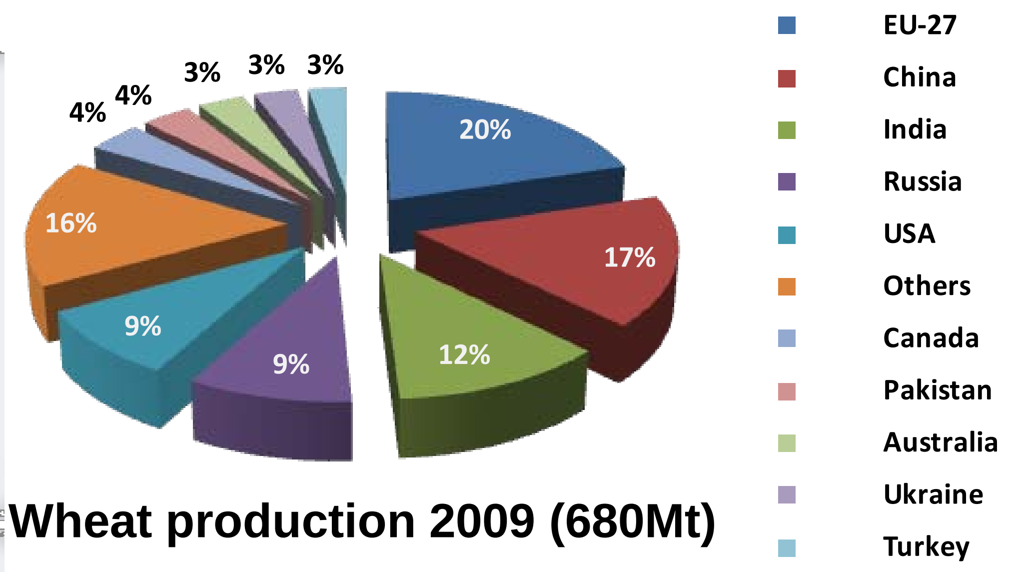
TriticeaeGenome

Genomics for Triticeae improvement for food, feed, and non-food uses

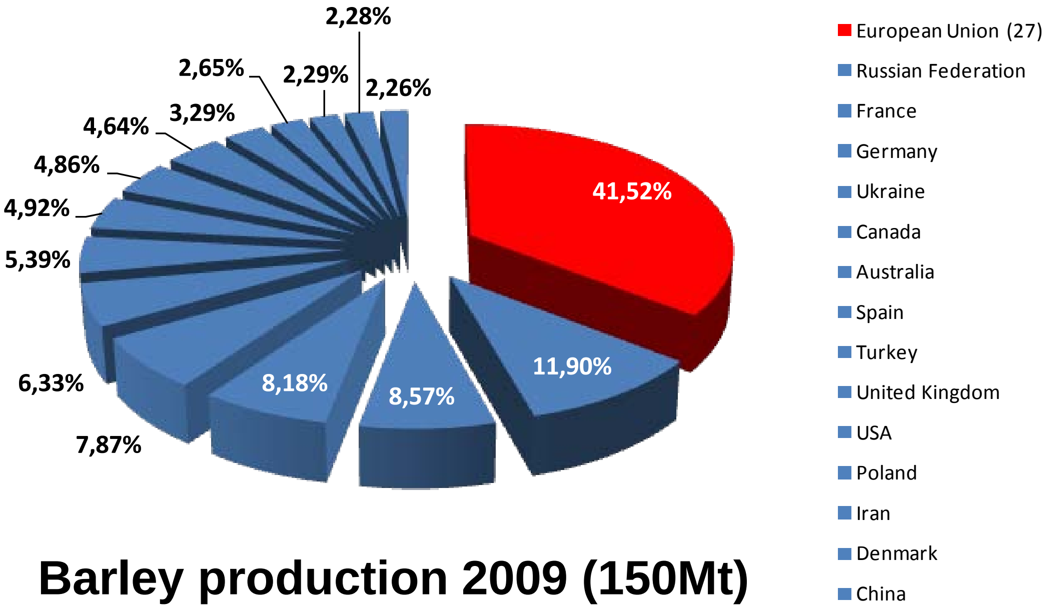
Journées INRA Céréales à Pailles
March 29-30, 2011 (Changins)

SEVENTH FRAMEWORK PROGRAMME

Wheat and barley are the most important cereal crops in Europe



Wheat production 2009 (680Mt)



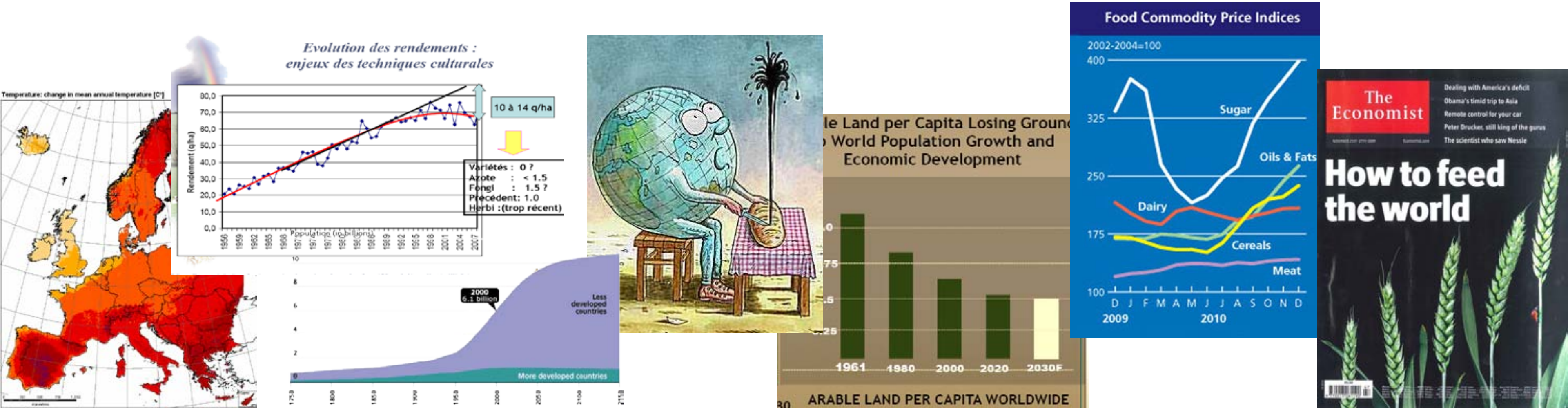
Barley production 2009 (150Mt)

Triticeae production is facing great challenges

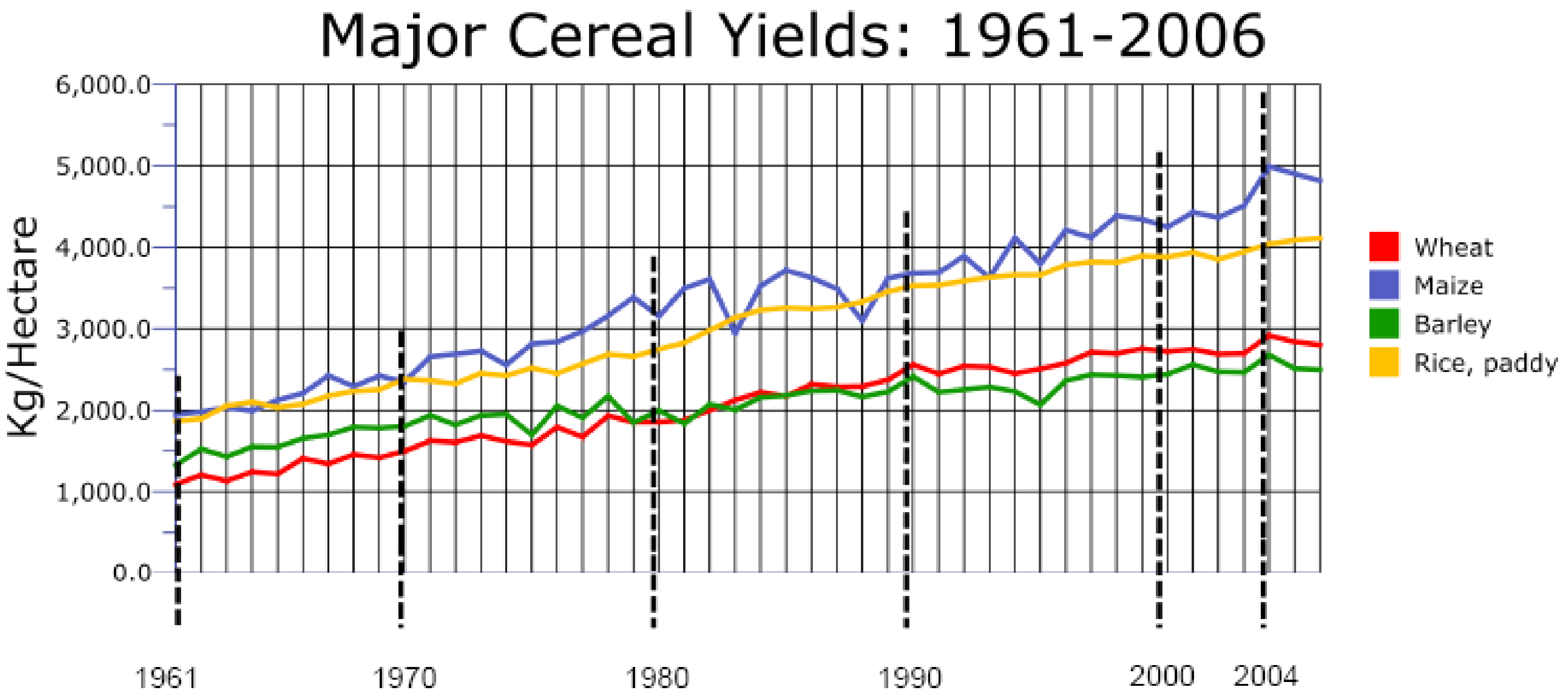
- **Provide consistently sufficient, high quality food and feed products as well as non food products through a sustainable agricultural system**

while

- **Increasing demand** (population, urbanization) = need to **increase production by 2%/year until 2050** (FAO)
- **Yield stagnation** in the past 10 years in main producing areas
- **Climate change**, reduced and unevenly distributed **water resources**, limited expansion of **arable lands**
- Need to **reduce environmental impact** of agricultural production (e.g. ECOPHYTO 2018)
- **Agricultural policies** difficult to coordinate, agricultural research is not a priority



Triticeae improvement lags behind the other cereals



Data Source: FAOSTAT, 2008.

- ➢ Relative yield improvement (in kg/ha) in four major cereal crops over the past 45 years

Target traits for Triticeae improvement

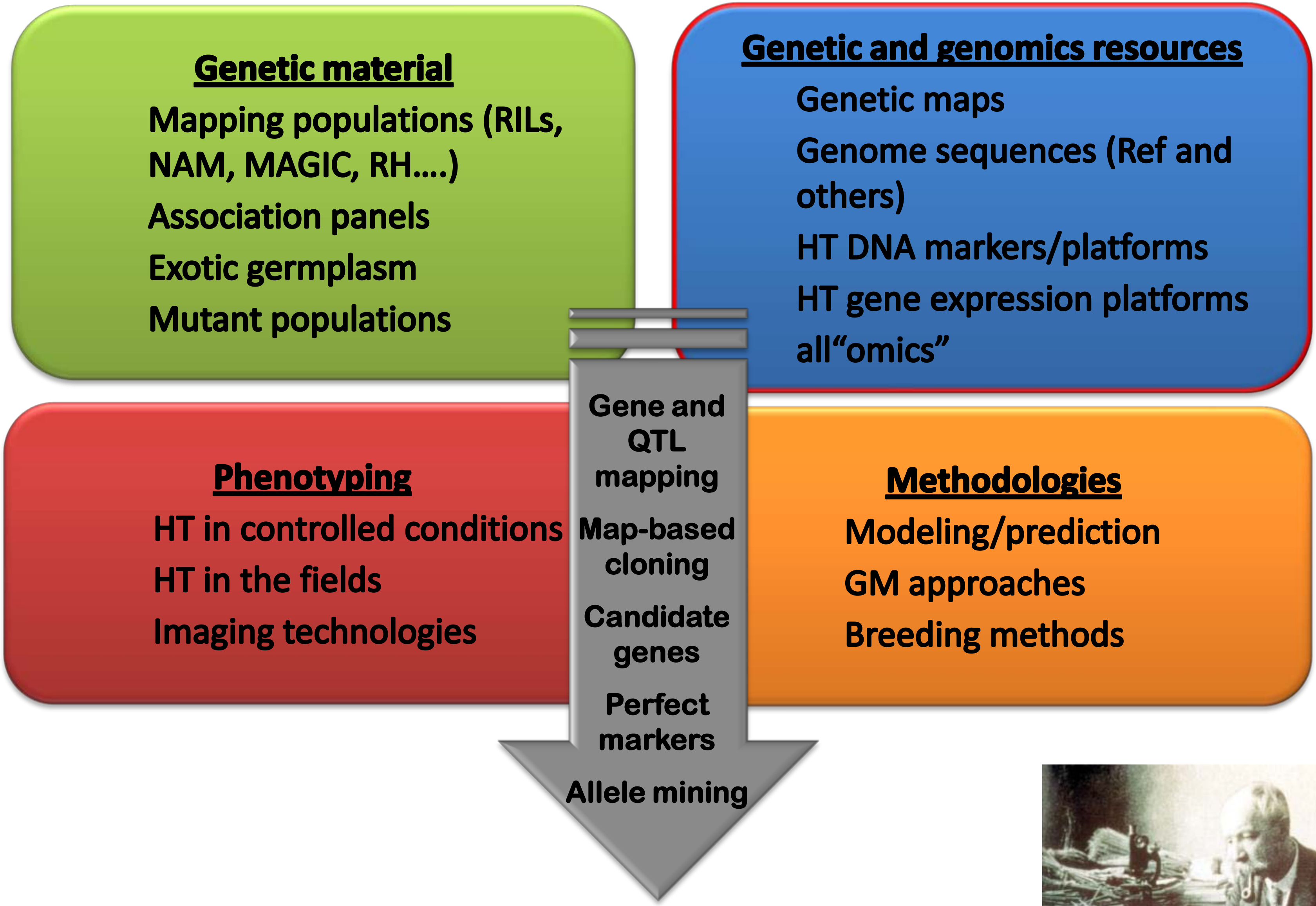
- **Yield potential and yield stability**
  - ✓ Photosynthesis efficiency
  - ✓ Harvest Index
  - ✓ Reduced inputs (fertilizers, pesticides..)

- **Adaptation to climate change**
  - ✓ Avoidance
  - ✓ Tolerance (Drought, heat, cold..)
  - ✓ Post stress recovery…

- **Durable resistance to biotic stress**
  - ✓ Usuals suspects (virus, fungi)
  - ✓ new pests and diseases
  - ✓ invasive species

- **Quality of grain and coproducts**
  - ✓ Grain protein content, malting quality, foam stability
  - ✓ Starch , straw
  - ✓ Food safety -Allergenicity-mycotoxin contamination..

The future is an integrated toolbox



Genetic material

Mapping populations (RILs, NAM, MAGIC, RH....)

Association panels

Exotic germplasm

Mutant populations

Genetic and genomics resources

Genetic maps

Genome sequences (Ref and others)

HT DNA markers/platforms

HT gene expression platforms

all“omics”

Phenotyping

HT in controlled conditions

HT in the fields

Imaging technologies

Methodologies

Modeling/prediction

GM approaches

Breeding methods

Gene and QTL mapping

Map-based cloning

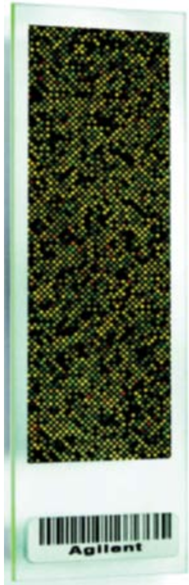
Candidate genes

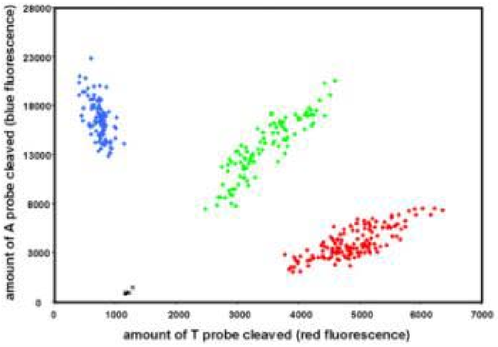
Perfect markers

Allele mining

Improved Triticeae germplasm

The triticeae tool box





Molecular markers

- ✓ Wheat : 1634 RFLPs/2946 SSRs/2000 DArTs/>1000 ISBPs/9000 SNPs
- ✓ Barley: 2956 RFLPs/ 972 SSRs/ 2085 DArTs/3072 SNPs

ESTs and microarrays

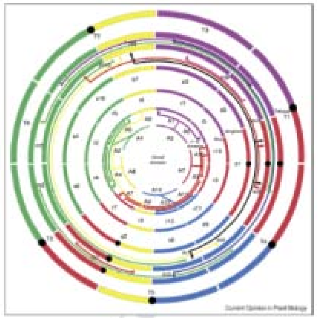
- ✓ > 1 million of wheat ESTs / > 500K barley ESTs
- ✓ Affymetrix 55K wheat and 53K barley GeneChip genome arrays
- ✓ Agilent 44K wheat and 40K barley gene expression microarrays

BAC libraries

- ✓ Wheat : 6 ABD-genome, 1 AB-genome, 2 A-genome, 1 S-genome, 2 D-genome libraries and Chromosome (arm) specific libraries
- ✓ Barley: > 3 whole genome BAC libraries from different cultivars (different enzymes)

Genetic resources

- ✓ Populations
- ✓ Germplasm collections
- ✓ Mutant collections



Gene validation

- ✓ transient (VIGS) transformation
- ✓ stable (biolistic, *A. tumefaciens*) transformation

Grass comparative genomics

- ✓ Rice, sorghum, maize, Brachypodium

triticeae Genome

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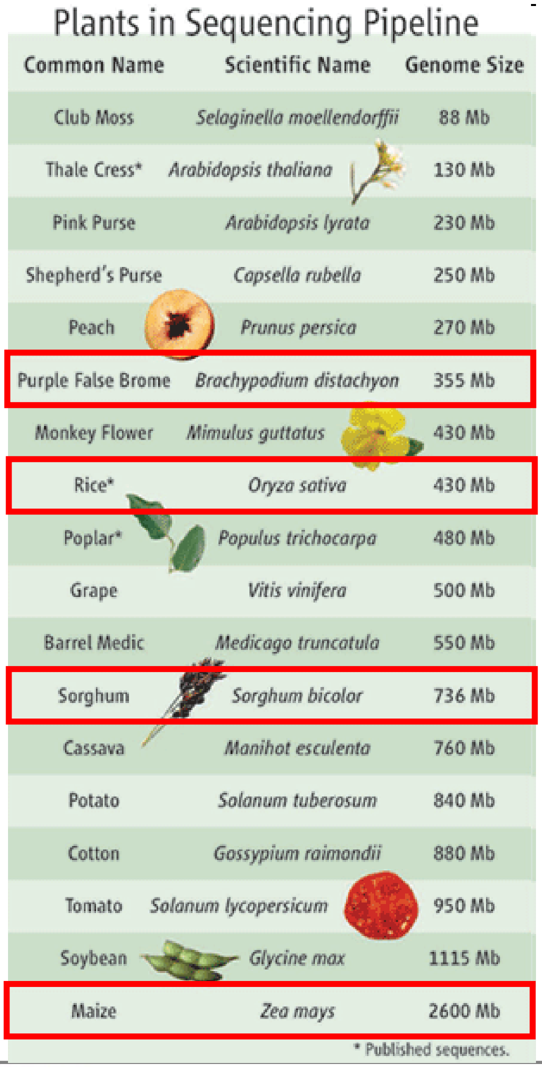
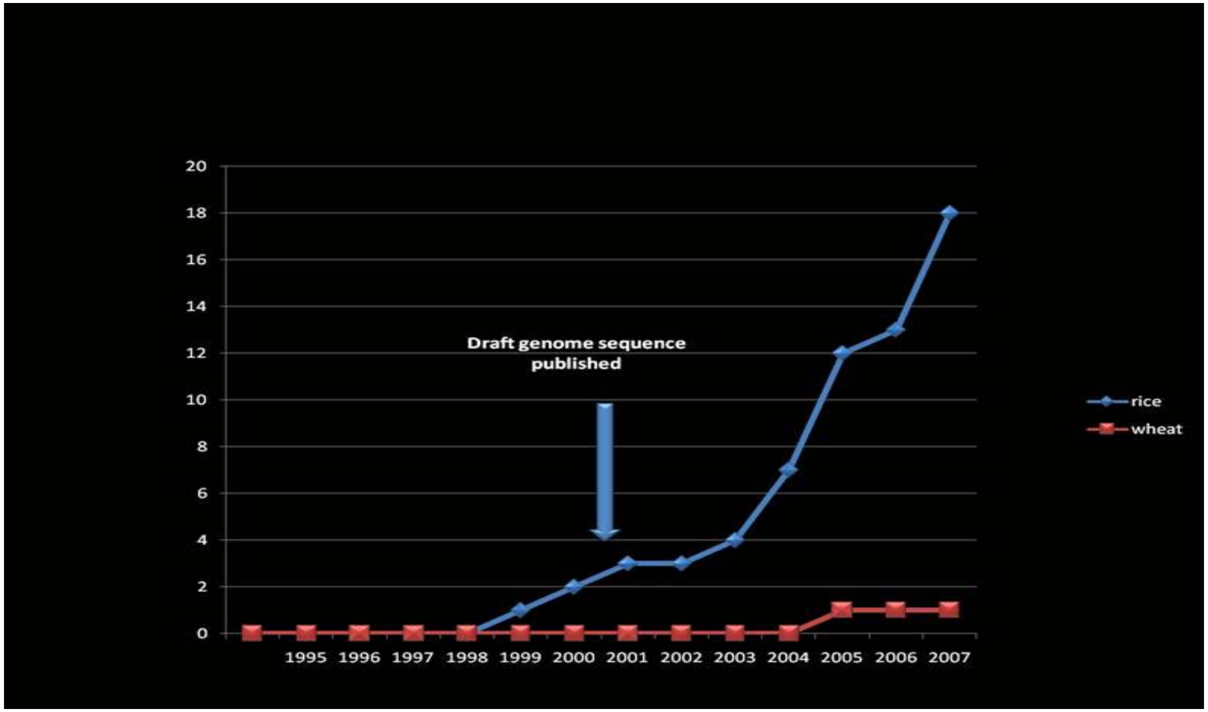
But constantly lagging behind other crops for the development of sequence based resources



Plants in Sequencing Pipeline

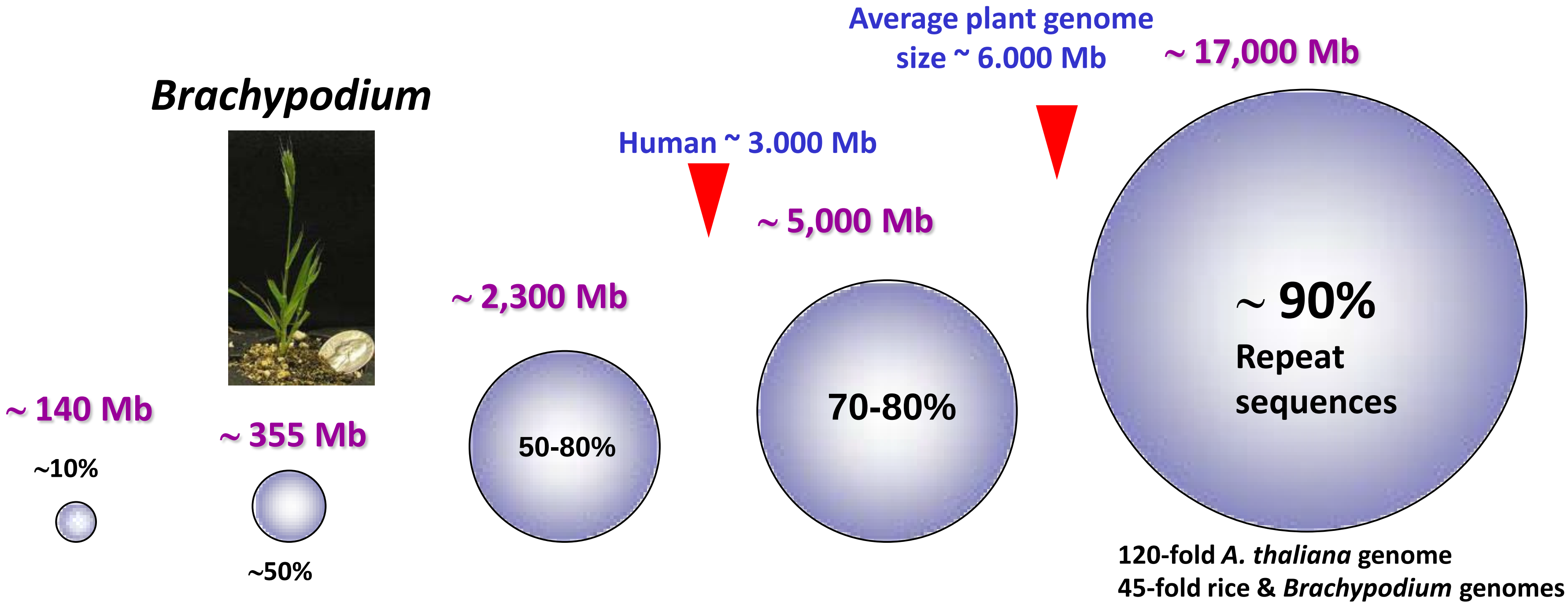
Common Name	Scientific Name	Genome Size
Club Moss	*Selaginella moellendorffii*	88 Mb
Thale Cress*	*Arabidopsis thaliana*	130 Mb
Pink Purse	*Arabidopsis lyrata*	230 Mb
Shepherd's Purse	*Capsella rubella*	250 Mb
Peach	*Prunus persica*	270 Mb
Purple False Brome	*Brachypodium distachyon*	355 Mb
Monkey Flower	*Mimulus guttatus*	430 Mb
Rice*	*Oryza sativa*	430 Mb
Poplar*	*Populus trichocarpa*	480 Mb
Grape	*Vitis vinifera*	500 Mb
Barrel Medic	*Medicago truncatula*	550 Mb
Sorghum	*Sorghum bicolor*	736 Mb
Cassava	*Manihot esculenta*	760 Mb
Potato	*Solanum tuberosum*	840 Mb
Cotton	*Gossypium raimondii*	880 Mb
Tomato	*Solanum lycopersicum*	950 Mb
Soybean	*Glycine max*	1115 Mb
Maize	*Zea mays*	2600 Mb

* Published sequences.



- ➢ **SNP based arrays for genetic analyses**
  - MaizeSNP50 Illumina BeadChip
  - Numerous rice chips
- ➢ **NGS resequencing projects**

The Challenges……



Average plant genome size ~ 6.000 Mb

~ 17,000 Mb

Brachypodium

Human ~ 3.000 Mb

~ 5,000 Mb

~ 2,300 Mb

~ 90% Repeat sequences

~ 140 Mb

~ 355 Mb

70-80%

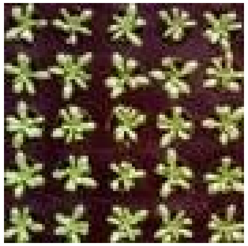
50-80%

~10%

~50%

120-fold *A. thaliana* genome
45-fold rice & *Brachypodium* genomes

A. thaliana **(2x)**



Rice(2x)

Maize (2x)

Barley (2x)

Bread wheat (6x)

The Triticeae genomes are a challenge for genomic studies and sequencing

TriticeaeGenome

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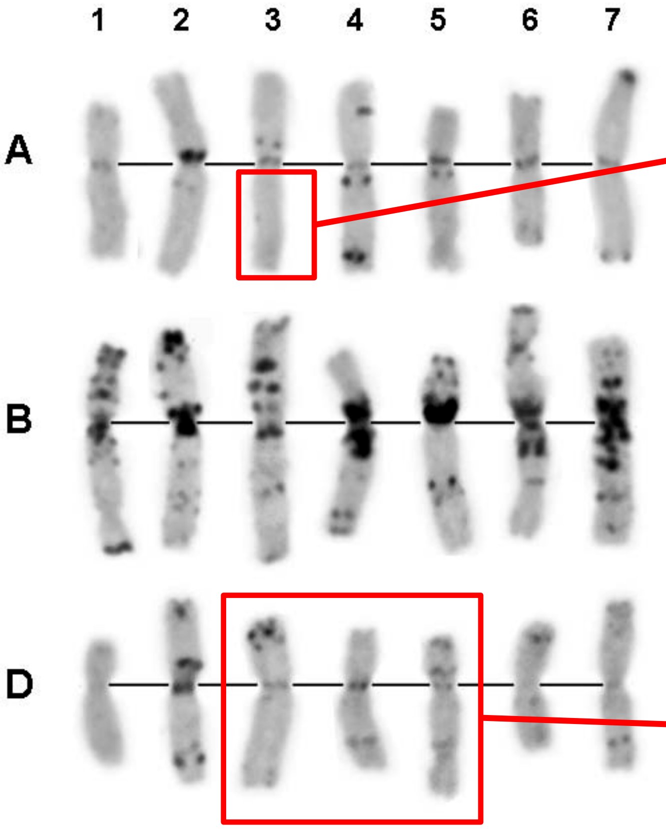
Working together on the Challenge……

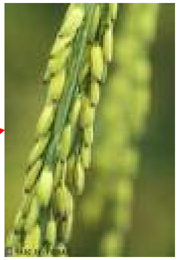
Bread wheat

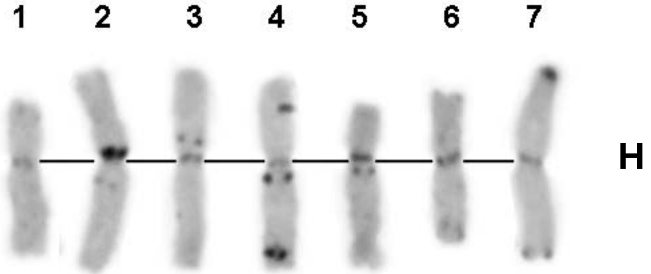
The “Giant” Genome : 17 Gb

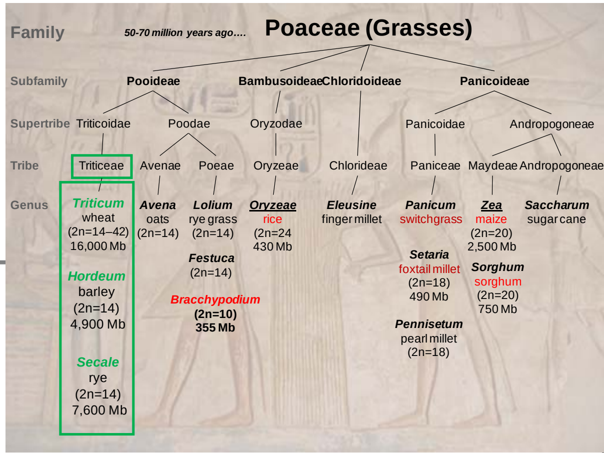
Barley

The “brother” genome: 5 Gb









Family *50-70 million years ago….* **Poaceae (Grasses)**

Subfamily **Pooideae** **Bambusoideae** **Chloridoideae** **Panicoideae**

Supertribe Triticoidae Poodae Oryzodae Panicoidae Andropogoneae

Tribe Triticeae Avenae Poeae Oryzeae Chlorideae Paniceae Maydeae Andropogoneae

Genus

Triticum wheat (2n=14–42) 16,000 Mb

Hordeum barley (2n=14) 4,900 Mb

Secale rye (2n=14) 7,600 Mb

Avena oats (2n=14)

Lolium rye grass (2n=14)

Festuca (2n=14)

Bracchypodium **(2n=10) 355 Mb**

Oryzeae rice (2n=24 430 Mb

Eleusine finger millet

Panicum switchgrass

Setaria foxtail millet (2n=18) 490 Mb

Pennisetum pearl millet (2n=18)

Zea maize (2n=20) 2,500 Mb

Sorghum sorghum (2n=20) 750 Mb

Saccharum sugar cane

European Triticeae Genomics Initiative

1st Workshop at the 4th Plant Genome European Meeting
Amsterdam, Sep 21st, 2005

Why and how to build up a network of excellence on Triticeae genomics in Europe?

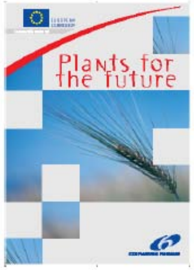
Nils Stein, Catherine Feuillet

Plant GEMs Amsterdam 2005
Plant Genomics European Meetings

Actions in 2005-2006

- Visit heads of the Food and Biotech departments at the EU commission in Bruxelles to present our vision
- Submit a white paper and a letter of intent (Dec2005/Feb2006)

"A European network for understanding and improving key traits for European agriculture through the development of Triticeae genomics" supported by 28 public institutions (research centers, universities, consortia) and 31 private companies (breeding, food processing……) to the EU commission and to the technology platform "Plants for the Future"


Plants for the future

- National feedbacks on strategic research agenda of PFF (through the INRA) (December 2005)
- Answer EPSO survey on priorities (June 2006)

"Unlocking the Triticeae genomes to improve key traits for a sustainable and competitive European agriculture"

- Apply for a COST action (Tritigen) (September 2006)
- EOI to Eurobiofund (ESF) (September 2006)

"Integrated physical maps of the Triticeae chromosome groups 1 and 3 as the foundation for gene isolation, evolutionary studies, and genome sequencing"

- Presentation of the ETGI at different meetings (Plant GEM)

SEVENTH FRAMEWORK
PROGRAMME

FP7 launched on 22nd December 2006/project submission 2nd May 2007

KBBE-2007-1-2-02: “Genomics for cereal improvement for food, feed and non-food uses“

This project will assemble the knowledge required, and use modern breeding techniques, including genetic engineering, to produce cereal crops (from the Triticeae tribe) with improved composition and characteristics that will satisfy the proven needs of consumers, processors and producers. In addition to developing new knowledge in the areas of genetics and genomics, the project will build on existing resources inside and outside Europe. To assure dissemination and transfer of the results, industrial, farmers’ and consumers’ representatives should be included from the project’s inception. Participation in international genomics programmes and collaboration with ICPC target countries is encouraged.

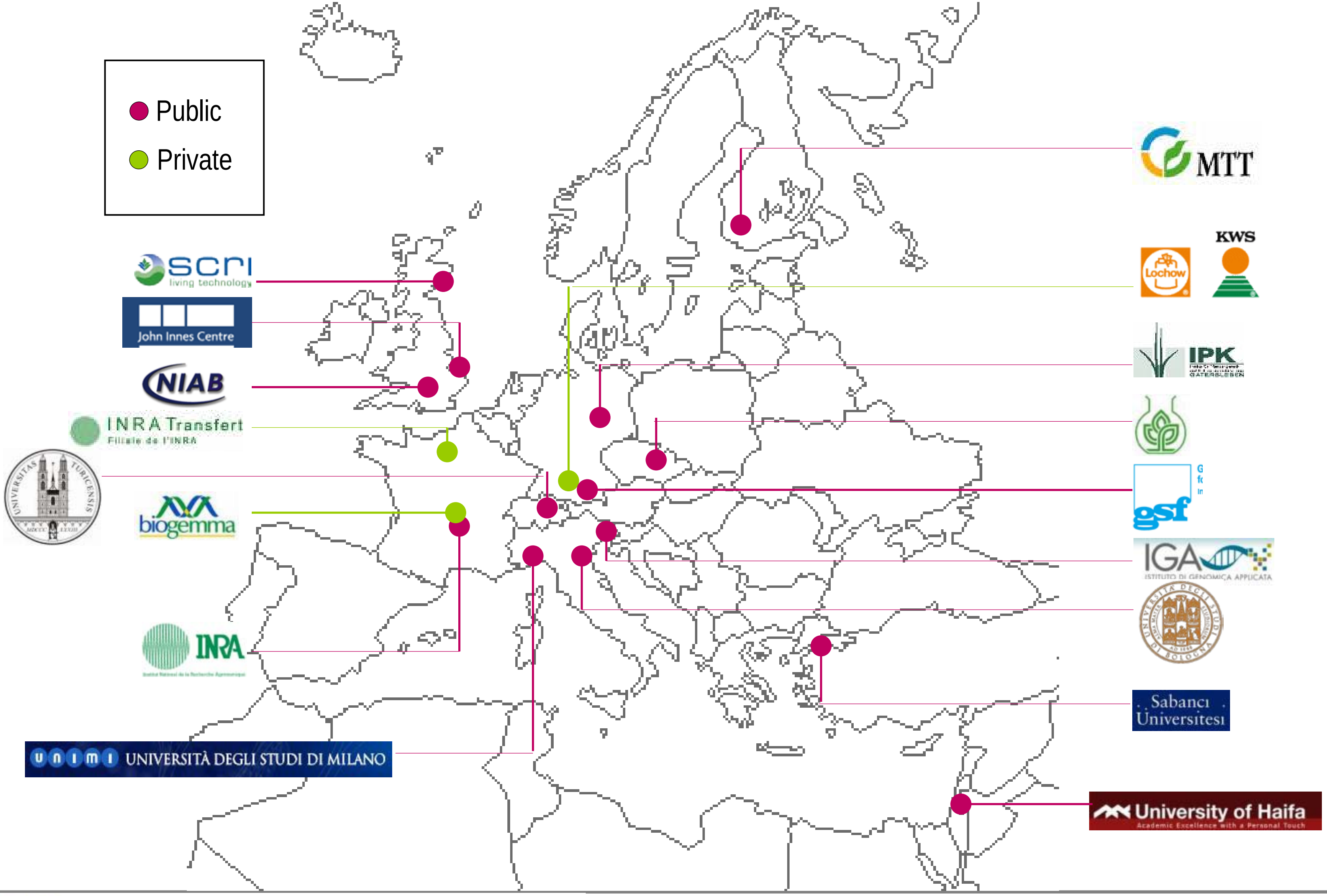
Triticeae Genome wants to

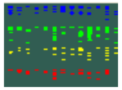
Achieve significant progress in Triticeae genomics and support efficient breeding of improved varieties for European agriculture

through

- **5 Work Packages that integrate fundamental and applied research**
- **The integration wheat and barley genomics to capitalize on synergies between these 2 essential Triticeae species**
- **A collaboration between 14 public research institutes, 2 private breeding companies and 1 managing body, all recognized for their excellence worldwide**
- **A project of 7.5 M€ supported by the EU commission (5.3 M€) and the individual partners institutes and companies**
- **A network of international collaborators and a complete coordination with other international initiatives**

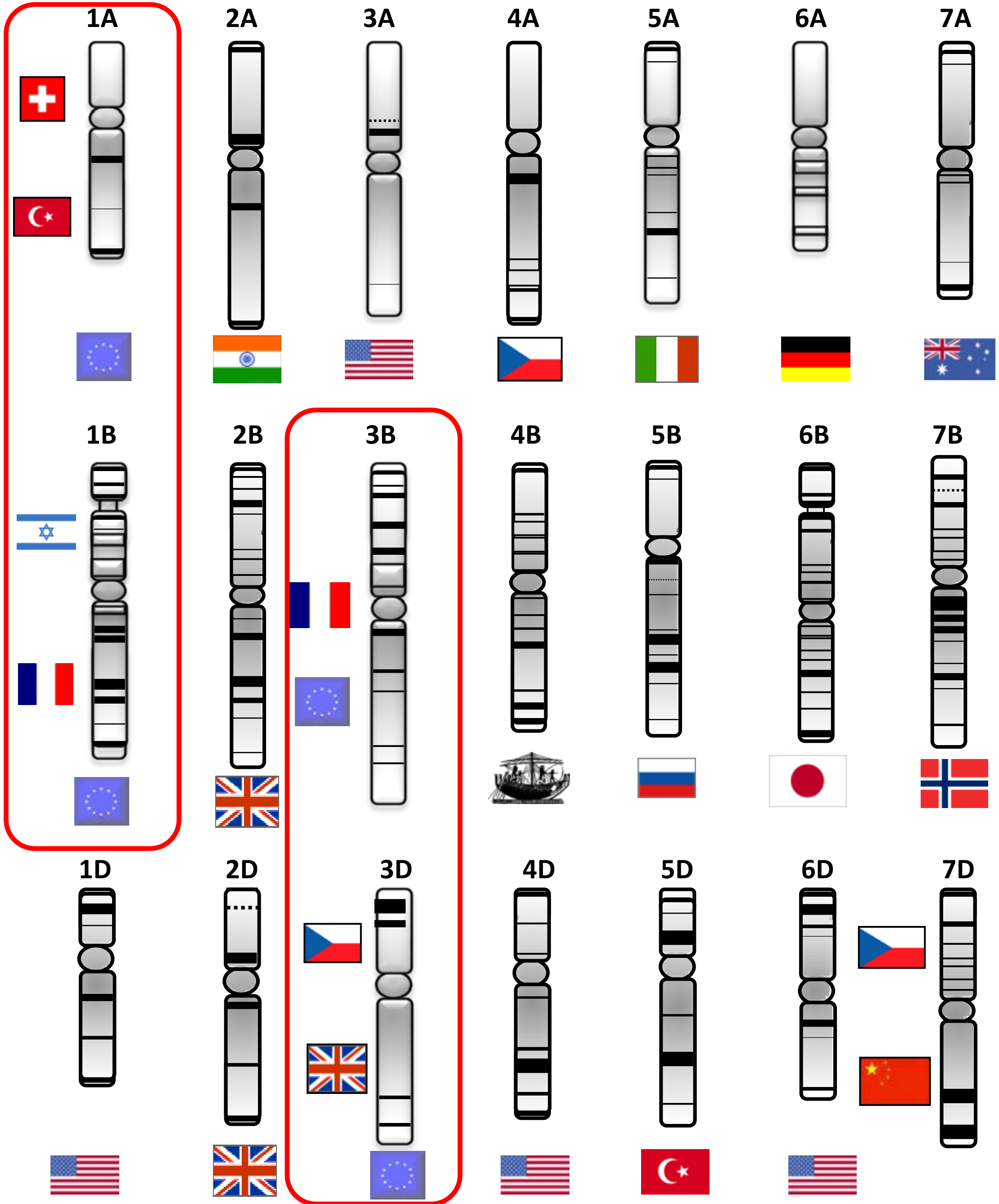
17 European Partners





WP1: Physical mapping of chromosomes 1 / 3

IWGSC

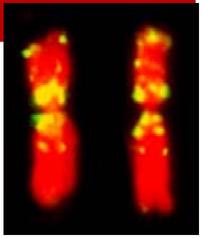


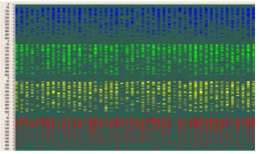
Triticeae Genome

T. aestivum

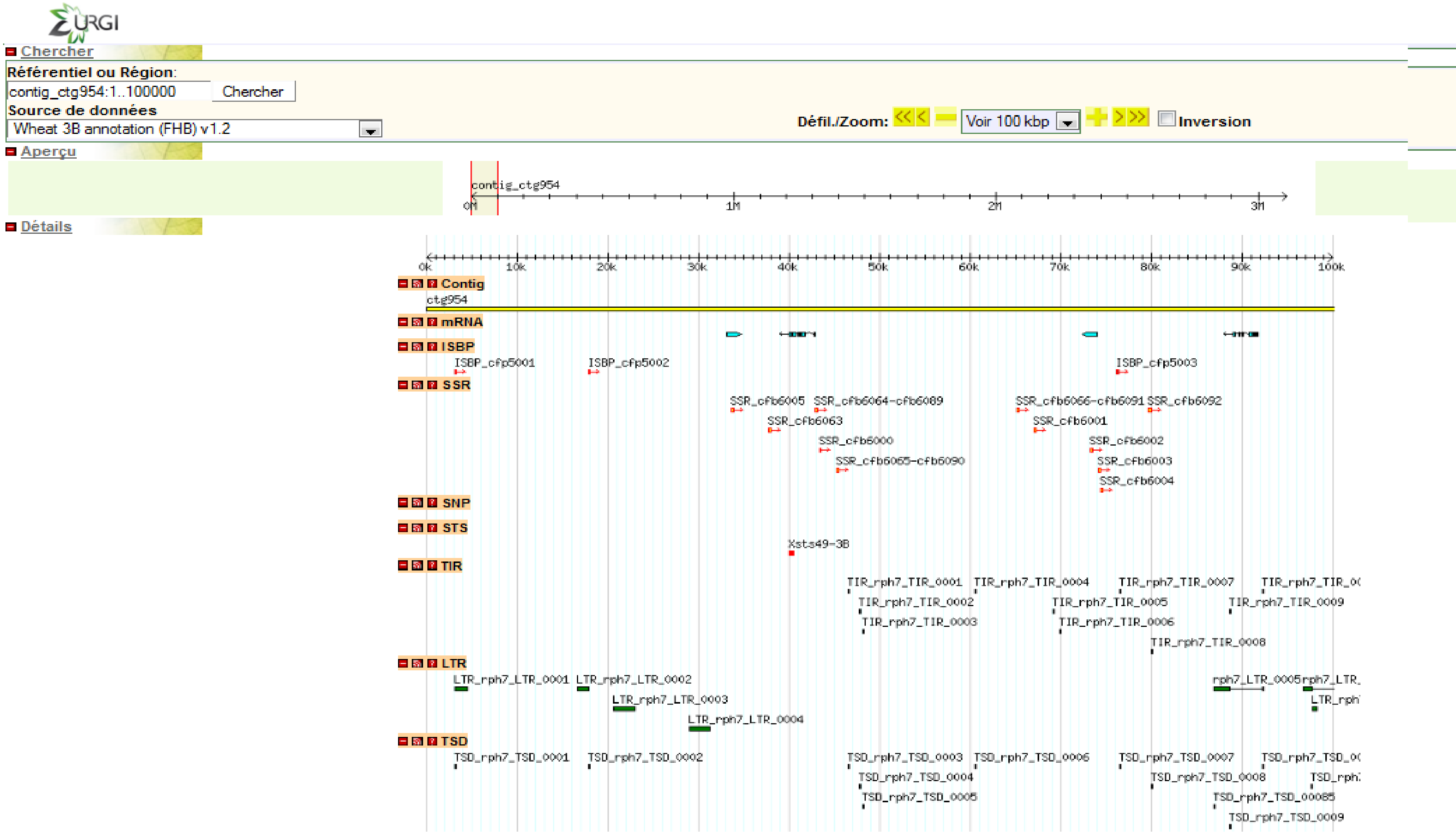
cv Chinese Spring

WP1: Establishment of genomic resources for physical mapping (INRA)





WP1 Results



Chercher

Référentiel ou Région: contig_ctg954:1..100000

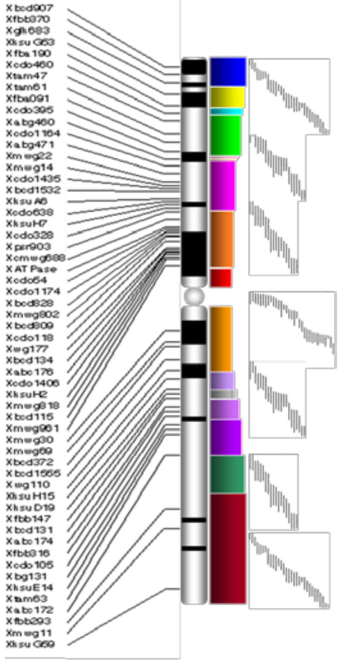
Source de données: Wheat 3B annotation (FHB) v1.2

Défil./Zoom: Voir 100 kbp

☐ Inversion

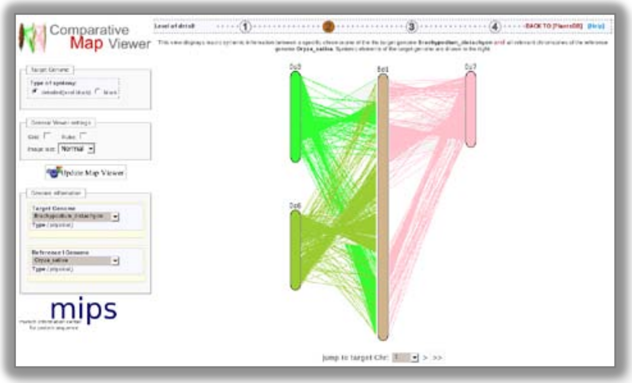
Safar et al. Cytogenetic and Genome Research, 2010

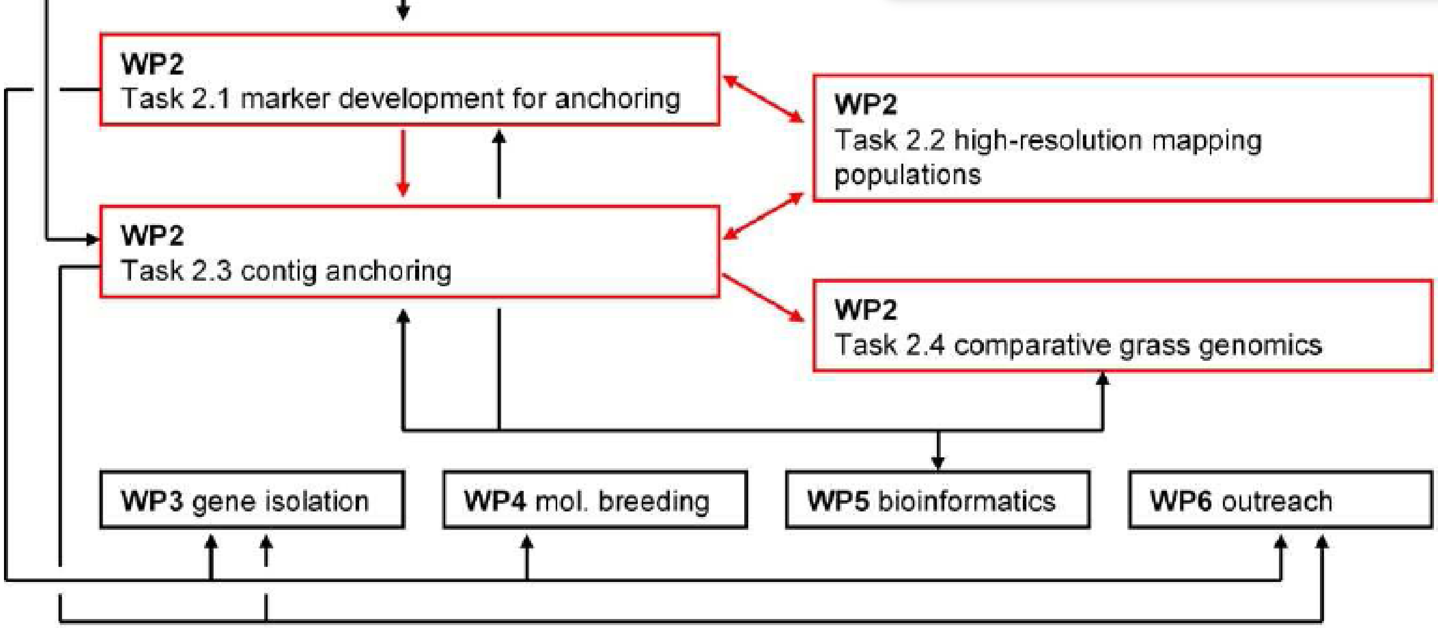
WP2: Construction of anchored physical maps (IPK)



WP1 genomic resources for physical mapping
BAC libraries, FPC, BES

external resources
barley: BAC libraries, FPC (Leibniz Pakt f. Forschung)
barley: BES (ERA-PG BARCODE)
wheat/barley: genetic maps, marker resources





WP2
Task 2.1 marker development for anchoring

WP2
Task 2.2 high-resolution mapping populations

WP2
Task 2.3 contig anchoring

WP2
Task 2.4 comparative grass genomics

WP3 gene isolation

WP4 mol. breeding

WP5 bioinformatics

WP6 outreach

Triticeae Genome

SEVENTH FRAMEWORK PROGRAMME

WP2 : Results

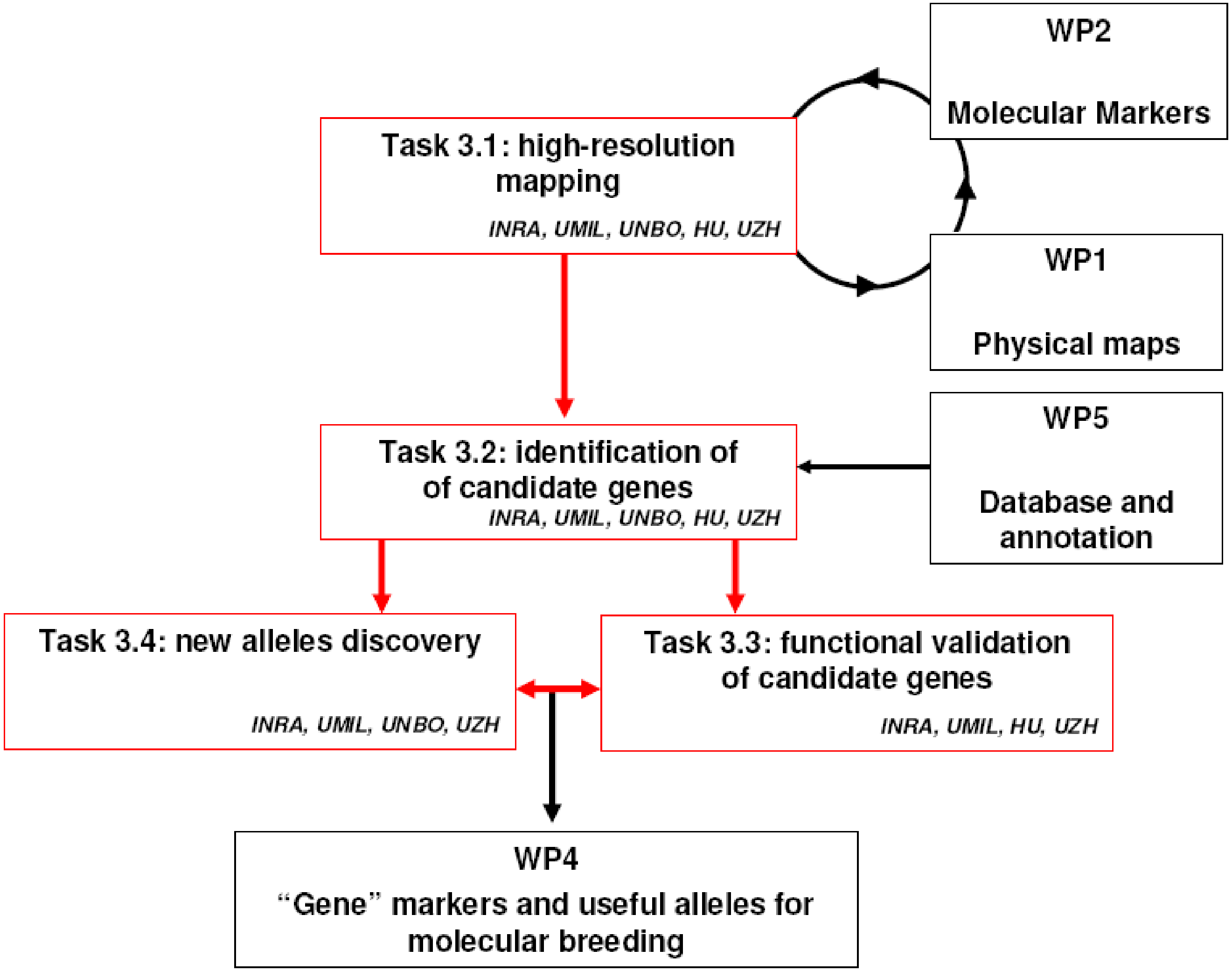
- **A TG database** with all potential **markers** for group 1 and group 3 chromosomes including:
  - ✓ Existing markers from 16 wheat genetic maps, 3 barley genetic maps, wheat cytogenetic maps. In total **more than 10’000 wheat markers, 7000 barley markers, 500 wheat QTLs** are available to support anchoring and map-based cloning
    - ▪ http://urgi.versailles.inra.fr/index.php/urgi/Species/Wheat
    - ▪ http://mips.helmholtz-muenchen.de/plant/barley/index.jsp
  - ✓ **New marker resources**: from 454 sequence survey of group 1/3 sorted chromosomes (SSR, ISBPs) as well as whole genome gene-based markers (SNPs and COS)

- **High-resolution mapping populations** in wheat (2000 RILs; Re x Cs) and barley (4000 RILs, Morex x Barke) for meiotic anchoring of the physical maps underway (F6/F7).

- **High throughput methodologies for anchoring :** BAC pool hybridizations on transcript arrays in barley and wheat

Rustenholz et al, 2010, BMC genomics 11:714
Liu et al, 2011, Biotechniques 50:165

WP3 : Improving wheat and barley yield, quality and resistance through gene isolation (UNIML)



WP2

Molecular Markers

Task 3.1: high-resolution mapping

INRA, UMIL, UNBO, HU, UZH

WP1

Physical maps

WP5

Database and annotation

Task 3.2: identification of of candidate genes

INRA, UMIL, UNBO, HU, UZH

Task 3.4: new alleles discovery

INRA, UMIL, UNBO, UZH

Task 3.3: functional validation of candidate genes

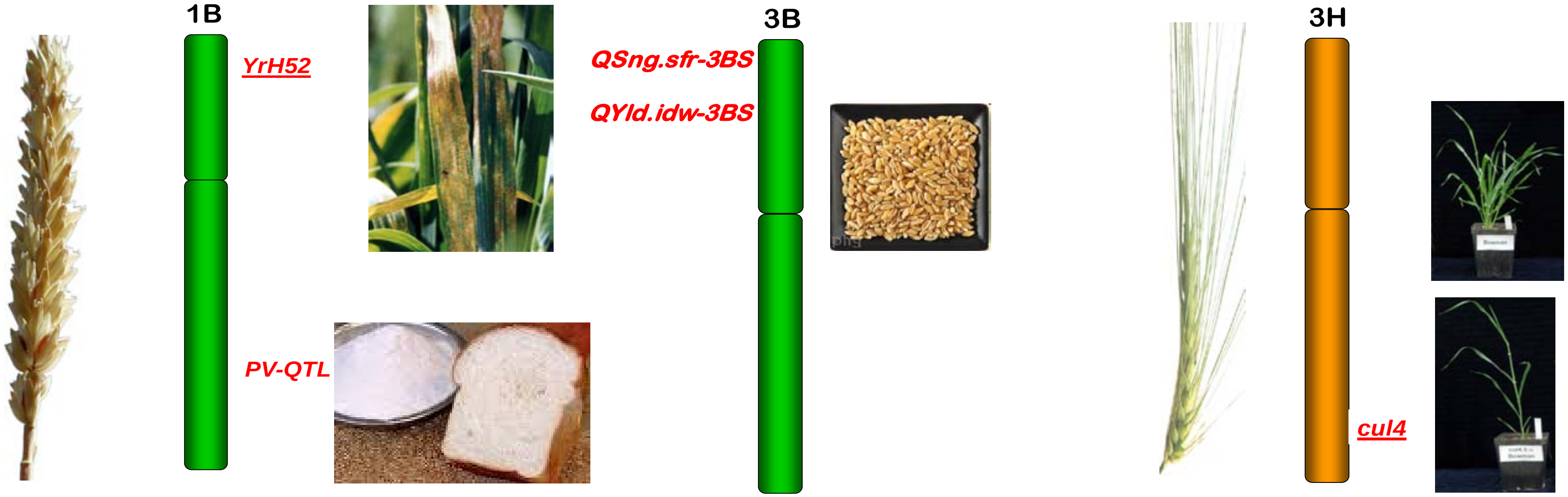
INRA, UMIL, HU, UZH

WP4

"Gene" markers and useful alleles for molecular breeding

WP3 : Results

- **Glume blotch** (*Qsng.sfr-3BS*) and **stripe rust*** (*YrH52-1BS*) disease R genes
- QTL for **grain yield*** (*QYld.idw-3BS*) in durum wheat
- QTL for **Pentosan Viscosity** (*PV-1BL*)
- Gene (*cul4-3HL*) involved in the determination of **plant architecture**



✓ **Fine genetic mapping** with confidence intervals < 2 cM to 10 cM using high resolution mapping populations (RILs, HIFs, Nils) and association genetics.

✓ **Physical contigs** (WP1/2) established for all genes and **candidate genes** identified for 2 (Cul4 and PV)

✓ **Functional validation tools** (VIGS, biolistic/ Agrobacterium transformation) available

WP4 : Molecular Breeding (BGA)

WP4

BGA, INRA

Task 4.1
Development of trait specific markers
Marker development for target traits on chromosome 1&3

NIAB, BGA

Task 4.2
Association genetics
Genotyping with markers from T1 and others already available and yield phenotyping (2 years*3 locations) of wheat diversity panel

WP1-WP2
Wheat and barley markers and genomic information
WP5
Comparative genomics with other cereal genomes

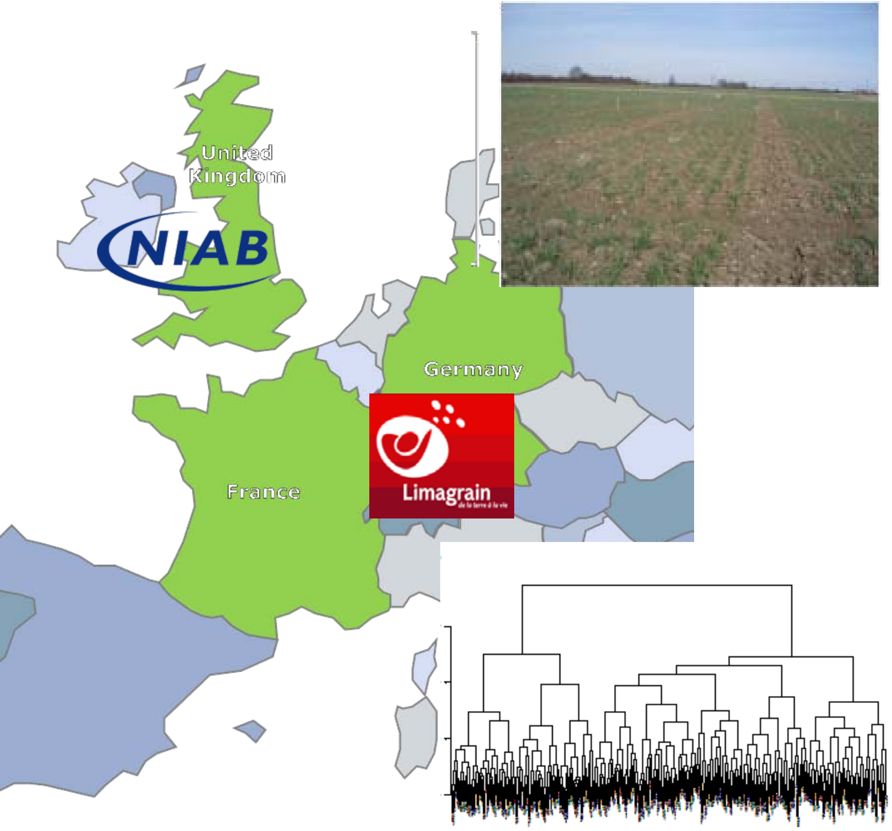
Markers associated with traits of agronomic interest in Wheat

Breeding

WP4 : Results

Task 4.2 Association genetics

- **Creation** of a **European** diversity panel of **376 lines** for **association mapping** (selected from a list of 730 from France, UK, Germany)



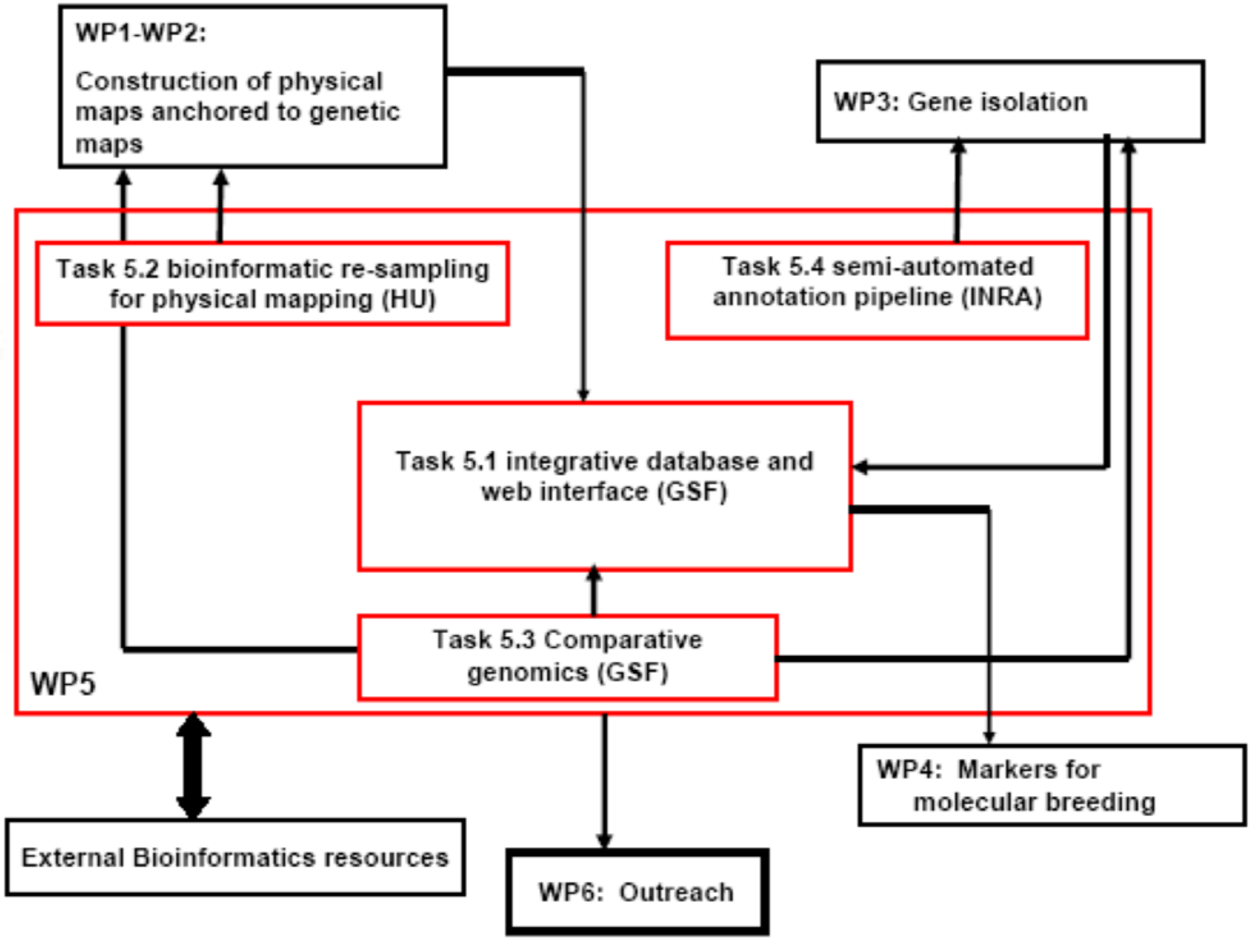
- **Phenotyping:** in the fields (2 years, 3 locations):
  - o yield + yield components
  - o adaptation
  - o morphological traits

- **Genotyping**:
  - 48 SSR markers
  - 2500 DArT markers
  - Target genes (Ppd, Rht, Q, Vrn, Tillering)

➢ Structure of the panel

➢ Association genetics underway

WP5 : Bioinformatics for Triticeae improvement (MIPS)



WP1-WP2:

Construction of physical maps anchored to genetic maps

WP3: Gene isolation

Task 5.2 bioinformatic re-sampling for physical mapping (HU)

Task 5.4 semi-automated annotation pipeline (INRA)

Task 5.1 integrative database and web interface (GSF)

Task 5.3 Comparative genomics (GSF)

WP5

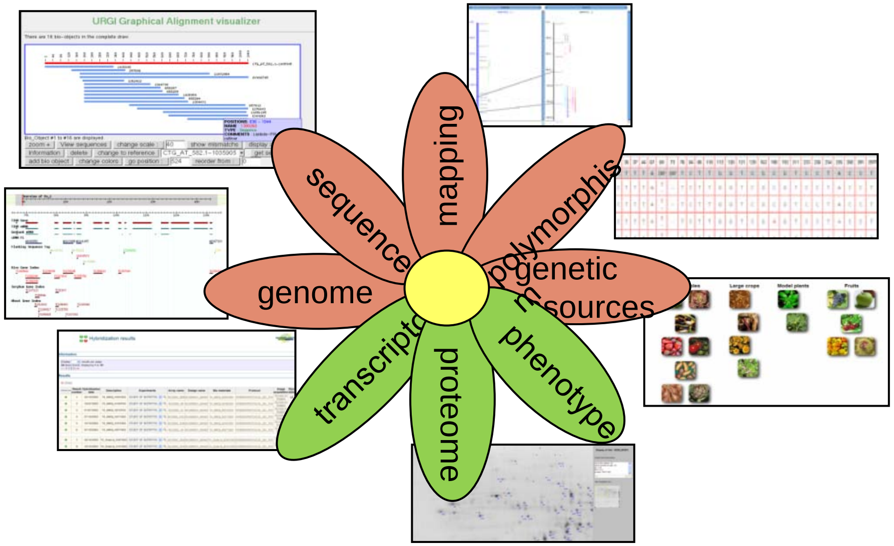
WP4: Markers for molecular breeding

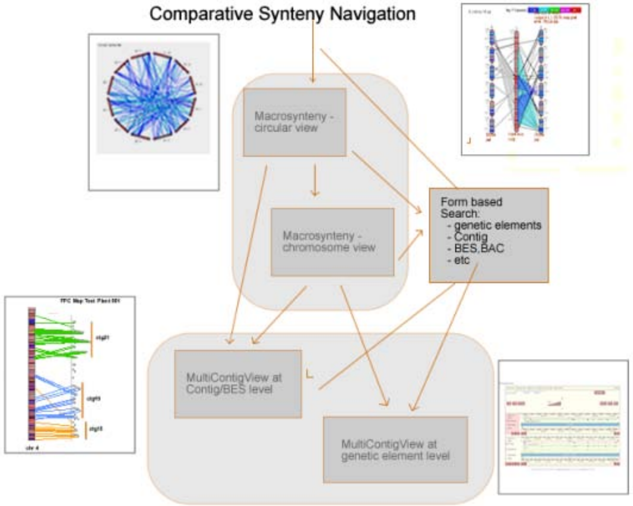
External Bioinformatics resources

WP6: Outreach

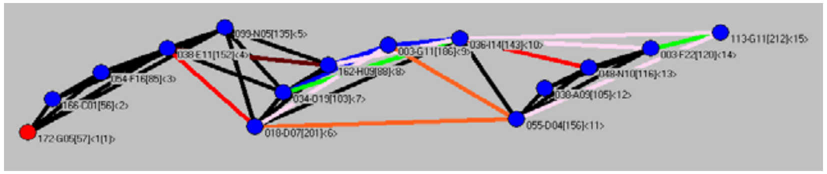
WP5 : Results

- **Integrative Databases for wheat and barley maps**

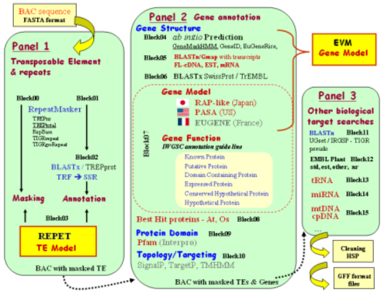




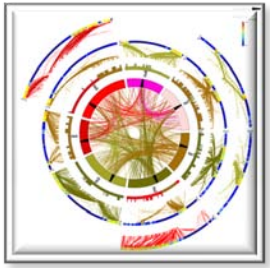
- **New algorithm for physical map assembly (LTC)**



- **Improved annotation pipeline (Triannot)**



- **Comparative map viewer (Crowsnest)**



Frenkel et al . BMC bioinformatics 2010

WP6 : Dissemination (MTT)

For many years the size and complexity of the wheat, barley and rye genomes have hampered the development of genomics and its application to produce Triticeae crops with improved composition and characteristics. Recently, however, new and more efficient scientific capabilities and resources have been developed that allows robust genomic programs to be established for the Triticeae.

TriticeaeGenome project (Genomics for Triticeae improvement) is designed to achieve significant progresses in Triticeae genomics and support efficient breeding of improved varieties for the European agriculture. This European project was launched on 1st June 2008, for a duration of 4 years, and mobilises 14 European research institutes and 2 industrial partners, from 9 different countries. TriticeaeGenome will receive 5.3 million Euros in funding over a four-year period, from the 7th European Union Framework Programme under the "Food, Agriculture and Fisheries, Biotechnology" priority.

Attend the TriticeaeGenome Training Courses !

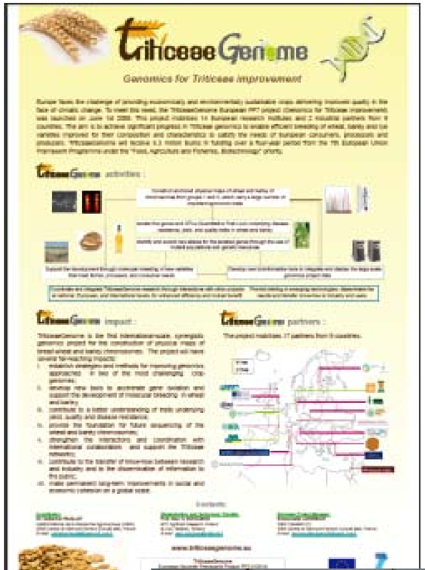
Last news and informations

Aug-5-2010 - TriticeaeGenome project article in the Annual International Innovation report 2010
TriticeaeGenome project article by Research Media

Apr-12-2010 - 2nd TriticeaeGenome Annual Meeting at Sabanci University + 1st EAB meeting (Istanbul, Turkey)
2nd TriticeaeGenome Annual Meeting at SU (Istanbul, Turkey)

Jan-12-2010 - Guidelines for physical map assembly available
Guidelines for physical map assembly available

This project is supported by the European Commission under the 7th Framework Programme for Research and Technological Development



TriticeaeGenome

Genomics for Triticeae improvement

TriticeaeGenome activities :

TriticeaeGenome impact :

TriticeaeGenome partners :

www.triticeaegenome.eu

Partners

The TriticeaeGenome project mobilises 17 partners from 9 countries.

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TriticeaeGenome
European Seventh Framework Project FP7-212019
Food, Agriculture and Fisheries, Biotechnology

TriticeaeGenome

Genomics for Triticeae improvement

www.triticeaegenome.eu

... the face of climatic change. To meet ... 1st 2008. This project mobilises 14 ... Triticeae genomics to enable efficient ... European consumers, processors and producers. TriticeaeGenome will receive 5.3 million Euros in funding over a four-year period from the 7th European Union Framework Programme under the "Food, Agriculture and Fisheries, Biotechnology" priority.

TriticeaeGenome activities :

Construct anchored physical maps of wheat and barley of chromosomes from groups 1 and 3, which carry a large number of important agronomic traits

Isolate five genes and QTLs (Quantitative Trait Loci) underlying disease resistance, yield, and quality traits in wheat and barley

Identify and exploit new alleles for the isolated genes through the use of mutant populations and genetic resources

Support the development through molecular breeding of new varieties that meet farmer, processor, and consumer needs

Develop new bioinformatics tools to integrate and display the large scale genomics project data

Coordinate and integrate TriticeaeGenome research through interactions with other projects at national, European, and international levels, for enhanced efficiency and mutual benefit

Provide training in emerging technologies, disseminate the results and transfer know-how to industry and users

TriticeaeGenome impact:

TriticeaeGenome is the first international-scale, synergistic genomics project for the construction of physical maps of bread wheat and barley chromosomes. The project will have several far-reaching impacts: (i) establish strategies and methods for improving genomics approaches in two of the most challenging crop genomes; (ii) develop new tools to accelerate gene isolation and support the development of molecular breeding in wheat and barley; (iii) contribute to a better understanding of traits underlying yield, quality and disease resistance; (iv) provide the foundation for future sequencing of the wheat and barley chromosomes; (v) strengthen the interactions and coordination with international collaborators and support the Triticeae networks; (vi) contribute to the transfer of know-how between research and industry and to the dissemination of information to the public; (vii) make permanent long-term improvements in social and economic cohesion on a global scale.

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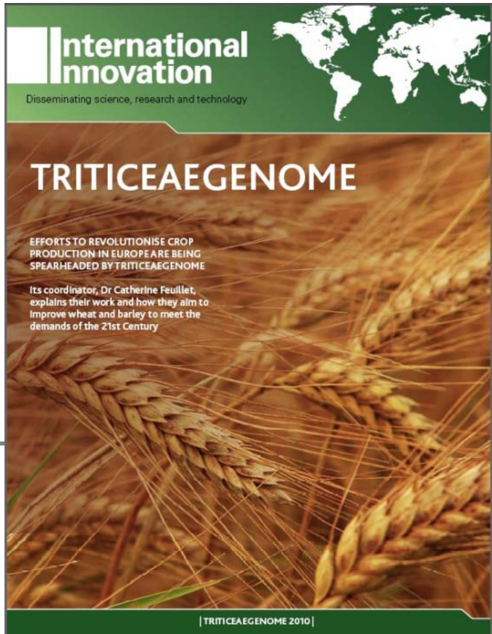

International Innovation

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TRITICEAEGENOME

EFFORTS TO REVOLUTIONISE CROP PRODUCTION IN EUROPE ARE BEING SPEARHEADED BY TRITICEAEGENOME

Its coordinator, Dr Catherine Feuillet, explains their work and how they aim to improve wheat and barley to meet the demands of the 21st Century

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SEVENTH FRAMEWORK PROGRAMME