



The IWGSC: A Genome Sequence Based Platform to Accelerate Wheat Improvement

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Executive Director
IWGSC

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St. Petersburg, Russian Federation

3 June 2010



EVERSOLE ASSOCIATES

Enabling Science and Technology





The International Wheat Genome Sequencing Consortium (IWGSC)

An internationally coordinated effort to sequence the bread wheat genome and create a platform for accelerating wheat improvement.

- Launched in 2005 (PAG meeting)
initiative of Kansas wheat growers



The Challenges

- **One Goal**: Sustainably produce a consistent, high quality supply of food, feed and nonfood products
- **A unique context in human history**:
 - Increasing demand requires 2% production increase/year through 2050
 - Increasing competition – food/nonfood
 - Uncertain climatic changes – extremes
 - New pests and diseases
 - Yield stagnation over the past 10 years
 - Limited opportunity for expansion of land
 - Trait discovery to commercialization for wheat = 10-20 years; corn – 4-6 years



Monsanto's Genomics Pipeline for Corn, Rice, Soybeans. . .

Sequencing
Genomic and cDNA

Sequence Bioinformatics
Discover & Annotate Genes

Expression Analysis
Functional Predictions

Phenotypic Testing
Translate Models to Crops

Billions of Bases

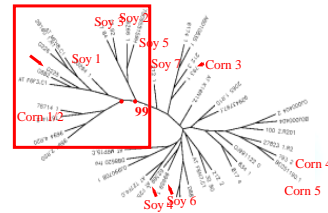
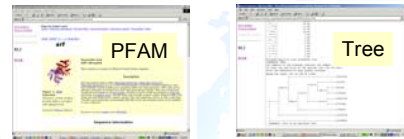
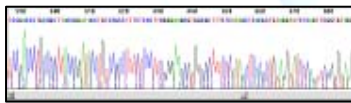
100,000's of Genes

10,000's of Genes

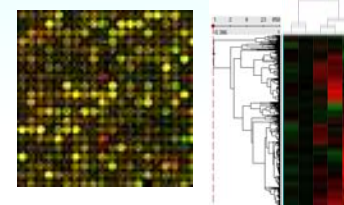
1,000's of Genes

```

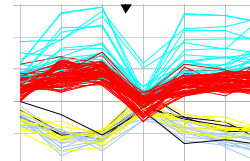
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GGCGCTAGATCGATCGATCGATC
GATTCAGACTGGAAGTCATGCT
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GGCGCTAGATCGATCGATCGATC
GATTCAGACTGGAAGTCATGCT
    
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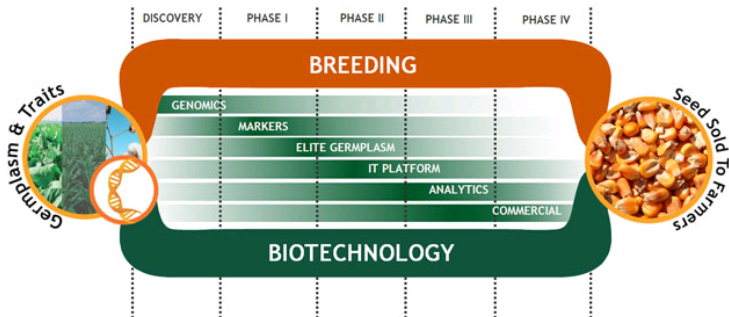
Gene Relationships



Rain ⚡



Monsanto Transcript Profiling:
Corn, Soy, Rice, Arabidopsis



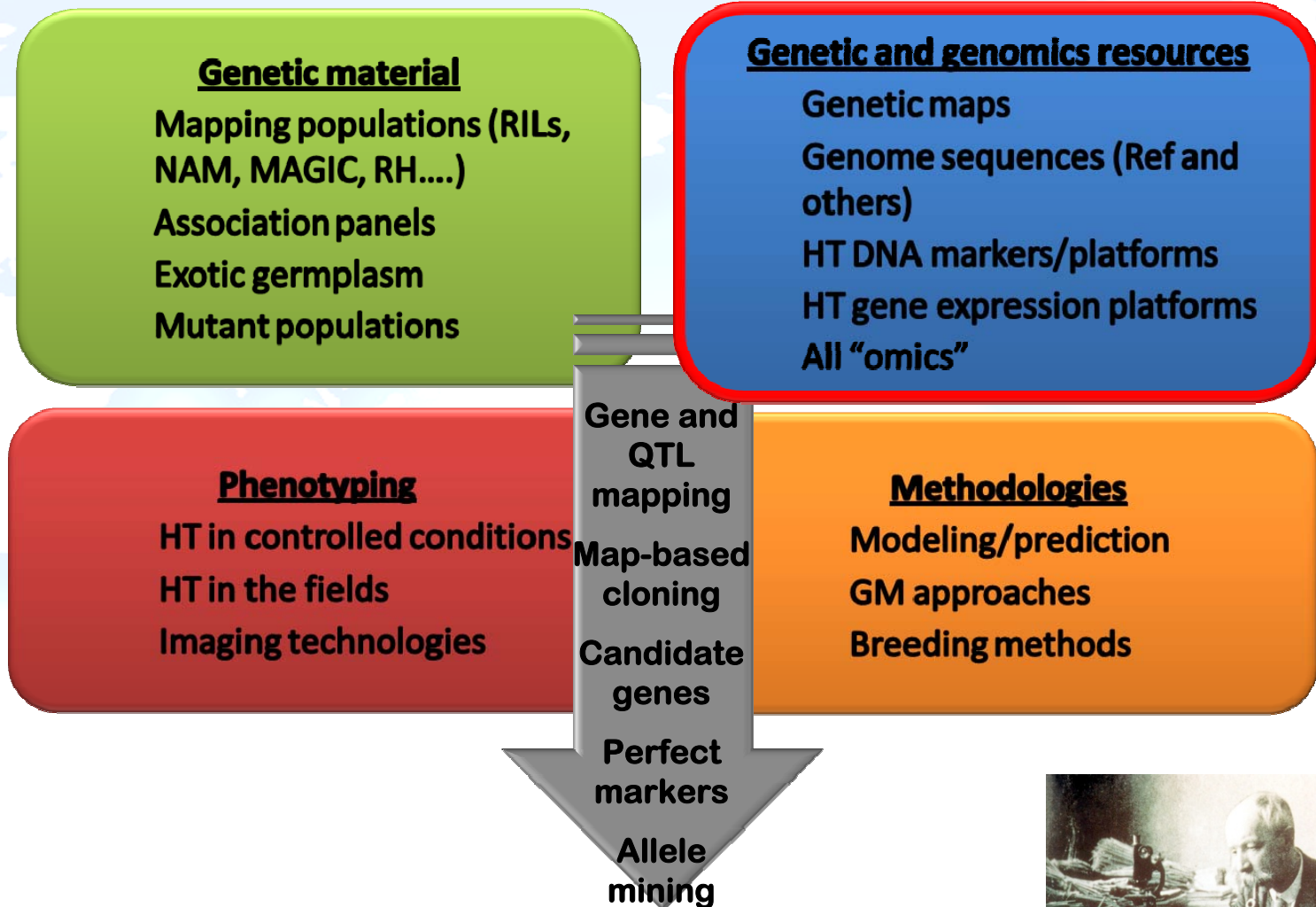
Courtesy: J. Rapp



A genome sequence platform

- Framework for understanding genetic variation – link traits to precise genomic locations, genes, and regulatory elements
- Unlimited source of markers
- Characterize alleles and eliminate linkage drag
- Platform for re-sequencing
- Facilitates QTL and gene cloning

Wheat's future – an integrated toolbox



Improved wheat germplasm

Courtesy of C. Feuillet



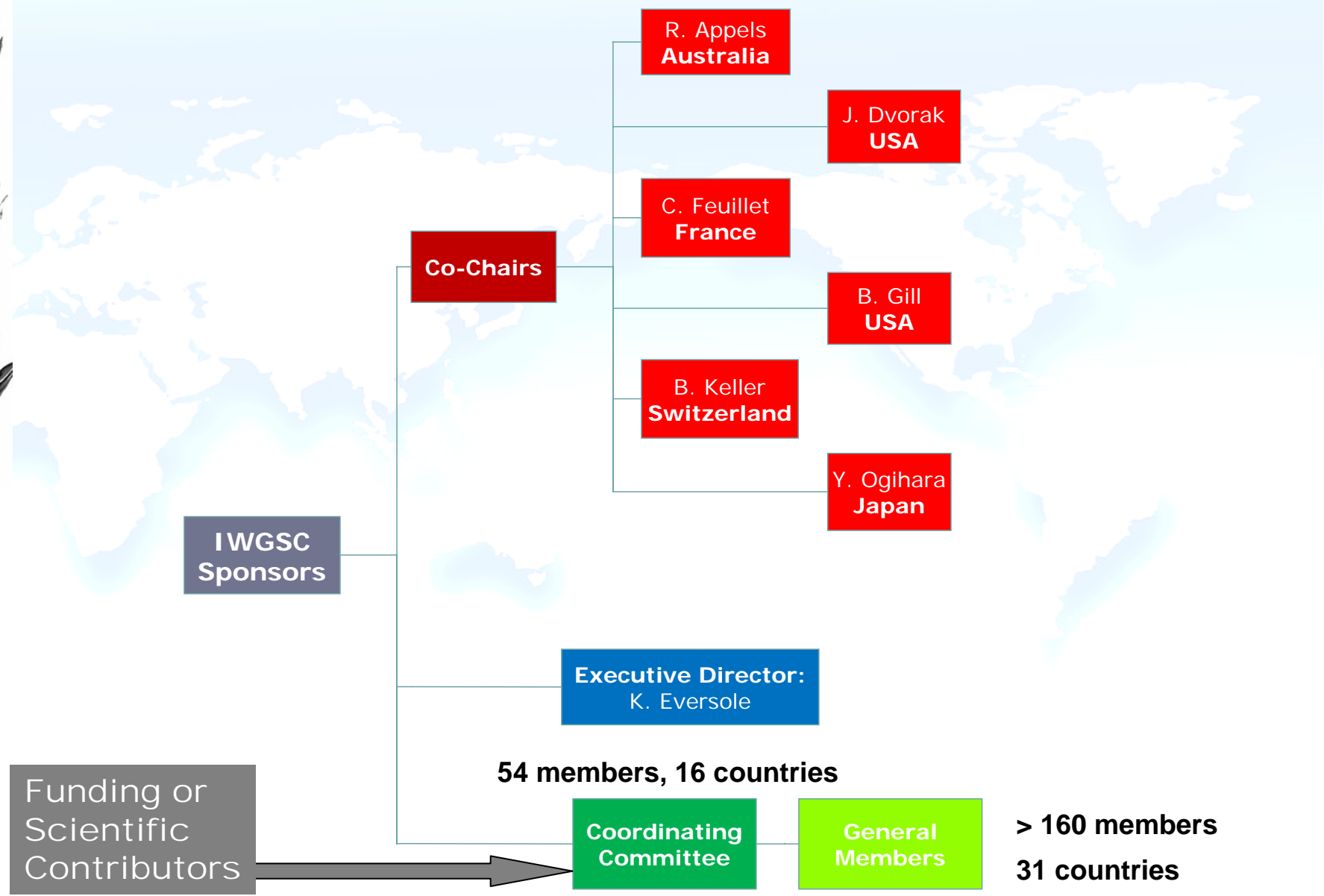


International Wheat Genome Sequencing Consortium (IWGSC)

An international, public-private collaboration focused on building the tools and resources for sequence enabled wheat breeding

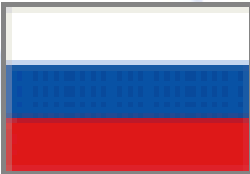
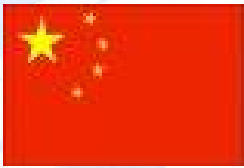
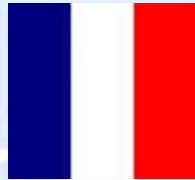
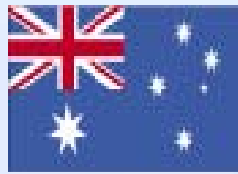


IWGSC





IWGSC Coordinating Committee



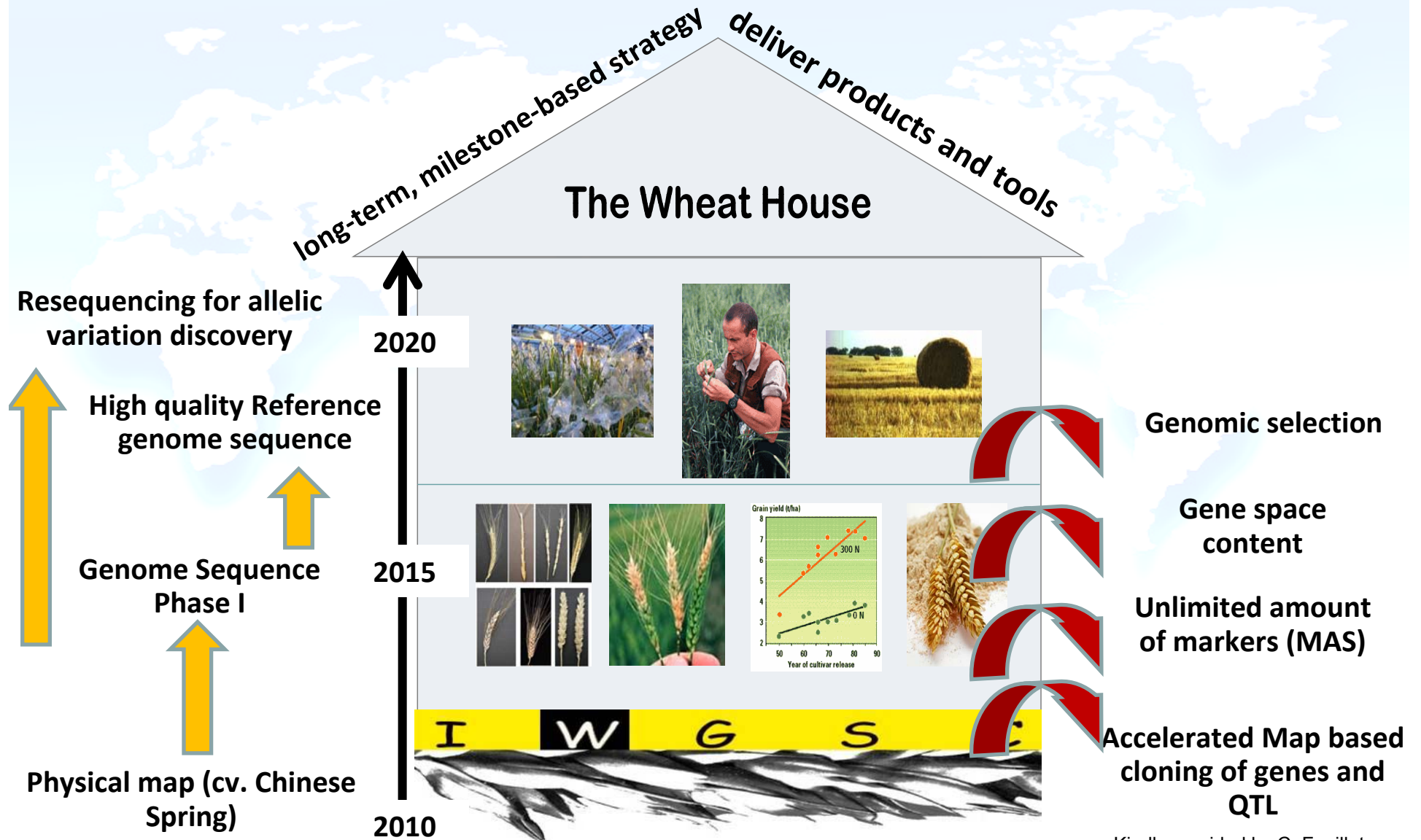
54 members, 16 countries



Vision: 21st Century Tools for Wheat

- A long-term, milestone-based strategy that delivers products and tools while working towards the ultimate goal of enabling profitability and sustainability throughout the industry
 - Physical map of bread wheat genome
 - Genome sequence launching pad
 - Robust bioinformatics tools
 - Whole genome enabled functional genomics
 - Accelerated breeding platforms

IWGSC Vision: Breeders, Agronomists, and Industry have state-of-the-art tools and technologies equal to those of other crops

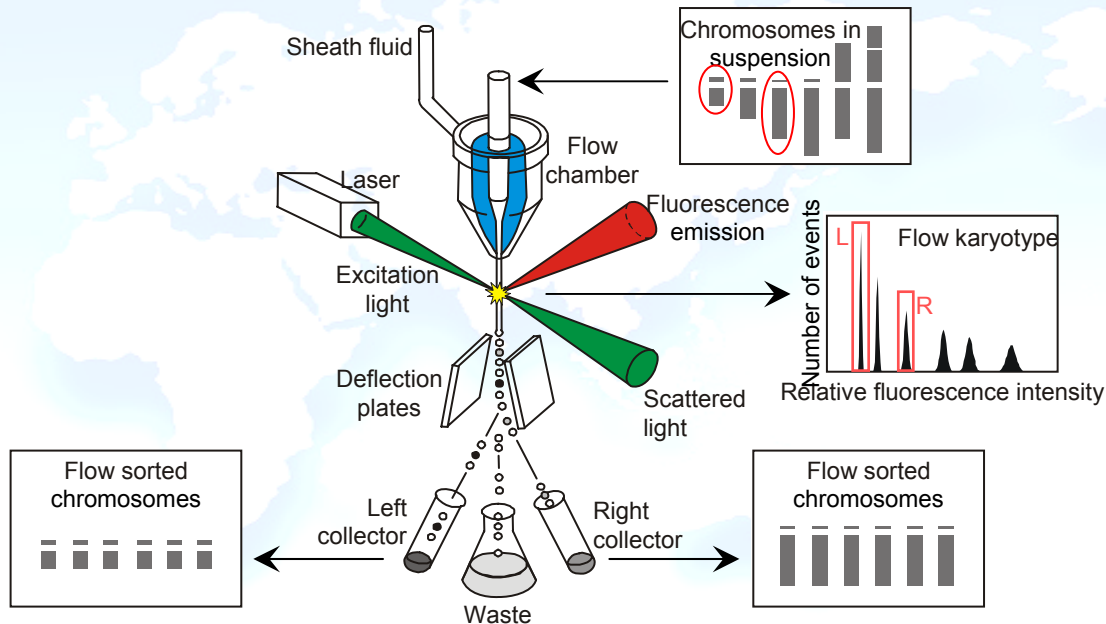


Kindly provided by C. Feuillet

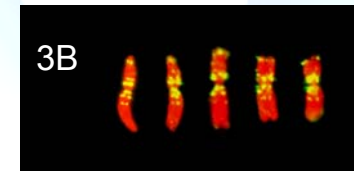
Convergence of efficient, cost-effective technologies

1. Chromosome sorting

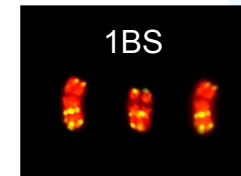
Institute of Experimental Botany
Jaroslav Dolezel



- 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 (http://lmcc.ieb.cz/genomic_resources/)

- 3B (Safar et al, 2004)

- To date, 12 chromosome/arm specific libraries are ready to be used

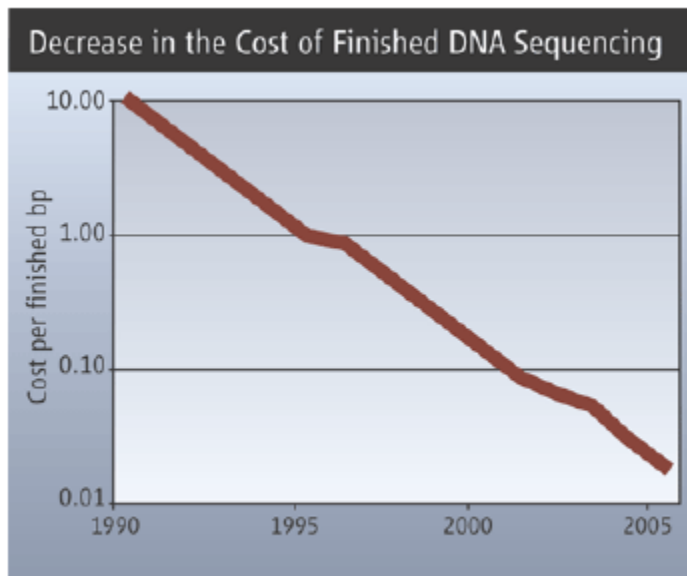
Advanced sequencing technologies

2. Next Generation Sequencing

GENE SEQUENCING

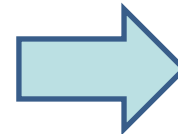
The Race for the \$1000 Genome

Fast, cheap genetic analyses will soon become a reality, and the consequences—good and bad—will affect everybody



(R. Service, 2006)

A wheat genome
sequence for less
than 10 million Euros



But which kind of
sequence? For whom
and for what?



IWGSC Roadmap for Wheat

I·T·M·I

MANAGEMENT OFFICE
Australian Centre Plant Functional Genomics
Plant Genomics Centre
Plant 4, Glen Osmond SA 5064
Ph: 01 8 6363 7423
Fax: 01 8 6363 7423
Email: peter.langridge@cepfg.com.au

International • Triticeae • Mapping •
Initiative

2006 ITMI Summer Workshop
Victor Harbor, Australia

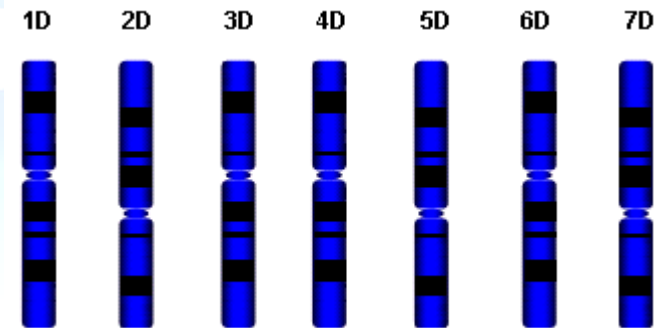
- Complete *Ae. tauschii* physical map
- Develop physical maps of individual Chinese Spring chromosomes to provide a sequencing substrate
- Gain sponsorship of individual chromosomes at the international level

2006



Wild diploid relatives D & A Genome Projects

- ***Ae. tauschii* D genome physical map funded**
 - Jan Dvorak, USA



- **Sequencing**

- ***Ae. tauschii* D-Genome:**

- NSF Proposal submitted – J. Dvorak
- BGI Solexa 40x coverage (gene space only, not linked to any map, not available so far)

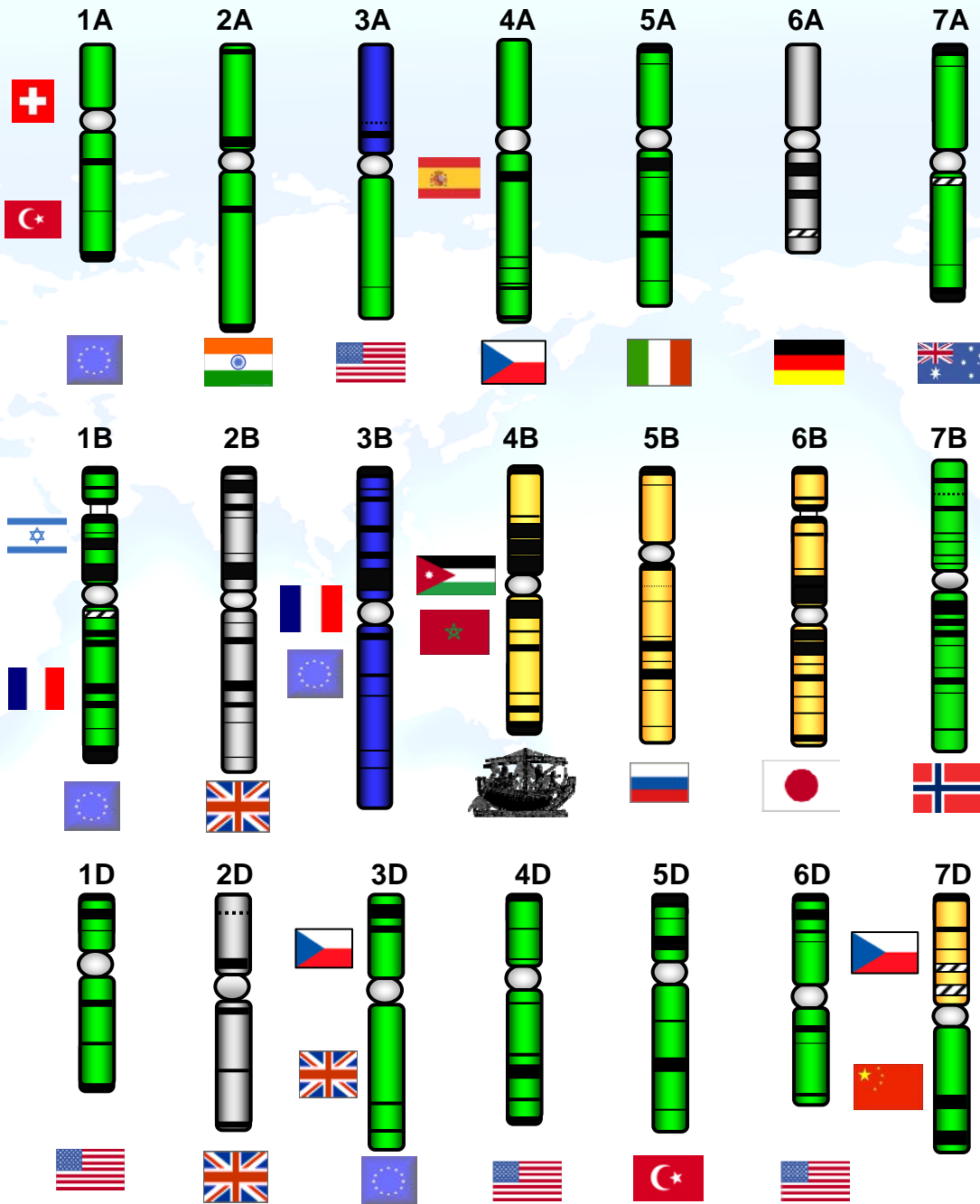
- ***T. urartu* A-Genome:**

- BGI Solexa 40x coverage (gene space only, not linked to any map, not available so far)

Physical mapping and low coverage sequencing



2010



T. aestivum
cv Chinese Spring

Some
funding

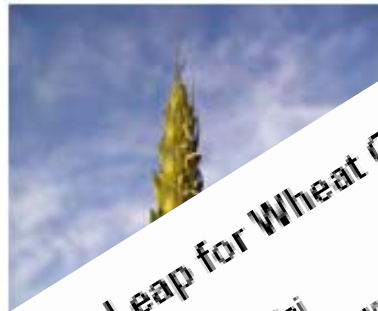
Funded

Finished

A Physical Map of the 1-Gigabase Bread Wheat Chromosome 3B

Etienne Paux,¹ Pierre Sourdille,¹ Jérôme Salse,¹ Cyrille Saintenac,¹ Frédéric Choulet,¹ Philippe Leroy,¹ Abraham Korol,² Monika Michalak,³ Shahryar Kianian,³ Wolfgang Spielmeier,⁴ Evans Lagudah,⁴ Daryl Somers,⁵ Andrzej Kilian,⁶ Michael Alaux,⁷ Sonia Vautrin,⁸ Hélène Bergès,⁸ Kellye Eversole,⁹ Rudi Appels,¹⁰ Jan Safar,¹¹ Hana Simkova,¹¹ Jaroslav Dolezel,¹¹ Michel Bernard,¹ Catherine Feuillet¹

SCIENCE VOL 322 3 OCTOBER 2008



A Giant Leap for Wheat Genome

By Elizabeth Pennisi
ScienceNOW Daily News
2 October 2008

GenomeWeb Daily News

National Association of Wheat Growers
www.wheatworld.org

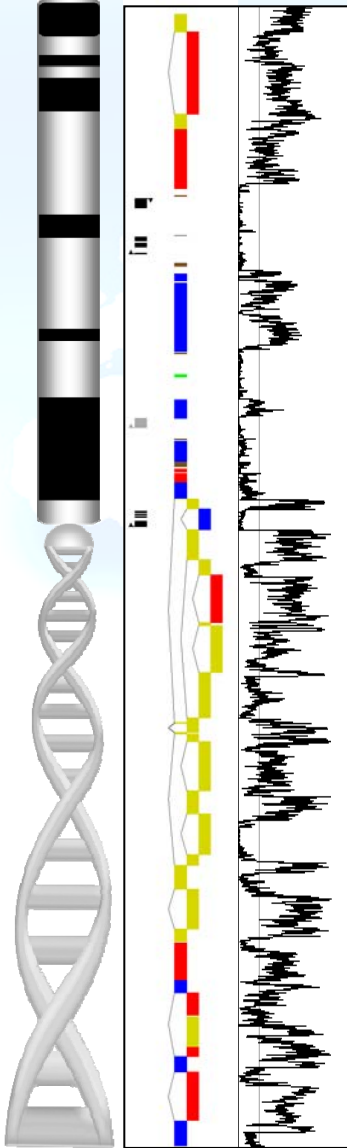
Breakthrough in Wheat Genome Mapping Reported

October 03, 2008

International Research Team Maps Largest Wheat Chromosome En Route to Sequencing

October 2, 2008
By Andrea Anderson,
a GenomeWeb staff reporter

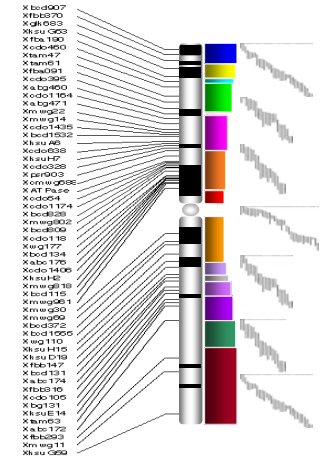
Utility of 3B Physical Map



- ✓ **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
- ✓ **Genomics-based tools for wheat breeding & improvement**
 - Positional cloning of genes underlying QTLs
 - Molecular markers (SNPs, ISBPs...)
 - New genotyping strategies

3B Physical Map Immediate Applications

- Gene catalog - 40 genes and QTLs identified
- 17 contigs representing 16.8 Mb anchored with markers flanking or cosegregating with 16
- Average contig size of ~900 kb is accelerating high resolution genetic mapping - positional cloning e.g., Sr2, Fhb1, Yr, Yield



Gene name	Deletion bin	Distal marker	Ctg name	Ctg length (kb)	Proximal marker	Ctg name	Ctg length (kb)
Lr27	3BS3-0.87-1.00	gwm533	ctg344	1400	gwm493	ctg918	630
Sr2	3BS8-0.78-0.87	CA640157	ctg11	1600	BE591959	ctg918	630
Sc	3BS8-0.78-0.87	CA640157	ctg11	1600	BE591959	ctg918	630
Pbc	3BS8-0.78-0.87	CA640157	ctg11	1600	BE591960	ctg918	630
Fhb1(QFhs.ndsu.3B)	3BS8-0.78-0.87	STS189	ctg954	3200	STS206	ctg954	3200
Rht5	3BS8-0.78-0.87	Barc102	ctg11 (glk683)	1600	-	-	-
Pm13	3BS8-0.78-0.87	gwm533	ctg344	1400	-	-	-
Yrns-B1	3BS8-0.78-0.87	gwm493	ctg918	630	gwm1329	ctg608	450
stb2	3BS8-0.78-0.87	gwm533	ctg344	1400	gwm493	ctg918	630
QSng.sfr-3BS	3BS8-0.78-0.87	gwm389/barc75	ctg825/ctg960	400/350	cf79/barc133	ctg666/ctg287	720/980
Grain Yield QTL	3BS8-0.78-0.87	gwm1034	ctg 541	980	gwm493	ctg918	630
BrA3	3BS4-0.55-0.56	Wmc43	ctg392	600	gwm264	ctg108	695
S-B1	3BS1-0.33-0.55	Xgwm685	NC	NC	gwm566	ctg695	200
Qkb.cnl-3B	3BS1-0.33-0.55	ATPase-3B	NC	NC	cdo1164	NC	NC
tsn2	3BS5-0.20-0.33	gwm285	ctg407	1500	wmc366.2	NC	NC
QTLPhs	3BL7-0.63-1.00	gwm403	NC	NC	bcd131	NC	NC
R-B1	3BL7-0.63-1.00	bcd131	NC	NC	abc174	NC	NC
Qsf.spa.-3B	3BL7-0.63-1.00	gwm247	ctg165	700	gwm114	NC	NC
stb14	3BL7-0.63-1.00	wmc500	ctg848	990	wmc632	NC	NC

▶ **cloning underway**

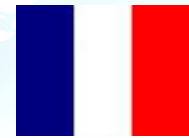
Kindly provided by C. Feuillet



Multi-Phase Sequencing Strategy

- Phase I – High quality sequences of individual chromosomes with physical maps

- 3B Funded – began February 2010



- 7B funded



The Research Council of Norway



- Other proposals pending

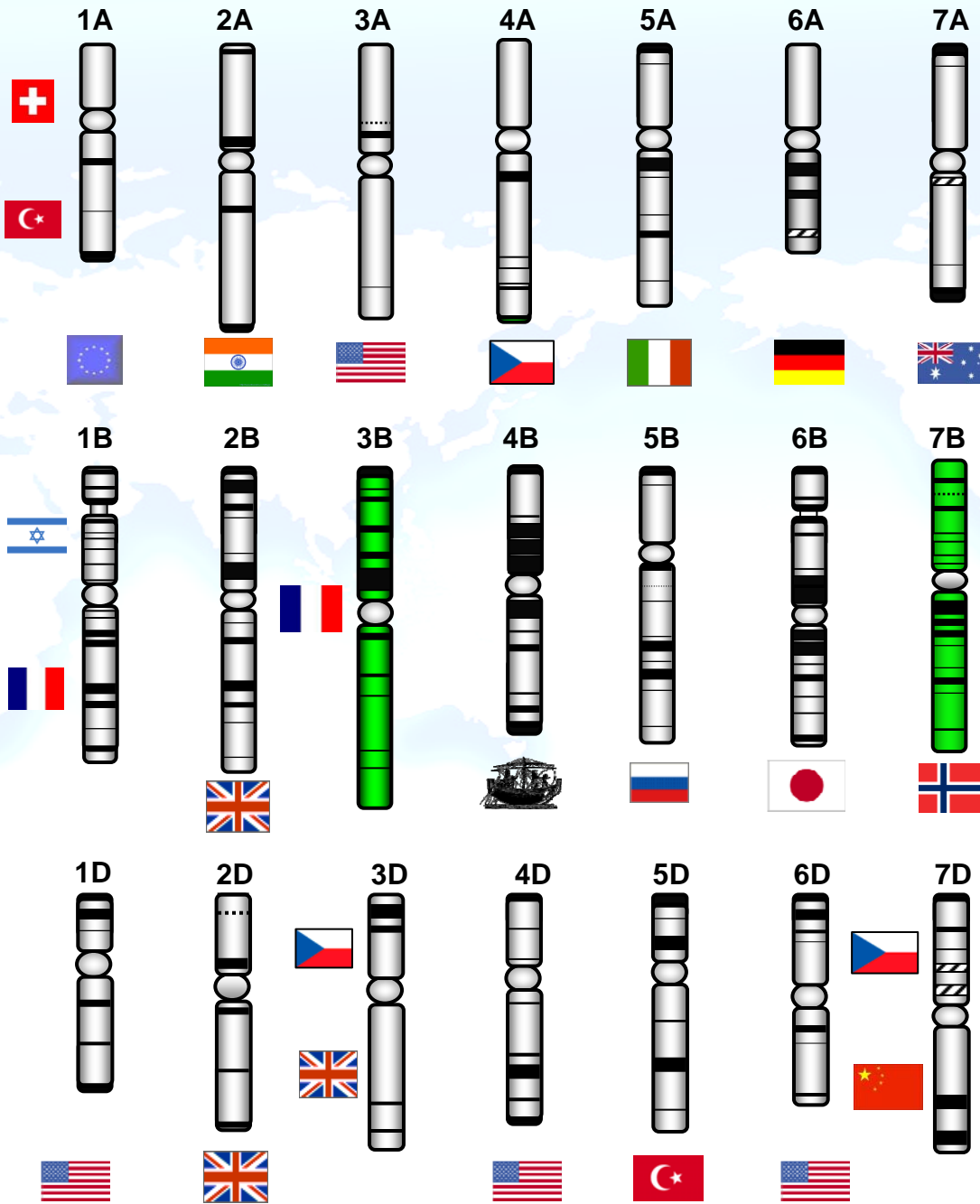
- Phase II – Rough draft sequence of Chinese Spring

- Phase III – High quality, gold standard reference sequence of bread wheat





Chromosome Complete Sequencing



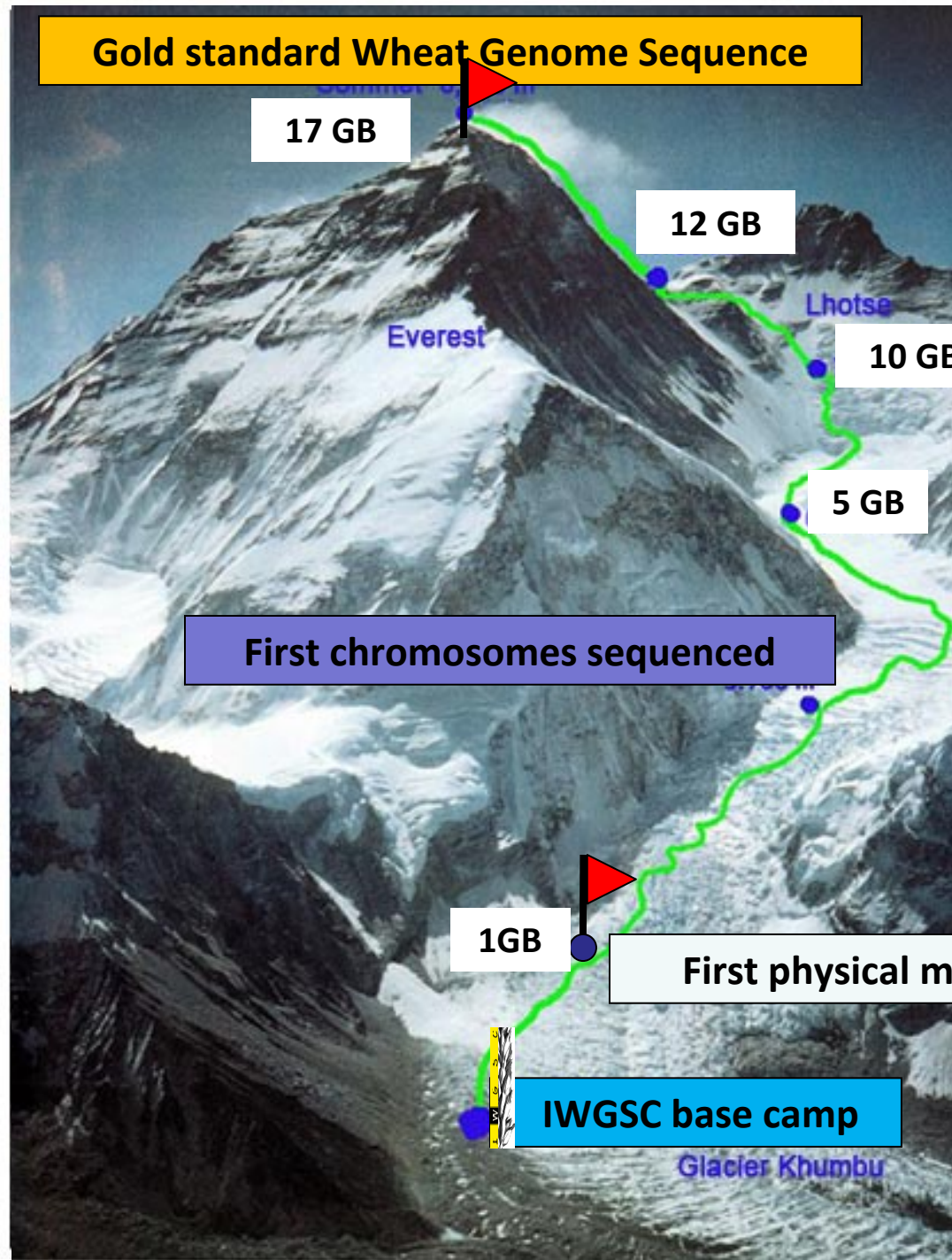
2010

Funded

T. aestivum
cv Chinese Spring

www.wheatgenome.org

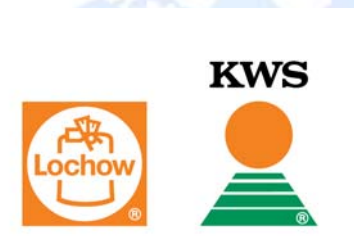
"The Team"



"The Sponsors"



Acknowledgements: IWGSC Sponsors





Thank you for your attention

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www.wheatgenome.org