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PROFESSIONAL EXPERIENCE:

2016-	Shanghai Normal University	Professor
2014- 2016	Chinese Academy of Sciences	Professor
2011- 2014	Chinese Academy of Sciences	Associate Professor
2011- 2011	Chinese Academy of Sciences	Assistant Professor

EDUCATION BACKGROUND:

2006- 2011	Chinese Academy of Sciences	Ph.D. in Genetics
2002- 2006	Fudan University	B.S. in Biological Science

Research Interests:

1. Genetic analysis of complex traits in crops
2. The genetic mechanisms of heterosis in crops
3. Bioinformatics methods for genomics and genetics studies

Publications (#co-first authors; *corresponding authors)

1. Liu H, Wang Q, Chen M, Ding Y, Yang X, Liu J, Li X, Zhou C, Tian Q, Lu Y, Fan D, Shi J, Zhang L, Kang C, Sun M, Li F, Wu Y, Zhang Y, Liu B, Zhao XY, Feng Q, Yang J, Han B, Lai J, Zhang X-S*, **Huang X***. Genome-wide identification and analysis of heterotic loci in three maize hybrids. ***Plant Biotech J.*** doi: 10.1111/pbi.13186 (2019).
2. Wang C, Tang S, Zhan Q, Hou Q, Zhao Y, Zhao Q, Feng Q, Zhou C, Lyu D, Cui L, Li Y, Miao J, Zhu C, Lu Y, Wang Y, Wang Z, Zhu J, Shangguan Y, Gong J, Yang S, Wang W, Zhang J, Xie H, **Huang X***, Han B*. Dissecting a heterotic gene through GradedPool-Seq mapping informs

a new rice-improvement strategy. ***Nat. Commun.*** 10:2982 (2019).

3. Wang A, Hou Q, Si L, **Huang X**, Luo J, Lu D, Zhu J, Shangguan Y, Miao J, Xie Y, Wang Y, Zhao Q, Feng Q, Zhou C, Li Y, Fan D, Lu Y, Tian Q, Wang Z, Han B*. The PLATZ transcription factor GL6 affects grain length and number in rice. ***Plant Physiol***. doi: 10.1104/pp.18.01574 (2019).
4. Chen K, Guo T, Li X-M, Zhang Y-M, Yang Y-B, Ye W-W, Dong N-Q, Shi C-L, Kan Y, Xiang Y-H, Zhang H, Li Y-C, Gao J-P, **Huang X**, Zhao Q, Han B, Shan J-X, Lin H-X*. Translational Regulation of Plant Response to High Temperature by a Dual Function $tRNA^{His}$ Guanylyltransferase in Rice. ***Mol. Plant*** doi.org/10.1016/j.molp.2019.04.012 (2019)
5. Chen Erwang, **Huang X***, Tian Z, Wing R.A*, Han B*. The Genomics of *Oryza* Species Provides Insights into Rice Domestication and Heterosis. ***Annu. Rev. Plant Biol.*** 70:639-665 (2019).
6. Liu Jie, Li M, Zhang Q, Wei X, **Huang X***. Exploring the molecular basis of heterosis for plant breeding. ***J Integr Plant Biol.*** doi.org/10.1111/jipb.12804 (2019)
7. Zhou Xiaoyi, **Huang X***. Genome-wide Association Studies in Rice: How to Solve the Low Power Problems? ***Mol. Plant*** 12:10-12 (2019)
8. Yang Jun*, **Huang X***. A new high-quality genome sequence in soybean. ***SCIENCE CHINA Life Sciences*** 61:1604-1605 (2018).
9. Wei Xin*, **Huang X***. Identification of a seed dormancy gene in soybean sheds light on crop domestication. ***SCIENCE CHINA Life Sciences*** 61:1439-1441 (2018).
10. Zhao Qiang#, Feng Q#, Lu H, Li Y, Wang A, Tian Q, Zhan Q, Lu Y, Zhang L, Huang T, Wang Y, Fan D, Zhao Y, Wang Z, Zhou C, Chen J, Zhu C, Li W, Weng Q, Xu Q, Wang ZX, Wei X, Han B, **Huang X***. Pan-genome analysis highlights the extent of genomic variation in cultivated and wild rice. ***Nat Genet.*** 50: 278-284 (2018).
11. Gong Junyi#, Miao J#, Zhao Y, Zhao Q, Feng Q, Zhan Q, Cheng B, Xia J, **Huang X***, Yang S* and Han B*. Dissecting genetic basis of grain shape and chalkiness traits in hybrid rice using multiple collaborative populations. ***Mol. Plant*** 10: 1353-1356 (2017).
12. Fang Lei#, Gong H#, Hu Y#, Liu C#, Zhou B, Huang T, Wang Y, Chen S, Fang DD, Du X, Chen H, Chen J, Wang S, Wang Q, Wan Q, Liu B, Pan M, Chang L, Wu H, Mei G, Xiang D, Li X, Cai C, Zhu X, Chen ZJ, Han B, Chen X, Guo W, Zhang T*, **Huang X***. Genomic insights into divergence and dual domestication of cultivated allotetraploid cottons. ***Genome Biol.*** 18:33 (2017)
13. Chen Erwang, **Huang X***, Han B*. How can rice genetics benefit from rice-domestication study? ***Natl. Sci. Rev.*** 3: 278-280 (2016).
14. **Huang Xuehui***. From genetic mapping to molecular breeding: genomics have paved the highway. ***Mol. Plant*** 9: 959-960 (2016).
15. **Huang Xuehui***#, Yang S#, Gong J #, Zhao Q, Feng Q, Zhan Q, Zhao Y, Li W, Cheng B, Xia J, Chen N, Huang T, Zhang L, Fan D, Chen J, Zhou C, Lu Y, Weng Q, Han B*. Genomic architecture of heterosis for yield traits in rice. ***Nature*** 537:629-633 (2016).
16. **Huang Xuehui***, Zhang Q, Han B. Comparative population genomics reveals strong divergence and infrequent introgression between Asian and African rice. ***Mol. Plant*** 8: 958-960 (2015).
17. **Huang Xuehui*** and Han B*. Rice domestication occurred through single origin and multiple introgressions. ***Nat. Plants*** 2: 15207 (2015).

18. Wei Xin[#], Liu K[#], Zhang Y[#], Feng Q[#], Wang L, Zhao Y, Li D, Zhao Q, Zhu X, Zhu X, Li W, Fan D, Gao Y, Lu Y, Zhang X, Tang X, Zhou C, Zhu C, Liu L, Zhong R, Tian Q, Wen Z, Weng Q, Han B, **Huang X**[*], Zhang X[*]. Genetic discovery for oil production and quality in sesame. ***Nat. Commun.*** 6:8609 (2015).
19. **Huang Xuehui**[*], Yang S[*], Gong J [*], Zhao Y[*], Feng Q, Gong H, Li W, Zhan Q, Cheng B, Xia J, Chen N, Hao Z, Liu K, Zhu C, Huang T, Zhao Q, Zhang L, Fan D, Zhou C, Lu Y, Weng Q, Wang Z-X, Li J, Han B[*]. Genomic analysis of hybrid rice varieties reveals numerous superior alleles that contribute to heterosis. ***Nat. Commun.*** 6:6258 (2015).
20. **Huang Xuehui**[*] and Han B[*]. Natural variations and genome-wide association studies in crop plants. ***Annu. Rev. Plant Biol.*** 65: 531-551 (2014).
21. Jia Guanqing[#], **Huang X** [#], Zhi H[#], Zhao Y[#], Zhao Q, Li W, Chai Y, Yang L, Liu K, Lu H, Zhu C, Lu Y, Zhou C, Fan D, Weng Q, Guo Y, Huang T, Zhang L, Feng Q, Hao H, Liu H, Lu P, Zhang N, Li Y, Guo E, Wang S, Wang S, Liu J, Zhang W, Chen G, Zhang B, Li W, Wang Y, Li H, Zhao B, Li J[*], Diao X[*], Han B[*]. A haplotype map of genomic variations and genome-wide association studies of agronomic traits in foxtail millet (*Setaria italica*). ***Nat. Genet****.* 45: 957-961 (2013).
22. **Huang Xuehui**, Lu T, Han B[*]. Resequencing rice genomes: an emerging new era of rice genomics. ***Trends Genet.*** 29: 225-232 (2013).
23. Han Bin[*], **Huang X**[*]. Sequencing-based genome-wide association study in rice. ***Curr. Opin. Plant Biol.*** 16: 133-138 (2013).
24. **Huang Xuehui**[*] and Han B[*]. A crop of maize variants. ***Nat. Genet****.* 44: 734-735 (2012).
25. **Huang Xuehui**[#], Kurata N[#], Wei X[#], Wang Z-X[#], Wang A, Zhao Q, Zhao Y, Liu K, Lu H, Li W, Guo Y, Lu Y, Zhou C, Fan D, Weng Q, Zhu C, Huang T, Zhang L, Wang Y, Feng L, Furuumi H, Kubo T, Miyabayashi T, Yuan X, Xu Q, Dong G, Zhan Q, Li C, Fujiyama A, Toyoda A, Lu T, Feng Q, Qian Q, Li J, Han B[*]. A map of rice genome variation reveals the origin of cultivated rice. ***Nature*** 490: 497-501 (2012).
26. **Huang Xuehui**[#], Zhao Y[#], Wei X[#], Li C, Wang A, Zhao Q, Li W, Guo Y, Deng L, Zhu C, Fan D, Lu Y, Weng Q, Liu K, Zhou T, Jing Y, Si L, Dong G, Huang T, Lu T, Feng Q, Qian Q, Li J, Han B[*]. Genome-wide association study of flowering time and grain yield traits in a worldwide collection of rice germplasm. ***Nat. Genet****.* 44: 32-39 (2012).
27. **Huang Xuehui**[#], Wei X[#], Sang T[#], Zhao Q[#], Feng Q[#], Zhao Y, Li C, Zhu C, Lu T, Zhang Z, Li M, Fan D, Guo Y, Wang A, Wang L, Deng L, Li W, Lu Y, Weng Q, Liu K, Huang T, Zhou T, Jing Y, Li W, Lin Z, Buckler ES, Qian Q, Zhang Q, Li J, Han B[*]. Genome-wide association studies of 14 agronomic traits in rice landraces. ***Nat. Genet****.* 42: 961-967 (2010).
28. **Huang Xuehui**[#], Feng Q[#], Qian Q[#], Zhao Q[#], Wang L[#], Wang A[#], Guan J, Fan D, Weng Q, Huang T, Dong G, Sang T, Han B[*]. High-throughput genotyping by whole-genome resequencing. ***Genome Res****.* 19: 1068-76 (2009).
29. **Huang Xuehui**, Lu G, Zhao Q, Liu X, Han B[*]. Genome-wide analysis of transposon insertion polymorphisms reveals intraspecific variation in cultivated rice. ***Plant Physiol****.* 148: 25-40 (2008).
30. Lu Tingting[#], **Huang X**[#], Zhu C[#], Huang T, Zhao Q, Xie K, Xiong L, Zhang Q, Han B[*]. RICD: a rice indica cDNA database resource for rice functional genomics. ***BMC Plant Biol****.* 8: 118 (2008).
31. Ying Jie-Zheng, Ma M, Bai C, Huang X, Liu JL, Fan YY, Song XJ. TGW3, a Major QTL that

Negatively Modulates Grain Length and Weight in Rice. ***Mol. Plant*** 11: 750-753. (2018).

32. Li Yan, Xiao J, Chen L, **Huang X**, Cheng Z, Han B, Zhang Q*, Wu C*. Rice Functional Genomics Research: Past Decade and Future. ***Mol. Plant*** 11: 359-380. (2018).
33. Sun S, Wang T, Wang L, Li X, Jia Y, Liu C, **Huang X**, Xie W, Wang X. Natural selection of a GSK3 determines rice mesocotyl domestication by coordinating strigolactone and brassinosteroid signaling. ***Nat. Commun.*** 9: 2523 (2018).
34. Zhang Lin$^{\#}$, Yu H$^{\#}$, Ma B, Liu G, Wang J, Wang J, Gao R, Li J, Liu J, Xu J, Zhang Y, Li Q, **Huang X**, Xu J, Li J, Qian Q, Han B, He Z, & Li J. A natural tandem array alleviates epigenetic repression of *IPA1* and leads to superior yielding rice. ***Nat. Commun.*** 8: 14789 (2017).
35. Si Lizhen, Chen J, **Huang X**, Gong H, Luo J, Hou Q, Zhou T, Lu T, Zhu J, Shangguan Y, Chen E, Gong C, Zhao Q, Jing Y, Zhao Y, Li Y, Cui L, Fan D, Lu Y, Weng Q, Wang Y, Zhan Q, Liu K, Wei X, An K, An G, Han B*. OsSPL13 controls grain size in cultivated rice. ***Nat. Genet.*** 48: 447-456 (2016).
36. Liu Hongjun, Shi J, Sun C, Gong H, Fan X, Qiu F, **Huang X**, Feng Q, Zheng X, Yuan N, Li C, Zhang Z, Deng Y, Wang J, Pan G, Han B, Lai J, Wu Y*. Gene duplication confers enhanced expression of 27-kDa γ-zein for endosperm modification in quality protein maize. ***Proc. Natl. Acad. Sci. USA***. 113: 4964-1969 (2016).
37. Ohyanagi Hajime, Ebata T, **Huang X**, Gong H, Fujita M, Mochizuki T, Toyoda A, Fujiyama A, Kaminuma E, Nakamura Y, Feng Q, Wang ZX, Han B, Kurata N*. OryzaGenome: Genome Diversity Database of Wild Oryza Species. ***Plant Cell Physiol.*** 57:e1 (2016).
38. Li Xin-Min, Chao DY, Wu Y, **Huang X**, Chen K, Cui LG, Su L, Ye WW, Chen H, Chen HC, Dong NQ, Guo T, Shi M, Feng Q, Zhang P, Han B, Shan JX, Gao JP, Lin HX*. Natural alleles of a proteasome α2 subunit gene contribute to thermotolerance and adaptation of African rice. ***Nat. Genet.*** 47:827-833 (2015).
39. Chen Chen, Chen H, Lin YS, Shen JB, Shan JX, Qi P, Shi M, Zhu MZ, **Huang X**, Feng Q, Han B, Jiang L, Gao JP, Lin HX*. A two-locus interaction causes interspecific hybrid weakness in rice. ***Nat. Commun.*** 5: 3357 (2014).
40. Peng Zhenhua$^{\#}$, Lu Y$^{\#}$, Li Y$^{\#}$, Zhao Q$^{\#}$, Feng Q$^{\#}$, Gao Z$^{\#}$, Lu HY, Hu T, Yao N, Liu K, Li Y,Fan D, Guo G, Li W, Lu Y, Weng Q, Zhou C, Zhang L, Huang T, Zhao Y, Zhu C, Liu X, Yang X, Wang T, Miao K, Zhuang Z, Cao X, Tang W, Li G, Liu Y, Chen J, Liu Z, Yuan L, Liu Z, **Huang X**, Lu T, Fei B, Ning Z, Han B*, Jiang Z*. The draft genome of the fast-growing non-timber forest species moso bamboo (Phyllostachys heterocycla). ***Nat. Genet.*** 45: 456-461 (2013).
41. Luo Jianghong$^{\#}$, Liu H$^{\#}$, Zhou T$^{\#}$, Gu B$^{\#}$, **Huang X**, Shangguan Y, Zhu J, Li Y, Zhao Y, Wang Y, Zhao Q, Wang A, Wang Z, Sang T, Wang Z, Han B*. An-1 encodes a basic helix-loop-helix protein that regulates awn development, grain size, and grain number in rice. ***Plant Cell*** 25:3360-3376 (2013).
42. Li Sujuan, Yan S, Wang A, Zou G, **Huang X**, Han B, Qian Q, Tao Y*. Identification of QTLs associated with tissue culture response through sequencing-based genotyping of RILs derived from 93-11 3 Nipponbare in rice (*Oryza sativa*). ***Plant Cell Rep.*** 32: 103-116 (2012).
43. Wang Lu$^{\#}$, Wang A$^{\#}$, **Huang X**, Zhao Q, Dong G, Qian Q, Sang T, Han B*. Mapping 49 quantitative trait loci at high resolution through sequencing-based genotyping of rice recombination inbred lines. ***Theor. Appl. Genet.*** 122:327-340 (2011).

44. Xie Weibo, Feng Q, Yu H, **Huang X**, Zhao Q, Xing Y, Yu S, Han B, Zhang Q*. Parent-independent genotyping for constructing an ultrahigh-density linkage map based on population sequencing. ***Proc. Natl. Acad. Sci. USA***. 107: 10578-10583 (2010).
45. Zhao Qiang, **Huang X**, Lin Z, Han B*. SEG-Map: A novel software for genotype calling and genetic map construction from next-generation sequencing. ***Rice*** 3: 98-102 (2010).
46. Lu Tingting#, Lu G#, Fan D, Zhu C, Li W, Zhao Q, Feng Q, Zhao Y, Guo Y, Li W, **Huang X**, Han B*. Function annotation of the rice transcriptome at single-nucleotide resolution by RNA-seq. ***Genome Res.*** 20: 1238-1249 (2010).
47. 中国科学家绘制籼稻高质量参考基因组序列图谱 **黄学辉*** 植物学报, 52: 1-3 (2017)
48. 水稻复杂性状研究的新途径：水稻重要农艺性状全基因组关联分析 侯青青，司丽珍，**黄学辉***，韩斌* 生命科学, 28: 1250-1257 (2016)
49. **Huang Xuehui*** and Han B*. Chapter 3: Natural variation and sequencing-based genetics studies. “Genetics and Genomics of Rice” Springer Press (2013).
50. **Huang Xuehui*** and Han B*. Chapter 25: Genome-wide association mapping of complex traits in rice. “Rice Genomics, Genetics and Breeding” Springer Nature Press (2018).
51. Wei Xin* and **Huang X***. Chapter 1: Origin, Taxonomy and Phylogenetics of Rice. “Rice: Chemistry and Technology, 4th Edition” Elsevier Press (2018).