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**I. SPECIAL REPORTS*****MINUTES OF THE NATIONAL WHEAT IMPROVEMENT COMMITTEE (NWIC) MEETING.******13 January, 2006.******San Diego, CA, USA.******Attendance.***

**NWIC Members and Proxies:** Allan Fritz, Brett Carver, Jim Peterson (Chair), Jim Anderson, Harold Bockelman, Joe Anderson, Xianming Chen, Kim Garland Campbell, Robert Graybosch (Secretary), Ruth Dill-Macky, Marty Carson, David Marshall, Yue Jin, John Burns, Jackie Rudd, Ben Edge, Luther Talbert, and Kay Simmons (ad hoc).

**Guests:** Ann Marie Thro, Ed Kaleikau, Guihua Bai, Dave Matthews, Jeff Entman, Floyd Dowell, Mike Davis, Rollin Sears, Gina Brown-Guedira, Victoria Carollo, Jorge Dubcovsky, others.

***Approval of Minutes.***

Minutes from the January 2005 meeting, as published in the *Annual Wheat Newsletter*, were approved without revision.

***Increased funding for wheat research included in U.S. FY2006 budget.***

Jim Peterson. The U.S. government provided additional funding for the following wheat/barley research projects in 2006:

- a. National Stripe Rust Initiative, \$500,000.
- b. Regional Small Grain Genotyping Centers
  - i. \$178,000 Raleigh
  - ii. \$150,000 Manhattan
  - iii. \$175,000 Pullman (New funding via Stripe Rust Initiative)
- c. Karnal bunt research, Manhattan, KS, \$80,000
- d. BYDV, West Lafayette, IN, \$75,000
- e. Genetic Resource Enhancement, Aberdeen, ID, \$100,000
- f. Cereal Crops Unit, Madison, WI, \$250,000
- g. ARS Buildings and Facilities
  - i. Plant Biosciences, Pullman – \$3.625 M
  - ii. Ag Res Center, Fargo, \$3.7M for plan and design
- h. Other USDA items:
  - i. USDA–ARS Request for emergency action and funding to initiate stem rust screening in Kenya: 1-yr temporary funding of \$180,000, 2nd year of funding has been allocated
  - ii. USDA–CSREES Special Research Grants
    1. Managing Karnal Bunt of wheat – \$260K

***Update on USDA–ARS positions and activities.***

Kay Walker Simmons. ARS continues support of existing and new research activities, both within ARS and in partnership with State Agricultural Experiment Stations. Highlighted activities included the Wheat Scab Initiative, the Wheat Rust Initiative, newly initiated stem rust screening nursery in Kenya (cooperative with CIMMYT). ARS mandated a

budget recession in 2006 to set aside funds for reconstruction of facilities destroyed by Hurricane Katrina. External reviews of USDA–ARS National Programs 301, 302, and 303 (<http://www.ars.usda.gov/research/programs.htm>) were conducted in 2005.

### ***U.S. Plant Breeding Coordination Committee, USDA–CSREES–NRI.***

Ann Marie Thro and Ed Kaleikau USDA–CSREES. Establishment of the U.S. Plant Breeding Coordination Committee ([http://www.csrees.usda.gov/nea/plants/in\\_focus/ptbreeding\\_if\\_multistate.html](http://www.csrees.usda.gov/nea/plants/in_focus/ptbreeding_if_multistate.html)) was described. The committee has the goal of establishing national goals in plant breeding. CSREES is supporting the wheat and barley CAP grants (<http://maswheat.ucdavis.edu/Meetings/CAP2005/>).

### ***National Barley Improvement Committee/American Malting Barley Association report.***

Mike Davis. Scab continues to have a major impact on malting barley quality in the U.S. Trade barriers and energy prices also are exerting negative effects on the domestic barley industry. The NBIC and AMBA remain supportive of all U.S. wheat research activities.

### ***Update on activities of the Wheat Crop Germplasm Committee.***

Kim Garland Campbell. The Wheat CGC met on 12 January. More than 400 new PI numbers were added to the USDA–ARS–NSGC, housed at Aberdeen, ID, during 2005. Regional nursery entries are under-represented. Breeders submitting materials to the USDA–ARS coordinated regional performance nurseries are encouraged to submit these materials to the Small Grains Collection. Additional items may be found in the minutes published elsewhere in the AWN.

### ***Wheat CAP (Coordinated Agricultural Project) on wheat translational genomics.***

Jorge Dubcovsky. The Wheat CAP grant program, a multi-state project aimed at the integration of functional genomics and wheat breeding, was funded by a USDA–CSREES–NRI grant. Activities were initiated with a coordination meeting held at the PAG meeting in January, 2006. For additional information see: <http://maswheat.ucdavis.edu/Meetings/CAP2005/>.

### ***National Association of Wheat Growers.***

Jeff Entman. NAWG has expressed concern over the future of wheat biotechnology and the continued loss of wheat acreage in the U.S. NAWG will meet with U.S. Wheat to discuss these issues.

### ***Regional reports.***

**Hard winter wheat region.** Brett Carver. Stripe rust was deemed responsible for an estimated 5–15% production loss in the region in 2005. Hessian fly has been increasing in importance as a pest, especially in Oklahoma and Kansas. Dr. Okky Chung has retired from her position as director of the Hard Wheat Quality Laboratory in Manhattan, KS, and a search for replacement is underway. Dr. Gina Brown-Guedira departed from the USDA–ARS at Manhattan, KS, to assume the position of director of the Small Grains Genotyping Laboratory at Raleigh, NC. Replacement of the position at Manhattan is anticipated.

**Spring wheat region.** Marty Carson/Yue Jin. Fusarium head blight and leaf rust continue to plague producers in the region. Construction of an addition to the Cereal Disease Laboratory in St. Paul, MN, has been completed and the facility will be commissioned shortly. Jeffrey Stein has assumed the position of Small Grains Pathologist at South Dakota State University.

**Eastern soft wheat region.** Dave Marshall/Joe Anderson. Stripe rust now is a recurring rather than periodic problem in wheat production in the southern and eastern U.S. Meera Kweon has assumed a position as Research Food Technologist, and Edward Souza has been appointed Research Leader at the USDA–ARS Soft Wheat Quality Laboratory at Wooster, OH.

**Pacific Northwest region.** Kim Garland Campbell/ Xianming Chen. Stripe rust now is common in 35 states, now present in locations from which historically it has been absent. Dr. Chen provided an update on stripe rust screening activities, now benefiting breeding programs throughout North America. The wheat crop in the PNW now contains large plantings of wheat cultivars incorporating Clearfield® technology. Dr. Mike Flowers joined the Oregon State University Department of Crop and Soil Science as an Extension Cereal agronomist.

### ***CIMMYT/NWIC interactions.***

Jim Peterson. The NWIC contacted the US Agency for International Development expressing the concern of U.S. wheat researchers regarding staffing reductions and impact of budget reductions on the scope of the CIMMYT wheat research activities. A positive response to the concern was received from AID. NWIC and CIMMYT co-sponsored a pre-conference workshop at the International Wheat Workers convention in Argentina, primarily to discuss joint activities on the control of Fusarium head blight, stripe and stem rust.

### ***GrainGenes (<http://wheat.pw.usda.gov/GG2/index.shtml>).***

Victoria Carollo. Current curator roles at GrainGenes are held by Dave Matthews, wheat maps, ancillary databases and projects, collaboration with Gramene; Victoria Carollo, barley maps, references, QTL, plant ontology, outreach; and Gerard Lazo, rye and oat maps, bioinformatics. Conversion to a relational database has been completed. Current projects under development include a web page to track stem rust race Ug99, SNP reports, and a complete collection of Triticeae QTL (in collaboration with Gramene). New wheat maps for 2005 include:

- a. BAC contigs from the D genome.
- b. Quality QTLs in the ITMI Synthetic X Opata population.
- c. Wheat, Grandin X BR34 map.
- d. QTL for wheat spindle streak mosaic virus resistance.
- e. Wheat physical/genetic integration map.
- f. Wheat physical SSR map.
- g. 1DS, *Ae. tauschii* AUS X CPI highly recombinogenic regions at seed storage protein loci on 1DS.
- h. 1DS *Ae. tauschii* RGA markers linked to *Lr21*.
- i. 3A, SxY, QTL milling yield, Schomburgk X Yarralinka population.

### ***Small Grains Genotyping Laboratories.***

Guihua Bai, Gina Brown-Guedira, Kim Garland Campbell, and Jim Anderson provided updates on status and activities of the four USDA–ARS Regional Small Grains Genotyping laboratories. For additional information see:

- a. <http://www.cropsci.ncsu.edu/sggenotyping/>
- b. <http://www.ars.usda.gov/Research/docs.htm?docid=9899>

### ***Other USDA–ARS informational items.***

Floyd Dowell, Engineering Research Unit, USDA–ARS Grain Marketing and Production Research Center presented an update on “Applications of Single Kernel Sorting to Breeding Programs” and described the status of his laboratory and research unit.

USDA–ARS Regional Wheat Quality Laboratories, and their need for additional resources and financial resources, were discussed. NWIC remains supportive of these laboratories.

Harold Bockelman, USDA-ARS, Aberdeen, ID, described the need for a position at Aberdeen that would utilize molecular technologies in the characterization of materials housed in the USDA-ARS National Small Grains Collection.

**Rust initiatives.** Kay Walker Simmons, Jim Peterson, Yue Jin, X. Chen, and others. The initiation of a Global Rust Initiative (<http://www.globalrust.org/>), with seed funding from the Rockefeller Foundation, was described. Yue Jin stressed the need to extend stem rust screening beyond USDA-ARS regional nursery entries and to start evaluating earlier generation materials from breeding programs. Funding for the U.S. stripe rust initiative was approved for FY2005. A steering committee was appointed, with members being: Jim Peterson, Dave Marshall, K. Garland Campbell, Pat Hays, and X. Chen. The need was discussed for a new, comprehensive Cereal Rust Initiative. The initiative should support research on epidemiology, gene pyramiding, and adult plant resistance. Allan Fritz, Kansas State University, moved the NWIC support the “Cereal Rust Initiative” as drafted by C. James Peterson. Motion was seconded by Joe Anderson, and was passed by vote of NWIC members.

**NWIC By-laws (see p. 10).** Modified by-laws were presented by R. Graybosch. Joe Anderson moved the revised by-laws be accepted by the NWIC; Brett Carver seconded; motion passed.

**AWN report.** Brett Carver. The Annual Wheat Newsletter remains solvent. Otherwise, you might not be reading this.

### *Informational items.*

**Patent application, Fusarium head blight resistance in durum wheat.** A discussion was held on patent application US2005/0273875A1, “Fusarium resistant tetraploid wheat.” The NWIC expressed concern over the potential impact of this patent application, if granted, on issues such as gene deployment and germ plasm exchange. A subcommittee will be established to further investigate the topic.

NWIC informational visit to Washington D.C. and Beltsville, MD, will occur in early March, 2006.

**Research priorities.** The NWIC voted to endorse, in order of preference, the following research priority areas. Increased emphasis and funding for these areas is encouraged.

- a. National Rust Initiative
- b. Regional Small Grains Genotyping Labs
- c. Wheat Quality Enhancement
- d. Small Grains Germplasm Enhancement, Aberdeen, ID

NWIC meeting, December, 2006: The next NWIC meeting will be held 13 December, 2006, in Raleigh, NC, in association with the National Scab Forum.

R. Graybosch, Secretary, NWIC.

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*Note of Appreciation*

The National Wheat Improvement Committee (hereafter designated NWIC) wishes to acknowledge former NWIC Chair Dr. David van Sanford's contributions to the National Wheat Improvement Committee, 2001–2005.

- a. WHEREAS, Dr. David van Sanford volunteered his time, exceeding all expectations of service as member of the NWIC for five years, and contributing significantly to the advancement of wheat improvement research, and;
- b. WHEREAS, as Chair of NWIC from 2001 to 2005 provided exemplary leadership raising national awareness and mobilizing support of two initiatives dedicated to Karnal bunt and stripe rust;
- c. WHEREAS, his steadfast drive and vision led to continued expansion of cereal genomics research, most notably his dedication to establishment of the USDA–ARS wheat genotyping centers;
- d. THEREFORE, be it resolved that the NWIC collectively expresses its most sincere appreciation to Dr. van Sanford for his distinguished service and innumerable contributions to the National Wheat Improvement community.

### *U.S. National Wheat Improvement Committee*

The National Wheat Improvement Committee (hereafter designated NWIC) was formerly organized in Fargo, ND, 22 January, 1959. The original 'rules of procedure' were published in the *Annual Wheat Newsletter*, Volume VI, 1959. Bylaws (revised January 2006) are as follows:

1. Members: The NWIC shall consist of a chair plus 16 regional representatives. The USDA–ARS National Program Leader overseeing Grain Crops investigations shall serve as an *ad hoc* (nonvoting) member. Regional representatives shall be derived from each of the following wheat regional programs (committees):
  - a. Eastern/Southern Soft Wheat Workers
  - b. Spring Wheat Workers
  - c. Hard Winter Wheat Improvement Committee (Great Plains Wheat Workers)
  - d. Western Wheat Workers
2. Regional representatives shall be the four USDA–ARS Wheat Regional Nursery Coordinators (*ex officio*) and three additional representatives from each region. Procedures for election of regional representatives shall be at the discretion of each regional committee.
3. Proxy representation: If an NWIC member is unable to attend the annual meeting, a proxy may be designated. The proxy shall have full voting power. Voting at NWIC meetings is restricted to members or designated proxies.
4. Officers: The officers of the NWIC shall be a chair and a secretary.
  - a. The chair shall be duly elected by current NWIC members. Any individual actively engaged in U.S. wheat improvement is eligible for election as chair. Prior service of at least one term as an NWIC member is suggested as a prerequisite for nomination. Nominations for chair shall be solicited from current NWIC members, with elections held every three years. The term shall be for 3 years and shall commence on 1 January 1 subsequent to the year of election. The chair is eligible for re-election, and there are no term limits. If a chair is elected from current NWIC members, the regional committee shall appoint a successor to fulfill the remainder of the individual's term.
  - b. A secretary shall be appointed by the chair, and shall be selected from current NWIC members. The secretary shall serve a term concomitant with that of the chair. Minutes of each NWIC meeting shall be published in the *Annual Wheat Newsletter*.
5. Meetings: The NWIC shall hold at least one meeting per year, preferably at the time of a major wheat workers meeting. Special meetings may be called by the chair.
6. Quorum: A quorum shall consist of not fewer than nine members and shall include at least 1 representative from each of the four wheat regions.
7. Committee: The chair shall appoint such committees as deemed necessary to conduct activities of the NWIC. Personnel on such committees need not be limited to NWIC members.

*Members of the National Wheat Improvement Committee  
July 2006.*

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**WHEAT WORKER'S CODE OF ETHICS**

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This seed is being distributed in accordance with the 'Wheat Workers' Code of Ethics for Distribution of Germ Plasm', developed and adopted by the National Wheat Improvement Committee on 5 November, 1994. Acceptance of this seed constitutes agreement.

1. The originating breeder, institution, or company has certain rights to the material. These rights are not waived with the distribution of seeds or plant material but remain with the originator.
2. The recipient of unreleased seeds or plant material shall make no secondary distributions of the germ plasm without the permission of the owner/breeder.
3. The owner/breeder in distributing seeds or other propagating material grants permission for its use in tests under the recipient's control or as a parent for making crosses from which selections will be made. Uses for which written approval of the owner/breeder is required include:
  - (a) Testing in regional or international nurseries;
  - (b) Increase and release as a cultivar;
  - (c) Reselection from within the stock;
  - (d) Use as a parent of a commercial F1 hybrid, synthetic, or multiline cultivar;
  - (e) Use as a recurrent parent in backcrossing;
  - (f) Mutation breeding;
  - (g) Selection of somaclonal variants; or
  - (h) Use as a recipient parent for asexual gene transfer, including gene transfer using molecular genetic techniques.
4. Plant materials of this nature entered in crop cultivar trials shall not be used for seed increase. Reasonable precautions to ensure retention or recovery of plant materials at harvest shall be taken.

## II. ANNOUNCEMENTS

### **INTERNATIONAL WHEAT GENOME SEQUENCING CONSORTIUM (IWGSC) [www.wheatgenome.org](http://www.wheatgenome.org)**

The mission of the International Wheat Genome Sequencing Consortium is to advance agricultural research for wheat production and utilization by developing DNA-based tools and resources that result from the complete sequence of the common (hexaploid) wheat genome and to ensure that these tools and the sequence are available for all to use without restriction and without cost. Information in this report can be found at the IWGSC website: [www.wheatgenome.org](http://www.wheatgenome.org).

#### ***Purpose of the IWGSC.***

The International Wheat Genome Sequencing Consortium (IWGSC) is a collaboration focused on building the foundation for advancing agricultural research for wheat production and utilization by developing DNA-based tools and resources that result from the complete genome sequence of common (hexaploid) wheat. The IWGSC was established to facilitate and coordinate international efforts toward obtaining the complete sequence of the common wheat genome. To this end, the IWGSC will continue to refine the strategic roadmap, integrate existing international resources, and develop a sequencing strategy that will capture international participation and a broad funding base.

Membership in the IWGSC is open to any individual, laboratory, or entity with an active interest in meeting the objectives of the IWGSC; that can contribute substantially to this effort in resource development, sequence activity, annotation, scientific expertise, or funding; and that agrees to comply with the guidelines and spirit of this agreement. The IWGSC will complement the IGROW effort in which obtaining the sequence and annotation for wheat is a discrete objective in furthering our understanding of wheat at the genome, molecular, and physiological levels.

#### ***Goals.***

The principal goal of the IWGSC is to obtain a publicly available, complete sequence of common (hexaploid) wheat since it is grown on over 95 % of the wheat growing area and the complete sequence of this particular wheat holds the key to genetic improvements that will allow growers to meet the growing demands for high quality food produced in an environmentally sensitive, sustainable, and profitable manner. Having the complete genome sequence of bread wheat will accelerate improvement of this important crop, yielding the greatest rewards for economic development and global food security.

The IWGSC has selected the specific cultivar, Chinese Spring (common wheat) as the source for the project as it has available already ample genetic and molecular resources (Gill et al. 2004, *Genetics* 168: 1087-1096). The IWGSC understands that sequencing the large wheat genome (five times that of the human genome) represents a challenging endeavor. Sequencing costs have been decreasing steadily during the last two decades and technology is continuously improving. Thus, the IWGSC believes that its goal of obtaining a complete sequence of common wheat for a reasonable price is achievable in the foreseeable future. Therefore, the following short- and mid-term goals will be pursued towards reaching the final objective of sequencing the complete bread wheat genome.

**Short-term goals of the IWGSC.** Develop a physical map for common wheat that is linked to the genetic map and assess alternative approaches for sequencing wheat.

**Mid-term goals of the IWGSC.** Sequence the genic regions of common wheat, link the sequence to the physical and genetic maps, annotate the genic regions, and obtain full-length cDNAs for all expressed genes.

**Long-term goals of the IWGSC.** Complete sequence of the common wheat genome and high quality annotation of the genome.



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***Recommended Approach to Sequence the Wheat Genome.***

At this time, the precise method to sequence the ~17 Gb hexaploid wheat genome is not known. The hexaploid nature of the genome, coupled with the repetitive nature of the genome, will present technical challenges in current methodologies. Several methods or combinations of approaches have been proposed (Gill et al. 2004, *Genetics* **168**: 1087-1096) including whole genome shotgun sequencing, enrichment methods such as methylation filtration or high Cot, and/or clone-by-clone sequencing. However, regardless of any method(s) selected, we currently have only limited data on the landscape of the wheat genome. Thus, as proposed by Gill et al. (2004), there will be three phases to sequencing the wheat genome. The first phase or pilot phase is designed to test genomic methods/approaches on the hexaploid wheat genome. The primary purpose of the pilot phase will be to obtain data for the assessment phase in which the effectiveness of these methods are determined.

The pilot phase has several clear goals:

1. ascertain the gene enrichment capabilities of methylation filtration and high Cot cloning;
2. construct and assess the quality of chromosome-specific, and chromosome-arm specific BAC libraries;
3. develop BAC fingerprint contig maps for each chromosome;
4. assess the distribution of genes across the genome;
5. investigate the ability to differentiate homologous sequences; and
6. develop bioinformatics tools for a semi-automated annotation of large sequences.

After sufficient pilot data have been obtained, an assessment of the pilot phase will be performed. The assessment phase will involve determining which method(s) can be used in a cost effective manner to generate the sequence of the wheat genome. Although it is anticipated that funding for the full genome sequence of wheat may not be available immediately, selection of the methods to sequence the wheat genome should be compatible with future efforts in which the complete genome sequence is obtained.

After a full assessment, the project will move to the scale-up phase in which the optimal methods are deployed on the whole genome. The scale-up phase involves obtaining the genome sequence and annotation. As noted, this may be in stages with an initial goal of sequencing the genic space and a subsequent goal of completing the sequence.

A first pilot project led by the INRA in France has been initiated in 2004 to assess point 3 using the largest wheat chromosome (chr. 3B, 1GB = 2x the rice genome) of hexaploid wheat as a model. The 68,000 BAC clones of a 3B chromosome specific BAC library (Safar et al. 2004, *Plant J* **39**:960-968) have been fingerprinted using an improved SNAPshot protocol for BAC fingerprinting and high-throughput facilities at the French National Sequencing Center (Genoscope). A first contiguing phase (2,500 contigs) has been recently achieved and the anchoring of the physical contigs to the genetic map is currently underway. Fingerprinting and FPC analysis have been achieved within 6 months by a postdoc and a technician for a total cost of about 180,000 USD. This demonstrates the feasibility of the chromosome specific approach for the hexaploid wheat genome.

**Next steps: Priority Research Projects.** The international IWGSC believes that we must begin well-coordinated, clearly articulated projects that will lay the foundation for sequencing the common wheat genome. During 2005, the IWGSC strongly supports these high priority proposed projects and urges funding agencies to provide funding this year for these projects:

1. Construction and large-scale sequencing of Cot-based cloning and methylation filtration libraries from Chinese Spring;
2. Large scale sequencing (> several Mb) of physical BAC contigs from hexaploid wheat (from Minimal Tilling Path at different regions (gene rich/gene poor) on 3B and possibly from other loci on the genome for which large contigs (> 1Mb) have been generated; and
3. Construction of physical maps (BAC fingerprinting) from already available (1BS and (1D, 6D, 4D)) chromosome-specific libraries.

***Organization.***

The IWGSC is led by six co-chairs, an executive director, and the coordinating committee (see chart). The six co-chairs

are representative of Australasia (R. Appels and Y. Ogihara), Europe (C. Feuillet and B. Keller), and the USA (B. Gill and J. Dvorak). Kellye Eversole serves as the executive director.

The Coordinating Committee is responsible for:

- Coördinating activities within the IWGSC and pertinent outside genome efforts,
- Allocating responsibilities/tasks to IWGSC members,
- Assessing and reporting on progress, and
- Monitoring data release activities.

### ***Funded projects.***

**Characterizing the wheat genome by random sample sequencing, National Science Foundation Funded Wheat Pilot Project 2005**, PIs and Co-PIs: J. Bennetzen, K. Devos, and P. SanMiguel (USA). The nuclear DNA of bread wheat cultivar Chinese Spring will be investigated to determine the content and distribution of genes and other sequences in the large genome of this polyploid species. A total of 220 large fragments of wheat DNA, cloned into a BAC vector, will be randomly selected and subjected to DNA sequence analysis. The sequence analysis will be done at a low redundancy to maximize the data generated per unit cost. These 220 BACs also will be located to wheat chromosome maps by a novel PCR strategy so that the relationship between chromosomal location and DNA sequence content can be assessed. Two gene enrichment techniques, high Cot analysis and hypomethylated partial restriction analysis, which have been proven in maize, will be tested for their efficacy in wheat. All generated sequences will be analyzed for gene and repetitive DNA content. Abundant repeats also will be characterized for their degree and nature of sequence divergence and their possible differential distribution across the wheat chromosomes. These experiments and analyses will determine the basic molecular characteristics of the wheat genome, provide insights into the nature of sequence evolution in this polyploid cereal, and lay the foundation for future genomic characterizations of wheat. Access to project outcomes and all data and analyses will be made available through a project website (accessible via <http://www.genetics.uga.edu/jlblab/index.html>), public databases, and publication in peer-reviewed scientific journals.

**Chromosome 3B, a model to study the structure, function and evolution of the wheat genome, Agence Nationale de la recherche (ANR) Funded Wheat Pilot Project 2005**, PIs and Co-PIs: C. Feuillet, J. David, I. Bonnin and O. Panaud (France). Improvement of bread wheat quality and yield in the context of sustainable agriculture has to be achieved in the next decades to meet human needs by 2050. Significant advances in the understanding of the wheat plant biology as well as in the management and exploitation of genetic resources are necessary to address this challenge. Genomic analyses can support this effort through a better understanding of the organisation, function, and evolution of this large and complex genome. Recent advances in wheat genomics already have led to better marker-assisted selection and to the positional cloning of a number of genes of agronomic interest. However, this knowledge remains too limited and larger scale studies are needed now to develop more efficient tools and strategies to support wheat improvement. Although the size and the complexity of the wheat genome do not allow yet detailed studies at the scale of the whole genome, recently it has become possible to work on single chromosomes. This project aims to exploit the first physical map of chromosome 3B of bread wheat that is under construction currently in the coördinating laboratory as a model to study the structure, function, and evolution of the wheat genome. This unique resource will allow us to address a number of important biological questions, such as:

The organization of the gene space and the duplication of the genome. These studies focus on characterizing the gene islands (distribution along the chromosome, gene density within and outside islands), identifying ancestral genome duplications through comparative analyses with rice, and studying their impact on gene function and evolution.

The recombination and its effect on genome evolution. Analyses will be performed in different genetic contexts (homology, homoeology, ploidy) and at different scales (whole chromosome, saturated deletion bins, and targeted sequenced regions) to study the recombination frequency and distribution as well as the effect of recombination on gene and genome evolution. Moreover, linkage disequilibrium and its use in association genetics will be evaluated.

The mechanisms of rearrangements that have shaped the wheat genome during evolution. As a model, we will study the evolution of the disease resistance locus *Rph7* in grasses. Rearrangement mechanisms leading to deletion and/or translocation of genes as well as gene sequence evolution at this locus will be studied through intraspecific (rice sub-species; wheat homoeologous chromosomes) and interspecific (barley, *Brachypodium*, rye-grass, maize, sorghum) comparative analyses.