Wang Lab

Research interests

- **Exploration of genes or cis-regulatory elements determining important plant (crop) traits and their regulation mechanisms**

We are interested in applying genetic and epigenomic profiling methods to discover gene or non-coding regulatory elements across diverse plant species including cotton, rice, common/hairy vetch, and *Brassicaceae* vegetables. These methods include ATAC-seq, ChIP-seq at whole-genome or single-cell levels. Integrating with genome-editing technologies we are beginning to edit cis-regulatory elements to new germplasms with improved traits.

- **Structure and evolution of plant centromeres**

The centromere is a chromosomal region that plays a key role in faithful segregation of chromosomes during cell division. In contrast to the centromere's conserved cellular function, centromeric DNA is highly diverse, which has been one of the most intriguing enigmas in biology. We are interested in studying the structure, function, and evolution of plant centromeric chromatin. We will use the chromatin immunoprecipitation combing with next-generation sequencing (ChIP-seq) to identify the functional centromere chromatin in plants, and to elucidate the structure, function, and evolution of plant centromere chromatin. And one of our long-term goals is to develop plant artificial chromosomes to help the genetic improvement in crops.

- **Plant molecular cytogenetic**

Fluorescence in situ hybridization (FISH) is a reliable cytological technique for chromosome identification and further fully characterizing the genome. Based on this tech, we will make efforts on the studies of plant genome karyotyping, chromosomal evolution and structural diversity, chromosomal spatial organization, and chromatin epigenetic modification.

Selected Publications

1. Wang BH, Ji MJ, Fang H, Gu HJ, Mehari TG, Han JL, Feng WX, Huo XH, Zhang JX, Chen Y, Zhang J, Ditta A, Khan MKR, Paterson AH, Chee PW, **Wang K** (2024) An analysis of lncRNAs related to fiber quality and the discovery of their target genes in a line with introgression. Theor Appl Genet 137:40
2. Yu G, Sun B, Zhu Z, Mehareb EM, Teng A, Han J, Zhang H, Liu J, Liu X, Raza G, Zhang B, Zhang Y, **Wang K** (2024) Genome-wide DNase I-hypersensitive site assay reveals distinct genomic distributions and functional features of open chromatin in autopolyploid sugarcane. The Plant Journal 117:573-589
3. Ding W, Zhu Y, Han J, Zhang H, Xu Z, Khurshid H, Liu F, Hasterok R, Shen X, **Wang K** (2023) Characterization of centromeric DNA of Gossypium anomalum reveals

sequence-independent enrichment dynamics of centromeric repeats. Chromosome Res 31:12

4. **Wang K**, Zhang H, Khurshid H, Esh A, Wu C, Wang Q, Piperidis N (2023) Past and recent advances in sugarcane cytogenetics. The Crop Journal 11:1-8
5. Yu GR, Ye F, Zhang X, Cai J, Zhu WL, Zhang H, Chen SB, Han JL, **Wang K** (2023) Characterization of open chromatin in response to cold reveals transcription factor association with preferred binding distances in cassava. Industrial Crops and Products 202:117055
6. Zhang X, Meng Z, Han J, Khurshid H, Esh A, Hasterok R, **Wang K** (2023) Characterization of meiotic chromosome behavior in the autopolyploid Saccharum spontaneum reveals preferential chromosome pairing without distinct DNA sequence variation. The Crop Journal 11:1550-1558
7. Xu Z, Chen J, Meng S, Xu P, Zhai C, Huang F, Guo Q, Zhao L, Quan Y, Shangguan Y, Meng Z, Wen T, Zhang Y, Zhang X, Zhao J, Xu J, Liu J, Gao J, Ni W, Chen X, Ji W, Wang N, Lu X, Wang S, **Wang K**, Zhang T, Shen X (2022) Genome sequence of Gossypium anomalum facilitates interspecific introgression breeding. Plant Commun 3:100350
8. **Wang K**, Cheng H, Han J, Esh A, Liu J, Zhang Y, Wang B (2022) A comprehensive molecular cytogenetic analysis of the genome architecture in modern sugarcane cultivars. Chromosome Res 30:29-41
9. Han J, Lopez-Arredondo D, Yu G, Wang Y, Wang B, Wall SB, Zhang X, Fang H, Barragán-Rosillo AC, Pan X, Jiang Y, Chen J, Zhang H, Zhou B-L, Herrera-Estrella L, Zhang B, **Wang K** (2022) Genome-wide chromatin accessibility analysis unveils open chromatin convergent evolution during polyploidization in cotton. Proceedings of the National Academy of Sciences 119:e2209743119
10. Huang Y, Ding W, Zhang M, Han J, Jing Y, Yao W, Hasterok R, Wang Z, **Wang K** (2021) The formation and evolution of centromeric satellite repeats in Saccharum species. ***Plant J*** 106:616-629
11. Wang Q, Yu G, Chen Z, Han J, Hu Y, **Wang K** (2021) Optimization of protoplast isolation, transformation and its application in sugarcane (Saccharum spontaneum L). ***The Crop Journal*** , 9:133-142
12. Wang Y, **Wang K** (2021) Genome-wide identification of DNase I hypersensitive sites in plants. Current Protocols 1:e148
13. Meng Z, Wang Q, Khurshid H, Raza G, Han J, Wang B, **Wang K** (2021) Chromosome painting provides insights into the genome structure and evolution of sugarcane. Front Plant Sci 12:731664
14. Han J, Wang P, Wang Q, Lin Q, Chen Z, Yu G, Miao C, Dao Y, Wu R, Schnable JC, Tang H, **Wang K** (2020) Genome-wide characterization of DNase I-hypersensitive sites and cold response regulatory landscapes in grasses. ***Plant Cell*** 32:2457-2473
15. Meng Z, Han J, Lin Y, Zhao Y, Lin Q, Ma X, Wang J, Zhang M, Zhang L, Yang Q, **Wang K** (2020) Characterization of a Saccharum spontaneum with a basic chromosome number of x = 10 provides new insights on genome evolution in genus Saccharum. ***Theor Appl Genet*** 133:187-199

16. Lin Q, Wang S, Dao Y, Wang J, **Wang K** (2020) The *Arabidopsis thaliana* trehalose-6-phosphate phosphatase gene *AtTPPI* enhances drought tolerance by regulating stomatal apertures. ***J Exp Bot*** 71:4285-4297
17. Huang Y, Chen H, Han J, Zhang Y, Ma S, Yu G, Wang Z, **Wang K** (2020) Species-specific abundant retrotransposons elucidate the genomic composition of modern sugarcane cultivars. ***Chromosoma*** 129:45-55
18. Hasterok R, **Wang K**, Jenkins G (2020) Progressive refinement of the karyotyping of Brachypodium genomes. New Phytol, DOI 10.1111/nph.16342
19. Zhang L, Chen F, Zhang X, Li Z, Zhao Y, Lohaus R, Chang X, Dong W, Ho SYW, Liu X, Song A, Chen J, Guo W, Wang Z, Zhuang Y, Wang H, Chen X, Hu J, Liu Y, Qin Y, **Wang K**, Dong S, Liu Y, Zhang S, Yu X, Wu Q, Wang L, Yan X, Jiao Y, Kong H, Zhou X, Yu C, Chen Y, Li F, Wang J, Chen W, Chen X, Jia Q, Zhang C, Jiang Y, Zhang W, Liu G, Fu J, Chen F, Ma H, Van de Peer Y, Tang H (2020) The water lily genome and the early evolution of flowering plants. Nature 577:79-84
20. Wang S, Jin W, **Wang K** (2019) Centromere histone H3- and phospholipase-mediated haploid induction in plants. ***Plant Methods*** 15:42
21. Yu G, Wang J, Miao L, Xi M, Wang Q, **Wang K** (2019) Optimization of Mature Embryo-Based Tissue Culture and Agrobacterium-Mediated Transformation in Model Grass Brachypodium distachyon. ***Int J Mol Sci*** 20:5448
22. Lin Q, Yang J, Wang Q, Zhu H, Chen Z, Dao Y, **Wang K** (2019) Overexpression of the trehalose-6-phosphate phosphatase family gene AtTPPF improves the drought tolerance of Arabidopsis thaliana. ***BMC Plant Biol*** 19:381
23. Wang S, Ouyang K, **Wang K** (2019) Genome-wide identification, evolution, and expression analysis of *TPS* and *TPP* gene families in *Brachypodium distachyon*. ***Plants*** 8:362
24. Li Z, **Wang K** (2019) Genome-Wide Identification of Regulatory DNA Elements in Crop Plants. In: Vaschetto LM (ed) Cereal Genomics: Methods and Protocols. Springer US, New York, NY, pp 85-99
25. Zou J, Mao L, Qiu J, Wang M, Jia L, Wu D, He Z, Chen M, Shen Y, Shen E, Huang Y, Li R, Hu D, Shi L, **Wang K**, Zhu Q, Ye C, Bancroft I, King GJ, Meng J, Fan L (2019) Genome-wide selection footprints and deleterious variations in young Asian allotetraploid rapeseed. Plant Biotechnol J 17:1998-2010
26. Hu Y, Chen J, Fang L, Zhang Z, Ma W, Niu Y, Ju L, Deng J, Zhao T, Lian J, Baruch K, Fang D, Liu X, Ruan YL, Rahman MU, Han J, **Wang K**, Wang Q, Wu H, Mei G, Zang Y, Han Z, Xu C, Shen W, Yang D, Si Z, Dai F, Zou L, Huang F, Bai Y, Zhang Y, Brodt A, Ben-Hamo H, Zhu X, Zhou B, Guan X, Zhu S, Chen X, Zhang T (2019) Gossypium barbadense and Gossypium hirsutum genomes provide insights into the origin and evolution of allotetraploid cotton. Nat Genet 51:739-748
27. Zhang J, Zhang X, Tang H, Zhang Q, Hua X, Ma X, Zhu F, Jones T, Zhu X, Bowers J, Wai CM, Zheng C, Shi Y, Chen S, Xu X, Yue J, Nelson DR, Huang L, Li Z, Xu H, Zhou D, Wang Y, Hu W, Lin J, Deng Y, Pandey N, Mancini M, Zerpa D, Nguyen JK, Wang L, Yu L, Xin Y, Ge L, Arro J, Han JO, Chakrabarty S, Pushko

M, Zhang W, Ma Y, Ma P, Lv M, Chen F, Zheng G, Xu J, Yang Z, Deng F, Chen X, Liao Z, Zhang X, Lin Z, Lin H, Yan H, Kuang Z, Zhong W, Liang P, Wang G, Yuan Y, Shi J, Hou J, Lin J, Jin J, Cao P, Shen Q, Jiang Q, Zhou P, Ma Y, Zhang X, Xu R, Liu J, Zhou Y, Jia H, Ma Q, Qi R, Zhang Z, Fang J, Fang H, Song J, Wang M, Dong G, Wang G, Chen Z, Ma T, Liu H, Dhungana SR, Huss SE, Yang X, Sharma A, Trujillo JH, Martinez MC, Hudson M, Riascos JJ, Schuler M, Chen LQ, Braun DM, Li L, Yu Q, Wang J, **Wang K**, Schatz MC, Heckerman D, Van Sluys MA, Souza GM, Moore PH, Sankoff D, VanBuren R, Paterson AH, Nagai C, Ming R (2018) Allele-defined genome of the autopolyploid sugarcane Saccharum spontaneum L. Nat Genet 50:1565-1573

28. Sharma A, Song J, Lin Q, Singh R, Ramos N, **Wang K**, Zhang J, Ming R, Yu Q (2018) Comparative analysis of homologous sequences of Saccharum officinarum and Saccharum spontaneum reveals independent polyploidization events. Front Plant Sci 9:1414
29. Liu S, Xue C, Fang Y, Chen G, Peng X, Zhou Y, Chen C, Liu G, Gu M, **Wang K**, Zhang W, Wu Y, Gong Z (2018) Global Involvement of Lysine Crotonylation in Protein Modification and Transcription Regulation in Rice. Mol Cell Proteomics 17:1922-1936
30. Dong G, Shen J, Zhang Q, Wang J, Yu Q, Ming R, **Wang K**, Zhang J (2018) Development and applications of chromosome-specific cytogenetic BAC-FISH Probes in S. spontaneum. Front Plant Sci 9:218
31. Meng Z, Zhang Z, Yan T, Lin Q, Wang Y, Huang W, Huang Y, Li Z, Yu Q, Wang J, **Wang K** (2018) Comprehensively characterizing the cytological features of Saccharum spontaneum by the development of a complete set of chromosome-specific oligo probes. ***Front Plant Sci*** 9:1624
32. Han J, Zhang Z, **Wang K** (2018) 3C and 3C-based techniques: the powerful tools for spatial genome organization deciphering. ***Mol Cytogenet*** 11:21
33. Li Y, Zuo S, Zhang Z, Li Z, Han J, Chu Z, Hasterok R, **Wang K** (2018) Centromeric DNA characterization in the model grass Brachypodium distachyon provides insights on the evolution of the genus. ***Plant J*** 93:1088-1101
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36. Han J, Masonbrink RE, Shan W, Song F, Zhang J, Yu W, Wang K, Wu Y, Tang H, Wendel JF, **Wang K** (2016) Rapid proliferation and nucleolar organizer targeting centromeric retrotransposons in cotton. ***Plant J*** 88:992-1005
37. Shan W, Jiang Y, Han J, **Wang K** (2016) Comprehensive cytological characterization of the *Gossypium hirsutum* genome based on the development of a set of chromosome cytological markers. ***The Crop Journal*** 4:256-265

38. **Wang K**, Yu W (2016) Chromosome Preparation in Rice (Oryza sativa). In: Gary Stacey, Birchler J, Ecker J, Martin C, Stitt M, Zhou J-M (eds) Current Protocols in Plant Biology. John Wiley & Sons, Inc., Hoboken, New Jersey, USA, pp 67-77
39. Han J, Zhou B, Shan W, Yu L, Wu W, **Wang K** (2015) A and D genomes spatial separation at somatic metaphase in tetraploid cotton: evidence for genomic disposition in a polyploid plant. ***Plant J*** 84:1167-1177
40. Gent JI, **Wang K**, Jiang J, Dawe RK (2015) Stable patterns of CENH3 occupancy through maize lineages containing genetically similar centromeres. ***Genetics*** 200:1105-1116
41. **Wang K**, Wu Y, Zhang W, Dawe RK, Jiang J (2014) Maize centromeres expand and adopt a uniform size in the genetic background of oat. ***Genome Res*** 24:107-116
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44. Chen Y, Wang Y, **Wang K**, Zhu X, Guo W, Zhang T, Zhou B (2014) Construction of a complete set of alien chromosome addition lines from Gossypium australe in Gossypium hirsutum: morphological, cytological, and genotypic characterization. Theor Appl Genet 127:1105-1121
45. **Wang K**, Zhang W, Jiang Y, Zhang T (2013) Systematic application of DNA fiber-FISH technique in cotton. ***PLoS One*** 8:e75674
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47. Cook DE, Lee TG, Guo X, Melito S, **Wang K**, Bayless AM, Wang J, Hughes TJ, Willis DK, Clemente TE, Diers BW, Jiang J, Hudson ME, Bent AF (2012) Copy number variation of multiple genes at Rhg1 mediates nematode resistance in soybean. Science 338:1206-1209
48. Gong Z, Wu Y, Koblizkova A, Torres GA, **Wang K**, Iovene M, Neumann P, Zhang W, Novak P, Buell CR, Macas J, Jiang J (2012) Repeatless and repeat-based centromeres in potato: Implications for centromere evolution. Plant Cell 24:3559-3574
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52. **Wang K,** Guan B, Guo W, Zhou B, Hu Y, Zhu Y, Zhang T (2008) Completely distinguishing individual A-genome chromosomes and their karyotyping analysis by multiple bacterial artificial chromosome-fluorescence in situ hybridization. ***Genetics*** 178:1117-1122
53. Guan B, **Wang K**, Zhou BL, Guo WZ, Zhang TZ (2008) Establishment of a multi-color genomic in situ hybridization technique to simultaneously discriminate the three interspecific hybrid genomes in gossypium. J Integr Plant Biol 50:345-351
54. **Wang K**, Guo W, Zhang T (2007) Detection and mapping of homologous and homoeologous segments in homoeologous groups of allotetraploid cotton by BAC-FISH. ***BMC Genomics*** 8:178
55. **Wang K**, Guo W, Zhang T (2007) Development of one set of chromosome-specific microsatellite-containing BACs and their physical mapping in *Gossypium hirsutum* L. ***Theor Appl Genet*** 115:675-682
56. **Wang K**, Song X, Han Z, Guo W, Yu JZ, Sun J, Pan J, Kohel RJ, Zhang T (2006) Complete assignment of the chromosomes of *Gossypium hirsutum* L. by translocation and fluorescence in situ hybridization mapping. ***Theor Appl Genet*** 113:73-80
57. Song X, **Wang K**, Guo W, Zhang J, Zhang T (2005) A comparison of genetic maps constructed from haploid and BC_1 mapping populations from the same crossing between *Gossypium hirsutum* L. and *Gossypium barbadense* L. ***Genome*** 48:378-390

PhD and Postdoc positions in cotton research:

We are currently seeking international PhD students and Postdoc to join our research team, with a primary focus on plant (cotton, rice, common/hairy vetch, and *Brassicaceae* vegetables) genetics and genomics in Wang lab at Nantong University, China. This is an exciting opportunity to work on cutting-edge research projects that aim to advance our understanding of genetic mechanisms in plants. Successful candidates will have the chance to collaborate with leading scientists, utilize state-of-the-art facilities, and contribute to impactful discoveries in the field. If you are passionate about plant genetics and are looking for a dynamic and supportive research environment, we encourage you to apply and become part of our innovative team. Experimental skills, experience in cotton or crop genetics and the ability to work in a distributed team are required. Interested candidates are welcome to establish contact via email to kwang5@ntu.edu.cn