



位置：首页 > 研究队伍



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1987年获扬州大学农学系农学学士，1990年获扬州大学农学系作物遗传育种硕士，1999年获中国科学院遗传研究所理学博士，1999年至2002年在美国Wisconsin-Madison大学从事博士后研究。2002年12月入选中国科学院“百人计划”，终期考核为优秀。2003年获国家杰出青年基金资助，现为*Chromosome Research*杂志编委。主要研究内容包括：

#### 主要研究方向——植物减数分裂的遗传调控机制

减数分裂是配子形成过程中进行的一种特殊分裂方式，其特点是染色体复制一次，细胞分裂两次，形成了染色体数目减半的配子。雌雄配子受精形成合子，染色体又恢复到原来的数目。由于减数分裂过程中来自父母双方染色体的充分重组和精确分离，既保证物种遗传物质的相对稳定，也为有性后代提供丰富的遗传多样性。减数分裂过程是一极其复杂的生命过程，涉及减数分裂的启动，同源染色体的配对、联会、交换和分离等一系列染色体的变化过程，这些过程受许多基因的调控，一直成为生物科学的研究热点。我们以水稻作为模式生物，通过正向和反向两种途径，系统研究参与减数分裂过程的基因，了解它们的作用网络，为最终解析减数分裂调控的分子机理提供依据。

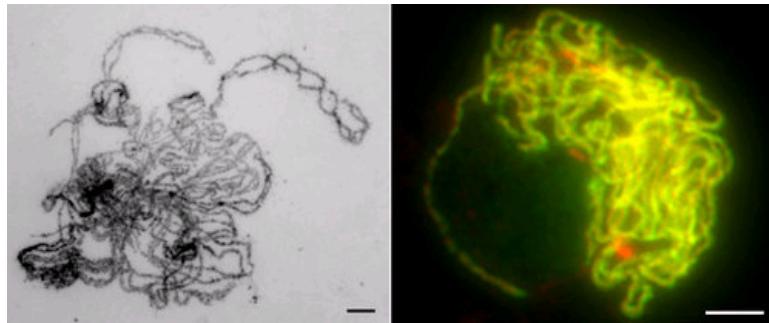


图1. 水稻联会复合体中央元件zep1突变体（左）及相关蛋白ZEP1的染色体定位（右）(Wang et al., Plant Cell, 2010)

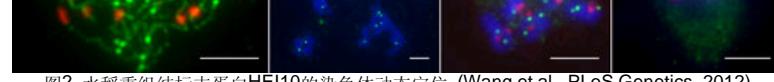


图2. 水稻重组结标志蛋白HEI10的染色体动态定位 (Wang et al., PLoS Genetics, 2012)

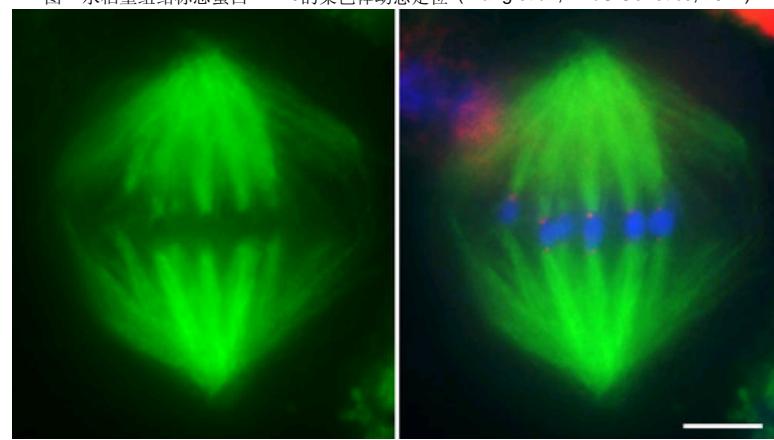


图3. 水稻减数分裂中期纺锤体与染色体间的相互作用 (Wang et al., Plant Cell, 2013)

回国后发表论文

### 一、减数分裂研究

1. Cheng ZK (2013). Analyzing meiotic chromosomes in rice. In *Methods in Molecular Biology: Plant Meiosis*.
2. Wang M, Tang D, Luo Q, Jin Y, Shen Y, Wang KJ, **Cheng ZK**. BRK1, a Bub1-related kinase, is essential for generating proper tension between homologous kinetochores at metaphase I of rice meiosis. *Plant Cell* (in press).
3. Luo Q, Tang D, Wang M, Luo WX, Zhang L, Qin BX, Shen Y, Wang KJ, Li YF, Cheng ZK. The role of OsMSH5 in crossover formation during rice meiosis. *Molecular Plant* 2012, doi: 10.1093/mp/sss145.
4. Hong LL, Tang D, Zhu KM, Wang KJ, Li M, and **Cheng ZK** (2012). Somatic and reproductive cell development in rice anther is regulated by a putative Glutaredoxin. *Plant Cell* 24: 577-588.
5. Wang K, Wang M, Tang D, Shen Y, Hu Q, Miao C, Lu T, **Cheng ZK** (2012). The role of rice HEI10 in the formation of meiotic crossovers. *PLoS Genet* 2012; 8: e1002809.
6. Hong LL, Tang D, Shen Y, Hu Q, Wang KJ, Li M, Lu TG, **Cheng ZK** (2012). MIL2 regulates early cell differentiation in the rice anther. *New Phytologist* 196: 402-413.
7. Ji JH, Tang D, Wang KJ, Wang M, Che LX, Li M, **Cheng ZK** (2012). OsCOM1 deficiency results in defective homologous recombination and in aberrant recombination between nonhomologous chromosomes in rice meiosis. *The Plant Journal* 72: 18-30.
8. Shen Y, Tang D, Wang KJ, Wang M, Huang J, Luo WX, Luo Q, Hong LL, Li M, and **Cheng ZK** (2012). The role of ZIP4 in homologous chromosome synapsis and crossover formation in rice meiosis. *Journal of Cell Science* 125: 2581-2591.
9. Che LX, Tang D, Wang KJ, Wang M, Zhu KM, Yu HX, Gu MH, **Cheng ZK** (2011). OsAM1 is required for leptotene-zygote transition in rice. *Cell Research* 21: 654-665.
10. Wang KJ, Wang M, Tang D, Shen Y, Qin BX, Li M, **Cheng ZK** (2011). PAIR3, an axis-associated protein, is essential for the recruitment of recombination elements onto meiotic chromosomes in rice. *Mol Biol Cell* 22: 12-19.
11. Wang M, Tang D, Wang KJ, Shen Y, Qin BX, Miao CB, Li, M, **Cheng ZK** (2011). OsSGO1 maintains synaptonemal complex stabilization in addition to protecting centromeric cohesion during rice meiosis. *The Plant Journal* 67: 583-594.
12. Shao T, Tang D, Wang KJ, Wang M, Che LX, Qin BX, Yu HX, Li M, Gu MH and **Cheng ZK** (2011). OsREC8 is essential for chromatid cohesion and metaphase I monopolar orientation in rice meiosis. *Plant Physiol.* 156: 1386-1396.
13. Wang M, Wang KJ, Tang D, Wei CX, Li M, Shen Y, Chi ZC, Gu MH, **Cheng ZK** (2010). The central element protein ZEP1 of the synaptonemal complex regulates the number of crossovers during meiosis in rice. *Plant Cell* 22: 417-430.
14. Yu HX, Wang M, Tang D, Wang KJ, Chen FL, Gong ZY, Gu MH, **Cheng ZK** (2010). OsSPO11-1 is essential for both homologous chromosome pairing and crossover formation in rice. *Chromosoma* 119: 625-636.
15. Wang KJ, Tang D, Wang M, Lu JF, Yu HX, Liu JF, Qian BX, Gong ZY, Wang X, Chen JM, Gu MH, **Cheng ZK** (2009). MER3 is required for normal meiotic crossover formation, but not for presynaptic alignment in rice. *Journal of Cell Science* 122: 2055-2063.

### 二、其它研究

16. Wu XR, Tang D, Li M, Wang KJ, **Cheng ZK**. Loose plant architecture 1, an INDETERMINATE domain protein involved in shoot gravitropism, regulates plant architecture in rice. *Plant Physiology*. 2012, DOI:10.1104/pp.112.208496.
17. Hong LL, Qian Q, Tang D, Wang KJ, Li M, and **Cheng ZK** (2012) A mutation in the rice chalcone isomerase gene causes the golden hull and internode1 phenotype. *Planta* 236: 141-151.
18. Shao T, Qian Q, Tang D, Chen J, Li M, **Cheng ZK**, Luo Q. (2012). A novel gene *IBF1* is required for the inhibition of brown pigment deposition in rice hull furrows. *Theor. Appl. Genet.* 125: 381-390.
19. Li M, Tang D, Wang KJ, Wu XR, Lu LL, Yu HX, Gu MH, Yan CJ and **Cheng ZK** (2011). Mutations in the F-box gene LARGER PANICLE improve the panicle architecture and enhance the grain yield in rice. *Plant Biotechnology Journal* 9: 2001-2012.
20. Qin BX, Tang D, Huang J, Li M, Wu XR, Lu LL, Wang KJ, Yu HX, Chen JM, Gu MH and **Cheng ZK** (2011). Rice OsGL1-1 is involved in leaf cuticular wax and cuticle membrane. *Molecular Plant* 4: 985-995.
21. Wang KJ, Tang D, Hong LL, Xu WY, Huang J, Li M, Gu MH, Xue YB, and **Cheng ZK** (2010). DEP and AFO regulate reproductive habit in rice. *PLoS Genet* 6: e1000818.
22. Zhu KM, Tang D, Yan CJ, Chi ZC, Yu HX, Chen JM, Liang JS, Gu MH, **Cheng ZK** (2010). ERECT PANICLE2 encodes a novel protein that regulates panicle erectness in *indica* rice. *Genetics* 184: 343-350.

23. Li M, Xiong GY, Li R, Cui JJ, Tang D, Zhang BC, Pauly M, **Cheng ZK** and Zhou YH (2009). Rice cellulose synthase-like D4 is essential for normal cell-wall biosynthesis and plant growth. *The Plant Journal* 60: 1055-1069.
24. Huang J, Zhang KW, Shen Y, Huang ZJ, Li M, Tang D, Gu MH, **Cheng ZK** (2009). Identification of a high frequency transposon induced by tissue culture, *nDaiZ*, a member of the *hAT* family in rice. *Genomics* 93: 274-281.
25. Zhang DF, Yang QY, Ding Y, Cao XF, Xue YB, **Cheng ZK** (2008) Cytological Characterization of the Tandem Repetitive Sequences and Their Methylation Status in the *Antirrhinum majus* Genome. *Genomics* 92: 107 - 114.
26. Zhang KW, Qian Q, Huang ZJ, Wang YQ, Li M, Hong LL, Zheng DL, Gu MH, Chu CC, and **Cheng ZK** (2006). *GOLD HULL AND INTERNODE2* (GH2) encodes a primarily multifunctional cinnamyl-alcohol dehydrogenase (CAD) in *Oryza sativa*. *Plant Physiol.* 140: 972-983.
27. Bao WD, Zhang WL, Yang QY, Zhang Y, Han B, Gu MH, Xue YB, and **Cheng ZK** (2006). Diversity of centromeric repeats in two closely related wild rice species, *O. officinalis* and *O. rhizomatis*. *Mol. Gen. Genomics* 275: 421-430.
28. Zhang WL, Yi CD, Bao WD, Liu B, Cui JJ, Yu HX, Cao XF, Gu MH, Liu M, and **Cheng ZK** (2005). The transcribed 165bp CentO satellite is the major functional centromeric element in the wild rice species *Oryza punctata*. *Plant Physiol.* 139: 306-315.
29. Zhang DF, Yang QY, Bao WD, Zhang Y, Han B, Xue YB and **Cheng ZK** (2005). Molecular cytogenetic characterization of the *Antirrhinum majus* genome. *Genetics* 169: 325-335.
30. Hong LL, Qian Q, Zhu KM, Tang D, Huang ZJ, Gao L, Li M, Gu MH, **Cheng ZK** (2010). ELE restrains empty glumes from developing into lemmas. *J. Genet. Genomics* 37: 101-114.
31. Huang J, Tang D, Shen Y, Qin BX, Hong LL, You AQ, Li M, Wang X, Yu HX, Gu M, **Cheng ZK** (2010). Activation of gibberellin 2-oxidase 6 decreases active gibberellin levels and creates a dominant semi-dwarf phenotype in rice (*Oryza sativa* L.). *J. Genet. Genomics* 37: 23-36.
32. Yu HX, Wang X, Gong ZY, Tang D, Gu MH, **Cheng ZK** (2008) Generating of rice *OsCENH3-GFP* transgenic plants and their genetic applications. *Chinese Science Bulletin* 53: 2981-2988.
33. Cui JJ, Fan SC, Shao T, Huang ZJ, Zheng DL, Tang D, Li M, Qian Q, **Cheng ZK** (2007). Characterization and fine mapping of the *ibf* mutant in rice. *J. Integr. Plant Biol.* 49: 678-685.
34. Tang XM, Bao WD, Zhang WL, **Cheng ZK** (2007). Identification of chromosomes from multiple rice genomes using a universal molecular cytogenetic marker system. *J. Integr. Plant Biol.* 49: 953-960.
- 三、合作论文**
35. The Tomato Genome Consortium (2012). The tomato genome sequence provides insights into fleshy fruit evolution. *Nature* 485: 635-641.
36. Xu J, Sun XJ, Jing YD, Wang M, Liu K, Jian YL, Yang M, Cheng ZK and Yang CL (2012). MRG-1 is required for genomic integrity in *Caenorhabditis elegans* germ cells. *Cell Research* 22:886 - 902.
37. Xu CH, **Cheng ZK**, and Yu WC (2012). Construction of rice minichromosomes by telomere mediated chromosomal truncation *The Plant Journal* 70: 1070-1079.
38. Li J, Jiang JF, Qian Q, Xu YY, Zhang C, Xiao J, Du C, Luo W, Zou GX, Chen ML, Huang YQ, Feng YQ, **Cheng ZK**, Yuan M, Chong K (2011). Mutation of rice BC12/GDD1, which encodes a kinesin-like protein that binds to a GA biosynthesis gene promoter, leads to dwarfism with impaired cell elongation. *Plant Cell* 23: 628-640.
39. Wang GX, He QY, Liu F, **Cheng ZK**, Talbert PB, Jin WW (2011). Characterization of CENH3 proteins and centromere-associated DNA sequences in diploid and allotetraploid *Brassica* species. *Chromosoma* 120: 353-365.
40. Gong ZY, Liu XX, Tang D, Yu HX, Yi CD, **Cheng ZK**, Gu MH (2011). Non-homologous chromosome pairing and crossover formation in haploid rice meiosis. *Chromosoma* 120: 47-60.
41. Chai CL, Fang J, Liu Y, Tong HN, Gong Y, Liu M, Wang YH, Qian Q, **Cheng ZK** and Chu CC (2011). *ZEBRA2*, encoding a carotenoid isomerase, is involved in photoprotection in rice. *Plant Mol. Biol.* 75: 211-221.
42. Lu F, Ammiraju J.S.S., Sanyal A., Zhang SL, Song RT, Chen JF, Li GS, Sui Y, Song X, **Cheng ZK**, de Oliveira A.C., Bennetzen J.L., Jackson S.A., Wing R.A., Chen MS (2009). Comparative sequence analysis of MONOCULM1-orthologous regions in 14 *Oryza* genomes. *PNAS* 106: 2071-2076.
43. Gao DY, Gill N, Kim HR, Walling JG, Zhang WL, Fan CZ, Yu YS, Ma JX, Miguel PS, Jiang N, **Cheng ZK**, Wing RA, Jiang JM and Jackson SA (2009). A lineage-specific centromere retro-transposon in *Oryza brachyantha*. *The Plant Journal* 60: 820-831.
44. Shang JJ, Tao Y, Chen XW, Zou Y, Lei CL, Wang J, Li XB, Zhao XF, Zhang MJ, Lu ZK, Xu JC, **Cheng ZK**, Wan JM and Zhu LH (2009). Identification of a new rice blast resistance gene, *Pid3*, by genome wide comparison of paired-nucleotide-bindingsite – Leucine-rich repeat genes and their pseudogene alleles between the two sequenced rice genomes. *Genetics* 182: 1303-1311.
45. Cheng XD, Zhang DF, **Cheng ZK**, Keller B, Ling HQ (2009). A new family of *Ty1-copia*-Like retrotransposons originated in the tomato genome by a recent horizontal transfer event. *Genetics* 181: 1183-1193.
46. Xue YB, Zhang YJ, Yang QY, Li Q, **Cheng ZK**, Dickinson, HG (2009). Genetic features of a pollen-part mutation suggest an inhibitory role for the *Antirrhinum* pollen self-incompatibility determinant. *Plant Mol. Biol.* 70: 499-509.
47. Mueller L. A., et al. (2009). A Snapshot of the Emerging Tomato Genome Sequence. *Plant Genome* 2: 78-92.
48. Chen SH, Yang Y, Shi WW, Ji Q, He F, Zhang ZD, **Cheng ZK**, Liu XN, Xu ML (2008). *Badh2*, encoding betaine aldehyde dehydrogenase, inhibits the biosynthesis of 2-acetyl-1-pyrroline, a major component in rice fragrance. *Plant Cell* 20: 1850-1861.
49. Yan S, Yan CJ, Zeng XH, Yang YC, Fang YW, Tian CY, Sun YW, **Cheng ZK**, Gu MH (2008). *ROLLED LEAF 9*, encoding a GARP protein, regulates the leaf abaxial cell fate in rice. *Plant Mol. Biol.* 68: 239 - 250.
50. Fang J, Chai CL, Qian Q, Li CL, Tang JY, Sun L, Huang ZJ, Guo XL, Sun CH, Liu M, Zhang Y, Lu QT, Wang YQ, Lu CM, Han B, Chen F, **Cheng ZK**, Chu CC (2008). Mutations of genes in synthesis of the carotenoid precursors of ABA lead to preharvest sprouting and photo-oxidation in rice. *The Plant Journal* 54: 177-189.
51. Ding Y, Wang X, Su L, Zhai JX, Cao SY, Zhang DF, Liu CY, Bi YP, Qian Q, **Cheng ZK**, Chu CC, Cao XF (2007). SDG714, a Histone H3K9 methyltransferase, is involved in Tos17 DNA methylation and transposition in rice. *Plant Cell* 19: 9-22.
52. Yang QY, Zhang DF, Li Q, **Cheng ZK**, Xue YB (2007). Heterochromatic and genetic features are consistent with recombination suppression of the self-incompatibility locus in *Antirrhinum*. *The Plant Journal* 51: 140 - 151.
53. Tang YL, Wen XG, Lu QT, Yang ZP, **Cheng ZK**, Lu CM (2007). Heat stress induces an aggregation of the light-harvesting complex of photosystem II in spinach plants.

54. Jiang L, Zhang W, Xia Z, Jiang G, Qian Q, Li A, **Cheng ZK**, Zhu L, Mao L, Zhai W. A paracentric inversion suppresses genetic recombination at the FON3 locus with breakpoints corresponding to sequence gaps on rice chromosome 11L. *Mol. Gen. Genomics* 2007, 277: 263-272.
55. Li L, Wang XF, Stolc V, Li XY, Zhang DF, Su N, Tongprasit W, Li SG, **Cheng ZK**, Wang J and Deng XW (2006). Genome-wide transcription analyses in rice using tiling microarrays. *Nature Genetics* 38: 124-129.
56. Wang Y, Tang XM, **Cheng ZK**, Mueller L, Giovannoni J and Tanksley SD (2006) Euchromatin and pericentromeric heterochromatin: Comparative composition in the tomato genome. *Genetics* 172: 2529-2540.
57. Ge CM, Cui X, Wang YH, Hu YX, Fu ZM, Zhang DF, Cheng ZK and **Jiayang Li**. (2006). *BUD2*, encoding an S-adenosylmethionine decarboxylase, is required for *Arabidopsis* growth and development. *Cell Research* 16: 446-456.
58. Mueller L. A., et al. (2005) The Tomato Sequencing Project, the first cornerstone of the International Solanaceae Project (SOL). *Comparative and Functional Genomics* 6: 153-158.
59. Jiao YL, Jia PX, Wang XF, Su N, Yu SL, Zhang DF, Ma LG, Feng Q, Jin ZQ, Li L, Xue YB, **Cheng ZK**, Zhao HY, Han B, and Deng XW (2005). A Tiling Microarray Expression Analysis of Rice Chromosome 4 Suggests a Chromosome-Level Regulation of Transcription. *Plant Cell* 17: 1641-1657.
60. Lee HR, Zhang WL, Langdon T, Jin WW, Yan HH, **Cheng ZK**, and Jiang JM (2005). ChIP cloning reveals rapid evolutionary patterns of centromeric DNA in *Oryza* species. *PNAS* 102: 11793-11798.
61. Nagaki K, Neumann P, Zhang DF, Ouyang S, Buell CR, **Cheng ZK**, and Jiang JM (2005). Structure, divergence, and distribution of the CRR centromeric retrotransposon family in rice. *Molecular Biology and Evolution* 22: 845-855.
62. Guyot R, Cheng XD, Su Y, **Cheng ZK**, Schlagenhauf E, Keller B and Ling HQ (2005). Complex Organization and Evolution of the Tomato, Pericentromeric Region at the FER Gene Locus1. *Plant Physiol.* 138: 1205-1215.
63. Nagaki K., **Cheng ZK**, Ouyang S., Talbert P.B., Kim M., Jones K.M., Henikoff S., Buell C.R., Jiang JM (2004). Sequencing of a rice centromere uncovers active genes. *Nature Genet.* 36: 138-145.
64. Zhang Y, Huang YC, Zhang L, Li Y, Lu TT, Lu YQ, Feng Q, Zhao Q, **Cheng ZK**, Xue YB, Rod A. Wing and Han B (2004). Structural features of the rice chromosome 4 centromere. *Nucleic Acids Research* 32: 2023-2030.
65. Yu YS et al., (2003). In-depth view of structure, activity, and evolution of rice chromosome 10. *Science*, 300: 1566-1569.
66. Liu DF, **Cheng ZK**, Liu GQ, Liu GZ, Wang Y, Zhao XF, Zhu LH (2003). Characterization and mapping of a lesion mimic mutant in rice (*Oryza sativa* L.). *Chinese Science Bulletin* 48(9): 892-896.



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