Curriculum vitae of Junming Li

1. EDUCATION

M.S., 1983-1986, Department of Agronomy,
Inner Mongolia College of Agriculture and Animal Husbandry,
Huhehot, Inner Mongolia, China

B.A., 1979-1983, Department of Agronomy,
Hebei Agricultural University,
Handan, Hebei, China

2. PROFESSIONAL EXPERIENCE

Jan. 2002-Present: Principal investigator, Center for Agricultural Resources Research,
Institute of Genetics and Developmental Biology,
Chinese Academy of Sciences, China

Mar. 2001- Dec. 2001: Professor, Shijiazhuang Institute of Agricultural Modernization,
Chinese Academy of Sciences, China

Mar. 1999- Feb. 2001: STA fellow, National Hokkaido Agriculture Research Centre,
Ministry of Agriculture, Forestry and Fishery, Memuro, Japan

Aug. 1992- Feb. 1999: Associate professor, Shijiazhuang Institute of Agricultural Modernization,
Chinese Academy of Sciences, China

(Apr. 1995—Sep. 1995, Visiting scholar, Purdue University, West Lafayette, Indiana, USA)

Apr. 1988- Jul. 1992: Assistant professor, Institute of Plant Genetics and Physiology,
Hebei Academy of Agricultural and Forestry Sciences, Shijiazhuang, China

Jul. 1986-Mar. 1988: Research Assistant, Institute of Cereal Crops,
Hebei Academy of Agricultural and Forestry Sciences, Shijiazhuang, China

3. HONORS AND ACADEMIC AWARDS

None.

4. MAJOR RESEARCH INTERESTS, SELECTED RESEARCH PROJECTS

(1) Major research interests and projects

① Wheat molecular chromosome engineering breeding

Distant hybridization or/and chromosome engineering breeding is a rapid, practical approach to transfer potentially useable alien chromatin from wild species into cultivated hexaploid wheat.

In our lab, *E. elongata*, *S. cereale* and *Ae. biuncialis* were successfully crossed with *T. aestivum* and a set of novel disease or/and drought resistant substitution and translocation lines were identified and used in breeding. With the aid of genome-wide molecular marker assisted selection, some elite varieties and lines with high yield potential, good industrial processing properties, strong disease resistance, and high nitrogen use efficiency (NUE) have derived from these alien translocation lines.

② Molecular genetic analysis of gene/QTL relevant to yield and NUE

Using forward and reverse genetics approach, we conducted gene/QTL identification, isolation and cloning of economic agronomic attributes such as wheat yield potential and NUE. We also used transgenics, RIL population and near inbred lines (NIL) to analyze the functioning of interesting gene/QTL and screened some superior allelic variation. We are mainly interested in understanding the molecular genetic basis of wheat yield and nitrogen use efficiency.

(2) Research background

Wheat is one of the leading crops worldwide. Huang-Huai Winter Wheat Region along the Yellow River, the most important wheat production zone of China, provides some 65% of commercial wheat products with 56% of total wheat growing area of the nation. Aiming to improve wheat yield potential, end-use quality, biotic stresses (mainly stripe rust and powdery mildew) and abiotic stresses (mostly drought, hot and dry wind) resistance, and water and nutrient use efficiency, we put efforts on introgression of alien chromatin through distant hybridization between cultivated wheat and *Triticinae* relatives such as *S. cereale*, *Ae. biuncialis* and *T. ponticum* (syn. *A. elongatum*) etc. and eventually obtained a set of novel disease/drought resistant addition, substitution and translocation lines by comprehensive application of C-banding, GISH, FISH and molecular markers. Some of these translocation lines were efficiently used in developing widely adapted, disease resistant, drought tolerant and productive wheat cultivars with appropriate industrial quality, one commercial wheat variety Kenong1006 were released in 2013 and grown in total over 30,000 hectare in the last two years.

In order to genetically investigate the characteristics of high yield potential and NUE of wheat Kenong9204 (in abbreviation Kn9204), we cloned six genes related to nitrogen metabolism pathway, investigated the function of *TaPIP1* and *TaNAS1* by transformation into *Arabidopsis*

thaliana, established mutant library of Kn9204 through ion beam irradiation, and screened knockout mutants of *TaGS2* and *TaPIP1*. We also developed a RIL population derived from Kn9204×Jing411, constructed genetic linkage map, identified QTLs related to plant architecture, yield and NUE. All the work above helps us to develop precise strategies of breeding ideal genotypes with desired agronomic attributes.

(3) Major research achievements

① N utilization and yield potential related gene cloning and functional analysis

***TaGS2*:** Glutamine synthetase is a key enzyme responsible of the first step of ammonium assimilation and transformation into glutamine. There are three homoeologous *TaGS2* gene (*TaGS2-A*, *B* and *D*) in hexaploid wheat (AABBDD), which located on the group two chromosomes, produced three corresponding proteins (TaGS2-A, B and D). This work was to characterize the three homoeologs of the glutamine synthetase plastic isoforms (GS2) and investigate the function of the three *TaGS2* homoeologs by a reverse genetics approach employing ion beam implantation in hexaploid wheat. A series of *TaGS2* deficient mutants were developed for three homoeologous *TaGS2* genes. The *gs2-a/b, gs2-b/d* and *gs2-a/d* double mutants displayed serious chlorophyll loss, protein degradation and yield decline. Furthermore, Reactive oxygen species (ROS), including O_2^- and H_2O_2, accumulated and the antioxidant enzyme activities increased in the leaves of *gs2* double mutants. It is interesting that the function/contribution of the three *TaGS*2 genes was different. Our data demonstrated that the *TaGS2-B* gene is comparatively the major contributors to the phenotype. Then, the different expression of three homoeologous *TaGS2* genes by qRT-PCR explained that knockout of *TaGS2-B* gene belongs to the more serious phenotype than the other two. The expression of *TaGS2-B* was 5-flod of *TaGS2-A* and 75-fold of *TaGS2-D* in wild-type plants.

***TaPIP1* and *TaNAS1*:** Full-length cDNA sequences and genomic DNA sequence of *TaPIP1* and *TaNAS1* were cloned from Kn9204. There are 2 introns in *TaPIP1*, and none in *TaNAS1*. Chromosome location analysis showed that *TaPIP1* and *TaNAS1* were assigned to chromosome 6A and 4D respectively. Quantitative reverse transcription-PCR revealed *TaPIP1* mainly expressed in the aboveground vegetative organs, while *TaNAS1* mainly expressed in vascular bundle developed tissue, such as stem and rachis, cob, etc. It was found that *TaPIP1* and *TaNAS1*

were both highly expressed in Kn9204 and could be induced by PEG6000, NaCl, ABA and H_2O_2 treatments, although the expression patterns were different under diverse abiotic stresses. Subcellular localization analysis showed that TaPIP1-GFP was localized to the membrane system; TaNAS1-GFP was mainly localized in both cytoplasm and nucleus.

Knockout mutants of *TaPIP1* were screened from the wheat Kn9204 mutant library, and *TaPIP1* and *TaNAS1* were respectively transformed into *A. thaliana* to obtain over-expression plants. The results proved that over-expression of *TaPIP1* or *TaNAS1* in transgenic *Arabidopsis* conferred higher salt tolerance than wild-type plants during germination stages. Over-expression of *TaPIP1* and *TaNAS1* in transgenic *Arabidopsis* also up-regulated the expression of stress associated genes, such as *FAD5*, *NHX1* and *DERB1A*. Moreover, stress-responsive genes such as *FRY1* and *SAD1* of the CDPK pathway were up-regulated in transgenic *Arabidopsis* plants over-expressing *TaNAS1*. The genes of *SOS2* and *SOS3* in SOS pathway, *FRY1* and *SAD1* in the CDPK pathway, *MEKK1* in MAPK pathway were all up-regulated in *Arabidopsis* plants when over-expressed *TaPIP1*.

② QTL mapping for plant type, yield and NUE in Kn9204

We developed a recombinant inbred line (RIL) population by crossing Kn9204 with J411. The original RIL population contained 427 RILs, and 188 of randomly sampled lines from the 427 KJ-RILs were used for molecular genetic map construction. A genetic map consisting of 591 loci distributed across 21 wheat chromosomes was constructed, including 295 PCR-based markers such as g-SSR, e-SSR, ISSR, STS, and SRAP, seven functional molecular markers, 287 DArT markers, and two morphological markers. Information on the genetic and physical positions of 118 markers is reported here for the first time. The map spanned 3930.7 cM, with one marker per 6.7 cM on average.

By combining molecular marker scores and the phenotypic values of the 188 KJ-RILs, QTL analysis revealed a total of 287 QTLs for 23 yield-related traits in eight environments. Of these, 16 QTLs were major stable QTL across environments that individually accounted for 10.67–35.14% of the phenotypic variations, and these QTLs are related to 12 traits including plant height (PH), heading date (HD), flag leaf width (FLW), flag leaf area (FLA), spike length (SL), penducle length (PL), spike exsertion length (SE), spikelet number per spike (SNPP), sterile spikelet number per spike (SSNPP), kernel number per spike (KNPS), kernel length (KL) and thousand-kernel weight

(TKW). Allelic effect analysis of these major stable QTL indicated that all these QTL are closely related to the corresponding traits.

Molecular markers flanking the important chromosomal regions are of great value in wheat breeding programs. For example, chromosomal region of *Xwmc601—wPt-5865* on 2DL contains QTL cluster related to HD, TKW and kernel size, which are all major stable QTL across environments; chromosomal region of *Xgpw2331—Xgpw7543* on 4AL harbored QTL cluster for consistently increasing KNPS, TKW, nitrogen contents and NUE across environments; chromosomal region of *wP-t6149—wPt-1046* on 4BL contains QTL cluster related to HD, PH, PL, KNPS, SSNPP, TKW, straw nitrogen contents and FLW, which are all major stable QTL across environments. It was noted that QTL clusters related to NUE and yield were detected on chromosomes 4AL and 4BL, and alleles from KN9204 of the corresponding QTLs could significantly improve the absorption and transportation of nitrogen. We speculated that 4AL and 4BL are genetic basis of high NUE and yield potential of KN9204. In addition, we detected QTLs related to PH, PL, SE, FLW and FLA in the interval of *Xwmc737—Xbarc198* on 6BS, which all showed stability across environments and exhibited phenotypic variance of >10% as major QTL.

It is noted that we identified two novel semi-dwarfing loci corresponding to two major stable QTL of *qPh-4B.5* and *qPh-6B.2*, respectively, which are closely linked with *Xcnl10* on 4B and *Xcnl113* on 6B. Both the two QTLs have not been documented previously and thus we speculated that they harbor two novel semi-dwarfing loci. The graphic genotypic map of KN9204 showed that the chromosomal regions of *qPh-4B.5* and *qPh-6B.2* are from Mianyang75-18 and Jimai38, respectively, both of which are ancestors of KN9204. Allelic effect analysis showed that alleles of KN9204 on the corresponding two loci could significantly reduce PH but have no negative effect on yield.

③ Enhancement of breeding materials with alien chromatin

Through distant hybridization and molecular chromosome engineering breeding, we transferred some alien gene/chromosome fragment of *S. cereale*, *Ae. biuncialis* and *T. ponticum* (syn. *A. elongatum*) etc. into common wheat and obtained a series of valuable breeding elements, new lines and varieties.

***T. aestivum-S. cereale* materials**：The original 1RS/1BL translocation lines lost their resistances to new races of stripe rust and powdery mildew. To develop new potentially usable

disease resistant germplasm, we made distant hybridization between *T. aestivum L.* cv. "Xiaoyan 6" and *S. cereale L.* cv. "German White" and consecutive selections in the descendant populations. One BC_2F_4 line BC01-7-1 was screened out and crossed with Kn9204, following backcrossing twice using Kn9204 as recurrent parent, and developed a line 9204R of satisfied agronomic attributes and disease resistance.

Meanwhile, we made backcross of Kn9204 and Gaomai5 with the former as recurrent parent to improve its bread-making properties and obtained a line 1006-18 of medium gluten strength. Using 1006-18 as maternal parent to cross with 9204R, we developed a new disease resistant variety Kenong1006 by pedigree method of breeding. It experienced three rounds of Hebei Provincial Performance Trial of Regional Nursery and was approved by Hebei Approval Committee of Crop Variety in 2013 (Registration No. JISHENMAI 2013003).

Wheat-Rye-*Thinopyrum ponticum* trigeneric materials: By crossing BE-1 (a *T. aestivum*–*Thinopyrum ponticum* partial amphiploid) with novel T1RS/1BL line 148 (derived from cross of *T. aestivum L.* cv. "Xiaoyan 6" and *S. cereale L.* cv. "German White"), we obtained Wheat-Rye-*Thinopyrum ponticum* trigeneric hybrid. Half of BC_1F_1 seeds of 148 as recurrent parent were irradiated by γ-ray. The semi-dwarf individuals were selected from the irradiated BC_1F_1 population, crossed with dwarf and early-matured variety kenong1095 and backcrossed twice. Pedigree method of breeding was applied in BC_2F_2 and subsequent generations. New trigeneric lines were selected possessing both rye and *T. ponticum* chromatin in the background of wheat. In 2010, one BC_2F_6 line, nominated as Kn2009, was highly resistant to both stripe rust and powdery mildew during the whole growth period. As HMW-Gs composition is 1/7+8/5+10, it manifested satisfied bread-making properties, such as sedimentation value 44.6mL, wet gluten content 37.5%, stability time 11.0 minutes. Owing to its excellent performance in yield trial, disease resistance test and bread-making quality evaluation, Kn2009 was adopted to take Hebei Provincial Wheat Performance Trial.

In 2011 pre-test of Hebei Provincial Performance Trial of Regional Nursery, Kn2009 averaged 7969.35 kg/ha (6.05% higher than control). In 2012 and 2013 formal test of the same trial it averaged 7511.1 kg/ha (3.43% higher than control) and 7498.2 kg/ha (2.96% higher than control) respectively. In 2014 large scale production trial it averaged 8784.0 kg/ha (5.36% higher than control). Up to now, Kn2009 have finished the official procedure for variety approval of

Hebei province and will be released this year.

***T. aestivum-Ae. biunaialis* materials:** *Aegilops biuncialis* (2n=4x=48) contains $U^bU^bM^bM^b$ genome. We crossed and backcrossed *Ae*. *biuncialis* with Chinese Spring (CS), and identified seven addition lines of $1U^b$, $2U^b$, $5U^b$, $6U^b$, $7U^b$, $1M^b$ and $3M^b$ respectively with the aid of C-banding and double color FISH. Using CS as control in PEG-stimulated osmotic stress and rain-fed field trial, four drought tolerant $6U^b$ and $7U^b$ addition lines Ae9013, Ae9041, Ae9061 and AD9004 were screened out according to their antioxidant enzyme (including catalase, peroxidase and superoxide dismutase) activity, photosynthetic characteristics (including stomatal conductance, intercellular CO_2 concentration, net photosynthetic rate and transpiration rate) and leaf water status (relative water content of intact leaf and rate of excised-leaf water loss) etc.

We backcrossed the drought tolerant $6U^b$ and $7U^b$ addition lines with modern varieties such as Kn199 and selected some elite BC_2F_3 and BC_1F_4 lines with both better drought tolerance and agronomic attributes through alternative selection under both normal irrigation and rain-fed nursery.

④ Molecular module pyramiding breeding

Scientists pursue to assemble more key gene/QTL of economic agronomic attributes using genome-wide MAS. To meet the demand of wheat breeding in our district, we are trying to pyramid superior alleles of interesting molecular module related to high yield potential, large root system and high NUE to obtain desirable lines.

Pyramiding of molecular module involved in yield potential: By screening molecular markers of *gwm131* and *cfe273* (close linkage with genes controlling kernel number per spike) and *cfd233, wmc17, gwm234, cfa2257* and *cfa2234* (close linkage with genes controlling thousand kernel weight), we found that genetic diversity existed in our varieties and advanced lines in the loci of *gwm131*, *cfe273* and *cfd233*. F_2 and advanced lines that aggregated superior alleles increasing kernel number per spike were identified.

Pyramiding of molecular module involved in large root system: By screening molecular markers of *gwm294, gwm332, cfa2257* (230bp), *cfa2040* and *barc267* (close linkage with genes controlling large root system), we identified that all advanced lines derived from the cross between *T. aestivum-Ae, biuncialis* alien additional lines and KN199 harbored superior alleles in the loci of *gwm332, cfa2257* (230bp) and *cfa2040*. We obtained BC_2F_3 and BC_1F_4 lines with superior alleles

in the loci of *gwm294* and *barc267*, which all showed excellent agronomic traits and adapted to both water deficient and irrigated farmland.

Pyramiding of molecular module involved in NUE: Using molecular markers of *GS2-A*、*GS2-B*、*GS2-D* and *Xgwm285* (close linkage with genes controlling NUE) etc., we analyzed the allelic variation in these NUE relevant loci among Kn9204 derived varieties and advanced lines and screened an elite line Kenong2011 (Kn2011) pyramiding multiple superior alleles of NUE relevant gene/QTL. Kn2011, possessing chromatin of P genome from *A. deserterm*, also expresses strong drought tolerance and was adopted to take Hebei Provincial Wheat Performance Trial.

In 2012 pre-test of Hebei Provincial Performance Trial of Regional Nursery, Kn2011 averaged 7900.5 kg/ha (5.18% higher than control). In 2013 and 2014 formal test of the same trial it averaged 7777.2 kg/ha (3.37% higher than control) and 9055.5 kg/ha (4.97% higher than control) respectively. Due to its excellent performance, Kn2011 will be put into next round of large scale production trial.

⑤ Genetic diversity analysis of Kenong-series varieties by genome-wide molecular marker screening

We screened KN9204, its ancestors and derivatives with 350 DArT molecular markers, which witnessed the rich genetic diversity among the Kenong-derived varieties. Clustering analysis based on the 350 DArT molecular markers showed that these derivatives could be classified into two major groups: one with high yield potential and high water and fertilizer use efficiencies represented by Kn2011 series, and one with high yield potential and good bread-making quality represented by Kn2009 series. The above findings provided genetic theoretical basis in determinant of hybridization combinations in wheat breeding programs.

(4) Current research and future directions

Wheat breeding nowadays faces two bottleneck problems of limited genetic resources and inefficient breeding methodology. It becomes ever increasingly difficult to develop variety with multiple desired agronomic attributes associated with yield, quality, resistance, water and nutrient use efficiency etc. It was a long time that none breakthrough variety released because of deficiency of genetic diversity. MAS currently used is mostly involved in single or a few major gene, but the attributes we concern are complicated quantitative and genetically governed by

multiple minor genes. For those traits easily affected by environment genetic modification in single or a few loci can not improve the whole characteristics.

Recent research revealed that molecular network regulation of most agronomic attributes is characterized by “module”. As the fulfillment of wheat genome sequencing, wheat molecular genetics and functionary genomics should advance by leaps and bounds. Data accumulation in transcriptionics, motablismics and phenomics enable SNP in whole genome easily to be developed into breeding selection markers and provide bountiful functional genes and markers for MAS. Genome-wide MAS is absolutely helpful to overcome the difficulty in genetic improvement of complex traits governed by multiple quantitative genes. Molecular module pyramiding, in particular, will dramatically increase the breeding efficiency in molecular improvement of complicated agronomic attributes including yield potential, end-use quality, biotic and abiotic stress resistance, water and nutrient use efficiency.

To solve the two bottleneck problems mentioned above, we will try our best to identify potentially useful germplasm and isolate economic genes for wheat breeding. Meanwhile，we will try to develop efficient breeding technology by incorporating genome-wide MAS, chromosome engineering and conventional breeding. What we will concern are as follows:

① Mechanism researches of yield potential and stress related gene

Modern bread wheat is an allohexaploid grass species that arose through hybridization of three related diploid grasses. The combination of several very similar genomes results in gene multiplication and redundancy. Expression divergences of homoeologs are frequently observed in wheat as well as in other polyploid plants. However, little is known about functional variances among homologous genes arising from polyploidy. Polyploidy has extensive effects on gene expression. There are three possible evolutionary fates for homoeologous genes in polyploids: retention of original or similar function, functional diversification and gene silencing. There are three homoeologous *TaGS2* gene (*TaGS2-A*, *B* and *D*) in hexaploid wheat. We will focus on the regulation mechanism of different expression of the three homoeologs.

To investigate the mechanisms of gene-specific higher expression of the *TaGS2-B* homoeologs, we first isolated the 5’ regions of the three *TaGS2* homoeologs. The 1000-bp region upstream of the ATG initiation codon of *TaGS2-A*, *TaGS2-B* and *TaGS2-D* were cloned. The 5’ regions showed 81% sequence similarities with each others. Sequence analyses indicated that the

TaGS2 genes had a >50% GC content and contained the criteria for CpG islands in the 5' region. Next, we will examine the methylation status of *TaGS2* using bisulfite sequence PCR analysis of CpG/CpNpG sites of the 5' upstream region. The methylated degrees of 5' region may be the reason for the difference expression of *TaGS2*.

We used real-time RT-PCR to examine the expression profiles of the *TaGS2* at different tissues in booting stages. The transcription level of *TaGS2* was low in root, stamen and pistil, but predominantly expressed in the green tissues, such as leaves. We assume that a substantial proportion of organ-specific regulation be mediated by an epigenetic mechanism. Next, we will analyze the epigenetic regulation mechanisms for the tissue-specific expression divergence of *TaGS2*.

Our study suggests that *TaPIP1* and *TaNAS1* may be involved in the salt tolerance signaling pathway. Next, we will search for the TaPIP1 /TaNAS1-interaction proteins by pull down system, and identify the special interaction between them using the yeast two hybrid systems.

② **Fine mapping of major stable QTLs related to wheat plant type, yield and nitrogen use efficiency in Kenong9204**

In the primary QTL mapping analysis of yield and NUE-related traits using the KJ-RIL populations, we have identified four important chromosomal regions that harbor genes controlling plant type, yield and NUE. In the interval of *Xwmc601— wPt-5865* on 2DL, a QTL cluster related to HD, TKW and kernel size were identified in multiple environments with large phenotypic contributions; we identified KJ058 and KJ135 as residue heterozygous lines (RHL) from the KJ-RILs, and the near isogenic lines (NILs) were thus obtained by selfing these two RHLs. In the interval of *Xgpw2331—Xgpw7543* on 4AL, a QTL cluster for consistently increasing KNPS, TKW, nitrogen contents and NUE across environments were identified; we identified KJ068, KJ150, KJ169, KJ380 and KJ387 as RHLs from the KJ-RILs, and the NILs were thus obtained by selfing these RHLs. Chromosomal region of *wPt-6149—wPt-1046* on 4BL contains QTL cluster related to HD, PH, PL, KNPS, SSNPP, TKW, straw nitrogen contents and FLW, which are all major stable QTL across environments; we identified KJ178 as RHL, and the NILs were thus obtained by selfing this RHL. We detected QTLs related to PH, PL, SE, FLW and FLA in the interval of *Xwmc737—Xbarc198* on 6BS, which all showed stability across environments and exhibited phenotypic variance of >10% as major QTL; we identified KJ010, KJ062, KJ081, KJ097 and

KJ135 as RHLs, and the NILs were thus obtained by selfing these RHLs.

Based on information of EST-SSR, STS and DArT flanking the target region and genomic sequence of wheat, *Brachypodium distachyon* and rice, more molecular markers will be developed and thus enrich the molecular genetic maps of the target regions. We will try to fine map the target genes, thus clone the target genes and characterize their functions in the end.

③ Molecular module assemble breeding of wheat complex agronomic attributes

To solve the current challenges in wheat production such as yield potential, end-use quality, biotic and abiotic stress resistance, water and nutrient use efficiency in Huang-Huai Winter Wheat Region simultaneously, it is essential to set up efficient breeding approach to incorporate multiple gene/QTL involved in complex agronomic attributes. Our strategies of breeding by molecular module assemble are to: assess both genotype and phenotype of the present materials of alien chromatin precisely and identify the potentially useable molecular module; take Kn9204 and its elite derivatives (including varieties and lines) as receptor, cross with the donor of different molecular module and backcross at least twice, selfing at least two generations to get uniform genotypes; detect genetic background and target molecular module through genome-wide molecular marker screening, identify single, double or triple, and multiple molecular module pyramiding genotypes of different attributes; characterize phenotype through alternative selection under both sufficient and insufficient nitrogen application and irrigation conditions at different locations, and develop breakthrough varieties and lines conferring desirable yield potential, satisfied bread- making properties, strong biotic and abiotic stress resistance, and high water and nutrient use efficiency.

5. FUNDING AND LABORATORY PERSONNEL

Funding: In total, we received grants 11.66 million RMB yuan, around 1.82 million US$ during the review period (from 2009 to 2013). The following table provides a list of grants.

Grant	Source	Duration	Project	Amount (million RMB)
2008GB24910477	MOST	2008- 2010	Nitrogen-using efficiency trial of winter wheat cultivar Kn199	0.70
KSCX2-YW-N-083	CAS	2009- 2010	Integrative extension of efficient production technologies for new varieties of major cereal crops	0.25

2009CB118300	MOST	2009- 2013	Molecular design and development of wheat varieties with high yield potential and super quality traits	1.65
KSCX2-EW-N-02	CAS	2010- 2014	Breeding of high-yielding, disease resistant and resource-using efficient wheat varieties	1.00
2011CB100104	MOST	2011- 2015	Applied basic research on the identification and establishment of wheat candidate founder parents	0.50
2011CB100304	MOST	2011- 2015		0.80
2011AA100103	MOST	2011- 2015	Research and utilization of efficient molecular chromosome engineering breeding technology	2.26
CARS-03	MA	2011- 2015	Luancheng Comprehensive Experiment Station in Wheat-industry Technology Research System	2.50
XDA08030107	CAS	2013- 2017	Molecular module design breeding of wheat complicated agronomic traits	2.00

CAS: Chinese Academy of Sciences; MA: Ministry of Agriculture of China;
MOST: Ministry of Science and Technology of China

Laboratory Personnel: There are 8 members in the lab now, including 4 permanent staff, 1 postdoctoral and 3 graduate students (2 PhD and 1 MSc students).

The following table provides a list of the researchers who have contributed to the research for the review period (from 2009 to 2013) in the laboratory.

Name	**Position**	**Period of staying in the group (current status)**
Mr. Junming Li	Principal investigator	2009 - present (in position)
Dr. Jun Ji	Research associate	2009 - present (in position)
Dr. Wei Zhang	Research assistant	2009 - present (in position)
Dr. Fa Cui	Research assistant	2011 - present (in position)
Ms. Yanlong Chen	Technician	2009 - 2011 (left)
Ms. Furong Li	Technician	2009 – 2011 (left)
Dr. Lijing Sun	Postdoctoral	2010 - 2012 (left)
Dr. Chunhua Zhao	Postdoctoral	2013 - present (in position)
Dr. Meicong Wang	PhD student	2008 - 2012 (graduated)
Dr. Hui Zhao	PhD student	2010 - 2013 (graduated)

Ms. Chunlin Chen	MSc student	2007 - 2010 (graduated)
Mr. Wenguang Wang	MSc student	2007 - 2010 (graduated)
Ms. Xiaoli Fan	MSc student	2008 - 2011 (graduated)
Ms. Hongxia Wang	MSc student	2009 - 2012 (graduated)
Ms. Xia Hong	MSc student	2010 - 2012 (graduated)
Ms. Xiaoli Fan	PhD student	2011 - present (in position)
Ms. Jie Han	PhD student	2013 - present (in position)
Ms. Mei Chen	MSc student	2013 - present (in position)

6. SELECTED PUBLICATIONS, PATENTS GRANTED, VARIETIES OBTAINED

(1) Selected Publications

① Hui Zhao, Wei Zhang, Jing Wang, Furong Li, Fa Cui, Jun Ji, Daowen Wang and **Junming Li**[*], Comparative study on drought tolerance of wheat and wheat-*Aegilops biuncialis* $6U^b$ addition lines. Journal of Food, Agriculture & Environment. 11, 1046-1052(2013).

② J Wang, W Zhang, H Zhao, FR Li, ZG Wang, J Ji, XQ Zhang, DW Wang and **JM Li**[*], Molecular cytogenetic characterization of the *Aegilops biuncialis* karyotype. Genetics and Molecular Research. 12, 683 - 692(2013).

③ Fa Cui, Chunhua Zhao, Jun Li, Anming Ding, Xingfeng Li, Yinguang Bao, **Junming Li**, Jun Ji, Honggang Wang, Kernel weight per spike: what contributes to it at the individual QTL level? Mol Breeding. 31, 265-278(2013).

④ Huilan Wu, Chunlin Chen, Juan Du, Hongfei Liu, Yan Cui, Yue Zhang, Yujing He, Yiqing Wang, Chengcai Chu, Zongyun Feng, **Junming Li** and Hongqing Ling, Co-Overexpression FIT with AtbHLH38 or tbHLH39 in Arabidopsis-Enhanced Cadmium Tolerance via Increased Cadmium Sequestration in Roots and Improved Iron Homeostasis of Shoots. Plant Physiology. 158, 790–800(2012).

⑤ Jun Ji，Aimin Zhang，Zhiguo Wang，Jing Wang，Wei Zhang，Dongcheng Liu，**Junming Li**[*], A wheat–*Thinopyrum ponticum*–rye trigeneric germplasm line with resistance to powdery mildew and stripe rust. Euphytica. 188, 199-207(2012).

⑥ Jun Ji, Xiaoli Guo, Fa Cui, Dongcheng Liu, Jiazhu Sun, Wei Zhang, Aimin Zhang, **Junming Li***, Variations in high-molecular-weight glutenin subunits in the main wheat growing zones in China. Australian J. of Crop Science. 6, 912-917(2012).

⑦ Zhiguo Wang, Donghe Xu, Jun Ji, Jing Wang, Meicong Wang, Hongqing Ling, Genlou Sun and **Junming Li***. Genetic analysis and molecular markers associated with *multi-gynoecia* (*Mg*) gene in Trigrain wheat. Canadian Journal of plant science. 89, 845-850(2009).

⑧ Ji J，J Wang, Q Zheng, **J.M. Li***, ZG Wang, XQ Zhang and AM Zhang. A powdery mildew resistant line with introgression of *Agropyron elongatum* chromatin. Cereal Research Communications. 37, 217-225(2009).

(2) Patent Granted

Title: A method for extraction of wheat glutenin subunits

Inventor: Jun Ji, Dongcheng Liu, Zhiguo Wang, **Junming Li**, Aimin Zhang

Grant No: ZL 2005 10048214.7

Publication date: 3 June, 2009

(3) Variety obtained

Title: Kenong 1006

Inventor: **Junming Li**, Jun Ji, Wei Zhang, ZhiguoWang, Jing wang, Aimin Zhang, Xiangqi Zhang, Furong Li, Yanlong Chen

Registration No: JISHENMAI 2013003

Authority Plant Protection Publication No: CNA009925E

7. EDITERIAL DUTIES

None.

8. INTERNATIONAL CONFERENCE ORGANIZATION

None.