

Baoxing Song

Surname: Song **Given name:** Baoxing **Birth place:** Shandong, P.R.CHINA
Birth day: 18/09/1987 **Sex:** Male **Nationality:** China

Research Experience

2014.02-2018.01 Bioinformatics and comparative genomics group, Department of Comparative Development and Genetics, Max Planck Institute for Plant Breeding Research
Postdoc

2014.02-2018.01 Bioinformatics and comparative genomics group, Department of Comparative Development and Genetics, Max Planck Institute for Plant Breeding Research
Ph.D. of botany

2011-2013.07 Functional Genomics Group, Qingdao Institute of Bioenergy and Bioprocess Technology, Chinese Academy of Sciences (CAS - QIBEBT)

2010.09-2013.07 College of Veterinary Medicine, Northwest A&F University
Master of Animal Biotechnology

2006.09-2010.07 Bioengineering department, Zhengzhou University
Bachelor of Science

Programming Skills

Perl, Java, R, Python, C/C++, LaTeX etc.

Publications

Plant (2014-2017 at Max Planck Institute for Plant Breeding Research):

- 1 **Baoxing Song**, Richard Mott, Xiangchao Gan. Recovery of missing causal candidates in *Arabidopsis thaliana* and *Drosophila melanogaster* through leveraging INDELs and integrated burden test. *Plos genetics* (accepted)

- 2 Xiangchao Gan, another 10 co-authors, **Baoxing Song**, another 18 co-authors, Miltos Tsiantis. The Cardamine hirsuta genome offers insight into the evolution of morphological diversity. *Nature Plants* 2(11) November 2016
- 3 Yong Xiang, **Baoxing Song**, Guillaume Née, Katharina Kramer, Iris Finkemeier, Wim Soppe. Sequence polymorphisms at the REDUCED DORMANCY5 pseudophosphatase underlie natural variation in Arabidopsis dormancy. *Plant physiology* 171(4):pp.00525.2016

Metagenome (2012-2014 at Chinese Academy of Sciences):

- 4 **Baoxing Song**, Xiaoquan Su, Jian Xu, Kang Ning. MetaSee: An interactive and extendable visualization toolbox for metagenomic sample analysis and comparison. *Plos One*. 2012.7(11):0048998.
- 5 Xiaoquan Su, **Baoxing Song**, Jian Xu, Qing Sang, Deli Zhang, Kang Ning. Meta-Mesh: metagenomic data analysis system. *Chinese journal of biotechnology* 30(1):6-17 (in Chinese)
- 6 Xiaoquan Su, Weihua Pan, **Baoxing Song**, Jian Xu, Kang Ning. Parallel-META 2.0: Enhanced Metagenomic Data Analysis with Functional Annotation, High Performance Computing and Advanced Visualization. *Plos One* (2014.9.e89323)

Proteome (2010-2014 at Northwest A&F University China):

- 7 **Baoxing Song**, Fen Wang, Yang Guo, Qing Sang, Min Liu, Dengyun Li, Wei Fang, Deli Zhang. Protein-protein interaction network-based detection of functionally similar proteins within species. *Proteins*, 2012, 80(7):1736-1743.
- 8 Fen Wang, Min Liu, **Baoxing Song**, Dengyun Li, Huimin Pei, Yang Guo, Jingfei Huang, Deli Zhang. Prediction and characterization of protein-protein interaction networks in swine. *Proteome Sci*, 2012,10(2).
- 9 **Baoxing Song**, Qing Sang, Fen Wang, Deli Zhang. PPI Network-Based Detecting of Proteins with Functional Similarity in a Species. *Acta Biophysica Sinica*, 2011,27(9):789-800. (In Chinese)
- 10 Fen Wang, **Baoxing Song**, Xing Zhao, Yaotian Miao, Dengyun Li, Na Zhou, Pengfei Jiang, Qing Sang, Jingfei Huang and Deli Zhang. Prediction and analysis of the protein-protein

interaction networks for chickens, cattle, dogs, horses and rabbits. *Current Bioinformatics*, 2016,11,131-142. (co-first author)

- 11 Fen Wang, **Baoxing Song**, Dengyun Li, Xing Zhao, Yaotian Miao, Pengfei Jiang, Deli Zhang. PPIPP: An online protein–protein interaction network prediction and analysis platform. *International Journal of Data Mining and Bioinformatics*, 14(4):305

Other (2010 Zhengzhou University):

- 12 Tianli Fan, Yu Xi, Dongsheng Yao, Tingting Zhao, **Baoxing Song**, Daheng Zhu. Study on Biosorption of Crystal Violet by Mycelial Pellets of *Aspergillus Terreus* M11. *Chemistry & Bioengineering*, 2010,27(3):77-79. (In Chinese)

Software:

- 13 Irisas -- Integrated region-based variants synchronization and Annotation for association studies:
<https://github.com/baoxingsong/Irisas>
- 14 AnnotationLiftOver -- This tool converts genome coordinates and gene structure annotation files between lines/accessions: <https://github.com/baoxingsong/AnnotationLiftOver>
- 15 Mlmm -- multiallelic linear mixed model for GWAS analysis:
<https://github.com/baoxingsong/mlmm>
- 16 MetaSee -- An Interactive and Extendable Visualization Toolbox for Metagenomic Sample Analysis and Comparison: <https://github.com/baoxingsong/MetaSee>

Academic Honors

2011.09	1 st prize for postgraduate in Northwest A&F University (1/3, one out of three could win this honor)
2011.09	Excellent student for postgraduate in Northwest A&F University (1/17)
2011.12	Excellent posters award of Graduate University of Chinese Academy of Sciences, graduate academic microbiology Forum 2011 (1/3)
2012.09	Zhengda 1 st Scholarship for postgraduate in Shanxi Province (1/17)

2012.10	Principal's Scholarship (1/300)
2012.12	Outstanding Graduate (1/17)
2012.12	National Scholarship (1/30, the highest honor of Chinese postgraduate students)
2013.06	Excellent Graduation Thesis of College of Veterinary Medicine
2013.06	Excellent Graduation Thesis of College of Northwest A&F University

Contact Information

E-mail: song@mpipz.mpg.de

Github: <https://github.com/baoxingsong>