PI's Curriculum Vitae

Wheat Genetic Improvement and Germplasm Enhancement

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Brief Introduction of Our Research Group : Website

1. EDUCATION

- Ph.D., 2006, Major: Plant Nutrition Genetics

  Research Center for Eco-environmental Sciences and Institute of Genetics and Developmental Biology (IGDB), Chinese Academy of Sciences (CAS), Beijing, China

  Dissertation: Studies on the Genetics of Nitrogen Uptake and Utilization Efficiency of Wheat (*Triticum aestivum* L.).
- M.S., 1989, Major: Plant Pathology

  Northwest A & F University, Yangling, Shaanxi, China
- B.A., 1986, Major: Plant Protection

  Northwest A & F University, Yangling, Shaanxi, China

2. PROFESSIONAL EXPERIENCE

- 2006-Present. Investigator, Center for Agricultural Resources (CAR, Shijiazhuang), Institute of Genetics and Developmental Biology (IGDB), CAS.
- 2002-2003. Chinese Academy of Sciences and Australia Academy of Sciences Exchange Visiting Scholar: Waite Campus, Adelaide University and South Australian Research and Development Institute (SARDI), Adelaide, Australia.

  Cooperative Research Center, Molecular Plant Breeding, CRC for MPB.

- 1997-2006. Associate Prof., Shijiazhuang Institute of Agricultural Modernization (SIAM) and CAR, IGDB, CAS.
- 1993-1997. Assistant Prof., SIAM, CAS.
- 1989-1993. Research Assistant, SIAM, CAS.

3. HONORS AND ACADEMIC AWARDS

In 2013, "the Evaluation, Innovation and Utilization of Important Breeding Target Traits in Wheat Germplasm Resources" was presented and as the sixth contributor, I won the first prize of Chinese Agricultural Science and Technology Award and the second prize of National Scientific and Technological Progress Award.

4. MAJOR RESEARCH INTERESTS, SELECTED RESEARCH PROJECTS, research background, major research achievements, current research and future directions.

Our research group is mainly interested in germplasm enhancement, desirable gene exploiting, pyramiding and utilization in wheat. The projects in this laboratory aim at transferring desirable genes from related species, landraces and introduced germplasms into common wheat by means of chromosome engineering, molecular and conventional breeding technologies, developing new germplasm and gene resources for wheat genetics and breeding. Currently, the main objectives focus on disease resistance, high nutrient use efficiency, resistance to abiotic stress and high yield using molecular cytogenetics, mapping genes/QTLs and developing molecular markers for important traits and breeding new wheat cultivars.

4.1 Research background

At present, breeding new wheat cultivars has been progressing at a relatively slow pace, the so called the difficult 'climbing' stage, although there have been a few breakthroughs in wheat yield, quality and disease resistance. Such slow development is mainly due to the narrow genetic base of the germplasms used in wheat breeding programs. The genetic uniformity of commercial cultivars in wheat production has already reached to more than 90%. The narrow genetic base and low genetic variation of wheat cultivars have not only limited further improvement of wheat yield and quality, but also rendered them more vulnerable to biotic and abiotic stresses, resulting in potentially serious problems to wheat production. Thus, it is urgent to develop a strategy for enhancing germplasm and breeding cultivars to increase genetic diversity. To broaden the genetic base and increase the genetic diversity of wheat, we mostly rely on discovering and transferring desirable genes from wheat-related species and landraces into common wheat. Through this approach, we will develop new desirable germplasms and cultivars. The results show that the contribution of the new germplasm to wheat yield increase could be more than 50%. Therefore, we should concentrate on the development, collection, identification and utilization of wheat germplasms.

North China is one of the major Chinese wheat production regions where fertilizer use efficiency is very low and water resources are limited. Furthermore, wheat is always exposed to severe threat of major diseases such as powdery mildew (*Blumeria graminis* f. sp. *tritici*), stripe rust (*Puccinia striiformis* f. sp. *tritici*) and leaf rust (*P. triticina* f. sp. *tritici*). Few high quality and strong gluten wheat cultivars have been favorably received by farmers or markets. In some medium- and low-yield regions, there is lack of salt- and barren-tolerant wheat cultivars, and wheat yield levels are very low. Therefore, there is a pressing need to increase the resistance or tolerance of wheat cultivars to diseases, abiotic stress and to improve quality, yield and fertilizer use efficiency, especially nitrogen use efficiency (NUE) in North China. Fortunately, there are abundant wheat germplasm resources in China and they can provide many important genes for genetic improvement of the target traits in wheat.

Many genes and quantitative trait loci (QTLs) controlling many traits in wheat have been identified and mapped. Along with rapid development of wheat genomics, more and more genes are being successfully isolated and cloned. This progress prompted us to exploit favorable genes, identify molecular markers for important traits, develope elite germplasms, and through pyramiding different genes make molecular genetic improvement for some important traits of released wheat cultivars in North China.

4.2 Major research achievements

Our research group has mainly conducted studies that involved the development of new wheat germplasm and gene resources with desirable diseases resistance, stress tolerance and high nutrient use efficiency to breed new wheat cultivars by means of distant hybridization, molecular chromosome engineering and conventional breeding technologies. As a major contributor, three new wheat cultivars at the national levels and three at the provincial levels were registered and released, including Kenong 199, Kenong 9204, Gaoyou 503, Kenong 1093, Kenong 213, and Xiaoyan 597. In the past five years, I have published 12 *SCI* papers as the first or the corresponding authors. Five national invention patents were granted and another two patents were announced. Our group has developed new wheat lines with desirable diseases resistance and stress tolerance, two of them have been tested in regional field trials for releasing as new cultivars. I won the first prize of Chinese Agricultural Technology Award and the second prize of National Scientific and Technological Progress Award (as the sixth contributor). The detailed progresses are shown below..

4.2.1 Development, collection, identification and utilization of wheat germplasm: Our research group has about 3000 wheat germplasms with various types of distinctive characteristic, they include wheat relatives and their derivative lines, rare species, Chinese landraces and introduced germplasms, which have laid a solid foundation for breeding disease-resistant, salt-tolerant and high nutrient-efficient wheat cultivars. Specifically, using the founder parent Xiaoyan 6 (susceptible to many diseases) as background, through distant hybridization and molecular chromosome engineering procedures, a series of new wheat-rye addition, substitution, translocation and introgression lines with desirable disease resistance and agronomic traits were developed and characterized by sequential GISH (genome *in situ* hybridization), multi-color FISH (fluorescence *in situ* hybridization) and PCR analyses. A part of these results have been published in 2013 *Chromosome Research* and 2009 *Plant Disease*. In addition, a series of new EST (expressed sequence tag) markers specific to rye chromosomes or chromosome arms were developed to rapidly and effectively detect rye chromosomes or chromosome segments that were introgressed into a wheat background. The results have been published in 2012 *Cytogenetic and Genome Research* and 2009 *Cereal Research Communications*.

Our research further indicated that wheat-rye 1R and 4R translocation lines, 2R substitution line, 6R and 5R addition lines, etc. carry new powdery mildew resistance (*Pm*) gene(s) different from the known *Pm* genes or gene combinations. In addition, 390 wheat-rye derivatives (triticale) were characterized by molecular cytogenetics, disease resistance and stress tolerance analyses, and then were crossed and backcrossed with the main cultivars in production. Combining PCR with GISH/FISH, alien translocation and introgression lines are being screened on a large-scale and identified in the BC_2F_4 populations. A series of elite wheat-rye germplasms are being developed. The new T1BL·1RS translocation line KM9603 has also been extensively used as a parent in wheat breeding programs for its disease-resistance and high-yield by many wheat breeders or breeding institutions. These studies were financially supported by the National High-Tech Research and Development Program (No. 2011AA1001) and National Natural Science Foundation (No. 31171550).

Fig. 1 Various kinds of wheat germplasm resources.

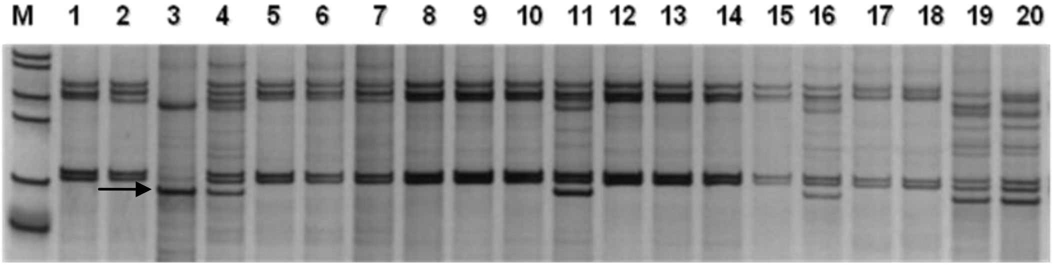

Fig. 2 The 4R wheat-rye translocation line WR41-1 was identified by using EST (expressed sequence tag) markers specific for rye chromosome 4R developed by ourselves. Arrows show the diagnostic DNA fragments.

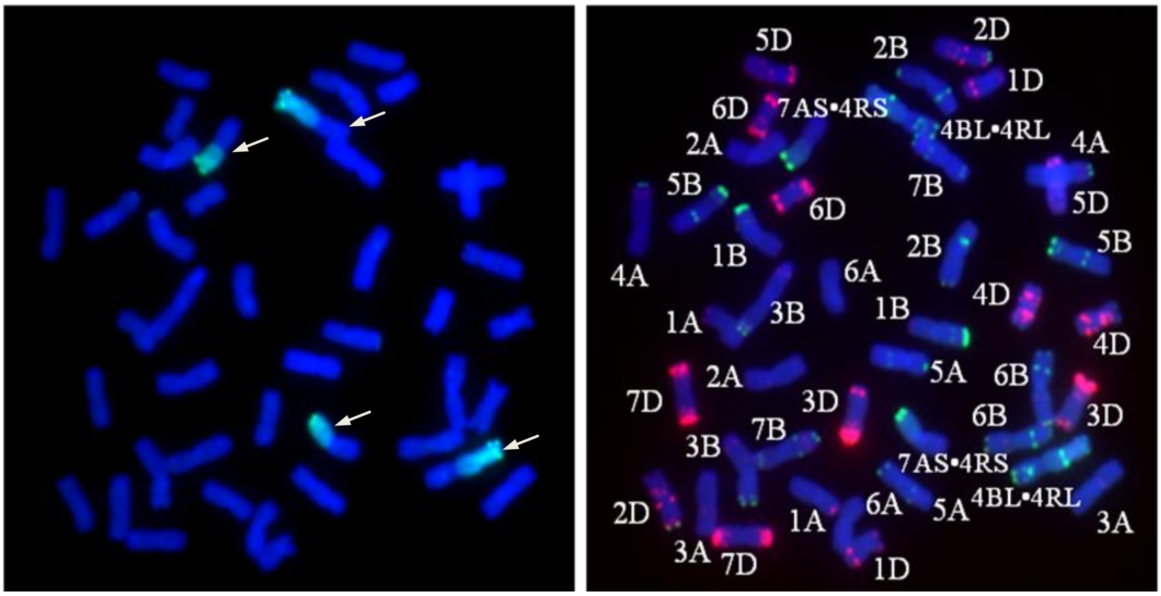

Fig. 3 The 4R wheat-rye translocation line WR41-1 was characterized by sequential genome *in situ* hybridization (GISH) (left) and multi-color fluorescence *in situ* hybridization (FISH) (right). Arrows show the translocated chromosomes.

4.2.2 Molecular identifications and utilizations of wheat resistance genes: More than 120 wheat germplasms with high resistance to powdery mildew, stripe rust or leaf rust were selected from 1300 wide hybridization germplasm, landraces and introduced cultivars. Of them, a wheat-*Agropyron cristatum* breeding line KM2939, displayed high powdery mildew resistance both at the seedling and the adult stages. The resistance gene *PmKM2939* was mapped to chromosome arm 5DS. It appears to be a new allele at the *Pm2* locus, and has been designated as *Pm2b* by the International Wheat Gene Nomenclature Committee. Two resistance genes *PmH962* and *PmLX66*, in the new distant hybridization germplasm H962R and a widely grown cultivar Liangxing 66, both showed a broad-spectrum of resistance to powdery mildew, and they were identified to be a new allele of *Pm5e* and a new allele of *Pm2*, respectively. A part of these results have been published in 2012 *Molecular Breeding*. The introduced cultivar C591 has a broad-spectrum of resistance to the stripe rust races currently prevalent in China. The stripe rust resistance gene *YrC591* was mapped onto chromosome arm 7BL with some closely linked markers. The result has been published in *Euphytica*.

In addition, the fine mapping of four *Pm* genes in landraces Niaomai, Dahongtou, Hongtoumai and Aiganmangmai are under way. In order to better use these resistance genes for wheat improvement, molecular markers closely linked to these genes were developed and identified for actual use in resistance breeding. At present, *PmKM2939* and *PmLX66* have been transferred into the main cultivars in production, and applied in the program of "Molecular Module Breeding of Wheat Resistant to Powdery Mildew" by using backcross and marker-assisted selection (MAS) strategy. These researches were financially supported by the National Natural Science Foundation (No. 31000709) and Strategically Special Leading Program of Science and Technology of Chinese Academy of Sciences (No. XDA08030107).

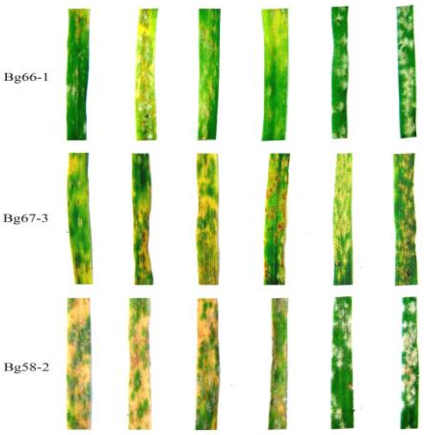

Fig. 4 Reactions of cultivar Liangxing 66 with *PmLX66* to different powdery mildew isolates with different infection patterns.

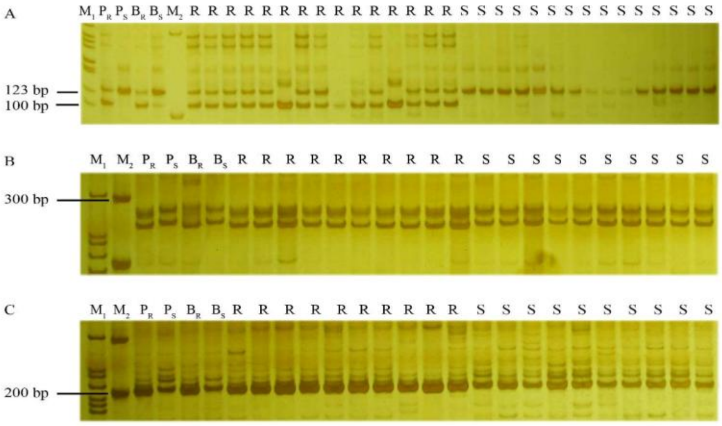

Fig. 5 Amplification profiles by markers *Xbarc44* (a), *Xcfd81* (b), and *SCAR203* (c) from Liangxing 66, Jingshuang 16, resistant and susceptible bulks, and selected F_2 plants of 'Jingshuang 16 × Liangxing 66' cross.

4.2.3 QTL mapping for yield, nitrogen- and phosphorus-related traits in wheat: Using a 'Xiaoyan 54 × Jing 411' RILs (recombinant inbred lines) population, we have conducted QTL analysis for grain yield, nitrogen (N)/phosphorus (P) utilization efficiency traits. By conditional analysis, spikelet number per spike was shown to be mostly influenced by P fertilization, whereas N fertilization had more effects on the expression of the QTLs for nitrogen concentration and utilization efficiency traits. QTLs involved in N and P interactions were also detected. The important QTL genomic regions were screened, included major QTLs that had large contributions, non-specific QTLs that were detected in various environments and pleiotropic QTLs that could affect various traits. The results are helpful for understanding the genetic basis of N utilization efficiency in wheat. In addition, we studied the relationships between N use efficiency and N uptake/utilization efficiency, five root traits involved in N uptake and discovered that a strong root system may contribute as a physiological basis for high nitrogen efficiency, and selected new wheat cultivars/lines with high N use efficiency. These results have been published in *Theoretical and Applied Genetics*, 2012 *Field Crops Research* and 2011 *Crop and Pasture Science*. This research was financially supported by National Basic Research Program (No. 2011CB100100) and National Nature Science Foundation (No. 31301400).

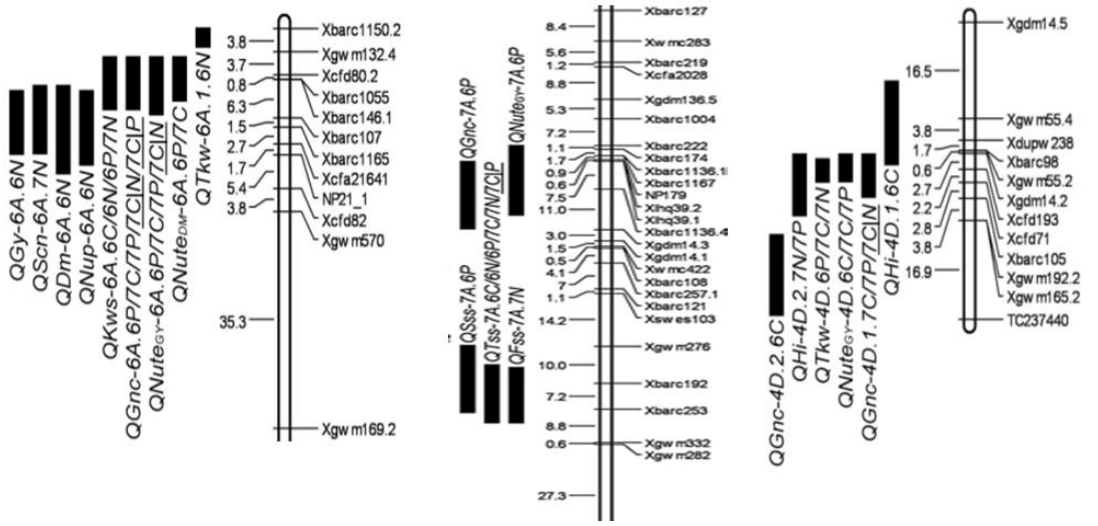

Fig. 6 Some important QTL loci.

4.2.4 QTL mapping for salt tolerance in wheat: Using two RIL populations 'Xiaoyan 54 × Jing 411' and 'Chuan 35050 × Shannong 483', QTLs related to salt tolerance were identified, among which some have been reported in previously studies, and the other were newly-detected loci. The results showed that additive and epistatic effects were common for both physiological and biomass traits, but the physiological traits rather than biomass traits are more likely to be involved in *Q* × *T* interactions at the seedling stage in wheat. Some QTLs for salt tolerance were detected in the two different genetic backgrounds. These QTLs and their closely linked markers, i.e., *Xcfd53*, *Xwmc112*, *Xwmc413* and *Xgwm6*, will facilitate MAS breeding and the identification of genes associated with salt tolerance in wheat. The results have been published in 2013 *Plant Breeding* and 2012 *Euphytica.* This research was financially supported by National Scientific and Technological Supporting Program (No. 2013BAD01B02) and the Knowledge Innovation Program of Chinese Academy of Sciences (No. KSCX2-EW-J-5).

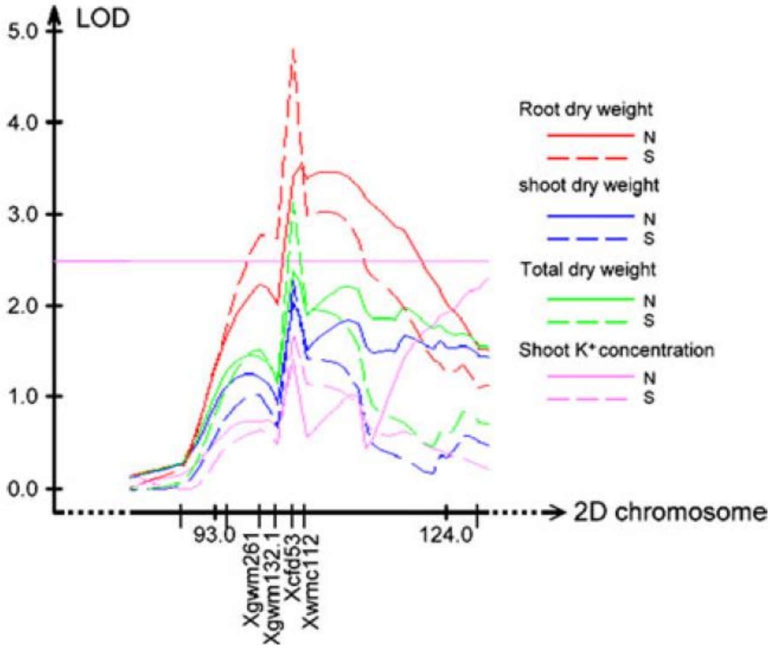

Fig. 7 The QTL cluster on chromosome 2D for biomass production. QTLs are indicated as LOD curves. N and S represent normal condition and salt stress treatments, respectively.

4.2.5 Breeding new wheat distant hybridization cultivars/lines: By combining distant hybridization and molecular chromosome engineering with conventional breeding technologies, we have selected a series of new wheat lines. The wheat-rye line KM9603 with a new T1BL 1RS translocation, has the multi-tiller characteristic, desirable disease resistance, good combining ability and high nitrogen use efficiency. By crossing KM9603 as a parent with wheat-*Agropyron elongatum* progenies (trititrigia) and wheat-*Ag. cristatum* progenies, respectively, three new wheat lines have been developed. Of them, line KM1572 has high resistance to powdery mildew, large spikes and high grain weight; while line KM187 has high resistance to powdery mildew and desirable tolerance to salt and barren stresses. The two lines show high-yield potential in yield comparison trials, and have been tested in regional field trials for releasing as new cultivars. Meanwhile, a series of new advanced lines with improved performances are being developed, and further systematic selection will be carried out to breed new wheat distant hybridization cultivars. This research was financially supported by the National High-Tech Research and Development Program (No. 2011AA1001) and the Science and Technology Service Network Initiative Program of Chinese Academy of Sciences (KFJ-EW-STS-056).

Fig. 8 Wheat new line KM1572.

Fig. 9 Wheat new line KM9603.

Fig. 10 Wheat new line KM187.

4.3 Current research and future directions

4.3.1 Identification and mapping of powdery mildew, stripe rust and leaf rust resistance genes and/or QTLs in wheat-related species and Chinese landraces

Chinese wheat landraces and related species are important gene resources. In order to exploit their favorable disease resistance genes and/or QTLs, about 1300 wheat landraces and wide hybridization germplasms were evaluated resistance to powdery mildew, stripe rust and leaf rust using the different isolates or races prevalent in China. At present, 120 resistant germplasms, including wheat-rye, wheat-*Ag. elongatum* and wheat-*Ag. cristatum* translocation and introgression lines, as well as Chinese landraces resistant to powdery mildew and/or rusts, have been screened and used to construct segregant populations with corresponding susceptible genotypes. More genetic and molecular mapping is still needed to identify resistance genes. The flanking markers tightly linked to the target genes can not only be applied in MAS breeding, but also will facilitate the fine mapping and map-based cloning of these genes. At present, we are transferring new powdery mildew resistant genes *PmKM2939 and PmLX66* to the main wheat cultivars in current production by using foreground selection for the two *Pm* genes and background selection for the whole-genome scan. Breeding wheat cultivars with desirable disease resistance and high-yield performance traits are in progress. These researches are financially supported by the National Scientific and Technological Supporting Program (No. 2013BAD01B02) and Strategically Special Leading Program of Science and Technology of Chinese Academy of Sciences (No. XDA08030107).

4.3.2 Molecular characterization on a large-scale and utilization of wheat-rye new germplasms

Using distant hybridization and chromosome engineering procedures, 278 advanced lines with different agronomic performance and types of disease resistance from crosses between wheat founder parent Xiaoyan 6 or its nullisomics lines and rye cultivar German White have been produced. In addition, 390 wheat-rye derivatives (triticale) have been characterized by molecular cytogenetics (Luo et al., 2014) and identified for their resistance to powdery mildew and rusts, salt and nutrient-deficient stresses. They were further crossed and backcrossed with the main cultivars in wheat production, so a large number of new wheat-rye lines have been produced. For better use of these wheat-rye lines in wheat breeding, molecular characterization on a large-scale by combining GISH/FISH with specific EST markers developed by ourselives, are in progress. From these lines, 6R and 5R wheat-rye addition lines, 2R substitution line, 1R and 4R translocation lines, etc. have been shown to possess new resistance genes for powdery mildew. Using the ^{60}Coγ radiation-induced approach and gametocidal chromosomes, small segment translocation and introgression lines resistant to powder mildew will be developed on a large-scale and identified by using PCR, GISH/FISH and resistance assessments and closely linked markers to the target resistant genes will be screened. These research works will continually provide new valuable germplasms and gene resources for wheat molecular breeding. These studies are financially supported by the National High-Tech Research and Development Program (No. 2011AA1001) and National Natural Science Foundation (No. 31171550).

4.3.3 Molecular marker assisted pyramiding genes/QTLs for disease resistance, superior kernel number and high molecular weight glutenin subunits (HMW-GS)

A new wheat-*Ag. cristatum* line PB3228 was developed that had large spike, superior kernels number and desirable adult plant resistance to powdery mildew. QTLs for kernel number per spike have been detected from PB3228, specifically a major QTL in the interval *Xbarc20-Xwmc238* on chromosome 4B (Wang et al. 2011). HMW-GS (1Dx5+1Dy10) have a positive influence on the end-use quality of wheat grains and contribute good bread-making quality. The markers specific for 1Dx5 and 1Dy10 can be used for molecular detection of HMW-GS 1Dx5+1Dy10. By crossing line PB3228 with bread wheat cultivar G8901, which has 1Dx5+1Dy10, but is highly susceptible to powdery mildew, we have developed 420 F_8 RILs. The RILs show segregated for kernel number per spike, subunit composition and adult plant resistance to powdery mildew in one field trial. We are now planning to conduct two-location and three-year field trials to map the adult plant resistant genes/QTLs for powdery mildew. Furthermore, RIL lines with pyramided HMW-GS (1Dx5+1Dy10), genes/QTLs for superior kernel number and powdery mildew resistance will be selected by MAS strategy. Wheat cultivars or advanced lines combining desirable disease resistance, promising quality and high-yield performance traits are expected to be obtained in the near future. This research is financially supported by the National Scientific and Technological Supporting Program (No. 2013BAD01B02).

4.3.4 Analysis and utilization of genetic effects and breeding effects for important genomic regions in wheat founder parents

Founder parents have played an important role for wheat breeding and production in China. They have not only been used to directly produce a lot of cultivars that have large planting area, but also result in many important breeding lines that were widely used. Identification and evaluation of the important genomic regions in the founder parents will facilitate understanding of the genetic basis for founder parents and provide guidelines for future wheat breeding.

Xiaoyan 6 is one of the most important founder parents, from which cultivar Xiaoyan 54 was derived by systematic selection. Using 'Xiaoyan 54 × Jing 411' RIL population, we have conducted a series of QTL analysis for traits associated with N and P utilization efficiency, salt tolerance and yield, and selected some important genomic regions and identified closely linked markers based on QTL mapping. Currently, we are conducting: (i) association mapping, to further validate the QTLs, identify and evaluate the alleles of the genomic regions to find the most important genomic regions and their most effective alleles; (ii) using SNP (single nucleotide polymorphism) marker, further analyze the inheritance and variation of the important genomic regions from the founder parents Xiaoyan 6 and Nanda 2419 to their derivative cultivars, and comparing the genomic regions of the two founder parents to find common and specific genomic regions between Xiaoyan 6 and Nanda 2419; (iii) constructing near-isogenic lines and backcrossed introgression lines of important genomic regions to be used in the fine mapping of important QTL and evaluate the breeding effects of the different alleles.

This research will understand at the molecular level how the founder parents have been produced in wheat breeding from various germplasms and will identify which genomic regions or loci from the founder parents have contributed to the wheat improvement. Meanwhile, we are also conducting limited backcrosses with the elite wheat cultivars as the recurrent parents to breed new wheat cultivars/lines containing the favorable alleles of important QTLs. This research is financially supported by National Basic Research Program (No. 2011CB100100) and National Nature Science Foundation (No. 31301400).

4.3.5 Breeding new wheat cultivars/lines through distant hybridization

By means of distant hybridization, molecular chromosome engineering and conventional breeding technologies, we have obtained a series of new wheat lines, such as wheat-rye line KM9603, wheat-rye-*Ag. elongatum* lines KM1572 and KM187, and wheat-rye-*Ag. cristatum* line KM1883, etc. Of them, lines KM1572 and KM187 have been permitted to participate in the Provincial Regional Nursery Trial and plan to complete the registration procedure for new cultivars in the next few years. The wheat-rye line KM9603 is one outstanding line from our germplasm materials. It has strong tillering and a compact plant type, etc. Line KM1883 is derived from line KM9603 and has superior kernel number characteristic from *Ag. cristatum*. By crossing KM1572 and KM1883 with the main wheat cultivars in production, respectively, a series of new advanced lines with improved performances are being developed. Further systematic selection will be carried out to breed new wide hybridization cultivars. In the near future, we will release some new wide hybrid cultivars. This research is financially supported by the National High-Tech Research and Development Program (No. 2011AA1001) and the Science and Technology Service Network Initiative Program of Chinese Academy of Sciences (KFJ-EW-STS-056).

5. FUNDING AND LABORATORY PERSONNEL(2009-2013)

5.1 Grant supports

- National Basic Research Program of China (the '973' Program)
  Genetic effect identification and evaluation of yield, nutrient use efficiency and water use efficiency related traits of wheat founder parents
  2009. 1-2015. 12, grant # 2011CB100100 1100,000 RMB Yuan
- National High-Tech Research and Development Program of China (the '863' Program)
  Wheat molecular chromosome engineering and functional gene breeding
  2011. 1-2015. 12, grant # 2011AA1001 1100,000 RMB Yuan
- National Scientific and Technological Supporting Program of China
  Identification and mapping of wheat disease resistance genes, germplasm enhancement and utilization
  2009. 1-2017. 12, grant # 2013BAD01B02 600,000 RMB Yuan
- General Research Program of National Natural Science Fundation of China (NNSFC)
  Molecular cytogenetic characterization and utilization of a new powdery mildew resistance gene of rye cultivar German white and development of small segment translocation lines
  2012. 1-2015. 12, grant # 31171550 600,000 RMB Yuan
- Strategically Special Leading Program of Science and Technology of Chinese Academy of Sciences (A)
  Molecular module breeding of wheat resistant to powdery mildew
  2013. 1-2017. 12, grant # XDA08030107 600,000 RMB Yuan (2013-2014)
- The Science and Technology Service Network Initiative Program of Chinese Academy of Sciences
  Development of wheat germplasm and cultivars with improved salt tolerance
  2014. 4-2016. 4, grant # KFJ-EW-STS-056 1100,000 RMB Yuan
- The Knowledge Innovation Program of Chinese Academy of Sciences

Development of wheat germplasm with improved disease resistance and yield

2011. 1-2013. 12, grant # KSCX2-EW-J-5 500,000 RMB Yuan

- Young Talents Fund Research Program of National Natural Science Fundation of China (NNSFC)

  Fine mapping and utilization of a new wheat stripe rust resistance gene *YrC591*

  2011. 1-2013. 12, grant # 31000709 200,000 RMB Yuan

- The Knowledge Innovation Program of Chinese Academy of Sciences

  Wheat genetic improvement and germplasm enhancement

  2009.1- Present 1,350,000 RMB Yuan for the members' salaries and daily operation of our research group

- Total: 7,150,000 RMB Yuan = 1,160,000 US $

  Note: 1US$ = 6.16 RMB Yuan (approximately)

5.2 Laboratory Members (2009-2013)

Our laboratory was founded in 2006, and so far, we have the following members:

- Investigator/Prof.: 1 (Investigator), Ph.D., Diaoguo An
- Research Assistants: 2, Ph.D., Hongxing Xu and Yunfeng Xu
- Graduate students: 15

  Ph.D. candidates: Pengtao Ma, Yanmin Qie, Jiang Huang, Ruifang Wang, Yunfeng Xu

  M.S. candidates: Dongdong Yin, Xiaohua Zhao, Qiaoling Luo, Hongxia Zhang, Feifei Ma and Huatian Zhao.

Visiting students: Jie Zhang (Henan University of Technology), Ping Zhang (Qinghai Normal University), Qing Liu and Wanwan Zhu (Henan Agricultural University).

6. SELECTED PUBLICATIONS, PATENTS GRANTED

6.1 Publication List (2009-2013)

1) **D. G. An***, Q. Zheng, Y. L. Zhou, P. T. Ma, Z. L. Lv, L. H. Li, B. Li, Q. L. Luo, H. X. Xu, Y. F. Xu, Molecular cytogenetic characterization of a new wheat–rye 4R chromosome translocation line resistant to powdery mildew. *Chromosome Research* **21**, 419-432 (2013).

2) Y. F. Xu, S. S. Li, L. H. Li, X. T. Zhang, H. X. Xu, **D. G. An***, Mapping QTLs for salt tolerance with additive, epistatic and QTL × treatment interaction effects at seedling stage in wheat. *Plant Breeding* **132**, 276-283 (2013).

3) H. X. Xu, D. D. Yin, L. H. Li, Q. X. Wang, X. Q. Li, X. M. Yang, W. H. Liu, **D. G. An***, Development and application of EST-based markers specific for chromosome arms of rye (*Secale cereale* L.). *Cytogenetic and Genome Research* **136**, 220-228 (2012).

4) J. Huang, Z. H. Zhao, F. J. Song, X. M. Wang, H. X. Xu, Y. Huang, **D. G. An***, H. J. Li*, Molecular detection of a gene effective against powdery mildew in the wheat cultivar Liangxing 66. *Molecular Breeding* **30**, 1737-1745 (2012).

5) Y. F. Xu, **D. G. An***, D. C. Liu, A. M. Zhang, H. X. Xu, B. Li, Molecular mapping of QTLs for grain zinc, iron and protein concentration of wheat across two environments. *Field Crops Research* **138**, 57-62 (2012).

6) Y. F. Xu, **D. G. An***, D. C. Liu, A. M. Zhang, H. X. Xu, B. Li, Mapping QTLs with epistatic effects and QTL × treatment interactions for salt tolerance at seedling stage of wheat. *Euphytica* **186**, 233-245 (2012).

7) R. F. Wang, **D. G. An***, C. S. Hu, L. H. Li, Y. M. Zhang, Y. G. Jia, Y. P. Tong, Relationship between nitrogen uptake and use efficiency of winter wheat grown in the North China Plain. *Crop and Pasture Science* **62**, 504-514 (2011).

8) Y. F. Xu, **D. G. An***, H. J. Li, H. X. Xu, Breeding wheat for enhanced micronutrients. *Canadian Journal of Plant Science* **91**, 231-237 (2011).

9) C. M. Wang, Q. Zheng, L. H. Li, Y. C. Niu, H. B. Wang, B. Li, X. T. Zhang, Y. F. Xu, **D. G. An***, Molecular cytogenetic characterization of a new T2BL·1RS wheat-rye chromosome translocation line resistant to stripe rust and powdery mildew. *Plant Disease* **93**, 124-129 (2009).

10) C. M. Wang, L. H. Li, X. T. Zhang, Q. Gao, R. F. Wang, **D. G. An***, Development and application of EST-STS markers specific to chromosome 1RS of *Secale cereale*. *Cereal Research communications* **37**, 13-21 (2009).

6.2 National Invention Patents Granted (2009-2013)

No.	Patent Name	Inventers	Application No.	Time Granted
1	EST-based markers specific for chromosome 1R and 6R of rye (*Secale cereale* L.) and their application.	**D. G. An**, D. D. Yin, H. X. Xu, L. H. Li	CN201210479074	2013.10.23
2	Development and application of rye EST-based markers specific for chromosomes of Rye (*Secale cereale* L.).	**D. G. An**, D. D. Yin, H. X. Xu, L. H. Li	CN201110092989	2012.12.12
3	Development and application of wheat EST-based markers specific for chromosomes of Rye (*Secale cereale* L).	H. X. Xu, D. D. Yin, **D. G. An**, L. H. Li	CN201110092988	2012.10.24
4	Development and application of EST-STS markers specific to chromosome 1RS of *Secale cereale*-I	C. M. Wang, **D. G. An**, Q. Gao	CN200710139507	2010.6.9
5	Development and application of EST-STS markers specific to chromosome 1RS of *Secale cereale*-II	C. M. Wang, **D. G. An**, Q. Gao	CN200710139509	2010.6.9