

宋庆鑫

教授 博士生导师

办公地址：南京农业大学理科楼 A626

联系电话：025-84395702

电子邮箱：qxsong@njau.edu.cn



个人简介：

2006 年本科毕业于沈阳农业大学，2006-2013 年在中国科学院遗传与发育生物学研究所攻读博士学位，期间主要研究种子油脂合成调控的分子机理。2013 年-2018 年，在美国德克萨斯大学奥斯汀分校从事博士后研究，主要从表观遗传修饰和转录调控网络两个角度研究杂种优势和多倍体化形成的遗传机制。2018 年 9 月作为南京农业大学高层次人才到农学院任教授。研究论文主要发表在《PNAS》、《Genome Biology》、《Nature Communications》、《PLoS Genetics》等国际知名期刊。

研究方向：

在自然进化和人工驯化过程中，作物的形态发生巨大变化。我们将综合利用生物信息学、群体遗传学、单细胞组学和表观遗传编辑等手段，研究表观遗传调控在多倍体作物进化和驯化中的作用以及鉴定与作物重要农艺性状相关的表观遗传位点。

课题组热烈欢迎对生物信息学和表观遗传学感兴趣的同学加入，希望帮助学生在生物学的多个维度得到全方位的锻炼，鼓励学生提出并开展自己感兴趣的科研项目，欢迎感兴趣的学生和我联系。

发表论文(#: co-first author)：

Song Q, Huang TY, Yu HH, Ando A, Mas P, Ha M, Chen ZJ. (2019) Diurnal regulation of SDG2 and JMJ14 by circadian clock oscillators orchestrates histone modification rhythms in Arabidopsis. *Genome Biology*. 20:170

Song Q, Ando A, Xu D, Fang L, Zhang T, Huq E, Qiao H, Deng XW, Chen ZJ. (2018) Diurnal down-regulation of ethylene biosynthesis mediates biomass heterosis. *PNAS*. 115: 5606-5611.

Song Q, Zhang T, Stelly D and Chen ZJ. (2017) Epigenomic and functional analyses revealed roles of epialleles in the loss of photoperiod sensitivity during domestication of allotetraploid cottons. *Genome Biology*. 18:99.

Song Q, Guan X and Chen ZJ. (2015) Dynamic Roles for Small RNAs and DNA Methylation during Ovule and Fiber Development in Allotetraploid Cotton. *PLoS Genetics* 11:e1005724.

Miller M[#], **Song Q**[#], Shi X, Juenger TE and Chen, ZJ. (2015) Natural variation in timing of stress-responsive gene expression predicts heterosis in intraspecific hybrids of Arabidopsis. *Nature Communications* 6:7453.

Song Q and Chen, ZJ. (2015) Epigenetic and developmental regulation in plant polyploids. *Current Opinion Plant Biology* 24:101-109.

Song QX[#], Li QT[#], Liu YF, Zhang FX, Ma B, Zhang WK, Man WQ, Du WG, Wang GD, Chen SY and Zhang JS. (2013) Soybean GmbZIP123 gene enhances lipid content in the seeds of transgenic Arabidopsis plants. *Journal of Experimental Botany* 64:4329-4341.

Song QX, Lu X, Li QT, Chen H, Hu XY, Ma B, Zhang WK, Chen SY and Zhang JS. (2013) Genome-wide analysis of DNA methylation in soybean. *Molecular Plant* 6:1961-1974.

Song QX, Liu YF, Hu XY, Zhang WK, Ma B, Chen SY and Zhang JS. (2011) Identification of miRNAs and their target genes in developing soybean seeds by deep sequencing. *BMC Plant Biology* 11:5.

Li QT, Lu X, **Song QX**, Chen HW, Wei W, Tao JJ, Bian XH, Shen M, Ma B, Zhang WK, Bi YD, Li W, Lai YC, Lam SM, Shui GH, Chen SY and Zhang JS. (2017) Selection for a Zinc-Finger Protein Contributes to Seed Oil Increase during Soybean Domestication. *Plant Physiology* 173:2208-2224.

Saski CA, Scheffler BE, Hulse-Kemp AM, Liu B, **Song Q**, Ando A, Stelly DM, Scheffler JA, Grimwood J, Jones DC, Peterson DG, Schmutz J and Chen ZJ. (2017) Sub genome anchored physical frameworks of the allotetraploid Upland cotton (*Gossypium hirsutum* L.) genome, and an approach toward reference-grade assemblies of polyploids. *Scientific Reports* 7:15274.

Zheng D, Ye W, **Song Q**, Han F, Zhang T and Chen ZJ. (2016) Histone Modifications Define Expression Bias of Homoeologous Genomes in Allotetraploid Cotton. *Plant Physiology* 172:1760-1771.

Ko DK, Rohozinski D, **Song Q**, Taylor SH, Juenger TE, Harmon FG and Chen ZJ. (2016) Temporal Shift of Circadian-Mediated Gene Expression and Carbon Fixation Contributes to Biomass Heterosis in Maize Hybrids. *PLoS Genetics* 12:e1006197.

Zhang T, Hu Y, Jiang W, Fang L, Guan X, Chen J, Zhang J, Saski CA, Scheffler BE, Stelly DM, Hulse-Kemp AM, Wan Q, Liu B, Liu C, Wang S, Pan M, Wang Y, Wang D, Ye W, Chang L, Zhang W, **Song Q**, Kirkbride RC, Chen X, Dennis E, Llewellyn DJ, Peterson DG, Thaxton P, Jones DC, Wang Q, Xu X, Zhang H, Wu H, Zhou L, Mei G, Chen S, Tian Y, Xiang D, Li X, Ding J, Zuo Q, Tao L, Liu Y, Li J, Lin Y, Hui Y, Cao Z, Cai C, Zhu X, Jiang Z, Zhou B, Guo W, Li R and Chen ZJ. (2015) Sequencing of allotetraploid cotton (*Gossypium hirsutum* L. acc. TM-1) provides a resource for fiber improvement. *Nature Biotechnology* 33:531-537.

Tuttle JR, Nah G, Duke MV, Alexander DC, Guan X, **Song Q**, Chen ZJ, Scheffler BE and Haigler CH. (2015) Metabolomic and transcriptomic insights into how cotton fiber transitions to secondary wall

synthesis, represses lignification, and prolongs elongation. *BMC Genomics* 16:477.

Guan X, **Song Q** and Chen ZJ. (2014) Polyploidy and small RNA regulation of cotton fiber development. *Trends Plant Science* 19:516-528.

Guan X, Nah G, **Song Q**, Udall JA, Stelly DM and Chen ZJ. (2014) Transcriptome analysis of extant cotton progenitors revealed tetraploidization and identified genome-specific single nucleotide polymorphism in diploid and allotetraploid cotton. *BMC Research Notes* 7:493.

Liu YF, Li QT, Lu X, **Song QX**, Lam SM, Zhang WK, Ma B, Lin Q, Man WQ, Du WG, Shui GH, Chen SY and Zhang JS. (2014) Soybean GmMYB73 promotes lipid accumulation in transgenic plants. *BMC Plant Biology* 14:73.

Zou HF, Zhang YQ, Wei W, Chen HW, **Song QX**, Liu YF, Zhao MY, Wang F, Zhang BC, Lin Q, Zhang WK, Ma B, Zhou YH, Zhang JS and Chen SY. (2013) The transcription factor AtDOF4.2 regulates shoot branching and seed coat formation in Arabidopsis. *Biochemical Journal* 449:373-378.

Ma B, He SJ, Duan KX, Yin CC, Chen H, Yang C, Xiong Q, **Song QX**, Lu X, Chen HW, Zhang WK, Lu TG, Chen SY and Zhang JS. (2013) Identification of rice ethylene-response mutants and characterization of MHZ7/OsEIN2 in distinct ethylene response and yield trait regulation. *Molecular Plant* 6:1830-1848.

Hao YJ, Wei W, **Song QX**, Chen HW, Zhang YQ, Wang F, Zou HF, Lei G, Tian AG, Zhang WK, Ma B, Zhang JS and Chen SY. (2011) Soybean NAC transcription factors promote abiotic stress tolerance and lateral root formation in transgenic plants. *Plant Journal* 68:302-313.

Hao YJ, **Song QX**, Chen HW, Zou HF, Wei W, Kang XS, Ma B, Zhang WK, Zhang JS and Chen SY. (2010) Plant NAC-type transcription factor proteins contain a NARD domain for repression of transcriptional activation. *Planta* 232:1033-1043.