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	发表文章
2008	<ul style="list-style-type: none"><li>● Zhang, Q.F., Li, J.Y., Xue, Y.B., Han, B. &amp; Deng, X.W. Rice 2020: A call for an international coordinated effort in rice functional genomics. <i>Molecular Plant</i>, doi:10.1093/mp/ssp043 (2008).</li><li>● Lu, T.T., Yu, S.L., Fan, D.L., Mu, J., Shangguan, Y.Y., Wang, Z.X., Minobe, Y., Lin, Z.X. &amp; Han, B. Collection and comparative analysis of 1888 full-length cDNAs from wild rice <i>Oryza rufipogon</i> Griff. W1943. <i>DNA Res.</i>, 15, 285-295 (2008). Summary PPT</li><li>● Huang, X.H., Lu, G.J., Zhao, Q., Liu, X.H. &amp; Han, B. Genome-wide analysis of transposon insertion polymorphisms reveals intra-specific variation in cultivated rice. <i>Plant Physiol.</i>, 148, 25-40 (2008). Summary PPT</li></ul>
2007	<ul style="list-style-type: none"><li>● Liu, X.H., Lu, T.T., Yu, S.L., Li, Y., Huang, Y.C., Huang, T., Zhang, L., Zhu, J.J., Zhao, Q., Fan, D.L., Mu, J., Shangguan, Y.Y., Feng, Q., Guan, J.P., Ying, K., Zhang, Y., Lin, Z.X., Sun, Z.X., Qian, Q., Lu, Y.P. &amp; Han, B. A collection of 10,096 <i>indica</i> rice full-length cDNAs reveals highly expressed sequence divergence between <i>Oryza sativa indica</i> and <i>japonica</i> subspecies. <i>Plant Mol Biol.</i> 65, 403-415 (2007).</li><li>● Han, B., Xue, Y.B., Li, J.Y., Deng, X.W. &amp; Zhang, Q.F. Rice functional genomics research in China. <i>Phi. Trans. R. Soc. B</i> 362, 1009-1021 (2007).</li><li>● The Rice Annotation Project. Curated genome annotation of <i>Oryza sativa ssp. japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i>. <i>Genome Research</i>. 17, 175-183 (2007).</li><li>● Wang, D.K., Pei, K.M., Fu, Y.P., Sun, Z.X., Li, S.J., Liu, H.Q., Tang, K., Han, B. &amp; Tao, Y.Z. Genome-wide analysis of the auxin response factors (ARF) gene family in rice (<i>Oryza sativa</i>). <i>Gene</i> 394, 13-24 (2007).</li></ul>
2006	<ul style="list-style-type: none"><li>● Hu, H., Mu, J., Zhang, H.J., Tao, Y.Z. &amp; Han, B. Differentiation of a Miniature Inverted Transposable Element (MI TE) System in Asian Rice Cultivars and Its Inference for a Diphyletic Origin of Two Subspecies of Asian Cultivated Rice. <i>Journal of Integrative Plant Biology</i> 48, 260-267 (2006).</li><li>● Stupar, R.M., Beaubien, K.A., Jin, W.W., Song, J.Q., Lee, M.K., Wu, C.C., Zhang, H.B., Han, B. &amp; Jiang, J.M. Structural Diversity and Differential Transcription of the Patatin Multicopy Gene Family During Potato Tuber Development. <i>Genetics</i> 172, 1263-1275 (2006).</li><li>● Bao, W.D., Zhang, W.L., Yang, Q.Y., Zhang, Y., Han, B., Gu, M.H., Xue, Y.B., &amp; Cheng, Z.K. Diversity of centromeric repeats in two closely related wild rice species, <i>Oryza officinalis</i> and <i>Oryzopsis hizomatis</i>. <i>Mol. Gen. Genomics</i> 275, 421-430 (2006).</li><li>● Lian, X.M., Wang, S.P., Zhang, J.W., Feng, Q., Zhang, L.D., Fan, D.L., Li, X.H., Yuan, D.J., Han, B. &amp; Zhang, Q.F. Expression profiles of 10,422 genes at early stage of low nitrogen stress in rice assayed using a cDNA microarray. <i>Plant Molecular Biology</i> 60, 617-631 (2006).</li></ul>

- Fan, C.C., Xing, Y.Z., Mao, H.L., Lu, T.T., Han, B., Xu, C.G., Li, X.H. & Zhang, Q.F. GS3, a major QTL for grain length and weight and minor QTL for grain width and thickness in rice, encodes a putative transmembrane protein. *Theor Appl Genet.* 112, 1164-71 (2006).

2005

- Qu, S.H., Liu, G.F., Zhou, B., Bellizzi, M., Zeng, L.R., Dai, L.Y., Han, B. & Wang, G.L. The Broad-Spectrum Blast Resistance Gene Pi9 Encodes a Nucleotide-Binding Site-Leucine-Rich Repeat Protein and Is a Member of a Multigene Family in Rice. *Genetics* 172, 1901-1914 (2005).
- Lan, L.F., Li, M.N., Lai, Y., Xu, W.Y., Kong, Z.S., Ying, K., Han, B. & Xue, Y.B. Microarray analysis reveals similarities and variations in genetic programs controlling pollination/fertilization and stress responses in rice (*Oryza sativa* L.). *Plant Molecular Biology* 59, 151-164 (2005).
- Wing, R.A., Ammiraju, J.S.S., Luo, M.Z., Kim, H.R., Yu, Y.S., Kudrna, D., Goicoechea, J.L., Wang, W.M., Nelson, W., Rao, K.R., Brar, D.S., Mackill, D.J., Han, B., Soderlund, C., Stein, L., SanMiguel, P. & Jackson, S. The *Oryza* Map Alignment Project: the golden path to unlocking the genetic potential of wild rice species. *Plant Molecular Biology* 59, 53-62 (2005).
- Stolc, V., Li, L., Wang, X.F., Li, X.Y., Su, N., Tongprasit, W., Han, B., Xue, Y.B., Li, J.Y., Snyder, M., Gerstein, M., Wang, J. & Deng, X.W. A pilot study of transcription unit analysis in rice using oligonucleotide tilling-path microarray. *Plant Molecular Biology* 59, 137-149 (2005).
- Zhang, D.F., Yang, Q.Y., Bao, W.D., Zhang, Y., Han, B., Xue, Y.B. & Cheng, Z.K. Molecular Cytogenetic Characterization of the *Antirrhinum majus* Genome. *Genetics* 169, 325-335 (2005).
- Lu, Y., Wu, Y.R. & Han, B. Anaerobic Induction of Isocitrate Lyase and Malate Synthase in Submerged Rice Plants Indicates the Important Metabolic Role of the Glyoxylate Cycle. *Acta Biochimica et Biophysica Sinica* 37, 406-414 (2005).
- Xie, K.B., Zhang, J.W., Xiang, Y., Feng, Q., Han, B., Chu, Z.H., Wang, S.P., Zhang, Q.F. & Xiong, L.Z. Isolation and annotation of 10828 putative full length cDNAs from *indica* rice. *Science in China Ser. C Life Sciences* 48, 445-451 (2005).
- Lian, X.M., Wang, S.P., Zhang, J.W., Feng, Q., Zhang, L.D., Fan, D.L., Li, X.H., Yuan, D.J., Han, B. & Zhang, Q.F. Expression profiles of 10,422 genes at early stage of low nitrogen stress in rice assayed using a cDNA microarray. *Plant Molecular Biology* 60, 617-631 (2006).
- International Rice Genome Sequencing Project. The map-based sequence of the rice genome. *Nature* 436, 793-800 (2005).
- Zhang, Y.J., Wu, Y.R., Liu, Y.L. & Han, B. Computational Identification of 69 Retroposons in *Arabidopsis*. *Plant Physiol* 138, 935-948 (2005).
- Zhang, J.W., Feng, Q., Jin, C.Q., Qiu, D.Y., Zhang, L.D., Xie, K.B., Yuan, D.J., Han, B., Zhang, Q.F. & Wang, S.P. Features of the expressed sequences revealed by a large-scale analysis of ESTs from a normalized cDNA library of the elite *indica* rice cultivar Minghui 63. *Plant J* 42, 772-80 (2005).
- Jiao, Y.L., Jia, P.X., Wang, X.F., Su, N., Yu, S.L., Zhang, D.F., Ma, L.G., Feng, Q., Jin, Z.Q., Li, L., Xue, Y.B., Cheng, Z.K., Zhao, H.Y., Han, B. & Deng, X.W. A Tiling Microarray Expression Analysis of Rice Chromosome 4 Suggests a Chromosome-Level Regulation of Transcription. *Plant Cell* 17, 1641-57 (2005).
- Zhang, D.F., Yang, Q.Y., Bao, W.D., Zhang, Y., Han, B., Xue, Y.B. & Cheng, Z.K. Molecular cytogenetics characterization of the *Antirrhinum majus* genome. *Genetics* 169, 325-335 (2005).

2004

- Lan, L.F., Chen, W., Lai, Y., Suo, J.F., Kong, Z.S., Li, C., Lu, Y., Zhang, Y.J., Zhao, X.Y., Zhang X.S., Zhang, Y.S., Han, B., Cheng, J. & Xue, Y.B. Monitoring of gene expression profiles and isolation of candidate genes involved in pollination and fertilization in rice (*Oryza sativa* L.) with a 10K cDNA microarray. *Plant Molecular Biology* 54, 471–487 (2004).
- Li, T. & Han, B. Dampable Waves along Nucleic Acid Sequences Mediating Nucleotides' Interactions. *DNA Sequence* 15, 135-140(2004).
- Hu, X., Hu, H., Hong, G.F. & Han, B. Identification and analysis of a group of highly conserved trs-like genes in rice. *Yi Chuan Xue Bao* 31,822-829 (2004).
- Hu, X., Hu, H., Hong, G.F. & Han, B. The structural, transcriptional and homology analysis of two frr genes in rice. *Zhi Wu Sheng Li Yu Fen Zi Sheng Wu Xue Xue Bao* 30, 105-114 (2004).
- Liu, X.H., Wang, H.W., Li, Y.M., Tang, Y.S., Liu, Y.L., Hua, X., Jia, P.X., Ying, K., Feng, Q., Guan, J.P., Jin, C.Q., Zhang, L., Lou, L.R., Zhou, Z. & Han, B. Preparation of single rice chromosome for construction of a DNA library using a laser microbeam trap. *Journal of Biotechnology* 109, 217–226 (2004).
- Zhang, Y., Huang, Y.C., Zhang, L., Li, Y., Lu, T.T., Lu, Y.Q., Feng, Q., Zhao, Q., Cheng, Z.K., Xue Y.B., Wing, R.A. & Han, B. Structural features of the rice chromosome 4 centromere. *Nucleic Acids Research* 32, 2023-2030 (2004).
- Wang, R., Hong, G.F. & Han, B. Transcript abundance of rml1, encoding a putative GT1-like factor in rice, is up-regulated by Magnaporthe grisea and down-regulated by light. *Gene* 324,105–115 (2004).
- Li, C., Zhang, Yu., Ying, K., Liang, X.L. & Han, B. Sequence variations of simple sequence repeats on chromosome-4 in two subspecies of the Asian cultivated rice. *Theor Appl Genet.* 108, 392–400 (2004).

## 2003

- Li, X.Y., Qian, Q., Fu, Z.M., Wang, Y.H., Xiong, G.S., Zeng, D.L., Wang, X.Q., Liu, X.F., Teng, S., Hiroshi, F., Yuan, M., Luo, D., Han, B. & Li, J.Y. Control of tillering in rice. *Nature* 422, 618-621 (2003).
- Li, Y.H., Qian, Q., Zhou, Y.H., Yan, M.X., Sun, L., Zhang, M., Fu, Z.M, Wang, Y.H, Han, B., Pang, X.M., Chen, M.S. & Li, J.Y. BRI TITTLE CULM1, which encodes a COBRA-like protein, affects the mechanical properties of rice plants. *Plant Cell* 15, 2020-2031 (2003).
- Han, B. & Xue, Y.B. Genome-wide intraspecific DNA-sequence variations in rice. *Current Opinion in Plant Biology* 6, 134-138 (2003).

## 2002

- Lai, Z., Ma, W., Han, B., Liang, L.Z., Zhang, Y.S., Hong, G.F. & Xue, Y.B. An F-box gene linked to the self-incompatibility (S) locus of *Antirrhinum* is expressed specifically in pollen and tapetum. *Plant Mol. Biol.* 50, 29-42 (2002).
- Feng, Q., Zhang, Y.J., Hao, P., Wang, S.Y., Fu, G., Huang, Y.C., Li, Y., Zhu, J.J., Liu, Y.L., Hu, X., Jia, P.X., Zhang, Y., Zhao, Q., Ying, K., Yu, S.L., Tang, Y.S., Weng, Q.J., Zhang, L., Lu, Y., Mu, J., Lu, Y.Q., Zhang, L., Yu, Z., Fan, D.L., Liu, X.H., Lu, T.T., Li, C., Wu, Y.R., Sun, T.G., Lei, H.Y., Li, T., Hu, H., Guan, J.P., Wu, M., Zhang, R.Q., Zhou, B., Chen, Z.H., Chen, L., Jin, Z.Q., Wang, R., Yin, H.F., Cai, Z., Ren, S.X., Lv, G., Gu, W.Y., Zhu, G.F., Tu, Y.F., Jia, J., Zhang, Y., Chen, J., Kang, H., Chen, X.Y., Shao, C.Y., Sun, Y., Hu, Q.P., Zhang, X.L., Zhang, W., Wang, L.J., Ding, C.W., Sheng, H.H., Gu, G.L., Chen, S.T., Ni, L., Zhu, F.H., Chen, W., Lan, L.F., Lai, Y., Cheng, Z.K., Gu, M.H., Jiang, J.M., Li, J.Y., Hong, G.F., Xue, Y.B. & Han, B. Sequence and analysis of rice chromosome 4. *Nature* 420, 336-40 (2002).
- Zhao, Q., Zhang, Y., Cheng, Z.K., Chen, M.S., Wang, S.Y., Feng, Q., Huang, Y.C., Li, Y., Tang, Y.S., Zhou, B., Chen, Z.H., Yu, S.L., Zhu, J.J., Hu, X., Mu, J., Ying, K., Hao, P., Zhang, L., Lu, Y.Q., Zhang, L., Liu, Y.L., Yu, Z., Fan, D.L., Weng, Q.J., Chen, L., Lu, T.T., Liu, X.H., Jia, P.X., Sun, T.G., Wu, Y.R., Zhang, Y.J., Lu, Y., Li, C., Wang, R., Lei, H.Y., Li, T., Hu, H., Wu, M., Zhang, R.Q., Guan, J.P., Zhu, J., Fu, G., Gu, M.H., Hong, G.F., Xue, Y.B., Wing, R., J, J.M. &

Han, B. A fine physical map of the rice chromosome 4. *Genome Research* 12, 817-23 (2002).

- Lei, H.Y., Zhou, B., Hong, G.F. & Han, B. Characterization of a S-locus-related receptor-like kinase cluster on rice chromosome 4. *Acta Botanica Sinica* 44, 1346-1350 (2002).
- Lei, H.Y., Zhou, B., Zhang, Y., Hong, G.F. & Han, B. Structural Analysis of a Gene Cluster Encoding DFR-like Proteins from Rice Chromosome 4. *Sheng Wu Hua Xue Yu Sheng Wu Wu Li Xue Bao* 34, 685-689 (2002).
- Hu, H., Li, T., Mu, J., Han, B. & Hong, G.F. A high efficient approach used for BAC-contig extension of *Oryza sativa* with PCR screening the BAC clone pools. *Sheng Wu Hua Xue Yu Sheng Wu Wu Li Xue Bao* 34, 358-364 (2002).
- Tang, Y.S., Li, Y., Zhu, J.J., Hu, X., Lin, Z.X., Han, B. & Hong, G.F. Colony PCR Apply to The Rice Genome Sequencing. *Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan* 29, 316-318 (2001).

2001

- Chen, Z.H., Zhou, B., Han, B., Qian, Y.M. & Hong, G.F. Structural Analysis of a Gene Cluster Encoding Two Cationic and Three Anionic Peroxidases from Rice Chromosome 4. *Sheng Wu Hua Xue Yu Sheng Wu Wu Li Xue Bao* 33, 163-172 (2001).
- Zhou, B., Chen, Z.H., Han, B. & Hong, G.F. Identification and Structural Analysis of a Class of Potentially Transposable Solo-LTR in Rice Genome. *Sheng Wu Hua Xue Yu Sheng Wu Wu Li Xue Bao* 33, 158-162 (2001).
- Yu, S.L., Lei, H.Y., Chang, W., Soll, D. & Hong, G.F. Protein phosphatase 2A : Identification in *Oryza sativa* of the gene encoding the regulatory A subunit. *Plant Mol Biol.* 45, 107-112 (2001).

2000

- Zhang, X.L. & Hong, G.F. Preferential Location of MI TEs in Rice Genome. *Sheng Wu Hua Xue Yu Sheng Wu Wu Li Xue Bao* 32, 223-228 (2000).

1997

- Hong, G., Qian, Y., Yu, S., Hu, X., Zhu, J., Tao, W., Li, W., Su, C., Zhao, H., Qiu, L., Yu, D., Liu, X., Wu, B., Zhang, X. & Zhao, W. A 120 kilobase resolution contig map of the rice genome. *DNA Seq.* 7, 319-35 (1997).
- Hong, G.F. A rapid and accurate strategy for rice contig map construction by combination of fingerprinting and hybridization. *Plant Mol Biol.* 35, 129-33 (1997).

1994

- Tao, Q., Zhao, H., Qiu, L. & Hong, G. Construction of a full bacterial artificial chromosome (BAC) library of *Oryza sativa* genome. *Cell Research* 4, 127-133 (1994).

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National Center for Gene Research, Chinese Academy of Sciences  
500 Cao Bao Road Shanghai 200233 P.R.China  
Phone: 86 21 54971303 Fax: 86 21 64825775  
E-mail: webmaster@ncgr.ac.cn