

CURRICULUM VITAE

Hongbin Zhang (H.-B. Zhang)

Professor of Plant Genetics, Genomics, Systems Biology and Molecular Breeding

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<http://scholar.google.com/citations?hl=en&user=ZplaeJgAAAAJ&sortby=pubdate&cstart=0&pagesize=20>

MAJOR ACHIEVEMENTS AND CONTRIBUTIONS TO SCIENCE AND TECHNOLOGY

1. ***Proposed and pioneered the discipline Systems Genomics and helped pioneer the discipline Systems Biology.*** Discovered that DNA in an organism is structured as a “Jigsaw puzzle”, demonstrated that the variation of the DNA “Jigsaw Puzzle” structure is the molecular basis of organisms’ variation, evolution, diversity and abundance, and also established the DNA “Jigsaw Puzzle” Structure Model (see below) is the molecular basis of Systems Genomics and Systems Biology.
2. ***Invented a genome-wide high-throughput gene/QTL cloning technology, *gExpress*.*** This technology allows genome-wide high-throughput and accurate cloning of genes controlling quantitative traits in any species, including plants, animals, humans and microbes, regardless of its genome size, genome complexity, ploidy level and availability of its genomic or molecular knowledge. Using the technology, hundreds of genes controlling quantitative traits can be cloned, including functional validation, within a few scientist-years. The throughput of the *gExpress* technology is >1,000-fold higher than those of the currently-used gene/QTL cloning methods, such as map-based cloning, gene mutagenesis, RNA interference (RNAi), gene overexpression and gene editing. The *gExpress* system has been filed in the United States Trademark and Patent Office for an intentional patent (Patent Serial No.: 62/298,606).
3. ***Genome-wide high-throughput cloning of genes controlling traits of importance in major crops.*** Cloned 20,688 genes controlling 23 agronomic traits from maize, cotton and chickpea, including 1,501 genes controlling maize inbred grain yield (*ZmINGY*); 181 genes controlling maize F₁ grain yield (*ZmFIGY*); 981 genes controlling maize grain yield heterosis (*ZmGYH*), 6,388 genes controlling 12 maize individual grain yield and quality component traits; 3,900 genes controlling five cotton fiber quality component traits, 185 genes controlling cotton fiber length heterosis, 3,140 genes controlling fiber yield, 1,420 genes controlling fiber percentage and 2,494 genes controlling cotton seed yield; and 498 genes controlling chickpea vernalization and flowering (*CVRN*). The number of the genes (20,688) that we have cloned so far is probably several-fold of the total number of genes/QTLs cloned from all species in the past 30 years worldwide.
4. ***Deciphered the molecular mechanisms underlying several biological phenomena.*** Through systems analysis of the above cloned genes, deciphered the molecular mechanisms of quantitative genetics, crop yield, crop quality, heterosis and polyploidization. These findings have currently been submitted or in preparation for publication.
5. ***Proposed and pioneered gene-based breeding (GBB).*** GBB is an innovative and extremely powerful and efficient molecular technology for enhanced and accelerated breeding in plants and animals by making full use of the genes controlling the targeted trait(s) through the entire process of plant and animal breeding, including parent selection, cross design and progeny selection. First proposed GBB and developed it in cotton and maize using the concepts of our DNA “Jigsaw Puzzle” structure model

(see below) and the genes that we cloned from the crops. Three genic datasets, (i) the number of favorable alleles, (ii) SNPs/InDels used as DNA markers and (iii) expression profiles and networks of the genes controlling the targeted traits are used to select breeding parents, design breeding crosses and make progeny selection for cultivar development. We showed that the grain yield or fiber length of a breeding line could be predicted in maize and cotton at an accuracy of $r > 0.80$ ($P = 0.0000$), approaching the maximal accuracy of phenotype prediction, for breeding selection, when one of the three genic datasets was used. When the prediction results of two or all of the three genic datasets were jointly used for progeny selection, the selection results of GBB were completely agreed (100%) with those selected by the current breeding progeny selection methods; therefore, GBB provides an extremely powerful and efficient method for enhanced crop breeding. Furthermore, we have also developed a rapid, high-throughput and economical assay method using modern high-throughput sequencing technology to facilitate deployment of GBB in practical breeding. The cost (including labor and supplies) of this assay method is <\$2.00 per sample for assaying 2,000 or more genes, with a throughput of 160,000 samples per sequencer run. This cost is only 1% – 2% of that for the genomic selection (GS) and this throughput is a few-fold higher than that of GS.

6. ***Re-established the molecular basis of biology: The DNA “Jigsaw Puzzle” Structure Model.*** Discovered that DNA is structured as a “Jigsaw Puzzle” in the genome of an organism and established the DNA “Jigsaw Puzzle” structure model as the new molecular basis of genetics and biology. This DNA structure model has been tested using a number of plant and animal species. Discovered that the variations of content, array or sequence, interaction and mutation (including gene mutation) of genome fundamental functional elements (FFE) (“Jigsaw Puzzle” elements), including genes (GEN), DNA transposable elements (DTE), retro-transposable elements (RTE), simple sequence repeats (SSR) and low complex repeats (LCR), are the molecular basis of living organism’s genetics, variation, diversity, abundance and complexity. Therefore, this discovery provides a novel and comprehensive molecular basis of genetics, variation, abundance, diversity and complexity of all living organisms, thus revolutionizing the knowledge, concepts and strategies currently used in biology, breeding and medicine. A book entitled “The Molecular Basis of Biology: DNA “Jigsaw Puzzle” Structure Model” about the findings currently is in preparation, invited by a world’s well-known publisher, Springer Verlag.
7. ***Discovered that the sizes (or numbers of genes) of gene (GEN) and nongene element (DTE, RTE, SSR and LCR) families varied significantly not only among within a species, but also within a bi-parental population; and that the variation of a gene family size is subject to natural and artificial selection, and associated with biology.*** Studies revealed that a majority of genes and nongene elements in the genome of a living organism, regardless of whether it is eukaryotic or prokaryotic, exist in multiple-copy families. Therefore, this discovery has laid an important molecular basis of living organism’s genetics, variation, diversity, abundance and complexity. Recently, this discovery has been supported by many studies with genome resequencing and assembly, and is named as “pan-genome”.
8. ***Discovered that species having same or very similar sets of genes and nongene elements may have different arrays of genes and nongene elements in their genomes (e.g., chicken vs. turkey).*** This discovery suggests that the position, array and re-array of the genome fundamental functional elements (FFE) are another molecular basis of living organism’s genetics, variation, diversity, abundance and complexity.
9. ***Discovered that the copy numbers of genes and nongene elements constituting a genome are correlated, forming a correlation network in the genome, and that the genetics and variation of the network is subject to natural and artificial selection and associated with biology.*** This discovery has, therefore, formed the third molecular basis of genetics, variation, diversity, abundance and complexity of living organisms.
10. ***Advanced the principles of gene research, and proposed and demonstrated use of gene transcripts as the basic functional unit for gene functional research and characterization.*** It has been

documented that a vast majority of genes in higher organisms are subjected to RNA alternative splicing and its pre-mRNA is spliced into one to hundreds of transcripts that may be translated into different proteins having different biological functions. Moreover, we found that the RNA alternative splicing pattern and resultant transcripts differ substantially among different tissues of a plant and across individuals within a bi-parental population. These discoveries have posed a great challenge for gene research and characterization. We discovered that it was impossible or extremely difficult to properly quantify the expressions of individual transcripts spliced from a gene or its overall expression using the widely-used Northern hybridization, microarray or genechip, quantitative real-time PCR, or serial analysis of gene expression, if it is subjected to RNA alternative splicing. This is because these technologies cannot well distinguish individual transcripts alternatively splice from a gene or paralogous gene(s). Shot-gun or full-length RNA-seq was the most proper to quantify the gene expressions of individual transcripts or genes. Therefore, we proposed for the first time that the gene individual transcripts should be used as the basic functional unit for gene functional research, expression regulation analysis, coding protein inference, metabolic pathway building and network construction.

11. ***Helped pioneer the discipline Genomics, especially the concepts and technology of one of the most significant findings in genomics research - the high-molecular-weight recombinant DNA technology.*** These include megabase-sized DNA preparation, manipulation and cloning, bacterial artificial chromosome (BAC) and transformation-competent binary BAC (BIBAC) library construction, manipulation and utilization. Using the technology, developed > 200 large-insert BAC and BIBAC libraries for different species, about ½ of all BAC and BIBAC libraries developed in the 20 years worldwide. The technology and BAC and BIBAC resources have been the foundation of modern genomics and genetics research worldwide and the technology has been used by a number of genome research companies, such as Bionano Genomics (San Diego, CA), 10x Genomics (Pleasanton, CA), BioPac Systems, Inc. (Goleta, CA) and Intact Genomics, Inc (Saint Louis, Mo).
12. ***Helped pioneer the concepts and technology of another most significant finding in genomics research - whole-genome integrative physical mapping with BACs and BIBACs.*** Using the technology, developed whole-genome BAC/BIBAC-based physical maps of *Arabidopsis*, indica rice, japonica rice, soybean, chicken, *Penicillium chrysogenum*, *Ustilago maydis*, *Phytophthora sojae*, red algae, turkey, horse Y chromosome, chickpea, and cotton, approximately 1/3 of the physical maps (40) published as of December 2012 worldwide. These physical maps have provided platforms and “freeways” essential for modern genomics, systems biology, genetics research and molecular breeding, including large-scale genome sequencing. The concepts, technologies and strategies of integrative physical mapping that we developed have been used worldwide in genome physical mapping of plants, animals and microbes.
13. ***Helped pioneer a multiple gene transformation system in plants using BIBAC as a tool.*** It combines molecular breeding, gene/QTL cloning, marker development and molecular farming into a single process, thus allowing high-throughput development of high-yielding and/or high-quality varieties, cloning of genes and QTLs of agricultural importance and development of molecular farming and production systems in agriculture in a single process, and allowing modern genomics research results to be translated into agricultural products rapidly and efficiently.
14. ***Isolation of agronomic genes*** - Many genes of agronomic importance are known only by phenotypes. We are among the few pioneer scientists worldwide who developed and used the approach of map-based cloning to isolate the genes, and cloned the gene controlling tomato fruit abscission zone development (j_1) using the approach.
15. ***Deciphered the phylogenies, and genome origin of wheat, cotton and related species (Triticum, Aegilops and Gossypium)*** – Re-constructed the phylogenies of diploid wheat and related species, and diploid cotton and related species, and determined the genome origin and evolution of the polyploid species of *Triticum*, *Aegilops* and *Gossypium*. The results have been widely accepted and used in the scientist community.

16. Developed millions of DNA markers, constructed genetic maps and mapped genes/QTLs in several crops:

Cotton: Developed nearly 1,000,000 genomic SNP markers and >4,000,000 genic SNP markers for cotton, constructed an integrated physical/genetic map of 145,396 SNP markers (17 kb/SNP) and mapped the QTLs controlling eight major fiber yield and quality traits.

Chickpea: Developed 320 SSR markers, constructed a BAC/BIBAC physical map and identified QTLs controlling several agronomic traits.

Maize: Developed >800,000 genic SNPs and mapped eQTLs/QTLs controlling 13 grain yield and quality traits.

Cowpea: Developed over 6,000 SNP markers, constructed a genetic map of 4,154 SNP markers and mapped the QTLs for numerous grain yield traits and abiotic stress tolerances.

17. Large-scale sequencing of agricultural genomes. Genome sequencing is crucial to deciphering many problems important to genetics, biology, physiology and breeding. Therefore, we have made significant efforts into genome sequencing of agricultural species. Led or helped *de-novo* sequence the genomes of *Phytophthora sojae*, *Phytophthora ramorum*, turkey, cassava, penaeid shrimp and Upland cotton; re-sequenced the genomes of 14 rice lines; sequenced and profiled the transcriptomes for 794 cotton, maize, wheat, chickpea and soybean lines; RAD-sequenced the genomes of 749 cotton, cowpea and rice lines.

18. Isolation and characterization of chromosome centromeres in crop plants. Chromosome centromeres are vital to chromosome behavior and genetic material transmission. Identified large-insert BACs and BIBACs derived from the centromeric regions and constructed BAC/BIBAC-based physical maps of all 12 indica rice chromosomes and all 12 japonica rice chromosomes. The centromere of chromosome 8 of the wild rice, *Oryza rufipogon*, has been sequenced.

EDUCATION

- **Ph.D.**, Genetics - Plant Molecular Genetics, University of California, Davis, California, 1990.
- **Study for Ph.D.** in Plant Biochemistry and Physiology, Utah State University, Logan, Utah, 10/1985 - 09/1986. Transferred to UC Davis, 10/1986.
- **M. S.**, Genetics, Chinese Academy of Agricultural Sciences, Beijing, China, 1984.
- **B. S.**, Plant Genetics and Breeding, Agricultural University of Hebei, Hebei, China, 1982.

PROFESSIONAL EMPLOYMENT

Professor, Plant Genomics, Systems Biology and Molecular Breeding, Texas A&M University, College Station, 2006 - present.

Director for Laboratory of Plant Genomics and Molecular Genetics, Texas A&M University, College Station, 1996 - present.

Director, the GENEfinder Genomic Resources Center, Texas A&M University, College Station, 1996 - present.

Associate Professor, Plant Genomics and Molecular Genetics, Texas A&M University, College Station, 2002 - 2005.

Assistant Professor, Plant Genomics and Molecular Genetics, Texas A&M University, College Station, 1996 - 2001.

Assistant Research Scientist, Plant Genomics and Molecular Genetics, Texas A&M University, College Station, Texas. 1994-1995

Postdoctoral Associate, Plant Molecular Genetics, Texas A&M University, College Station, Texas. 1992-1994.

Postdoctoral Associate, Plant Molecular Genetics, University of California, Davis, California. 1991-1992.

PROFESSIONAL ACTIVITIES

- Faculty of Genetics (GENE), Texas A&M University, 1997 - present.
- Faculty of Molecular and Environmental Plant Sciences (MEPS), Texas A&M University, 1996 - present.
- Faculty of Professional Program in Biotechnology (BIOT), Texas A&M University, 1999 - present.
- Faculty of Plant Breeding, Texas A&M University, 1997 - present.
- Member of American Association for the Advancement of Science. 1989 - present.
- Served/serve in a variety of committees at Texas A&M University, including those of Genetics executive committee, departmental faculty advisory committee, curriculum, faculty search, awards, student recruiting, tenure/promotion, and graduate fairs.

PROFESSIONAL SERVICES, AND NATIONAL AND INTERNATIONAL RECOGNITION

A. Professional services in the scientific community:

A-1. National and international peer-reviewed journals:

- Editor-in-Chief, *International Journal of Plant Genomics*, 2006 – 2009.
- Editor-in-Chief, *Journal of Agricultural Sciences*, 1989-1993.
- Associate Editor, *BMC Genomics*, 2011 – present.
- Editorial Board, *Agricultural Science & Technology*, 2008 – present.
- Editorial Board, *Acta Agronomica Sinica*, 2010 – present.
- Editorial Board, *Agrotechnology*, 2013 – present.
- Editorial Board, *The Crop Journal*, 2013- present.
- Editorial Board, *Journal of Cotton Research*, 2018- present.
- Editorial Board, *International Journal of Plant Genomics*, 2010 – 2017.
- Associate Editor, *Journal of Biomedicine and Biotechnology*, 1999 – 2006.
- Ad hoc reviewer of manuscripts for 33 journals: *Proc. Acad. Natl. Sci. USA*, *Nature Reviews Genetics*, *The Plant Cell*, *Genetics*, *Plant Physiol.*, *Bioinformatics*, *Gene*, *Genome*, *Genomics*, *BMC Genomics*, *Plant J.*, *Theor. Appl. Genet.*, *Plant Mol. Biol.*, *Mol. Breed.*, *Briefings in Functional Genomics & Proteomics*, *Plant Science*, *BMC Bioinformatics*, *Plant Cell Reports*, *Functional and Integrative Genomics*, *Mol. Plant-Microbe Interact.*, *BMC Plant Biology*, *Trends in Plant Science*, *Tree Genetics and Genomes*, *Genome Biol.*, *Physiologia Plantarum*, *BMC Research Notes*, *European J. of Plant Pathology*, *Molecular Biology and Evolution*, *Molecular Genetics and Genomics*, *Plant Methods*, *PLoS ONE*, *Plant Biotechnology Journal*, and *J. Heredity*.

A-2. National and international research funding organizations:

- The panel committee service: USDA/BARD (2011, 2012, 2013, 2014); Oklahoma Center for the Advancement of Science and Technology (OCAST) (2010 - 2019); National Natural Science Foundation of China (2011); CRDF (U.S. Civilian Research and Development Foundation) Global (2017, 2019).
- *Ad hoc* research proposal reviewer: USDA/NRI, U.S. National Science Foundation, Swiss Federal Institute of Technology Zurich, the Netherlands Foundation for the Advancement of Tropical Research (WOTRO), German Federal Ministry of Education and Research (BMBF); National Natural Science Foundation of China (NSFC); and the PLANT-KBBE Program

supported by the Ministries for Research from Spain, Germany and France; and Ministry of Education and Science of the Russian Federation.

A-3. National and international professional conferences:

- Co-chair, Systems Genomics Workshop, International Annual Plant & Animal Genome Conference, 2011- present.
- Co-chair, Analysis of Complex Genomes Workshop, International Annual Plant & Animal Genome Conference, 2012 – present.
- Co-chair, Large-insert DNA Library and Their Applications Workshop, International Annual Plant & Animal Genome Conference, 1998 – 2011.
- The Organization Committee of the 10th International Triticeae Genome Mapping Conference. Newark, Delaware, USA. June 14-16, 2000.

A-5. National and international public workshops:

- Invited instructor, the summer course “Construction of Large-insert BAC Libraries and Analysis of Complex Genomes”. The Chinese Academy of Tropical Agricultural Sciences, Haikou, Hainan, China. July 16 – 26, 2008.
- Organizer and instructor, the International Biotechnology Workshop – BAC Workshop II: BAC Cloning and Manipulation. Texas A&M University, College Station, Texas. June 8-17, 2000.
- Invited instructor, the BAC Biotechnology Workshop, Chinese Academy of Agricultural Sciences, Beijing, China. July 10-20, 2000.
- Invited instructor, the Workshop on BAC Technology. CSIRO, Queensland, Australia, June 2 – 11, 1999.
- Organizer and instructor, the international BAC Cloning and Library Construction Program. Texas A&M University. 10/1997.
- Co-organizer and instructor, the international BAC Workshop. Texas A&M University. June 3 - 10, 1995.

B. Invited presentations at national or international conferences (25):

1. “Genome-Wide High-throughput Cloning of the Genes Important to Plants, Animals and Humans: From Traits to Genes to Mechanisms to Trait Prediction to Gene-based Breeding/Medicine”. 2018 International Sesame Genetics and Breeding Symposium, Zhengzhou, China, August 23-24, 2018.
2. “Helping Feed the World through Gene-based Breeding”. 2017 China Summit Forum on Wheat Diseases and Control Technologies. Baoding, Hebei, China, August 25 – 27, 2017.
3. “Re-establishing the Molecular Mechanisms of Genetics and Biology: The DNA “Jigsaw Puzzle” Structure Model”. Symposium in Applications of New Biotechnologies in Crop Genetic Improvement. Shijiazhuang, Hebei, China, July 14, 2016.
4. “Modern Biotechnology: Opportunities, Challenges and Perspectives”. US-China Scientific and Technological Exchanges, Cooperation Development Forum. Zhangjiagang, Jiangsu, China, September 11-13, 2013.
5. “Re-establishing the Molecular Mechanisms of Genetics and Biology: The DNA “Jigsaw Puzzle” Structure Model”. 2012 International Conference on Ginseng, Jilin, China, September 4-8, 2012.
6. “The DNA ‘Jigsaw Puzzle’ Structure Model – The Molecular Basis of Biology”. Annual Conference of Zhejiang Association of Genetics, Lake of Thousand Islands, Zhejiang, China, December 2 – 4, 2011.
7. “Toward Comprehensive Understanding of the Chickpea Genome in Structure, Organization, and Function for Modern Crop Improvement”. The First International Chickpea Conference. Tel Aviv, Israel, March 18 – 22, 2011.

8. "How Does DNA Make the Abundant, Diverse and Complex Life World? The DNA "Jigsaw Puzzle" Structure Model". The Conference of Functional Genomics of Marine Life and Its Applications in Aquaculture and Medicine. Qingdao, China, June 30 – July 3, 2008.
9. "Beyond the double helix model: DNA structure revealed by comprehensive analysis of the *Arabidopsis thaliana* genome". The CAS Conferences on Marine Science and Technology, Qingdao, China, July 28 – August 1, 2006.
10. "Whole Genome Physical Mapping with BACs by Fingerprint Analysis: Lessons and Tips". The International Plant & Animal Genome Conference XIII. San Diego, CA, January 15-19, 2005.
11. "BAC Maps and Their Applications for Chicken Genomics Research". The Chicken Genome: New Tools and Concepts. Stowers Institute for the Medical Research, Kansas City, MO, April 29 – May 2, 2004.
12. "A BAC-based Physical Map of the Chicken Genome". The International Chicken Genome Conference". The Sanger Centre, Cambridge, UK. March 9 – 11, 2003.
13. "Toward development of a whole-genome, BAC/BIBAC-based integrated physical/genetic map of the cotton genome using the Upland cotton genetic standard TM-1: BAC fingerprinting and physical map contig construction". The 3rd International Cotton Genome Conference. Nanjing, China. June 2 – 7, 2002.
14. "Development of a BAC-based Physical Map of the Chicken Genome for High-throughput Gene Mapping and Cloning". Poultry Workshop, International Conference Plant & Animal Genome IX. January 13-17, 2001. San Diego, CA.
15. "Development and Applications of Genome-wide BAC/BIBAC-based Physical Maps for Accelerated Research of Agricultural Genomes". Large-insert DNA Libraries and Their Applications Workshop, International Conference Plant & Animal Genome IX. January 13-17, 2001. San Diego, CA.
16. "Development of a BAC/BIBAC-based Physical Map of the Soybean Genome for Accelerated Genome Research". Legume Workshop, International Conference Plant & Animal Genome IX. January 13-17, 2001. San Diego, CA.
17. "Genome-wide Physical Mapping with BACs". Annual Conference of Plant Genomics in China I, Dalian, China. July 24 – 27, 2000.
18. "Biotechnological Revolution is Coming". International Hi-Tech Conference. Beijing, China. May 5 – 10, 2000.
19. "The genome-wide Physical Maps of the Rice and Arabidopsis Genomes: Reliability and Accessibility". Large-insert DNA Libraries and Their Applications Workshop, International Conference Plant & Animal Genome VIII. January 9 –12, 2000. San Diego, CA.
20. "Strategy for Physical Mapping with DNA Fingerprinting Technique". International Triticeae Mapping Initiative 1999 Public Workshop, Viterbo, Italy. August 24 –28, 1999.
21. "BAC Technology – Current Status and Development". Public Workshop on Development and Applications of BAC Libraries, Caloundra, Australia. May 26, 1999.
22. "A Large-scale Plant Transformation- and Genome Sequence-ready Physical Map of the *Arabidopsis thaliana* Genome". Arabidopsis Workshop, International Conference Plant & Animal Genome VII. January 17 - 21, 1999. San Diego, CA
23. "Integrative Physical Mapping of Genomes with Large-insert Bacterial Clones: the Sequence-ready Physical Map of the Rice Genome". Large-insert DNA Libraries and Their Applications Workshop, International Conference Plant & Animal Genome VII. January 17 - 21, 1999. San Diego, CA
24. "Toward development of an Integrated Physical Map of the Rice Genome with Bacterial Artificial Chromosomes". The General Meeting of the International Program on Rice Biotechnology, September 15-19, 1997, Malacca, Malaysia.
25. "Construction and Characterization of Two Rice Bacterial Artificial Chromosome Libraries from the Parents of a Permanent Recombinant Inbred Mapping Population". Rice Workshop, International Conference Plant Genome III. January 15 – 19, 1995. San Diego, CA.

C. National and International visiting scientists hosted and trained:

- Hosted 69 visiting scientists from 17 countries of the world: 27 from USA, 21 from China, 3 from Turkey, 2 from each of Australia, Korea, Italy and Mexico, and 1 from each of Belgium, Canada, Israel, Japan, The Netherlands, Spain, Thailand, Vietnam, Pakistan and UK. 10/1996 - present.

AWARDS AND SCHOLARSHIPS

- Jastro-Shields Research Awards, 1988.
- Research Assistantship, University of California, Davis, 1988-1990.
- Tuition Fee Fellowship, University of California, Davis, 1988-1990.

TEACHING ACTIVITIES

A. Courses:

- Analysis of Complex Genomes (SCSC, GENE, MEPS and BIOT 654) (Lectures), graduate course, 3 credit hours, Texas A&M University, College Station, Texas. 2011 – present (8-year mean student evaluation: 4.69 of 5.00 = 93.8%, with a range from 4.39 – 4.88).
- Analysis of Complex Genomes (SCSC, GENE, MEPS and BIOT 655) (Labs), graduate course, 3 credit hours, Texas A&M University, College Station, Texas. 2011 – present (8-year mean student evaluation: 4.86 of 5.00 = 97.2%, with a range from 4.73 – 4.96).
- Analysis of Complex Genomes (AGRO, GENE and MEPS 655) (Lectures and Labs), graduate course, 3 credit hours, Texas A&M University, College Station, Texas. 1998 – 2010 (12-year mean student evaluation: 4.82 of 5.00 = 96.4%, with a range from 4.40 to 4.98)).
- Directed Studies in Genomics for graduate students (AGRO, GENE and MEPS-685), 1 – 3 credit hours, Texas A&M University, College Station, Texas. 1999 – present (12-year mean student evaluation: 4.82 of 5.00 = 96.4%).
- Graduate Research (AGRO, GENE and MEPS-677 and 691), 1 – 9 credit hours, Texas A&M University, College Station, 1997 – present (2-year mean student evaluation: 4.97 of 5.00 = 99.4%).
- Directed Studies in Genomics for undergraduate students (SCSC and GENE-485), 1 – 3 credit hours, Texas A&M University, College Station, Texas, 2000 – present.

B. Graduate students advised:

	Degrees	Status	Current positions
Boris Vinatzer	Ph.D.	Graduated in 2000	Professor
Yueh-Long Chang	Ph.D.	Graduated in 2001	Professor
Huaming Chen	M.S.	Graduated in 2000	Research associate
Limei He	M.S.	Graduated in 2000	Research manager
Teofila S. Santos	Ph.D.	Graduated in 2002	Unknown
Kejiao Ding	M.S.	Graduated in 2002	Lecturer
Laura Wakefield	M.S.	Graduated in 2002	Unknown
Xiaohua Fang	Ph.D.	Graduated in 2003	Professor
Yaning Li	Ph.D.	Graduated in 2004	Professor
Taesik Uhm	Ph.D.	Graduated in 2004	Research scientist
Ying Rong	M.S.	Graduated in 2004	Research associate
Greg Hess	M.S.	Graduated in 2005	Research associate
Hyun Jung Park	M.S.	Graduated in 2007	Postdoc
Yun-Hua Liu	M.S.	Graduated in 2008	Ph.D. student
Yen-Hsuan Wu	M.S.	Graduated in 2008	Research associate
James J. Huang	M.S.	Graduated in 2009	Ph.D. student

Hui Zhi	M.S.	Graduated in 2010	Ph.D. student
Fisher Chang	M.S.	Graduated in 2012	Research Associate
Yun-Hua Liu	Ph.D.	Graduated in 2014	Postdoctoral Scientist
Lorin Harvey	M.S.	Graduated in 2016	Ph.D. student
Kari L. Hugie	Ph.D.	Graduated in 2016	Research Geneticist
Jingjia Li	M.S.	Graduated in 2016	Ph.D. student
Murat Aci	M.S.	Graduated in 2018	Research associate
Gali Bai	M.S.	Graduated in 2020	Data Scientist
Drutdaman S. Bhangu	Ph.D.	Graduated in 2020	
Mehmet Dogan	M.S.	Graduated in 2020	
Mustafa Cilkiz	Ph.D.	09/17 – present	
Ozge Ekinci	M.S.	08/20 -	

C. Postdoctoral associates advised:

	Period	Current position
Yun-Hua Liu	09/2014 - present	
Delin Xu	10/2016 – 10/2018	Associate professor
Yang Zhang	09/2008 – 08/2011	Assistant research scientist
Xiaojun Zhang	05/2007 – 10/2008	Professor
Mi-Kyung Lee	05/2000 – 09/2005	Research scientist
Zhanyou Xu	01/2001 – 01/2003	Assistant research scientist
Chengwei Ren	09/2000 – 05/2004	Chief scientist and director
Shuku Sun	06/2001 – 06/2003	Vice president
Bo Yen	01/2001 – 08/2002	Professor and director
Liangtao Zhang (co-advisor)	09/2000 – 12/2002	Research scientist
Yueh-Long Chang	06/2001 – 01/2002	Professor
Padmavathi Nimmakayala	06/1999 – 05/2001	Associate professor
Paul P. Ling	12/1999 – 08/2000	Research geneticist
Chengcang Wu	05/1999 – 08/2002	CEO and president
Quanzhou Tao	09/1997 – 05/2000	Research scientist

D. Research scientists supervised:

Meiping Zhang	09/2011 - present	
Yang Zhang	09/2011 – 08/2015	Research Scientist
Mi-Kyung Lee	09/2005 – 05/2008	Research scientist
Chengcang Wu	09/2002 – 06/2004	CEO and president
Zhanyou Xu	01/2003 – 07/2004	Research associate

B. Undergraduate and unassigned graduate students supervised and trained:

Graduate students: James J. Huang, Hyun Jung Park, Cathy Dole, George Hodnett, Jeong-Soon Kim, Qin Ye, David Finlkestein, Jo Unsun, and Michel S. Zwick
Undergraduate students: Jessica Dodge, Jennifer Centrato, Kelli Black, Bettye Cox, Lucas Garcia, Xiomara Henriquez, Elizabeth Huff, Dustin Jordon, Steven Koether, Rika Lubis, Aaron Malet, Racheal Springman, and Carman Williams

C. Other activities related to teaching

Ms. Adriana Robbins (Spring 2006) – served as a mentor for University Graduate Teaching Advisor
 Ms. Yichun Yang (Spring 2007) – served as a mentor for University Graduate Teaching Advisor

G. Public workshops organized and/or instructed:

- The summer course “Construction of Large-insert BAC Libraries and Analysis of Complex Genomes”. The Chinese Academy of Tropical Agricultural Sciences, Haikou, Hainan, China. July 16 – 26, 2008.
- The International Biotechnology Workshop – BAC Workshop II: BAC Cloning and Manipulation. Texas A&M University, College Station, Texas. June 8-17, 2000.
- The BAC Biotechnology Workshop, Chinese Academy of Agricultural Sciences, Beijing, China. July 10-20, 2000.
- The Workshop on BAC Technology. CSIRO, Queensland, Australia, June 2 –11, 1999.
- The international BAC Cloning and Library Construction Program. Texas A&M University. 10/1997.
- The international biotechnology workshop: BAC Workshop. Texas A&M University. June 3 -10, 1995.
- Crop Genome Analysis, Texas A&M University, College Station, Texas, January 1995.

RESEARCH GRANT SUPPORTS (49)

- PI/co-PI of 49 projects with a total fund of \$24,632,442, of which \$10,258,656 are/were for Zhang laboratory

a. Current grant supports (1):

1. Other public and private organizations: BAC and BIBAC resources development, archiving and dissemination. 1996 – present (a collective amount of funding: \$1,756,084)

b. Previous grant supports (48):

1. Texas Corn Producers Board (TCPB): Enhanced Corn Breeding for Grain Yield Using the Genes Controlling the Targeted Traits, 02/2017 – 01/2019 (\$120,000).
2. Texas AgriLife Research Crop Improvement: Packaging the Toolbox of Gene-based Breeding (GBB), a Novel and Powerful Breeding Method for Enhanced and Accelerated Breeding in Maize, 09/2017 – 08/2019 (\$140,000).
3. Texas AgriLife Research Crop Improvement: Combining Gene-based Breeding (GBB) and High Throughput Phenotyping (HTP) to Advance Variety Selection in Cotton, 09/2017 – 08/2019 (\$140,000).
4. Cotton, Inc.: Predicting best models for whole genome sequencing as a selection tool in breeding upland cotton, 01/2016 – 12/2018 (\$150,000).
5. USDA/NIFA: Analysis of fiber traits and development of toolkits enabling enhanced fiber breeding in cotton using an integrated RAD-seq and RNA-seq Approach. 09/13 - 08/17 (\$500,000)
6. Texas A&M AgriLife Research Cotton Improvement Program: Gene-based selection for elite fiber quality and other important traits in upland cotton. 09/15-08/17 (\$100,000)
7. USDA/NIFA: Molecular mapping of genes for drought and heat tolerance in cowpea. 11/2013 – 12/2016 (\$499,660)
8. Texas A&M AgriLife Research Cotton Improvement Program: Genetic Markers for Upland Fiber Quality Traits to Maintain Texas Competitiveness. 09/13-08/15 (\$100,000)
9. Texas A&M AgriLife Research Monocot Improvement Program: Large-scale Cloning of the Genes Controlling Maize Grain Yield and Quality and Development of Gene-based Toolkits Enabling Enhanced Maize Breeding. 09/13-08/15 (\$83,520)
10. Texas A&M AgriLife Research Monocot Improvement Program: Genetic improvement of corn drought tolerance, insect resistance, mycotoxin resistance. 09/13-08/15 (\$83,520)
11. Monsanto: Sequencing the Upland cotton genome. 09/12-08/14 (\$12,076 in cash and \$1,000,000 in kind).

12. The U.S. Consortium for Plant Biotechnology Research: Integrative Genetic and Physical Mapping of Upland Cotton. 03/2013 - 02/2015 (\$736,582)
13. The U.S. Consortium for Plant Biotechnology Research: Deciphering Molecular Basis of Heterosis: Maize as a Model System. 03/2013 - 02/2015 (\$658,515)
14. Dow AgroScience: A minimal-tilling-path BIBAC map of the upland cotton genome. 01/2013 – 12/2015 (\$80,000)
15. USDA/BARD: Winter chickpea: towards a new winter pulse for the semiarid Pacific Northwest and wider adaptation in the Mediterranean basin. 09/11 – 08/14 (\$280,000)
16. Texas AgriLife Research Monocot Improvement Program: Toward Cloning the Genes and QTLs Controlling Major Agronomic Traits in Texas Monocot Crops. 09/2011 – 08/2013 (\$100,000)
17. Texas AgriLife Research Monocot Improvement Program: Discovering Traits and Genes for Drought Tolerance, CEW Resistance, and Ear Rot Resistance in Corn. 09/2011 – 08/2013 (\$100,000)
18. Texas AgriLife Research Cotton Improvement Program: High-throughput Cotton DNA Extraction Procedures and Chromosome Integrated Physical/Genetic Maps for Gene Discovery and Cloning, Germplasm Analysis and Marker-assisted Breeding. 09/2011 – 08/2013 (\$100,000)
19. Texas AgriLife Research Cotton Improvement Program: Genetic Markers for Upland Fiber Quality Traits to Maintain Texas Competitiveness. 09/2011 – 08/2013 (\$100,000)
20. USDA/NRI-Animal Genome: A Robust Integrated Map of the Turkey Genome. 01/08 – 12/11 (\$738,261)
21. Texas AgriLife Research Monocot Improvement Program: Discovering Traits and Genes Associated with Drought Tolerance in Corn. 09/09-08/11 (\$180,500)
22. Texas AgriLife Research Cotton Improvement Program: High-throughput and High-efficient Discovery of Genes/QTLs Important to Cotton Fiber Quality, Fiber Yield and Stress Tolerance. 09/09 – 08/11 (\$100,000)
23. Texas AgriLife Research Cotton Improvement Program: High-throughput platforms for cotton genome dissection and improvement. 09/09 – 08/11 (\$160,000)
24. NSF-Microbial Genome Sequencing: *Phytophthora sojae*: A high quality reference sequence for the Oomycetes. 10/07 – 09/11 (\$2,130,497)
25. USDA/NRI-1890 Grants: Syntenic analysis of cucurbit complex for widening genetic diversity and functional genomics of fruit quality and architecture. 09/07-08/11 (\$499,880)
26. USDA/CSREES - Develop and/or use molecular tools to identify and clone desirable genes from rangeland plants. 10/05-09/09 (\$311,213)
27. USDA/NRI - 1890 Research and Teaching Capacity Building Grants - Physical mapping of ready to transform BAC clones and eco-TILLING of sweetpotato germplasm for gene identification and genetic improvement of disease resistance and nutraceutical traits. 12/05-11/09 (\$499,840)
28. USDA/BARD: Integrative physical and genetic mapping of the chickpea genome for fine mapping and analysis of agronomic traits. 12/06 – 11/09 (\$300,000)
29. USDA/NRI – Animal Genomics: A physical and comparative map of the turkey genome. 09/05 - 08/07 (\$499,939)
30. NSF-Plant Genome: Plant centromere functions defined by tetrad analysis and artificial chromosomes. 06/99 - 05/04 (\$2,274,211)
31. NSF-Plant Genome: Assessment of the insular organization of the wheat D genome by physical mapping. 09/00-08/04 (\$4,435,924)
32. USDA/IFAFS-Animal Genome: Bridging genome sequence to the prevention of Marek's disease in poultry. 10/01 - 09/04 (\$1,600,000)
33. NSF-BAC Library Construction: BAC Libraries for fundamental studies in *Lepidoptera*. 08/2002 – 07/2004 (\$210,000)

34. USDA/ARS: Integrative physical mapping of the cultivated cotton genome. 10/2002 – 09/2003 (\$150,000)
35. USDA/NRI - Animal Genome: An integrated BAC map of the chicken genome. 02/00 -11/02 (\$650,000)
36. USDA/BARD: Genomics tools for legume agronomic gene mapping and cloning, and genome analysis: Chickpea as a model. 12/99 - 11/02 (\$250,000)
37. NSF-Plant Genome: Integrative physical mapping of the soybean genome 05/99 - 04/02 (\$1,303,664)
38. ISPOB: Soybean gene golfing: a tool for rapid cloning of agronomic genes. 12/98 - 11/2001 (\$460,000)
39. Dupont Ag Biotechnology: Development of an efficient approach to rapid mapping of grass ESTs and genes. 07/1998 - 06/2000 (\$30,000)
40. NIH: Development of a BAC library for *Ae. gamsiae*. 05/00 - 04/01 (\$60,000)
41. Dekalb Genetics, Inc.: maize genome research initiative. 01/98 - 12/99 (\$82,000)
42. NIH: Development of a BAC library for mosquito. 10/98 - 12/99 (\$80,000)
43. Texas Advanced Technology Program: The Texas A&M BAC Center for enhanced plant and animal genome research. 01/01/98 - 08/31/00 (\$234,626) (Zhang)
44. Texas Cotton Biotechnology Initiative: Identification and isolation of genes for nematode resistance in cotton. 01/01/1998 - 12/31/1999 (\$70,000)
45. Rockefeller Foundation: Characterization and chromosomal classification of two rice BAC libraries constructed from the parents of a permanent recombinant inbred mapping population. 07/1995 - 12/1998 (\$120,000)
46. Rockefeller Foundation: Rice Biotechnology Development and Transfer. 01/1996 - 10/1998 (\$24,900)
47. Rockefeller Foundation: The demonstration project for development of an integrated map of the rice genome for gene golfing. 07/1997 - 12/1998 (\$50,000)
48. USDA/NRI: Development of a BAC library for Jungle Fowl. 06/98 - 05/99 (\$50,000)

PATENTS, TECHNOLOGIES AND GENOMIC RESOURCES RELEASED

a. Invention Patents:

1. **Zhang H-B**, Zhang MP, Liu Y-H, Smith CW, Xu WW, Murray SC. 2016. Methods for Genome-Wide High-throughput Cloning of Genes Controlling Quantitative Traits. United States Letters Patent Serial No 62/298,606. Washington, DC: U.S. Patent and Trademark Office.
2. Leong SA, Chauhan RS, Farman ML, **Zhang H-B**. 2003. Chromosome region conferring resistance to rice blast, P00254US.
3. Gmitter Jr. FG, Deng Z, Huang S, **Zhang H-B**. 2002. Citrus tristeza virus resistance genes and methods of use, 60/336549US.
4. Gene-based breeding and toolkit for grain yield in maize (in preparation)
5. Gene-based breeding and toolkit for fiber quality in cotton (in preparation)
6. BIBACs as a tool for large-scale genome functional analysis, gene/QTL cloning, molecular breeding and molecular farming (in preparation)

b. Genomic Resources Released:

1. 120 large-insert, arrayed BAC and BIBAC libraries (<http://hbz7.tamu.edu>).
2. Indica rice BAC-based physical map and database at <http://hbz7.tamu.edu>;
3. Arabidopsis BAC/BIBAC, integrated physical, genetic and sequence map and database at <http://hbz7.tamu.edu>;
4. Soybean BAC/BIBAC-based physical map and database at <http://hbz7.tamu.edu>;
5. Chicken BAC-based physical map and database at <http://hbz7.tamu.edu>

6. Japonica rice BIBAC-based physical map and database at <http://pubs.nrc-cnrc.gc.ca/rp/rpsuppl/g07-006suppl.ppt>; <http://hbz7.tamu.edu>
7. The robust physical map of *Penicillium chrysogenum* at <http://nar.oupjournals.org/archive/index.dtl>
8. A BAC physical map of the *Ustilago maydis* genome at http://pubs.nrc-cnrc.gc.ca/cgi-bin/rp/rp2_tocs_e?gen_gen2-05_48
9. A BAC physical map of *Phytophthora sojae* at http://phytophthora.vbi.vt.edu/webfpc/WebAGCoL/contig_bac/WebFPC/ and http://phytophthora.vbi.vt.edu/webfpc/WebAGCoL/contig_bac/Data.
10. A draft BIBAC physical map of cotton at <http://cottondb.org/cdbpages/fpc.html>.
11. A BAC/BIBAC-based physical map of chickpea, *Cicer arietinum* L. at <http://www.biomedcentral.com/content/supplementary/1471-2164-11-501-s1.pdf>
12. 47,645 gene and BAC/BIBAC end sequences deposited at GenBank, including
 - 61 cotton disease resistance gene analogue sequences (AY600372v-AY600433)
 - 622 rice BAC end sequences (CG206233-CG206855)
 - 36,941 turkey BAC end sequences (ER942218-ER962259, FI503157-FI520055)
 - 246 *Heliconius erato* BAC end sequences (TI#: 908600791-908601036)
 - 299 *Heliopsis virescens* BAC end sequences (TI#: 908601037-908601335)
 - 273 *Manduca sexta* BAC end sequences (TI#: 908601336-908601608)
 - 9,223 Upland cotton BIBAC end sequences (dbGSS JY253441-JY262664)
 - 1,236 SSR markers
 - 1,003 cotton SSRs
 - 223 chickpea SSRs

c. Technologies Developed and Released

- Preparation of megabase-sized DNA, which have been widely used worldwide in preparation of megabase-sized nuclear DNA from plants, animals, insects, fishes and microbes (see MP Zhang et al. 2012 below)
- Megabase-sized recombinant DNA, including manipulation and cloning of large DNA fragment, and construction and manipulation of large-insert, arrayed bacterial artificial chromosome (BAC) and plant-transformation-competent binary BAC (BIBAC) libraries (see H-B Zhang et al. 2012 below)
- Whole-genome physical mapping with BACs and/or BIBACs (see Y Zhang et al. 2017 below)

PUBLICATIONS (395)

A. Peer-Reviewed, Refereed (SCI) Journals (116):

1. Zhang MP, Liu Y-H, Xu W, Smith CW, Murray SC, **Zhang H-B**. 2020. Analysis of the genes controlling three quantitative traits in three diverse plant species reveals the molecular basis of quantitative traits. *Scientific Reports* 10:10074. <https://doi.org/10.1038/s41598-020-66271-8>.
2. Angira B, Zhang Y, Scheuring CF, Zhang YD, Masor L, Coleman RJ, Liu Y-H, Singh BB, **Zhang H-B**, Hays DB, Zhang MP. 2020. Quantitative trait loci influencing days to flowering and plant height in cowpea, *Vigna unguiculata* (L.) Walp. *Mol Genet Genomics* (in press). <https://doi.org/10.1007/s00438-020-01680-y>
3. Zhang MP, Cui Y, Liu Y-H, Xu W, Sze S-H, Murray SC, Xu S, **Zhang H-B**. 2020. Accurate prediction of maize grain yield using its contributing genes for gene-based breeding. *Genomics* 112:225-236.
4. Wahl NJ, Murray SC, **Zhang H-B**, Zhang MP, Dickens CM, Isakeit TS. 2019. Maize kernel development stage the primary factor in differential gene expression in response to two methods of field inoculation with *Aspergillus flavus*. *bioRxiv* 617241.

5. Mugabe D, Coyne CJ, Piakowski J, Zheng P, Ma Y, Landry E, McGee R, Main D, Vandemark GJ, **Zhang H-B**, Abbo A. 2019. Quantitative trait loci for cold tolerance in chickpea. *Crop Sci* 59:1-10.
6. Song J-M, Arif M, Zhang MP, Sze S-H, **Zhang H-B**. 2019. Phenotypic and molecular dissection of grain quality using the USDA rice mini-core collection. *Food Chemistry* 284:312-322.
7. Zhang X, Yuan J, Sun Y, Li S, Gao Y, Yu Y, Liu C, Wang Q, Lv X, Zhang X, Ma KY, Wang X, Lin W, Wang L, Zhu X, Zhang C, Zhang J, Jin S, Yu K, Kong J, Xu P, Chen N, **Zhang H-B**, Sorgeloos P, Sagi A, Warren A, Liu Z, Wang L, Ruan J, Chu K, Liu B, Li F, Xiang J. 2019. Penaeid shrimp genome provides insights into benthic adaptation and frequent molting. *Nature Comm* 10:356.
8. Zhang MP, Liu Y-H, Chang C-S, Zhi H, Wang S, Xu W, Smith CW, **Zhang H-B**. 2019. Quantification of gene expression while taking into account RNA alternative splicing. *Genomics* 111:1517-1528.
9. van-Oss R, Gopher A, Kerem, Peleg Z, Lev-Yadun S, Sherman A, **Zhang H-B**, Vandemark G, Coyne CJ, Reany O, Abb S. 2018. Independent selection for seed free tryptophan content and vernalization response in chickpea domestication. *Plant Breed* 137:290-300.
10. Fu Y, Xia Z, Wang S, Chen X, Lu C, Luo M, **Zhang H-B**, Wang W. 2016. A bacterial artificial chromosome-based physical map of *Manihot esculenta* ssp. *flabellifolia*. *Frontiers of Agricultural Science and Engineering* 3:321-329.
11. Ji R, Wang Y, Cheng Y, Zhang M, **Zhang H-B**, Zhu L, Fang J, Zhu-Salzman K. 2016. Transcriptome analysis of green peach aphid (*Myzus persicae*): Insight into developmental regulation and inter-species divergence. *Front Plant Sci* 7:1562.
12. van-Oss R, Sherman A, Shtienberg D, **Zhang H-B**, Vandemark G, Coyne C, Abbo S. 2016. Vernalization response of domesticated x wild chickpea progeny is subject to strong genotype by environment interaction. *Plant Breeding* 135:102-110.
13. van-Oss R, Abbo S, Eshed R, Sherman A, Coyne C, Vandemark G, **Zhang H-B**, Peleg Z. 2015. Genetic relationship in *Cicer* sp. expose evidence for geneflow between the cultigen and its wild progenitor. *PLoS ONE* 10(10): e0139789.
14. Zhang MP, Rong Y, Lee M-K, Zhang Y, Stelly DM, **Zhang H-B**. 2015. Phylogenetic analysis of *Gossypium* L. using restriction fragment length polymorphism of repeated sequences. *Mol Genet Genomics* 290:1859-1872.
15. Wang W, Feng B, Xiao J, Xia Z, Zhou X, Li P, Zhang W, Wang Y, Møller BL, Zhang P, Luo M-C, Xiao G, Liu J, Yang J, Chen S, Rabinowicz PD, Chen X, **Zhang H-B**, Ceballos H, Lou Q, Zou M, Carvalho LJCB, Zeng C, Xia J, Sun S, Fu Y, Wang H, Lu C, Ruan M, Zhou S, Wu Z, Liu H, Kannangara RM, Jørgensen K, Neale RL, Bonde M, Heinz N, Zhu W, Wang S, Zhang Y, Pan K, Wen M, Ma P-A, Li Z, Hu M, Liao W, Hu W, Zhang S, Pei J, Guo A, Guo J, Zhang J, Zhang Z, Ye J, Ou W, Ma Y, Liu X, Tallon LJ, Galens K, Ott S, Huang J, Xue J, An F, Yao Q, Lu X, Fregene M, López-Lavelle LAB, Wu J, You FM, Chen M, Hu S, Wu G, Zhong S, Ling P, Chen Y, Wang Q, Liu G, Liu B, Li K, Peng M. 2014. Cassava genome from a wild ancestor to cultivated varieties. *Nat Comm* 5:5110.
16. Liu Y-H, Zhang MP, Huang JJ, **Zhang H-B**. 2014. DNA is structured as a linear “Jigsaw Puzzle” in the genomes of *Arabidopsis*, rice and budding yeast. *Genome* 57:9-19.
17. Qin J, Scheuring CF, Wei G, Zhi H, Zhang MP, Huang JJ, Zhou X, Galbraith DW, **Zhang H-B**. 2013. Identification and characterization of a repertoire of genes differentially expressed in developing top ear shoots between a superior hybrid and its parental inbreds in *Zea mays* L. *Mol Genet Genomics* 288:691-705.
18. Zhai J, Wang Y, Sun C, Jiang S, Wang K, Zhang Y, **Zhang H-B**, Zhang MP. 2013. A plant-transformation-competent BIBAC library of ginseng (*Panax ginseng* C. A. Meyer) for functional genomics research and characterization of genes involved in ginsenoside biosynthesis. *Mol Breeding* 31:685-692.
19. Lee M-K, Zhang Y, Zhang MP, Goebel M, Kim HJ, Triplett BA, Stelly DM, **Zhang H-B**. 2013. Construction of a plant-transformation-component BIBAC library and genome sequence analysis

- of polyploid Upland cotton (*Gossypium hirsutum* L.). BMC Genomics 14:208. doi:10.1186/1471-2164-14-208.
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 21. Zhang MP, Zhang Y, Scheuring CF, Wu C-C, Dong JJ, **Zhang H-B**. 2012. Preparation of megabase-sized DNA from a variety of organisms using the nuclei method for advanced genomics research. Nature Protocols 7:467-478.
 22. **Zhang H-B**, Scheuring CF, Zhang MP, Zhang Y, Wu C-C, Dong JJ, Li Y. 2012. Construction of BIBAC and BAC libraries from a variety of organisms for advanced genomics research. Nature Protocols 7:479-499.
 23. Kim HJ, Triplett BA, **Zhang H-B**, Lee M-K, Hinchliffe DJ, Li P, Fang DD. 2012. Cloning and characterization of homoeologous cellulose synthase catalytic subunit 2 genes from allotetraploid *Gossypium hirsutum*. Gene 494:181-189.
 24. Zhang X, Zhao C, Huang C, Duan H, Huan P, Liu C, Zhang X, Zhang Y, Li F, **Zhang H-B**, Xiang J. 2011. A BAC-based physical map of Zhikong scallop (*Chlamys farreri* Jones et Preston). PLoS ONE 6: e27612. doi:10.1371/journal.pone.0027612
 25. Zhang Y, Zhang X, O'Hare TH, Payne WS, Dong JJ, Scheuring CF, Zhang MP, Huang JJ, Delany M*, **Zhang H-B***, Dodgson JB* (*co-corresponding authors). 2011. A comparative physical map reveals the pattern of chromosomal evolution between the turkey (*Meleagris gallopavo*) and chicken (*Gallus gallus*) genomes. BMC Genomics 12:447.
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 27. Fu Y, Scheuring CF, **Zhang H-B**, Wang W. 2011. Construction and characterization of a BIBAC library of *Jatropha curcas* L. and identification of BIBAC clones containing genes associated with fatty acid metabolism. Mol. Breed. 28:559-567.
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