyue and Shizhong Xu. 2019. Statistics of Mendelian segregation – A mixture model. *Journal of Animal Breeding and Genetics*. 136(5): 341-350.
158. Hu, Xuehai, Weibo Xie, Chengchao Wu and Shizhong Xu. 2019. A directed learning strategy integrating multiple omic data improves genomic prediction. *Plant Biotechnology Journal*. 17(10):2011-2020.
159. Wang, Meiyue and Shizhong Xu. 2019. A coordinate descent approach for sparse Bayesian learning in high dimensional QTL mapping and genome-wide association studies. *Bioinformatics*. 35(21): 4327-4335
160. Ning, Chao, Dan Wang, Lei Zhou, Julong Wei, Yuanxin Liu, Huimin Kang, Shengli Zhang, Xiang Zhou, Shizhong Xu and Jian-Feng Liu. 2019. Efficient multivariate analysis algorithms for longitudinal genome-wide association studies. *Bioinformatics*. 35(23): 4879-4885.
161. Yao, Wen, Guangwei Li, Yanru Cui, Yiming Yu, Qifa Zhang and Shizhong Xu. 2019. Mapping quantitative trait loci using binned genotypes. *Journal of Genetics and Genomics*. 46(7): 343-352.
162. Lo, Sassoum, María Muñoz-Amatriaín, Samuel A. Hokin, Ndiaga Cisse, Philip A. Roberts, Andrew D. Farmer, Shizhong Xu and Timothy J. Close. 2019. A Genome-wide association and meta-analysis reveal regions associated with seed size in cowpea [*Vigna unguiculata* (L.) Walp]. *Theoretical and Applied Genetics*. 132(11): 3079-3087.
163. Zhang, Meiping, Yangru Cui, Yun-Hua Liu, Wenwei Xu, Sing-Hoi Sze, Seth Murray, Shizhong Xu and Hongbin Zhang. 2020. Accurate prediction of maize grain yield using its contributing genes for gene-based breeding. *Genomics*. 12(1): 225-236.
164. Cui, Yanru, Ruidong Li, Guanwei Li, Fan Zhang, Tiantian Zhu, Qifa Zhang, Jauhar Ali, Zhikang Li and Shizhong Xu. 2020. Hybrid breeding of rice via genomic selection. *Plant Biotechnology Journal*. 18(1):57-67.
165. Zhang, Wenchao, XinbinDai, Shizhong Xu and Patrick X. Zhao. 2020. GPU empowered pipelines for calculating genome-wide kinship matrices with ultra-high dimensional genetic variants and facilitating 1D and 2D GWAS. *NAR Genomics and Bioinformatics*. 2(1) 1 doi: 10.1093/nargab/lqz009.
166. An, Bingxing, Xue Gao, Tianpeng Chang, Jiangwei Xia, Xiaoqiao Wang, Jian Miao, Lingyang Xu, Lupei Zhang, Yan Chen, Junya Li, Shizhong Xu and Huijiang Gao. 2020. Genome-wide association studies using binned genotypes. *Heredity*. 124(2): 288-298.https://doi.org/10.1038/s41437-019-0279-y.

167. Wang, Meiyue, Ruidong Li and Shizhong Xu. 2020. Deshrinking ridge regression for genome-wide association studies. *Bioinformatics*. 36(14): 4154-4162, doi: 10.1093/bioinformatics/btaa345.
168. Wang, Dan, Hui Tang, Jianfeng Liu, Shizhong Xu, Qin Zhang, Chao Ning. 2020. Rapid epistatic mixed model association studies by controlling multiple polygenic effects. *Bioinformatics*. 36 (19):4833-4837. https://doi.org/10.1093/bioinformatics/btaa610
169. Hillis, David A, Liran Yadgary, George M. Weinstock, Fernando Pardo-Manuel de Villena, Daniel Pomp, Alexandra S. Fowler, Shizhong Xu, Frank Chan and Theodore Garland, Jr. 2020. Genetic basis of aerobically supported voluntary exercise: Results from a selection experiment with house mice. *Genetics*. 216(3): 781-804. https://doi.org/10.1534/genetics.120.303668
170. Liu, Yun-Hua, Yang Xu, Meiping Zhang, Yanru Cui, Sing-Hoi Sze, C Wayne Smith, Shizhong Xu, Hong-Bin Zhang. 2020. Accurate prediction of a quantitative trait using the genes controlling the trait for gene-based breeding in cotton. *Frontiers in Plant Science (Plant Breeding Section)*. 11:583277. doi: 10.3389/fpls.2020.583277.
171. Xu, Yang, Yue Zhao, Xin Wang, Ying Ma, Pengcheng Li, Zefeng Yang, Xuecai Zhang, Chenwu Xu and Shizhong Xu. 2021. Incorporation of parental phenotypic data into multi-omic models improves prediction of yield related traits in hybrid rice. *Plant Biotechnology Journal*. Feb;19(2):261-272. doi: 10.1111/pbi.13458. Epub 2020 Sep 2. PMID: 32738177; PMCID: PMC7868986.
172. Zhang, Wenchao, Yun Kang, Xinbin Dai, Shizhong Xu and Patrick X. Zhao. 2021. PIP-SNP: A pipeline for processing SNP data featured as linkage disequilibrium bin mapping, genotype imputing and marker synthesizing. *NAR Genomics and Bioinformatics*. 3(3): https://doi.org/10.1093/nargab/lqab060
173. Xie, Fangjie, Shibo Wang, William D. Beavis and Shizhong Xu. 2021. Estimation of genetic variance contributed by a quantitative trait locus — Correcting the bias associated with significance tests. *Genetics*. 219 (3), iyab115. DOI: 10.1093/genetics/iyab115.
174. Li, Dongdong, Zhiqiang Zhou, Xiaohuan Lu, Yong Jiang, Guoliang Li, Junhui Li, Haoying Wang, Shaojiang Chen, Xinhai Li, Tobias Würschum, Jochen C. Reif, Shizhong Xu, Mingshun Li and Wenxin Liu. 2021. Genetic dissection of hybrid performance and heterosis for yield-related traits in maize. *Frontiers in Plant Science, Section Plant Breeding*. Nov 30;12:774478. doi: 10.3389/fpls.2021.774478. PMID: 34917109; PMCID: PMC8670227.
175. Wang, Shibo, Fangjie Xie, and Shizhong Xu. 2022. Estimating Genetic Variance Contributed by a Quantitative Trait Locus: A Random Model Approach. *PLoS Computational Biology*. Mar 11;18(3):e1009923. doi: 10.1371/journal.pcbi.1009923

176 Zhou, Yao, Zhiyang Zhang, Zhigui Bao1, Hongbo Li, Yaqing Lyu, Yanjun Zan,Yaoyao Wu, Lin Cheng, Yuhan Fang, Kun Wu, Jinzhe Zhang, Hongjun Lyu, Tao Lin, Qiang Gao, Surya Saha, Lukas Mueller, Zhangjun Fei, Thomas Städler, Shizhong Xu, Zhiwu Zhang, Doug Speed & Sanwen Huang. 2022. Graph pangenome captures missing heritability and empowers tomato

breeding. *Nature* 606, 527—534 (2022).
https://doi.org/10.1038/s41586-022-04808-9

B Books

1. Xu, S. 2012. Principles of Statistical Genomics. Springer, New York. ISBN: 978-0-387-70806-5
2. Xu, S. 2022. Quantitative Genetics, Springer, New York. ISBN: 978-3-030-83939-0
3. Xu, S. 2032. Genetical Statistics.
4. Xu, S. 2042. Agricultural Statistics.

C Conference and Symposia Proceedings

1. Levy, M., S. Xu and J. E. Hamer. 1992. MGR-DNA fingerprinting for rice blast population analysis: SAS programs for inferring lineage phylogenies. *Proc. Intl. Rice Res. Conf., 21-25 April, 1992, I.R.R.I., Los Banos, The Philippines.*
2. Muir, W. M. and S. Xu. 1992. Separation of genetic gain from random genetic drift, inbreeding depression, and environmental trends in non-replicated selected populations with or without a control. In Proceedings, 41st National Breeders Round Table. Table. 24p. St. Louis, MO. 05/07/1992.

2b. Muir, W. M. and S. Xu. 1992. Estimation of response to selection and standard error with non-replicated selected populations. *Proceedings of the 41th National Breeders Round Table. May 7-8, St. Louis, Missouri.*

3. Muir, W. M. and S. Xu. 1992. Optimizing profits in breeding programs using selection index updating. *Proceedings of the XIX World's Poultry Congress, September 23, Amsterdam, The Netherlands*.
4. Xu, S., W. R. Atchley and W. M. Muir. 1994. Multistage selection incorporating information from relatives. *Proceedings of The 5th World Congress on Genetics Applied to Livestock Production*, *August 7-12, Guelph, Canada.* Vol. 18:463-466.
5. Smouse, P.E., C. J. Kobak and S. Xu. 1994. Some thoughts on information content in allozyme and DNA markers. In: *NOAA Tech. Memo. NMFS-NWFSC-17. Application of DNA Technology to the Management of Pacific Salman, Proceedings of the Workshop*, *March 22-23, 1993*, Seattle, Washington, Edited by L. K. Park, P. Moran and R. S. Waples, pp 121-126.
6. Xu, S. 1998. Mapping quantitative trait loci and marker assisted selection in small domesticated populations. p. 62-87, In *Research Council Secretariat of MAFF* (ed.), *Proceedings of the 6th MAFF International Workshop on genetic Resources – Genetic Diversity and Conservation of Genetic Resources*, National Institute of Agrobiological Resources, Tsukuba, Ibaraki, Japan, Nov. 4-5, 1998.

D Book Chapters

1. Xu, S. 1995. Sequential regression and its applications in biology. In *Animal Genetics and Breeding*, Edited by Y.C. Pan and Y.Q. Yang, Harbin Engineering University Press, pp 93-112.
2. Xu, S. 2002. Linkage analysis of quantitative traits. In Tao, J., Xu, Y., and Zhang, M. Q. (eds), *Current Topics in Computational Biology*, Tsinghua University Press and Massachusetts Institute of Technology, pp 175-199.
3. Xu, S. 2002. QTL analysis in plants. In Camp, N. and Cox, A (eds), *Quantitative Trait Loci: Methods and Protocols*, Humana Press, Totowa, NJ, pp 283-310.
4. Yi, N. and S. Xu. 2003. Designs and methods to detect QTLs for production traits based on random genetic models. In Muir, W. M. and Aggrey, S. E. (eds), *Poultry Genetics, Breeding and Biotechnology*, CABI Publishing Oxon, UK, pp 465-496.
5. Xu, C. and S. Xu. 2004. The extended sib-pair method for mapping QTL. In Saxton, R. (ed), *Genetic Analysis of Complex Traits Using SAS*. SAS Institute, Inc., Cary, North Carolina, Chapter 9: pp 201-223.
6. Jia, Zhenyu, Sha Tang, Dan Mercola and Shizhong Xu. 2008. Detection of quantitative trait associated genes using cluster analysis. *Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics (EvoBIO)*. *Lecture Notes in Computer Science (LNCS)*. Volume 4973/2008. doi: 10.1007/978-3-540-78757-0_8.
7. Jia, Zhenyu, Yipeng Wang, Kai Ye, Qilan Li, Sha Tang, Shizhong Xu and Dan Mercola. 2009. Association study between gene expression and multiple relevant phenotypes with cluster analysis. *Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics (EvoBIO). Lecture Notes in Computer Science (LNCS)*. Volume 5483/2009. doi: 10.1007/978-3-642-01184-9_1.

E Computer Programs

1. Xu, S. 1993. INDUPDAT: A SAS/IML program for selection index updating. *The Journal of Heredity*. 84:316.
2. Xu, C. and S. Xu. 2003. A SAS/IML program for mapping QTL in line crosses. *Proceedings of the Twenty-Eighth Annual SAS Users Group International Conference (SUGI)*, March 30-April 2, 2003, Cary, NC, SAS Institute, Inc., Paper 235-28:1-6.
3. Hu, Z. and S. Xu. 2009. PROC QTL – A SAS procedure for mapping quantitative trait loci. *International Journal of Plant Genomics*, Volume 2009, Article ID 141234, 3 pages, doi:10.1155/2009/141234.
4. Hu, Z., J. D. Ehlers, P. A. Roberts, T. J. Close, M. R. Lucas, S. Wanamaker, and S. Xu. 2012. ParentChecker: a computer program for automated inference of missing parental genotype calls and linkage phase correction. *BMC Genetics.* 13:9, doi:10.1186/1471-2156-13-9.
5. Xavier, Alencar, Shizhong Xu, William M. Muir and Katy Martin Rainey. 2015. NAM: association studies in multiple populations. *Bioinformatics.* 31(23):1-3 doi: 10.1093/bioinformatics/btv448

F Review Articles

1. Zhang, Y. –M. and S. Xu. 2005. Advanced statistical methods for detecting multiple quantitative trait loci. *Recent Research Development in Genetics and Breeding.* 2:1-23.
2. Xu, S. 2003. Advanced statistical methods for estimating genetic variances in plants. *Plant Breeding Reviews.* 22:113-163.
3. Che, X. and S. Xu. 2010. Bayesian data analysis for agricultural experiments. *Canadian Journal of Plant Science.* 90: 575-603.
4. Xu, S. and Z. Hu. 2010. Methods of plant breeding in the genome era. *Genetics Research.* 92:423-441, doi:10.1017/S0016672310000583.
5. Xu, Yang, Kexin Ma, Yue Zhao, Xin Wang, Kai Zhou, Guangning Yu, Cheng Li,Pengcheng Li, Zefeng Yang, Chenwu Xu and Shizhong Xu. 2021. Genomic selection: A breakthrough technology in rice breeding. *The Crop Journal*. 9(3): 669-677. https://doi.org/10.1016/j.cj.2021.03.008

G Notes and Comments

1. Xu, S. 2006. Separating nurture from nature in estimating heritability. *Heredity.* 97:256-257.