CURRICULUM VITAE

Personal Information

Name	Jun Zou	Gender	Female	
Position Title		Associate Professor, Ph. D supervisor		
Working Department		National Key Laboratory of Crop Genetic Improvement, College of Plant Science and Technology		
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Research Interest

- Germplasm innovation and intersubgenomic heterosis analysis of rapeseed
- QTL mapping, marker assisted selection and genome-wide selection in rapeseed
- Interspecific crosses and its consequence on genomic alterations of *Brassica* oilseeds
- Towards a stable new *Brassica* hexaploid species with different subgenome construction

Education & Working Experience

2012 - Present: Associate professor, National Key Laboratory of Crop Genetic Improvement, College of Plant Science & Technology, Huazhong Agricultural University, Wuhan, China

Sep 2015 - Sep 2016 and Oct 2014 - Dec 2014: Visiting scientist, Department of Plant Breeding, Justus Liebig University Giessen, Giessen, Germany

Concentrations: Analyzing genomic structural variation in synthesized tetraploids and hexaploids

Oct 2011 - Jan 2012: Visiting scientist, Wagga Wagga Agricultural Research Institute, NSW, Australia

Concentrations: Analyzing subgenomic differentiation in three tetraploid *Brassica* species through genetic comparative mapping with genotyping by sequencing technique

Jan 2010 - Feb 2012: Post doctor in National Key Laboratory of Genetic Improvement, Huazhong Agricultural University, China

Concentrations: Retrotransposon activity in the offspring and hybrids derived from interspecific hybridization; genetic mapping and association mapping analysis referring to oil content of *B. napus*; exploring intersubgenomic heterosis of new-type rapeseed.

Sep 2002 - Dec 2009: Ph. D in Developmental Biology, Huazhong Agricultural University

Thesis title: “Analyzing the genomic structural variation of new-type *Brassica napus* and its genetic improvement”.

Sep 1998 – Jun 2002: B. A. in Agronomy, Huazhong Agricultural University, China
Thesis title: “The genetic difference of boron uptake efficiency between two genotypes of *Arabidopsis thalian*”.

Publications

Published papers as the first and corresponding author ($^{\#}$co-first author, *corresponding)

Citation from *web of science*, 201911

2020

1）秦晗，张文姗，王猛，熊思灿，胡丹丹，孙秀丽，胡莲莲，孟金陵，邹珺*。四个芸薹属物种硫苷比较及特殊硫苷种间导入。植物遗传资源学报，2020，21(01):94-104.

2019

1) **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 G, Meng J, Fan L*. Genome-wide selection footprints and deleterious variations in young Asian allotetraploid rapeseed. **Plant Biotechnology Journal**, 2019, 17(10): 1998-2010. April 4 first online, https://doi.org/10.1111/pbi.13115

2) Hu D, Zhang W, Zhang Y, Chang S, Chen L, Chen Y, Shi Y, Shen J, Meng J, **Zou J***. Reconstituting the genome of a young allopolyploid crop, *Brassica napus*, with its related species. **Plant Biotechnology Journal**, 2019, 17 (6): 1106-1118. https://doi.org/10.1111/pbi.13041

2018

1）**Zou J**$^{\#}$*, H D$^{\#}$, Mason A, Shen X, Wang X, Wang N, Grandke F, Wang M, Chang S, Snowdon R, Meng J. Genetic changes in a novel breeding population of *Brassica napus* synthesized from hundreds of crosses between *B. rapa* and *B. carinata*. **Plant Biotechnology Journal**, 2018, 16(2), 507-519, doi: 10.1111/pbi.12791 (11 citation)

2）Luo Z$^{\#}$, Wang M$^{\#}$, Long Y, Huang Y, Shi L, Zhang C, Liu X, Fitt B, Xiang J, Mason A, Snowdon R, Liu P, Meng J, **Zou J***. Incorporating pleiotropic quantitative trait loci in dissection of complex traits: seed yield in rapeseed as an example. **Theor Appl Genet.**, 2018, 131(2), 497, equal to 2017, 130(8), 1569-1585, doi:10.1007/s00122-017-3005-2 (16 citation)

2017

1）Liu P[#], Zhao Y[#], Liu G, Wang M, Hu D, Hu J, Meng J, Reif JC*, **Zou J***. Hybrid Performance of an immortalized F_2 rapeseed population is driven by additive, dominance, and epistatic effects. Front. Plant Sci., 2017, 8:815. doi: 10.3389/fpls.2017.00815 (4 citations)

2）Zhang W[#], Hu D[#], Raman R, Guo S, Wei Z, Shen X, Meng J, Raman H*, **Zou J***. Investigation of the genetic diversity and quantitative trait loci accounting for important agronomic and seed quality traits in *Brassica carinata*. Front. Plant Sci.，2017, 8:615. doi: 10.3389/fpls.2017.00615 (3 citations)

2016

1）**Zou J**[#]*, Zhao Y[#], Liu P, Shi L, Wang X, Wang M, Meng J, Reif J*. Seed quality traits can be predicted with high accuracy in *Brassica napus* using genomic data. PLoS ONE, 2016, 11(11): e0166624. doi:10.1371/journal.pone.0166624 (8 citation)

2）Wei Z, Wang M, Chang S, Wu C, Liu P, Meng J, **Zou J***. Introgressing subgenome components from *Brassica rapa* and *B. carinata* to *B. juncea* for broadening its genetic base and exploring intersubgenomic heterosis. Front. Plant Sci., 2016, 7:1677. doi: 10.3389/fpls.2016.01677 (7 citations)

3）**Zou J**, Hu D, Liu P, Raman H*, Liu Z*, Liu X, Parkin IA, Chalhoub B, Meng J*. Co-linearity and divergence of the A subgenome of *Brassica juncea* compared with other *Brassica* species carrying different A subgenomes. BMC Genomics, 2016, 17(1):18. doi: 10.1186/s12864-015-2343-1 (9 citations)

2015-2012

1）Shen E[#], **Zou J**[#], Behrens F[#], Chen L, Ye C, Dai S, Li R, Ni M, Jiang X, Qiu J, Liu Y, Wang W, Zhu Q, Chalhoub B, Bancroft I, Meng J, Cai D*, Fan L*. Identification, evolution, and expression partitioning of miRNAs in allopolyploid *Brasscia napus*. Journal of Experimental Botany, 2015, 66(22): 7241-7253 doi:10.1093/jxb/erv420 (23 citations)

2）**Zou J**, Raman H*, Guo S, Hu D, Wei Z, Luo Zi, Long Y, Shi W, Fu Zhong, Du D, Meng J*. Constructing a dense genetic linkage map and mapping QTL for the traits of flower development in *Brassica carinata*. Theoretical and Applied Genetics, 2014, 127(7):

1593-1605 (18 citations)

Before 2012

1） **Zou J**$^{\#}$, Fu D$^{\#}$, Gong H, Qian W, Xia W, Pires C, Li R, Long Y, Mason A, Yang T, Lim Y, Beom S, Meng J*. *De novo* genetic variation associated with retrotransposon activation, genomic rearrangements and trait variation in a RIL population of *Brassica napus* derived from interspecific hybridization with *B. rapa*. The Plant Journal, 2011, 68(2):212-224 (51citations)

2） **Zou J,** Zhu J, Huang S, Tian E, Xiao Y, Fu D, Tu J, Fu T, Meng J*. Broadening the avenue of intersubgenomic heterosis for oilseed *Brassica*. Theoretical and Applied Genetics, 2010, 120: 283-290 (55 citations)

3） **Zou J**$^{\#}$, Jiang C$^{\#}$, Cao Z, Li R, Long Y, Chen S, Meng J*. Association mapping of seed oil content in different *Brassica napus* populations and its coincidence with QTL identified from linkage mapping. Genome, 2010, 53: 908-916 (51 citations)

4） Chen S$^{\#}$, **Zou J**$^{\#}$, Cowling W, Meng J*. Allelic diversity in a novel gene pool of canola-quality *Brassica napus* enriched with alleles from *B. rapa* and *B. carinata*. Crop & Pasture Science, 2010, 61, 483-492 (21 citations)

5） **Zou J**, Gong H, Yang Tae-Jin, Meng J*. Retrotransposons - a Major Driving Force in Plant Genome Evolution and a Useful Tool for Genome Analysis. J. Crop. Sci. Biotech., 2009, 12 (1):1-8 (16 citations)

6） **Zou J**, Fu D, Gong H, Tian E, Xiao Y, Huang S, Meng J*. How far we could go on modifying U's triangle for rapeseed breeding? The Fifteenth Biennial Australian Research Assembly On *Brassicas*: conference proceedings. Geraldton, Western Australia. November, 2007. Full paper and abstract: 126-130.

Book Chapter

Zou J, Meng J. Chapter 8, Rapeseed germplasm innovation and the utilization of heterosis. In: Tu JX (eds) The Biological Basis and Utilization of Rapeseed Heterosis. Science Publishers, Beijing, 9ISBN978-7-03-058545-5, 2018, pp 267-286

Zou J, Wang N, Meng J. Chapter 8, Mutagenesis. In: Edwards D, Batley J, Parkin IAP, Kole C (eds) Genetics, Genomics and Breeding of Oilseed Brassicas. Science Publishers, CRC press, USA, 2011, pp 158-173.

Additional Information

Oral presentation at international conferences in recent 5 years

1) Hu D, Jing J, Qin H, Zhang W, Zhang Y, Shen J, Meng J, **Zou J***. Expanding a novel gene pool of *Brassica napus* with massive introgression of related oilseed species and exploring its intersubgenomic heterosis. The 15th International Rapeseed Congress, BERLIN, Germany, 16.-19.06.2019
2) Hu D, Xue H, Chang S, Hu J, Zhang W, Meng J, **Zou J***. Development and evaluation of a novel gene pool of *Brassica napus* with introgression of genomic variation between and within related oilseed species. The 4th International Symposium on Genomics of Plant Genetic Resources, September 3-7, 2017, Giessen, Germany.
3) **Zou J***, Chang S, Meng J, Gäbelein R, Mason A. Investigation and improvement of the genome stability and genetic diversity of advanced allohexaploids derived from different interspecific cross origins. The 20th Crucifer Genetics Conference, *Brassica* 2016, and the 19th Australian Research Assembly, October 3-7, 2016, Melbourne, Australia.
4) **Zou J***, Meng J, Mason A, Liu P, Hu D, Wang M, Luo Z, Stein A, Samans B, Snowdon R. Understanding and exploring subgenomic variation in *Brassica* oilseeds. The Second Sino-German Symposium on Genetics and Biotechnology of Rapeseed, May 23-27, 2016, Kiel, Germany.
5) **Zou J***, Luo ZL, Xiang JX, Liu Pf, Wang XH, Niu XH, Shi L, Feng J, Long Y, Zhang CY, Meng J. Comprehensive linkages between SNP and various important agronomic traits in rapeseed via QTL analysis and whole-genome evaluation. The 14th International Rapeseed Congress, July 5-9, 2015, Saskatoon, Canada.
6) Hu D, **Zou J***, Liu P, Chen Y, Chen L, Xiao Y, Meng J. Creating a novel recurrent selection population in *Brassica napus* by massively introgressing subgenomic components from four oilseed *Brassica* species. The 14th International Rapeseed Congress, July 5-9, 2015, Saskatoon, Canada.

Other academic activities

1) Secretariat, the 19th Crucifer Genetics Workshop and Brassica 2014, 2014. 03.30-04.02, Wuhan, China
2) Secretariat, the National Doctoral Forum of Crop Genetic Improvement and Biological Seed Industry, 2012.11.03, Wuhan, China

3) Reviewers for the scientific journals, Plant Journal, Plant Genome, Plant Biotechnology, BMC plant biology, Theoretical and Applied Genetics, Plant Breeding, etc.

Supervision

Current: Nine MSc students and one Ph. D student

Previous: One Ph. D student, 9 MSc students, 19 undergraduate research project students

Teaching

Plant Breeding Principle, Molecular Plant Breeding, Plant Seed Production and Technology

Competitive Research Grant Funding

1) Principal investigator: NSFC project, The genome structural variation of the ‘New-type’ *Brassica napus* (2020-2023).
2) Principal investigator: NSFC-DFG project, The whole genome-wide pattern of heterosis associated with the allopolyploid chromosome collision (2019-2021).
3) Principal investigator: Cooperation research funded by NSW Department of Primary Industries, Australia, Resynthesis of *Brassica napus* with Shattering Resistance (2016-2021).
4) Participate: National Key Research and Development Program of China (No.2016YFD0101300), Elite hybrid breeding and utilization of rapeseed (2016-2020).
5) Participate: National Basic Research Program of China (Grant No. 2015CB150200), Dissecting the genetic basis of seed oil content of rapeseed (2015-2019).
6) Principal investigator: National Science Foundation of China for international cooperation and exchange (31410303006), The 19th Crucifer Genetics Workshop and Brassica 2014.
7) Principal investigator: National Science Foundation of China for young scientist (31100876), Genome stress induced by intercrosses characterized by transposon activity and its genetic effects (2012-2014).
8) Principal investigator: Transposon activity in new-type *Brassica napus* with introgression of subgenomic components, a project of Chinese Postdoctoral Foundation (2010-2011).