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ORIGINAL: English
DATE: December 8, 2011

INTERNATIONAL UNION FOR THE PROTECTION OF NEW VARIETIES OF PLANTS
GENEVA

WORKING GROUP ON BIOCHEMICAL AND MOLECULR TECHNIQUES, AND DNA-PROFILING IN PARTICULAR

Thirteenth Session
Brasilia, November 22 to 24, 2011

THE INTERNATIONAL WHEAT GENOME SEQUENCING CONSORTIUM (IWGSC): BUILDING THE FOUNDATION FOR A PARADIGM SHIFT IN WHEAT BREEDING

Document prepared by experts from the United States of America

The International Wheat Genome Sequencing Consortium (IWGSC): Building the Foundation for a Paradigm Shift in Wheat Breeding

Kellye Eversole
Executive Director
IWGSC

Breeders Day, UPOV Working Group
on Biochemical and Molecular Techniques

22 November 2011

Brasilia, Brazil

Eversole Associates
Enabling Science & Technology

The International Wheat Genome Sequencing Consortium

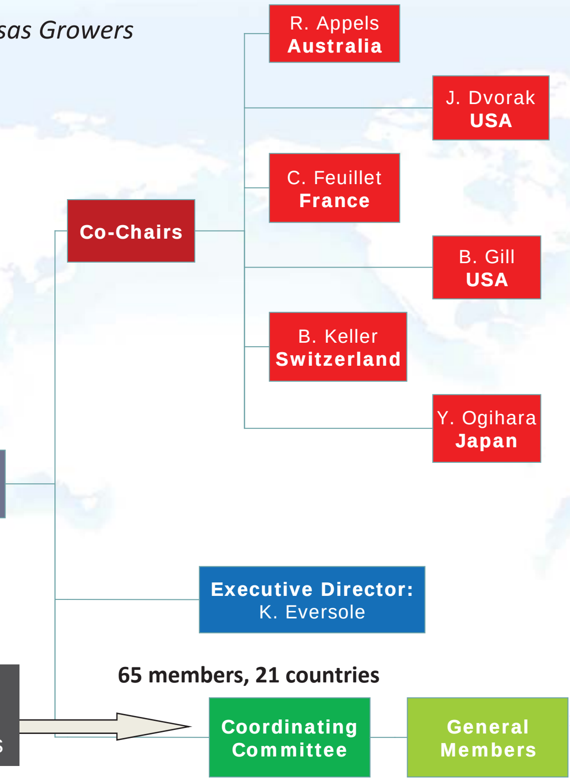
Launched in 2005 on the initiative of Kansas Growers

Sponsors

IWGSC Sponsors

21 Sponsors

Funding or Scientific Contributors



Co-Chairs

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Japan

Executive Director:
K. Eversole

65 members, 21 countries

Coordinating Committee

General Members

> 270 members
33 countries

www.wheatgenome.org

The International Wheat Genome Sequencing Consortium (IWGSC)

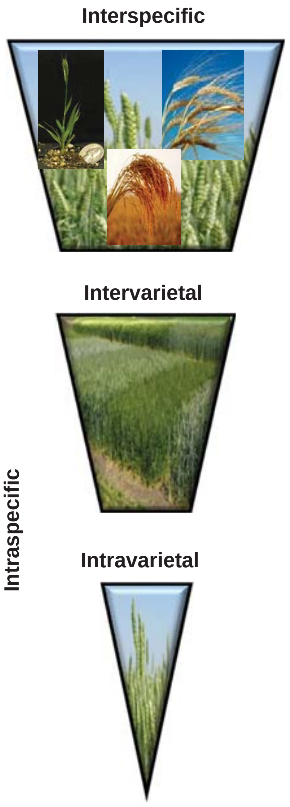
Who
- Growers, public/private breeders, plant scientists

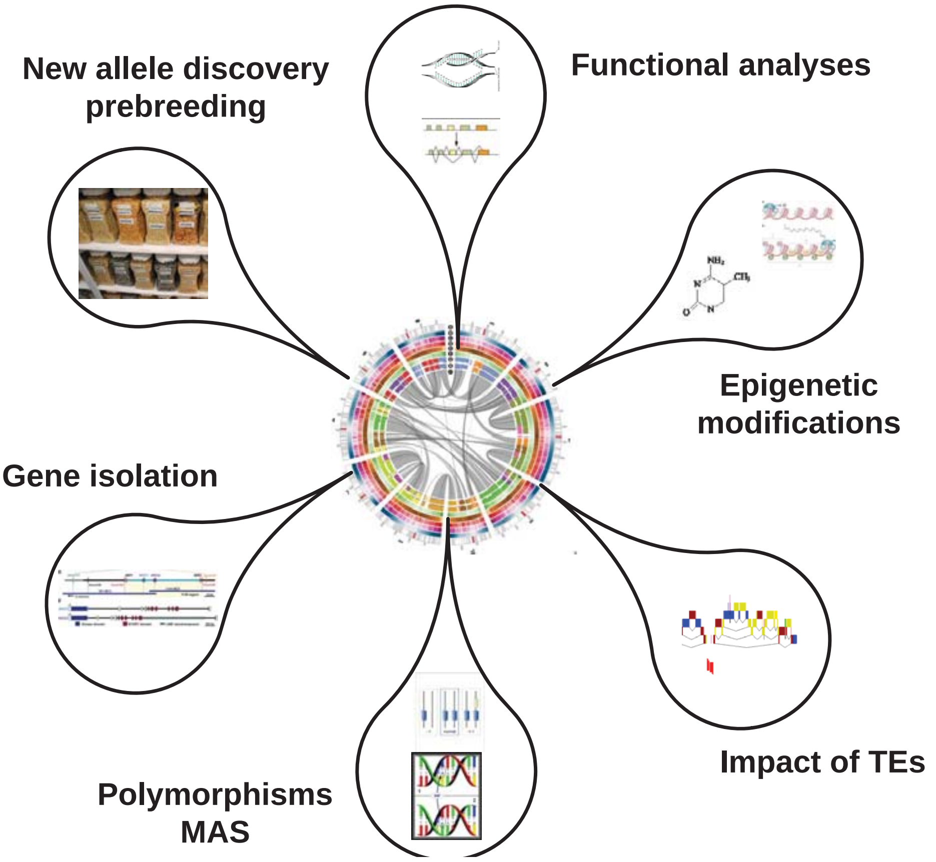
Purpose
- Accelerate wheat improvement
- Increase profitability throughout the industry

Vision
- High quality manually annotated genome sequence
- Anchored to the genetic maps

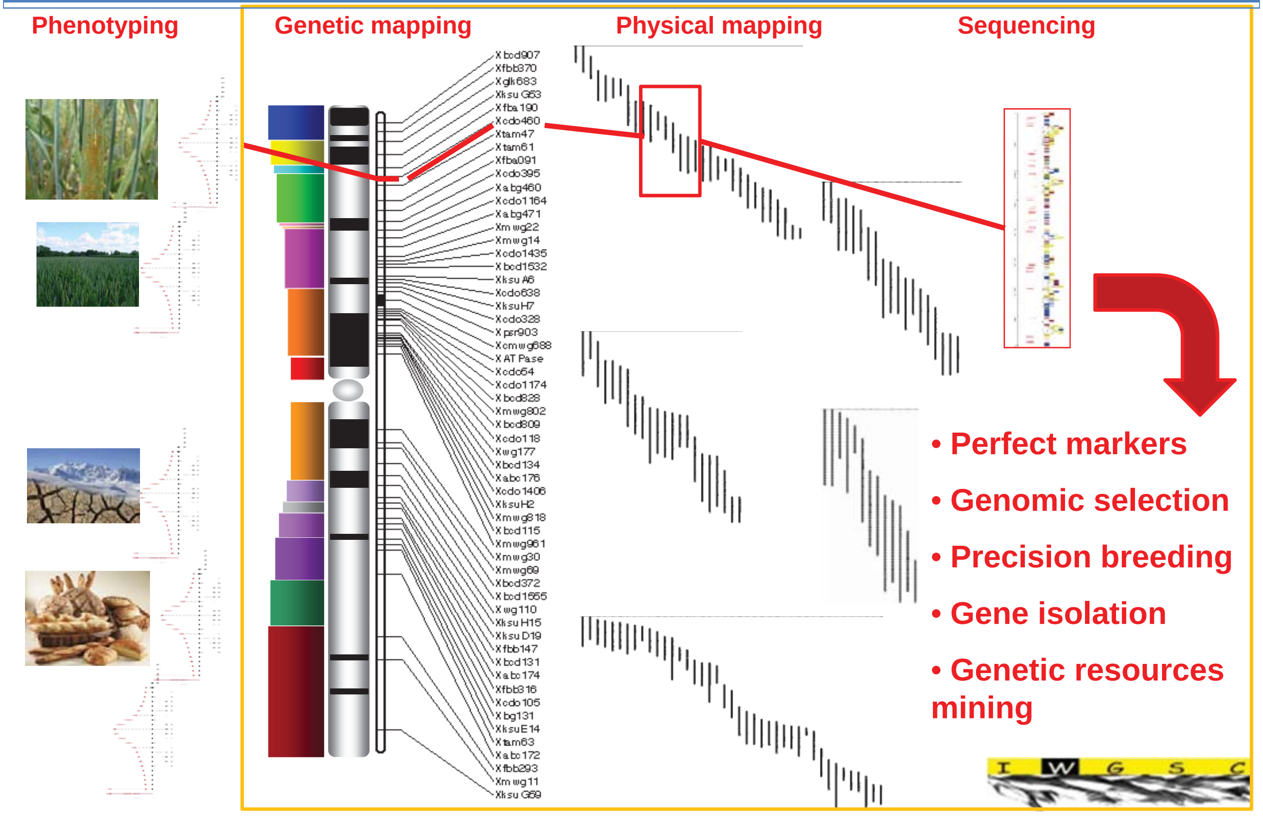
Strategy
- Milestone-based, adaptable
- Deliver products and tools to breeders along the way

A Genome Sequence for what?



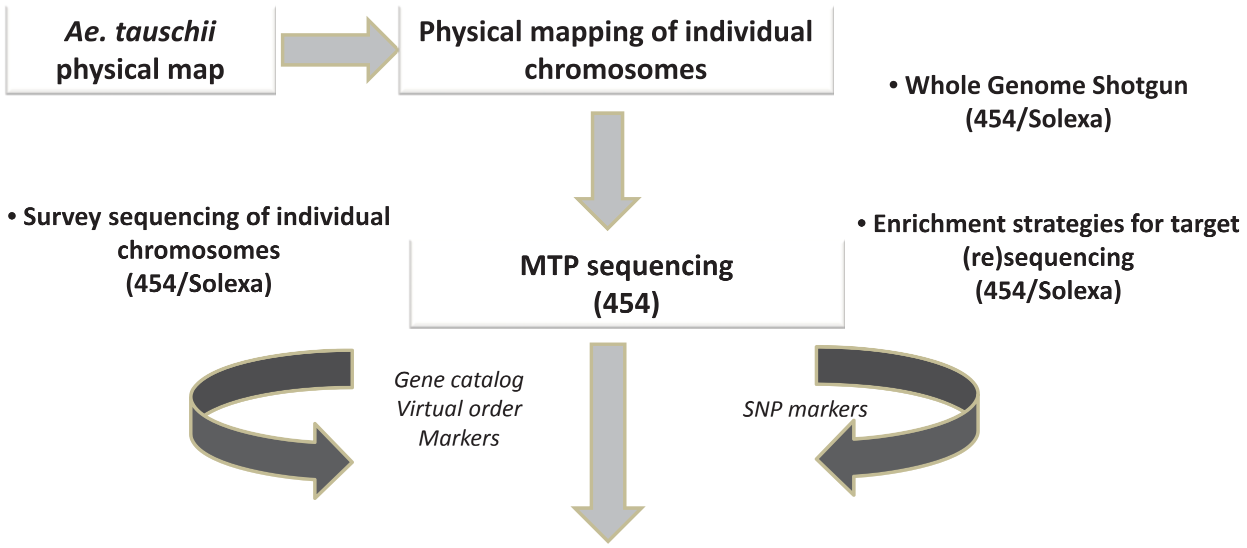


An integrated and ordered wheat genome sequence



- Perfect markers
- Genomic selection
- Precision breeding
- Gene isolation
- Genetic resources mining

Combined strategies to establish a Chinese Spring reference genome sequence



Ae. tauschii physical map

Physical mapping of individual chromosomes

- Whole Genome Shotgun (454/Solexa)

- Survey sequencing of individual chromosomes (454/Solexa)

MTP sequencing (454)

- Enrichment strategies for target (re)sequencing (454/Solexa)

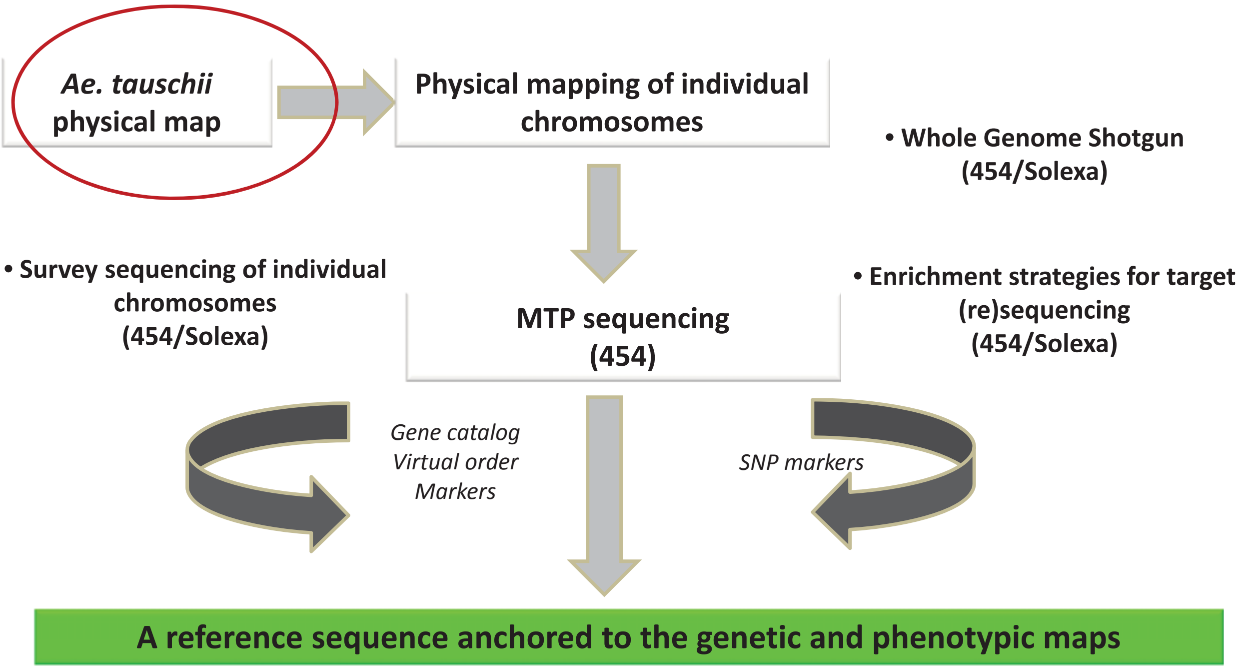
Gene catalog
Virtual order
Markers

SNP markers

A reference sequence anchored to the genetic and phenotypic maps

TGAC
The Genome Analysis Centre™

Combined strategies to establish a Chinese Spring reference genome sequence



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GENOSCOPE

IWGSC

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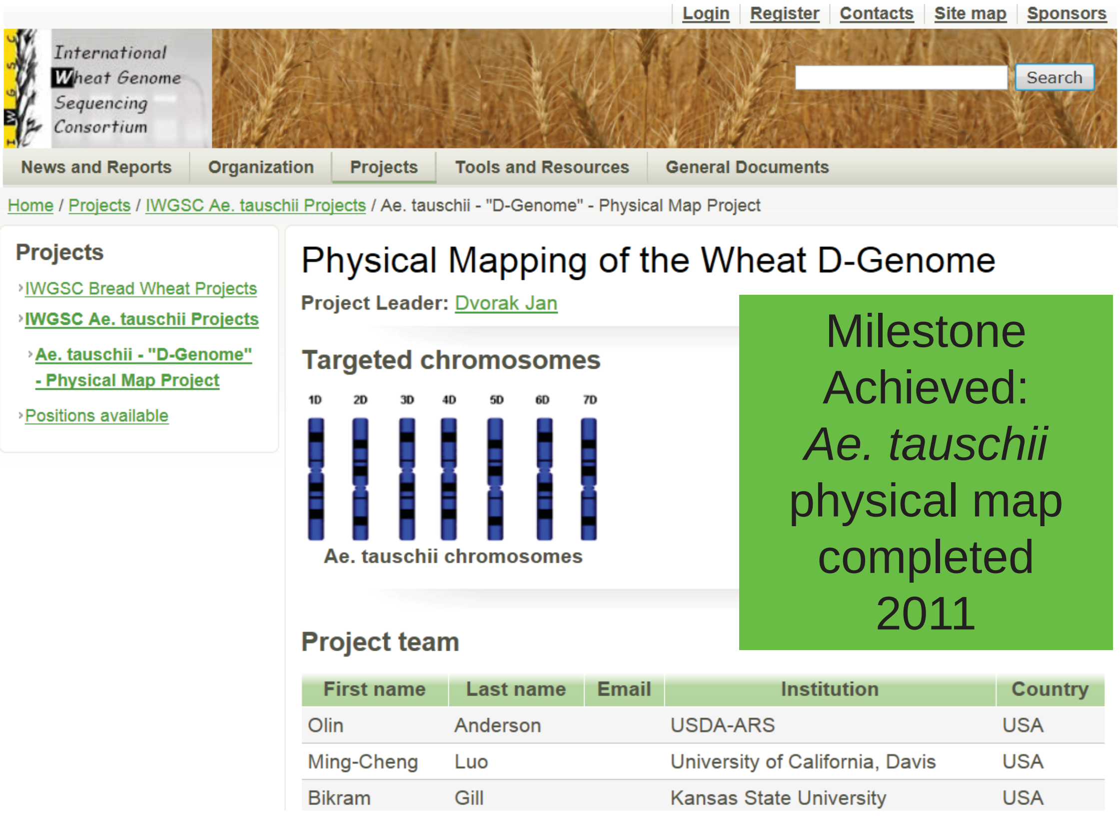


Home / Projects / IWGSC Ae. tauschii Projects / Ae. tauschii - "D-Genome" - Physical Map Project

Projects
- IWGSC Bread Wheat Projects
- **IWGSC Ae. tauschii Projects**
  - **Ae. tauschii - "D-Genome" - Physical Map Project**
- Positions available

Physical Mapping of the Wheat D-Genome

Project Leader: Dvorak Jan

Targeted chromosomes

Ae. tauschii chromosomes

Project team

First name	Last name	Email	Institution	Country
Olin	Anderson		USDA-ARS	USA
Ming-Cheng	Luo		University of California, Davis	USA
Bikram	Gill		Kansas State University	USA

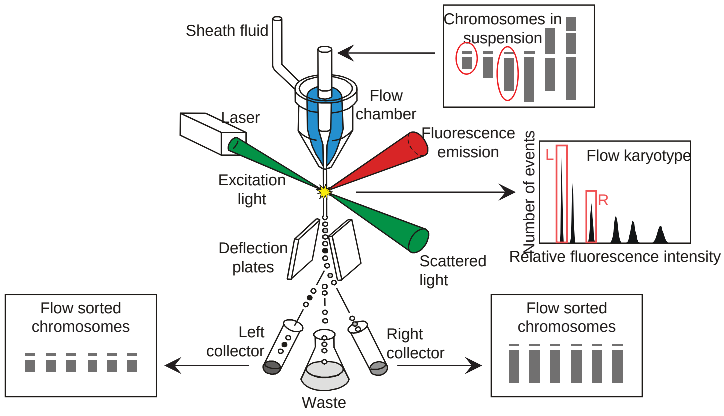
Milestone Achieved:
Ae. tauschii
physical map
completed
2011

www.wheatgenome.org

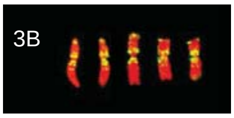
Bread Wheat: Chromosome-Based

Laboratory of
Molecular Cytogenetics and Cytometry
Institute of Experimental Botany AS CR

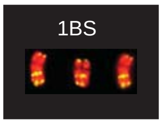
Chromosome sorting



- Chromosomes: 605 - 995 Mbp
(3.6 – 5.9% of the genome)



- Chromosome arms: 225 - 585 Mbp
(1.3 – 3.4% of the genome)

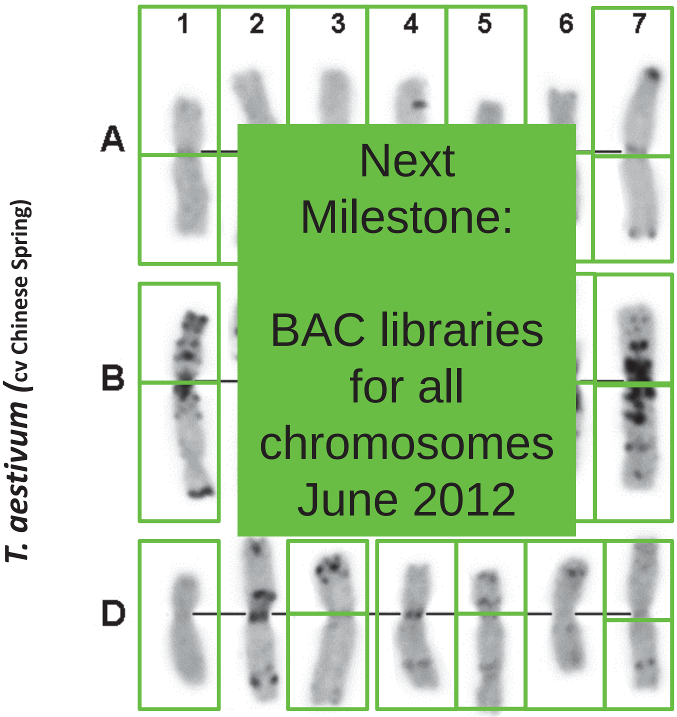


Chromosome specific BAC libraries

International
Wheat Genome
Sequencing
Consortium

Chromosome specific BAC libraries

Laboratory of
Molecular Cytogenetics and Cytometry
Institute of Experimental Botany AS CR



Next
Milestone:

BAC libraries
for all
chromosomes
June 2012

890,880 BAC clones
(1 arm remaining)

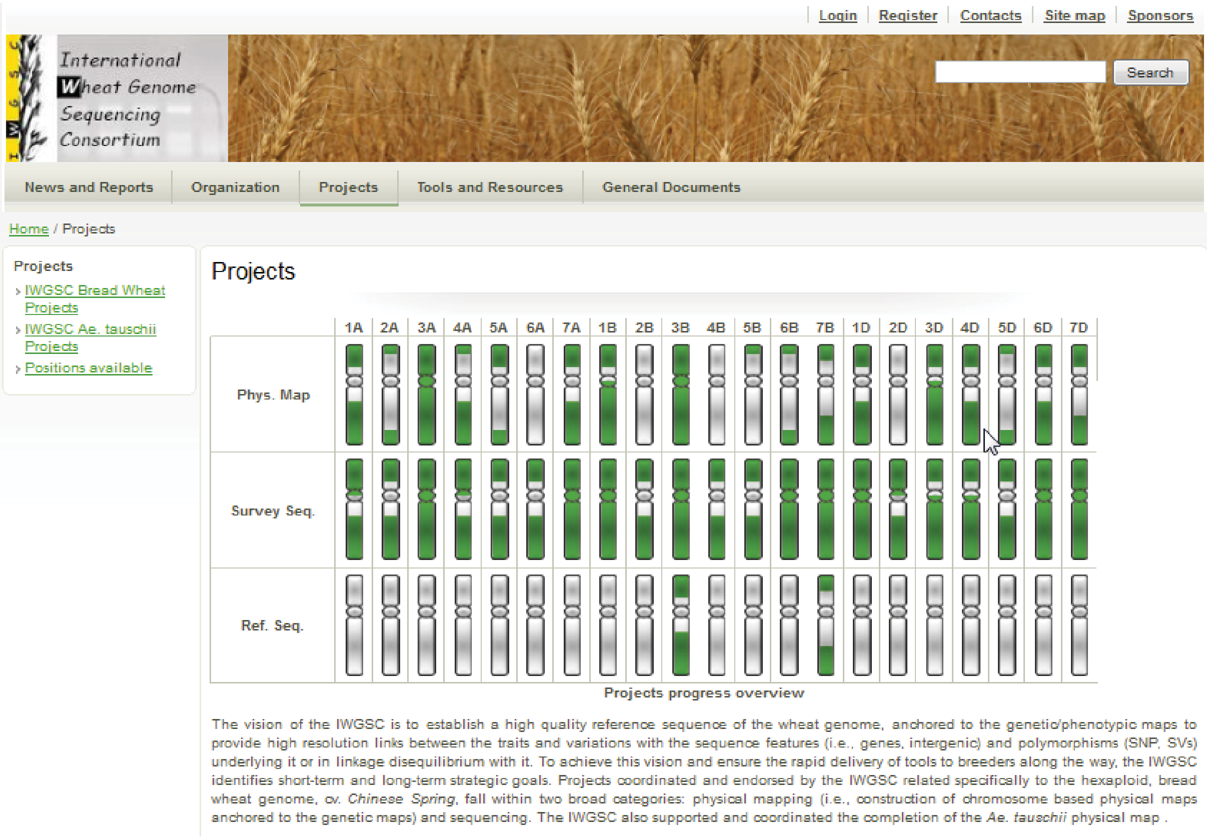
618,240 BAC clones
(5 arms remaining)

710,400 BAC clones
(2 arms remaining)

TOTAL (Oct 2011) : **2,219,520 BAC clones** (~ 16 x , 118 kb)

http://olomouc.ueb.cas.cz/dna-libraries/cereals

IWGSC



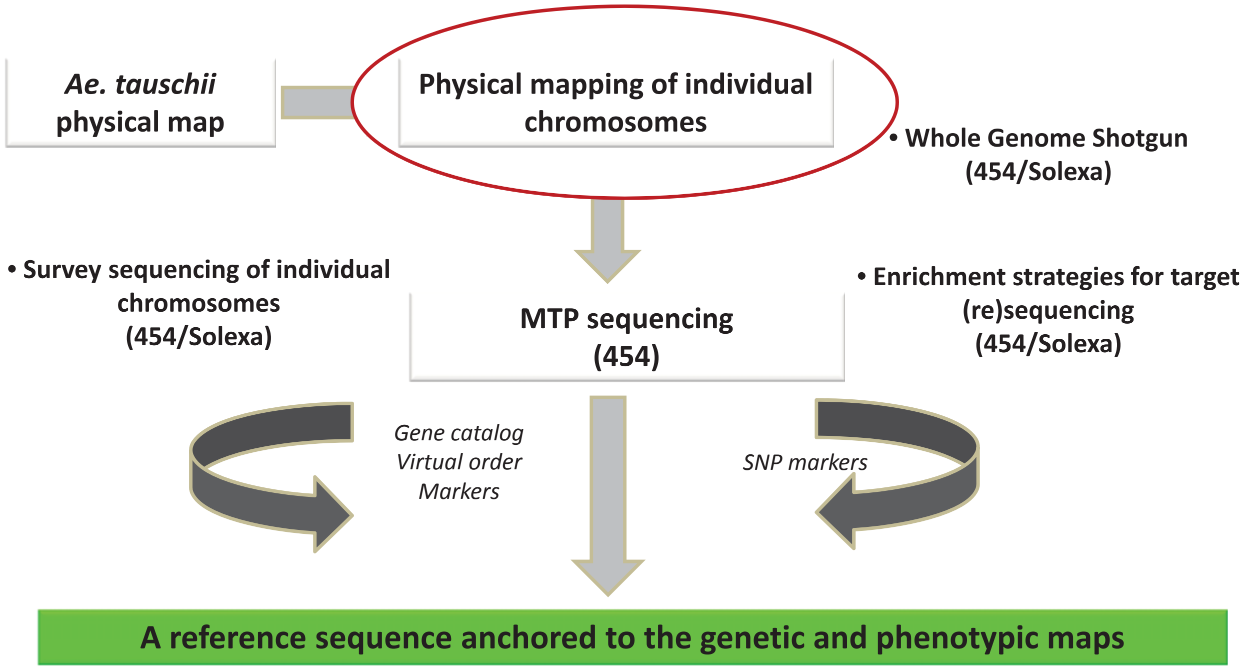
Projects

Projects progress overview

The vision of the IWGSC is to establish a high quality reference sequence of the wheat genome, anchored to the genetic/phenotypic maps to provide high resolution links between the traits and variations with the sequence features (i.e., genes, intergenic) and polymorphisms (SNP, SVs) underlying it or in linkage disequilibrium with it. To achieve this vision and ensure the rapid delivery of tools to breeders along the way, the IWGSC identifies short-term and long-term strategic goals. Projects coordinated and endorsed by the IWGSC related specifically to the hexaploid, bread wheat genome, cv. *Chinese Spring*, fall within two broad categories: physical mapping (i.e., construction of chromosome based physical maps anchored to the genetic maps) and sequencing. The IWGSC also supported and coordinated the completion of the *Ae. tauschii* physical map .

www.wheatgenome.org

Combined strategies to establish a Chinese Spring reference genome sequence



***Ae. tauschii* physical map**

Physical mapping of individual chromosomes

- **Whole Genome Shotgun (454/Solexa)**
- **Survey sequencing of individual chromosomes (454/Solexa)**

MTP sequencing (454)

- **Enrichment strategies for target (re)sequencing (454/Solexa)**

A reference sequence anchored to the genetic and phenotypic maps

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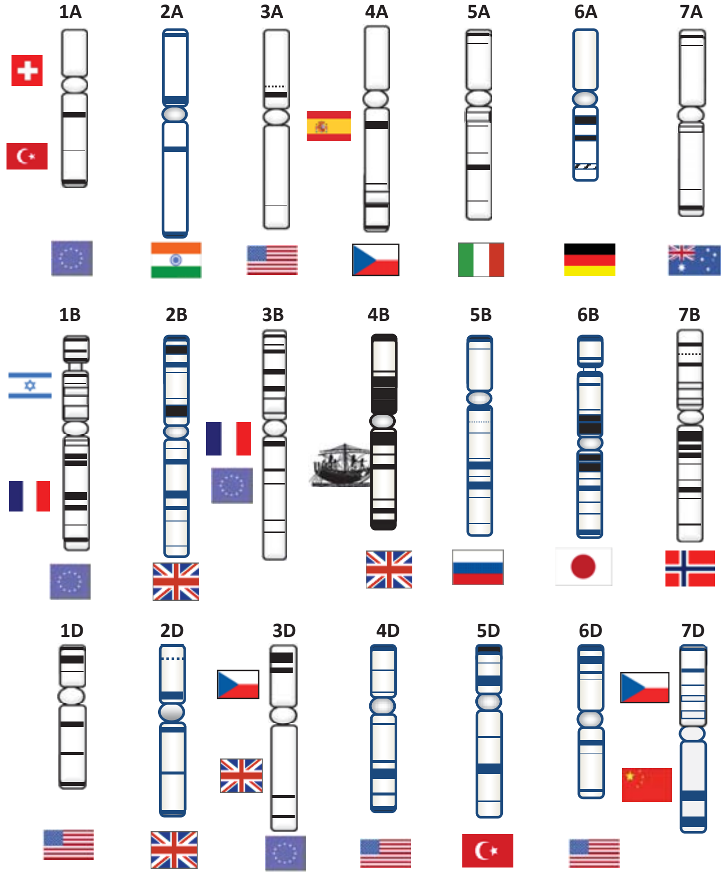
Physical mapping of the Bread Wheat Genome



2011

T. aestivum

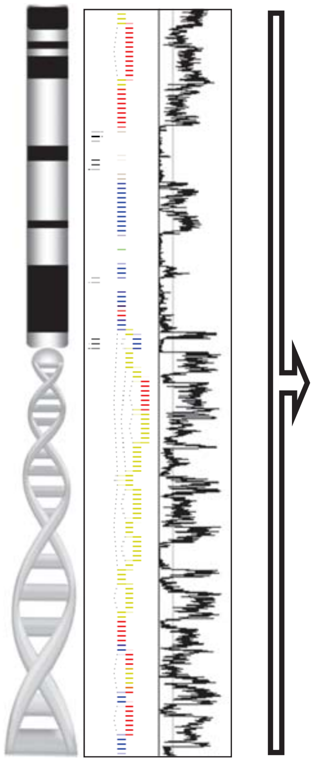
cv Chinese Spring

Milestone
Achieved:

Physical Maps
Funded for all
chromosomes
Sept 2011

Next Milestone:
All Physical Maps
Completed
2012/2013

Wheat Physical Maps - Applications



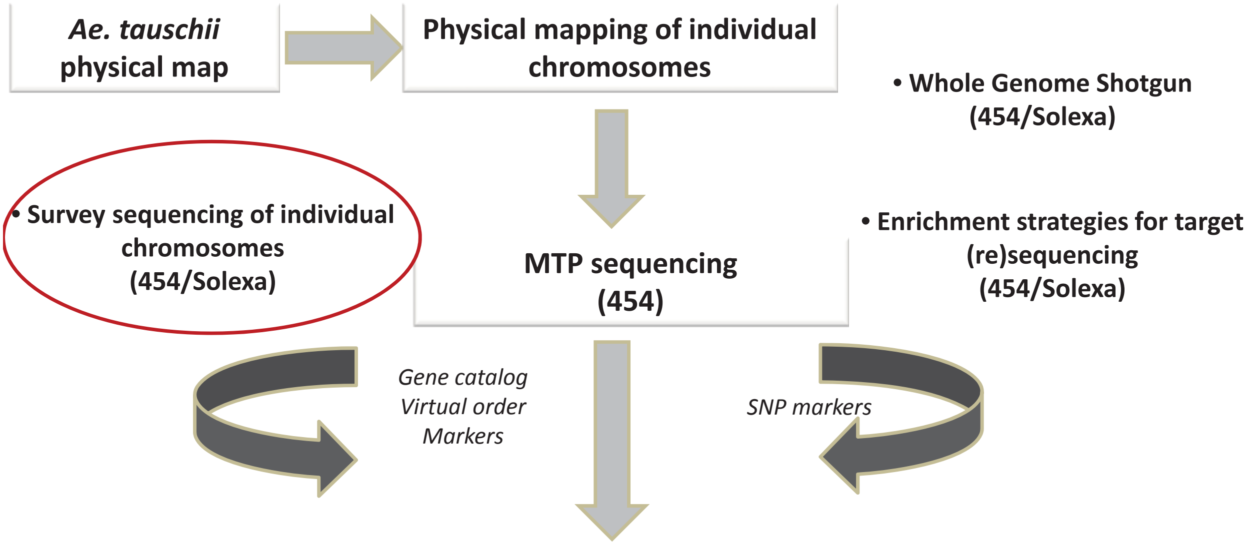
✓ **Structure, function & evolution of the wheat genome**

- **Gene space organization and regulation**
- **Synteny between homoeologous genomes and with other cereal genomes**
- Evolutionary mechanisms (gene movements, genome duplications, TE transposition…)
- Pattern of recombination and linkage disequilibrium
- **Whole Chromosome Sequencing**

✓ **Genomics-based tools for wheat breeding & improvement**

- Positional cloning of genes/QTLs underlying agronomically important traits
- Molecular markers (SNPs, ISBPs...)
- New genotyping strategies

Combined strategies to establish a Chinese Spring reference genome sequence



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Gene catalog
Virtual order
Markers

SNP markers

A reference sequence anchored to the genetic and phenotypic maps

GENOSCOPE

IWGSC

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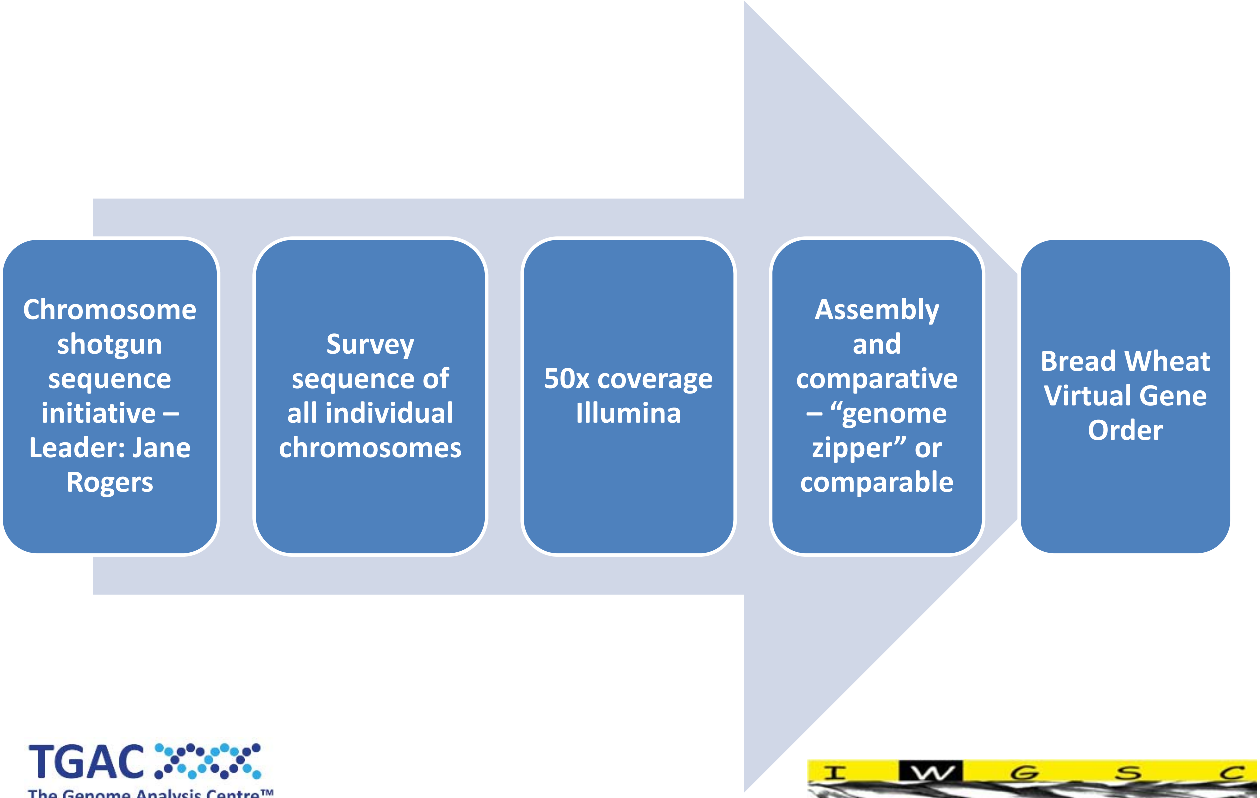
Survey Sequencing Initiative



- Chromosome shotgun sequence initiative – Leader: Jane Rogers
- Survey sequence of all individual chromosomes
- 50x coverage Illumina
- Assembly and comparative – “genome zipper” or comparable
- Bread Wheat Virtual Gene Order

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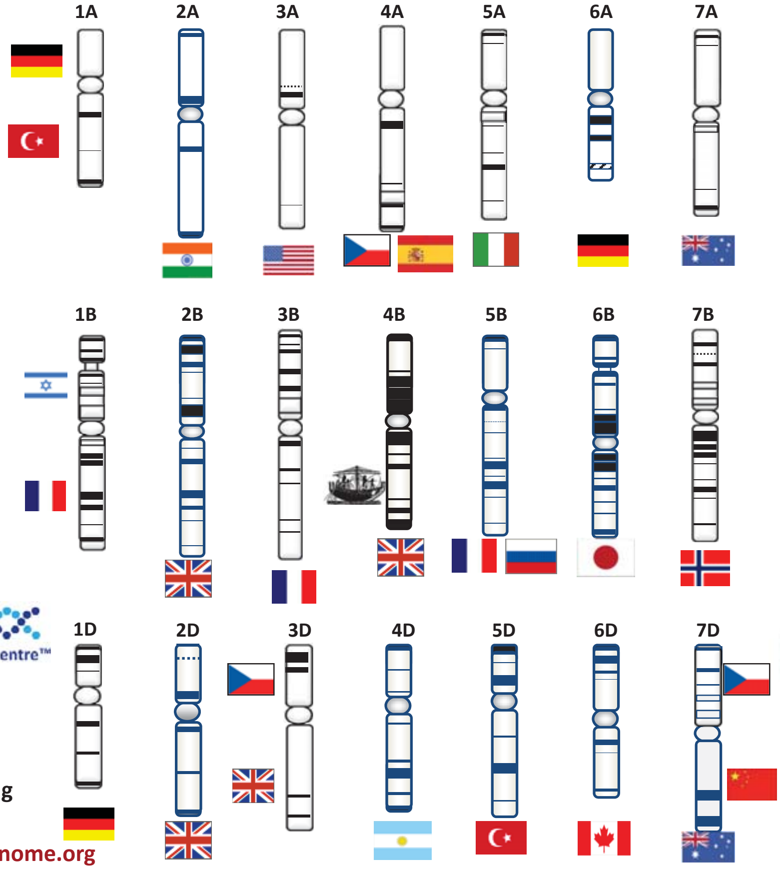
IWGSC

Survey sequencing of bread wheat genome

IWGSC



Funded with support from

Graminor

biogemma

INRA

Institute of Experimental Botany of the AS CR, v. v. i.

ICARDA

TGAC The Genome Analysis Centre™

T. aestivum

cv Chinese Spring

www.wheatgenome.org

Survey sequencing of bread wheat genome

IWGSC

Milestones Achieved:

- Illumina Sequence Coverage for all 21 chromosomes
- Assemblies of 29 chromosome arms completed

Next Milestones:

- Dec 2011 - Assemblies completed
- Jan 2012 - Genome zipper completed
- Mar 2012 - Main paper drafted

Funded with support from

Graminor

biogemma

INRA

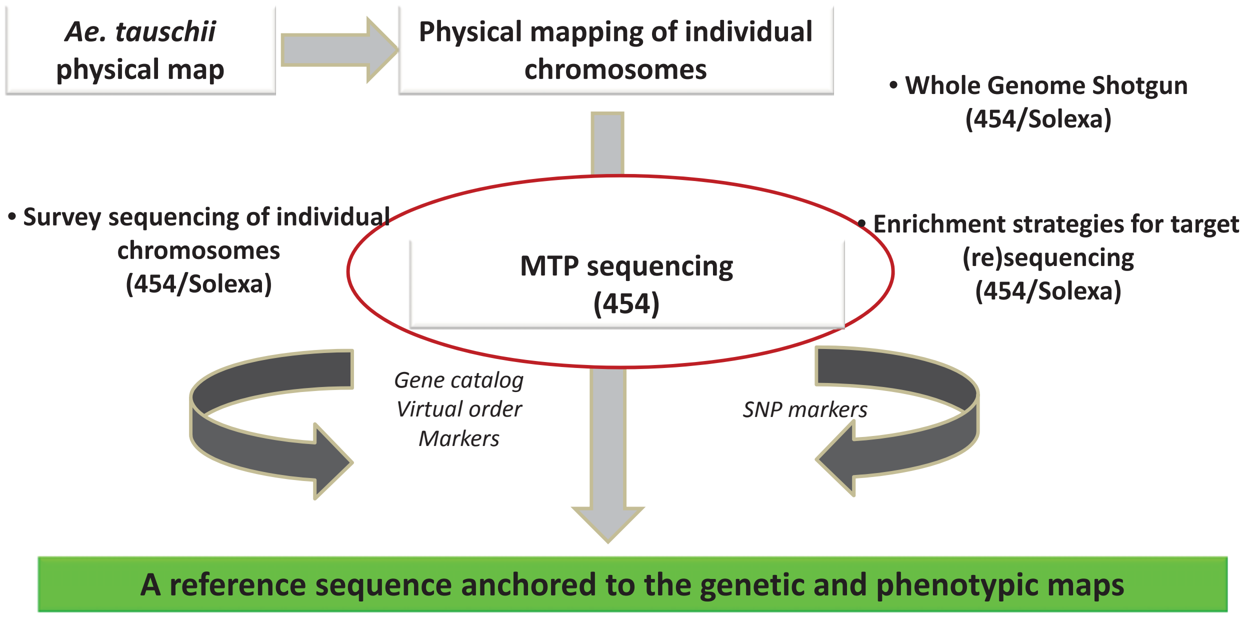
Institute of Experimental Botany of the AS CR, v. v. i.

ICARDA

2012 - What can you do with the chromosome-based survey sequence

- Annotate genes within contigs (intron-exon structure)
- Link features to chromosomes (within subgenomes)
- Localized synteny studies
- Gain approximate knowledge of some global figures –
  - Gene counts
  - Pseudogenes
  - Lineage specific genes
  - Comparative analysis of homoeologous genes

Combined strategies to establish a Chinese Spring reference genome sequence



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A reference sequence anchored to the genetic and phenotypic maps

MTP sequencing of the bread wheat genome

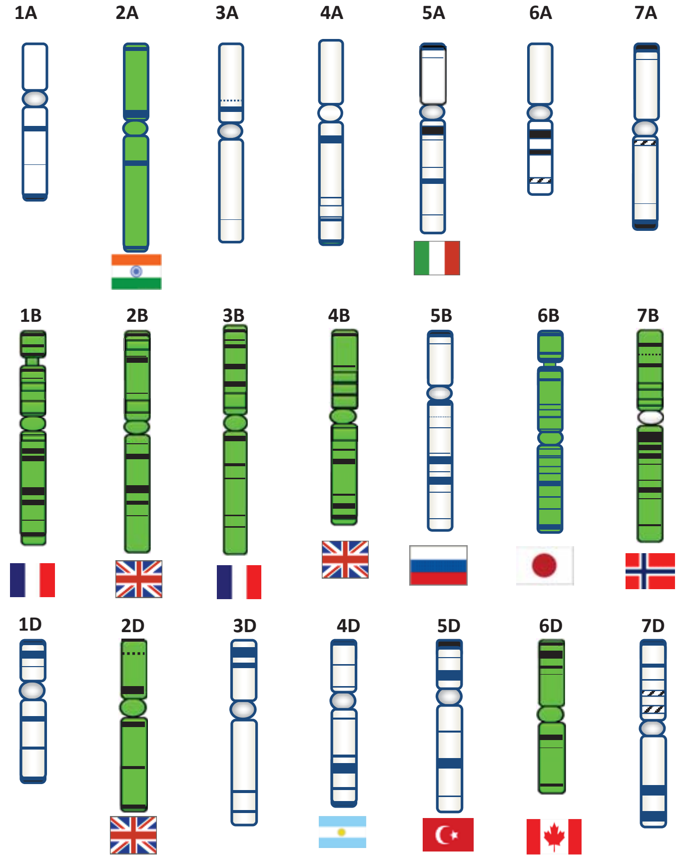
2011 Milestone :

One-third of chromosomes funded

T. aestivum

cv Chinese Spring

MTP sequencing of the bread wheat genome



Milestone Achieved:
10 chromosomes funded
Sept 2011

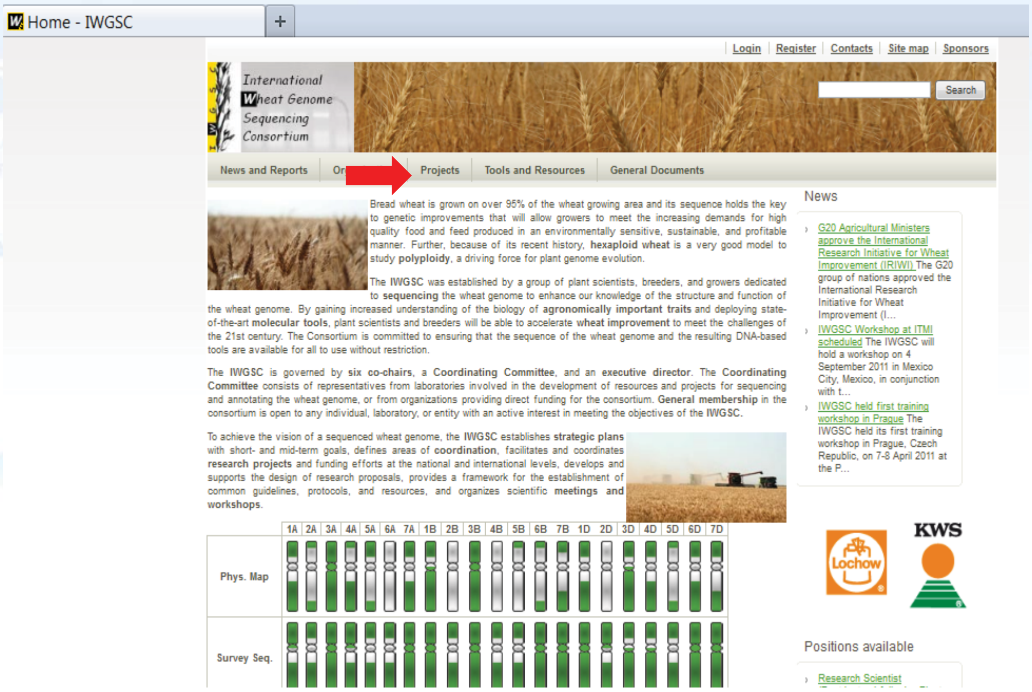
Now Seeking:
Project leaders and funders for remaining chromosomes

Next Milestone:
All chromosomes funded (2013)

T. aestivum

cv Chinese Spring

Where to find information



Bread wheat is grown on over 95% of the wheat growing area and its sequence holds the key to genetic improvements that will allow growers to meet the increasing demands for high quality food and feed produced in an environmentally sensitive, sustainable, and profitable manner. Further, because of its recent history, **hexaploid wheat** is a very good model to study **polyploidy**, a driving force for plant genome evolution.

The IWGSC was established by a group of plant scientists, breeders, and growers dedicated to **sequencing** the wheat genome to enhance our knowledge of the structure and function of the wheat genome. By gaining increased understanding of the biology of **agronomically important traits** and deploying state-of-the-art **molecular tools**, plant scientists and breeders will be able to accelerate **wheat improvement** to meet the challenges of the 21st century. The Consortium is committed to ensuring that the sequence of the wheat genome and the resulting DNA-based tools are available for all to use without restriction.

The IWGSC is governed by **six co-chairs**, a **Coordinating Committee**, and an **executive director**. The **Coordinating Committee** consists of representatives from laboratories involved in the development of resources and projects for sequencing and annotating the wheat genome, or from organizations providing direct funding for the consortium. **General membership** in the consortium is open to any individual, laboratory, or entity with an active interest in meeting the objectives of the IWGSC.

To achieve the vision of a sequenced wheat genome, the IWGSC establishes **strategic plans** with short- and mid-term goals, defines areas of **coordination**, facilitates and coordinates **research projects** and funding efforts at the national and international levels, develops and supports the design of research proposals, provides a framework for the establishment of common guidelines, protocols, and resources, and organizes scientific **meetings and workshops**.

News

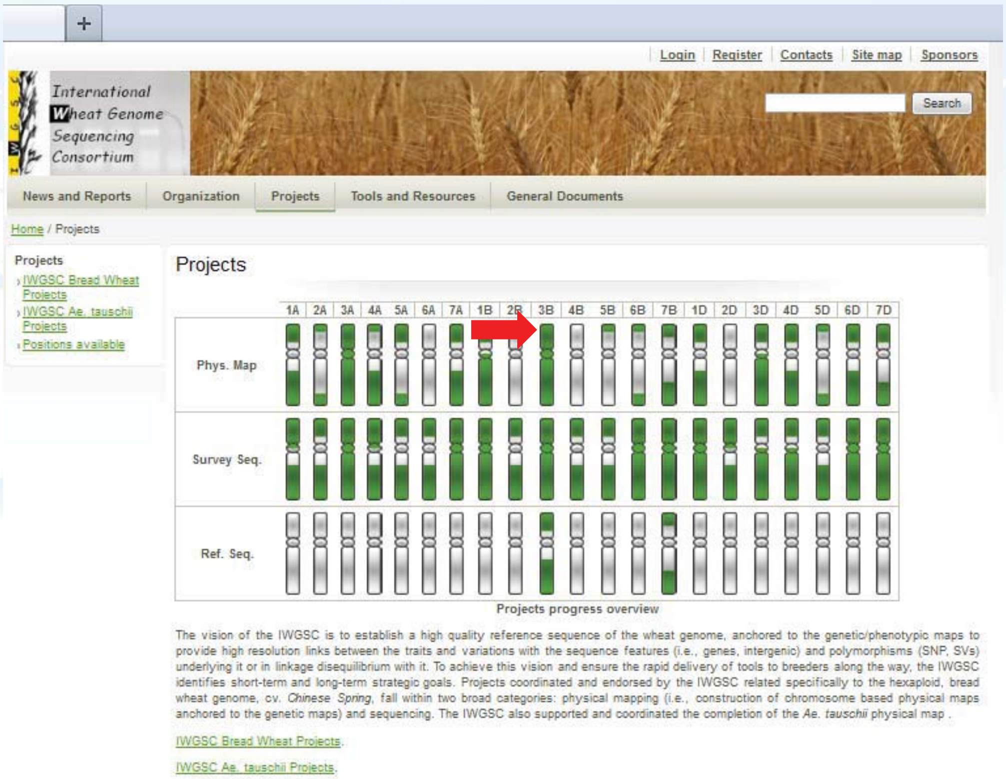
- G20 Agricultural Ministers approve the International Research Initiative for Wheat Improvement (IRIWI) The G20 group of nations approved the International Research Initiative for Wheat Improvement (I...
- IWGSC Workshop at ITMI scheduled The IWGSC will hold a workshop on 4 September 2011 in Mexico City, Mexico, in conjunction with t...
- IWGSC held first training workshop in Prague The IWGSC held its first training workshop in Prague, Czech Republic, on 7-8 April 2011 at the P...

Positions available

- Research Scientist

www.wheatgenome.org

Projects



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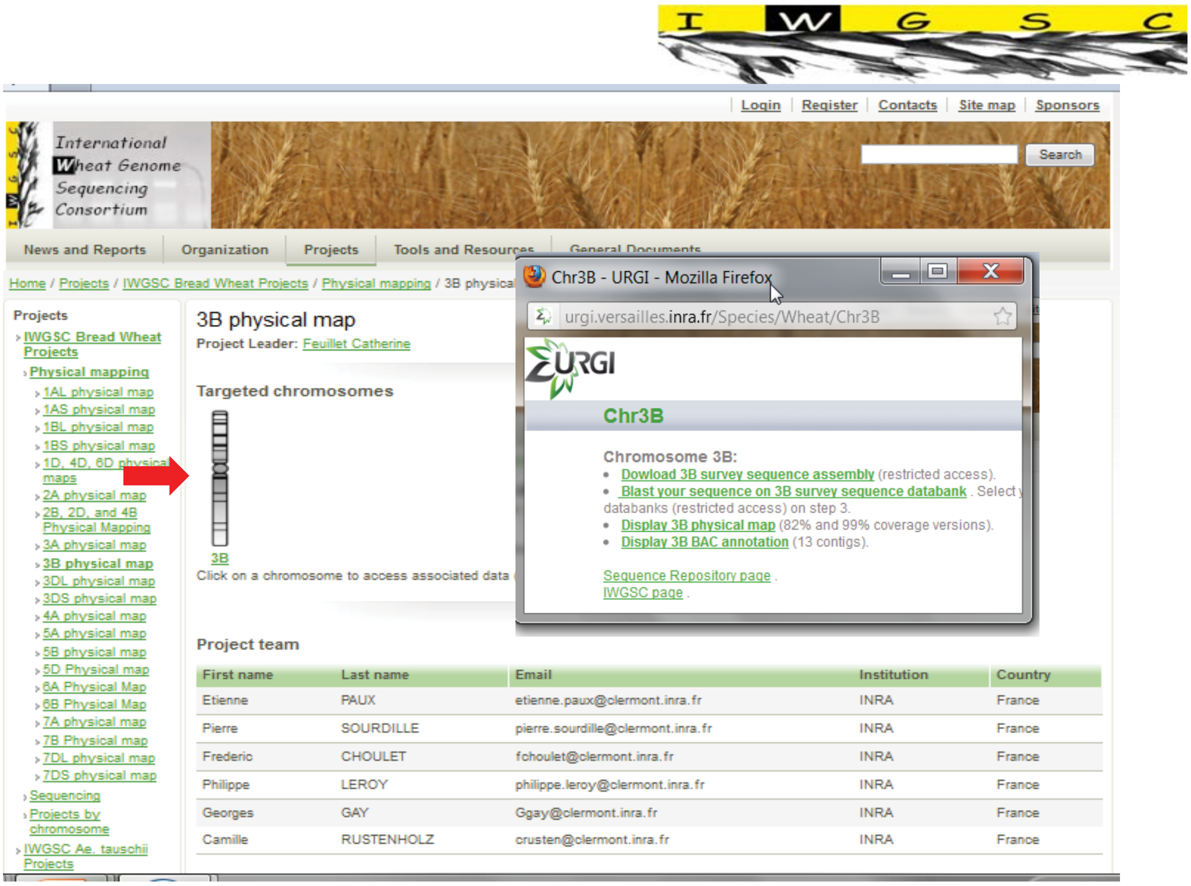
IWGSC Bread Wheat Projects.

IWGSC Ae. tauschii Projects.

www.wheatgenome.org



3B physical map

Project Leader: Feuillet Catherine

Targeted chromosomes

Click on a chromosome to access associated data

Chromosome 3B:

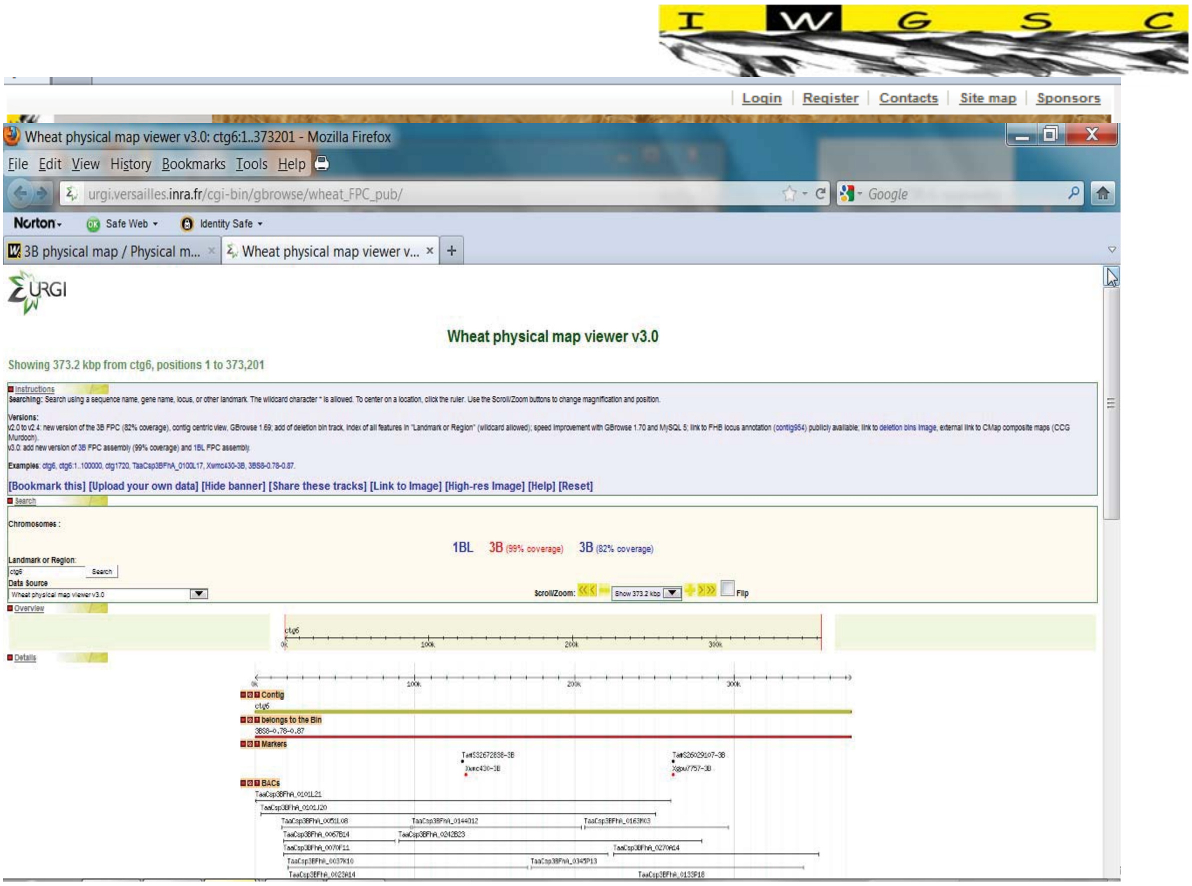
- Dowload 3B survey sequence assembly (restricted access).
- Blast your sequence on 3B survey sequence databank . Select y databanks (restricted access) on step 3.
- Display 3B physical map (82% and 99% coverage versions).
- Display 3B BAC annotation (13 contigs).

Sequence Repository page .
IWGSC page .

Project team

First name	Last name	Email	Institution	Country
Etienne	PAUX	etienne.paux@clermont.inra.fr	INRA	France
Pierre	SOURDILLE	pierre.sourdille@clermont.inra.fr	INRA	France
Frederic	CHOULET	fchoulet@clermont.inra.fr	INRA	France
Philippe	LEROY	philippe.leroy@clermont.inra.fr	INRA	France
Georges	GAY	Ggay@clermont.inra.fr	INRA	France
Camille	RUSTENHOLZ	crusten@clermont.inra.fr	INRA	France

www.wheatgenome.org



Wheat physical map viewer v3.0

Showing 373.2 kbp from ctg6, positions 1 to 373,201

Searching: Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed. To center on a location, click the ruler. Use the Scroll/Zoom buttons to change magnification and position.

Versions:
v2.0 to v2.4: new version of the 3B FPC (82% coverage), contig centric view, GBrowse 1.69; add of deletion bin track, index of all features in "Landmark or Region" (wildcard allowed); speed improvement with GBrowse 1.70 and MySQL 5; link to FHB locus annotation (contig954) publicly available; link to deletion bins image, external link to CMap composite maps (CCG Murdoch).
v3.0: add new version of 3B FPC assembly (99% coverage) and 1BL FPC assembly.

Examples: ctg6, ctg6:1..100000, ctg1720, TaaCsp3BFhA_0100L17, Xwmc430-3B, 3BS8-0.78-0.87.

[Bookmark this] [Upload your own data] [Hide banner] [Share these tracks] [Link to Image] [High-res Image] [Help] [Reset]

Chromosomes :

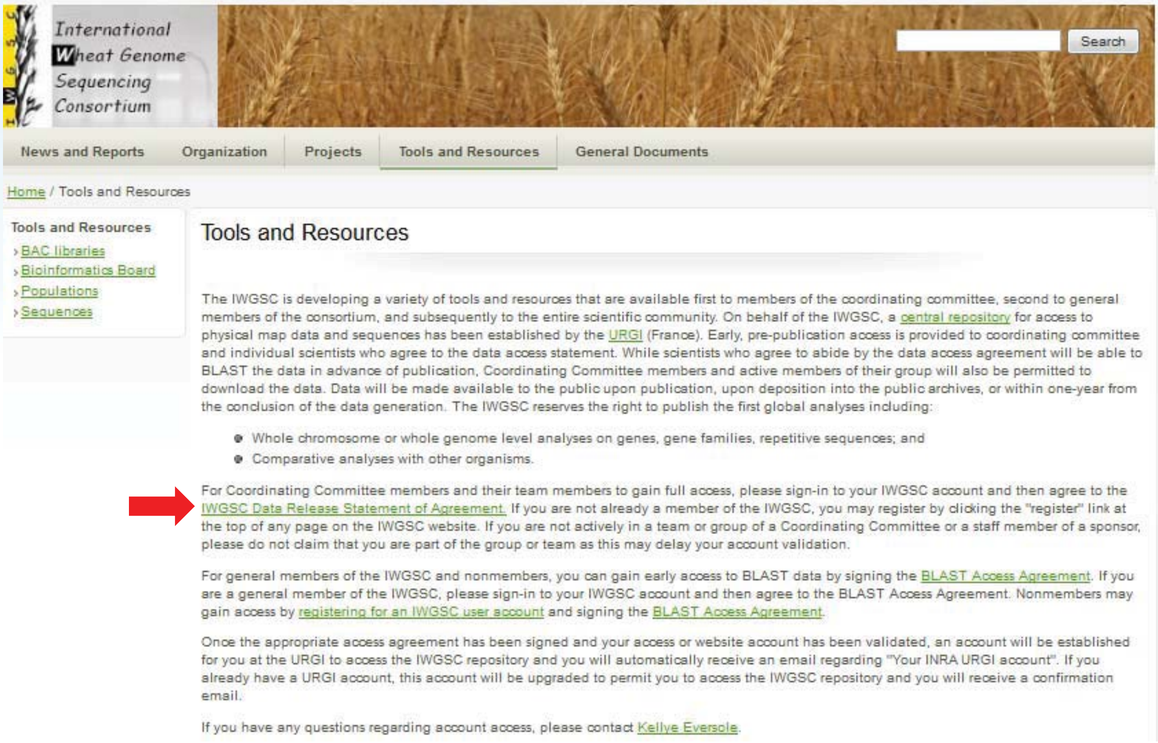
1BL 3B (99% coverage) 3B (82% coverage)

Landmark or Region: ctg6

Data Source: Wheat physical map viewer v3.0

www.wheatgenome.org

Gaining access



Tools and Resources

The IWGSC is developing a variety of tools and resources that are available first to members of the coordinating committee, second to general members of the consortium, and subsequently to the entire scientific community. On behalf of the IWGSC, a central repository for access to physical map data and sequences has been established by the URGI (France). Early, pre-publication access is provided to coordinating committee and individual scientists who agree to the data access statement. While scientists who agree to abide by the data access agreement will be able to BLAST the data in advance of publication, Coordinating Committee members and active members of their group will also be permitted to download the data. Data will be made available to the public upon publication, upon deposition into the public archives, or within one-year from the conclusion of the data generation. The IWGSC reserves the right to publish the first global analyses including:

- Whole chromosome or whole genome level analyses on genes, gene families, repetitive sequences; and
- Comparative analyses with other organisms.

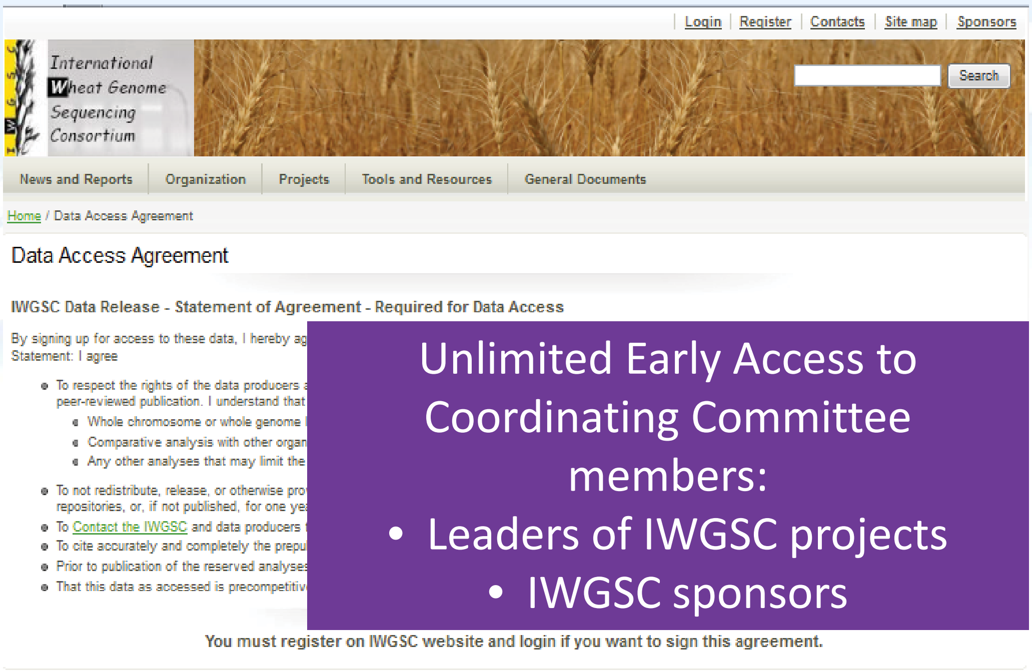
For Coordinating Committee members and their team members to gain full access, please sign-in to your IWGSC account and then agree to the IWGSC Data Release Statement of Agreement. If you are not already a member of the IWGSC, you may register by clicking the "register" link at the top of any page on the IWGSC website. If you are not actively in a team or group of a Coordinating Committee or a staff member of a sponsor, please do not claim that you are part of the group or team as this may delay your account validation.

For general members of the IWGSC and nonmembers, you can gain early access to BLAST data by signing the BLAST Access Agreement. If you are a general member of the IWGSC, please sign-in to your IWGSC account and then agree to the BLAST Access Agreement. Nonmembers may gain access by registering for an IWGSC user account and signing the BLAST Access Agreement.

Once the appropriate access agreement has been signed and your access or website account has been validated, an account will be established for you at the URGI to access the IWGSC repository and you will automatically receive an email regarding "Your INRA URGI account". If you already have a URGI account, this account will be upgraded to permit you to access the IWGSC repository and you will receive a confirmation email.

If you have any questions regarding account access, please contact Kellye Eversole.

Data Access Agreement



Data Access Agreement

IWGSC Data Release - Statement of Agreement - Required for Data Access

By signing up for access to these data, I hereby ag
Statement: I agree

- To respect the rights of the data producers a
  peer-reviewed publication. I understand that
    - Whole chromosome or whole genome
    - Comparative analysis with other organ
    - Any other analyses that may limit the
- To not redistribute, release, or otherwise pro
  repositories, or, if not published, for one yea
- To Contact the IWGSC and data producers
- To cite accurately and completely the prepu
- Prior to publication of the reserved analyses
- That this data as accessed is precompetitiv

Unlimited Early Access to Coordinating Committee members:
- Leaders of IWGSC projects
- IWGSC sponsors

You must register on IWGSC website and login if you want to sign this agreement.

2012 - Next Steps….

- Complete survey sequence initiative
- Complete MTP sequence, assembly, and annotation for chromosomes 3B, 7B
- Complete physical maps for all chromosomes
- Obtain funding for MTP sequencing of remaining 11 chromosomes

Perhaps a few other countries will take a chromosome ….??

Acknowledgements

Eduard. Akhunov	Kansas State University
Michael Alaux	INRA-URGI
Olin Anderson	ARS-USDA
Rudi Appels	Murdoch University
Jan Bartos	IEB
Hélène Berges	CNRGV-INRA
Delphine Fleury	ACPFG
G. Freyssinet	Limagrain
Jan Gielen	Syngenta
Bikram Gill	Kansas State University
Justin Gilpin	Kansas Wheat Commission
Magne Gullord	Graminor
Perry Gustafson	USDA-ARS
Dimah Habash	Secure Wheat

Darrell Hanavan	Colorado Wheat
Hirokazu Handa	NIAS
Marcelo Helguera	INTA
Pilar Hernandez	IAS (CSIC)
Kuldeep Singh	Punjab Agricultural University
Mark Sorrells	Cornell University
Roberto Tuberosa	University of Bologna
Miroslav Valarik	Institute of Experimental Botany
Song Weining	Norwest A&F University
Thomas Wicker	University of Zurich

IWGSC Coordinating Committee: Project Leaders & Sponsors

Sponsors

Thank you for your attention

eversole@eversoleassociates.com

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