



Lingling Chai

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Education Background

China Agricultural University, Dept. of plant science & breeding (Ph.D)

09/2012-now

Major: crop science

Jilin Agricultural University, Dept. of agronomy (B.S)

09/2008-07/2012

Major: agronomy,

Shandong Province Qihe County No.1 Middle School

09/2005-06/2008

Current Research

Genetic mapping of a major QTL controlling plant height and spike length.

In our previous study, two wheat genotypes with significant different plant height, that is ND3488 and ND459, have been employed to produce a genetic population with 191 recombinant inbred lines(RIL), and genetic linkage map has been constructed with 178 SSR markers and 1901 SNP markers. Using this genetic linkage map and phenotype data, a major environmentally stable QTL controlling plant height and spike length with no effect on kernel weight and kernel number per spike was detected on short arm of chromosome 2D (Huijie Zhai, 2014) .

Academic Achievements

- Xuejiao Cheng; **Lingling Chai**; Lu Xu; Huijie Zhai; Aiju Zhao; Huiru Peng; Yingyin Yao; Mingshan You; Qixin Sun; Zhongfu Ni. Identification and Characterization of a High Kernel Weight Mutant Induced by Gamma Radiation in Wheat (*Triticum aestivum* L.). *BMC Genetic*, 2015, 16:127.
- Hu ZR, Han ZF, Song N, **Chai LL**, Yao YY, Peng HR, Ni ZF, Sun QX. 2013. Epigenetic modification contributes to the expression divergence of three TaEXPA1 homoeologs in hexaploid wheat (*Triticum aestivum* L.). *New Phytologist*, 197:1344-1352.

Skills

- Experience with DNA & RNA extraction, DNA purification, batch primer design and PCR
- Experience with phenotyping wheat root related traits under water culture, such as primary root length and total root length
- Experience with phenotyping wheat grain related traits, namely TGW, grain length, width, circle and grain area
- Experience with greenhouse experiment and management
- Familiar with wheat breeding programs including parents selection, segregation population construction, and progeny line selection
- Experience with molecular marker enrichment for QTL regions based on collinearity between wheat and model genomes, namely, *Brachypodium*, rice and *Aegilops tauschii*



- Experience with field management including experimental design, crossing, phenotypic data collection and statistical analysis
- Computer proficiency in SPSS software for statistical analysis, WinQTL Cart, JoinMap 4.0, MapChart, software for QTL mapping, and Photoshop software for drawing.

Scholarship & Honors

- **Scholarship:** National Scholarship, National Excellent Scholarship, winner of Top Prize (for consecutive four years)
- **Honors:** Excellent Graduate of Jilin Province, Provincial Outstanding Student, Third-class Prize of National College English Contest, Outstanding member in Jilin Agricultural University