



19th International *Triticeae* Mapping Initiative

3rd COST Tritigen

Mining the Maize Genome

***The future impact of genomic-assisted
approaches on maize breeding***

Sébastien PRAUD

ARVALIS
Institut du végétal

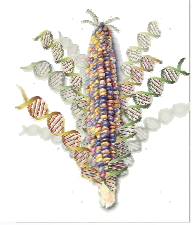
IRAGT

biogemma

GRUPE
EURALIS

Limagrain
from earth to life

In plants, how is used the genomic sequence?



Advance in genomics can contribute to crop improvement in two general ways



1-provide **general knowledge** on the maize genome organization and gene content



participate to the **global understanding of plant evolution and complex biological processes**

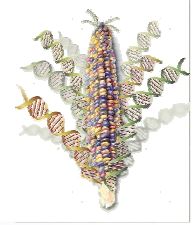
2-integrate genetic and genomic data to **identify key genes involved in traits' variations**



- provide new genomic powerful tools to **facilitate and stimulate germplasm and allelic diversity characterization** of key genes

- increase breeding efficiency** by marker-assisted selection based on the genomic tools provided by sequencing projects.

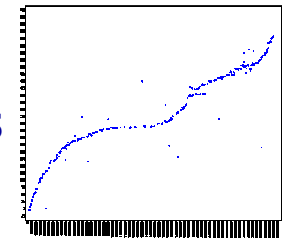
Outlines



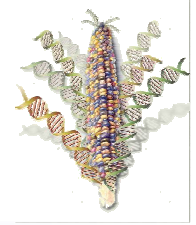
- Integration of Genetic and Genomic data



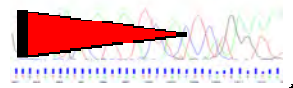
- How is the information used in genetic and in breeding programs



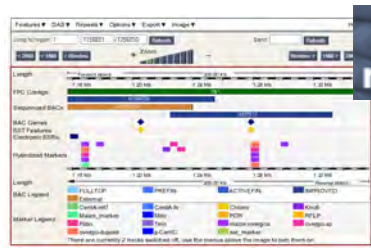
Integration of Genomic data: Data Flow



Genome Sequencing Center 



NCBI  Nucleotide
 GCATC CCGGG GGTG ATTA TATAGC TCGATG ATCT
 TTCTGACACAG CACTG GCGG ATAGGATC ATGATCTA
 CCCTACGTG CAGTGG GAGGAGG CCGG GATG CCGAG
 CACAC CAAT TCGGAGAGG GCGG GATG CCGG GCGAG



maizeSequence



EMBL-EBI 


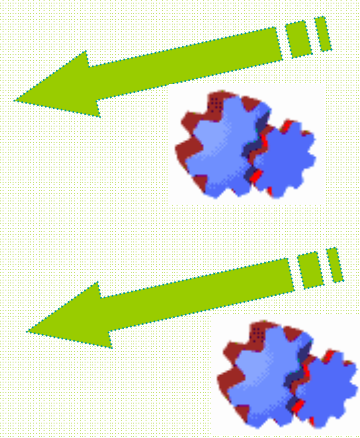
GGBrowser

Welcome on the textual part of the GnpMap interface. The extended query forms allow to search and retrieve precise information. Some of the result pages offer the ability to export the query results.

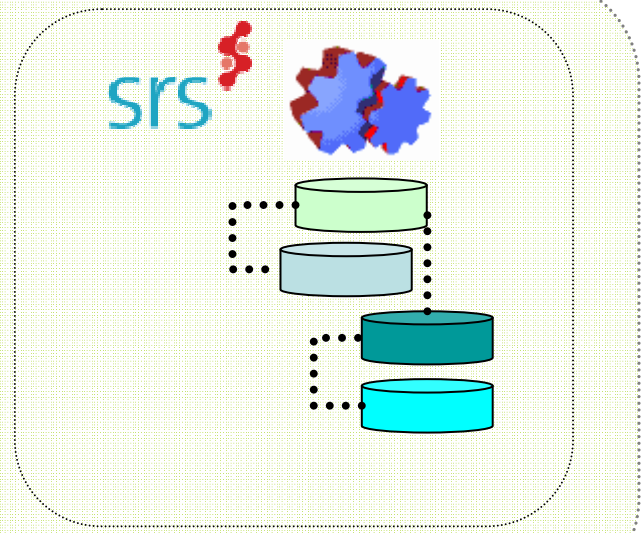
Query types


- [Query on loci](#)
- [Query on QTL](#)
- [Query on marker](#)
- [Query on pool](#)
- [Query on chromosome](#)
- [Query on map](#)
- [Query on trait](#)
- [Blast](#)
- [Keyword's lists for data submission](#)

Genetic maps

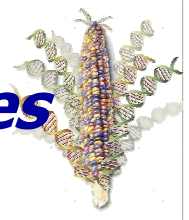



Specific rules  Clermont-Ferrand



Generic system 

Integration of Genomic data to identify key genes

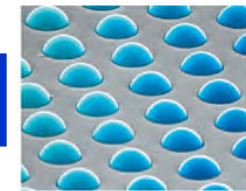


The assembled genome sequence provides a good basis for developing and locate precisely **a large number of markers in candidate genes** or within gene-rich regions that can, in a second time, be used in genetic studies.



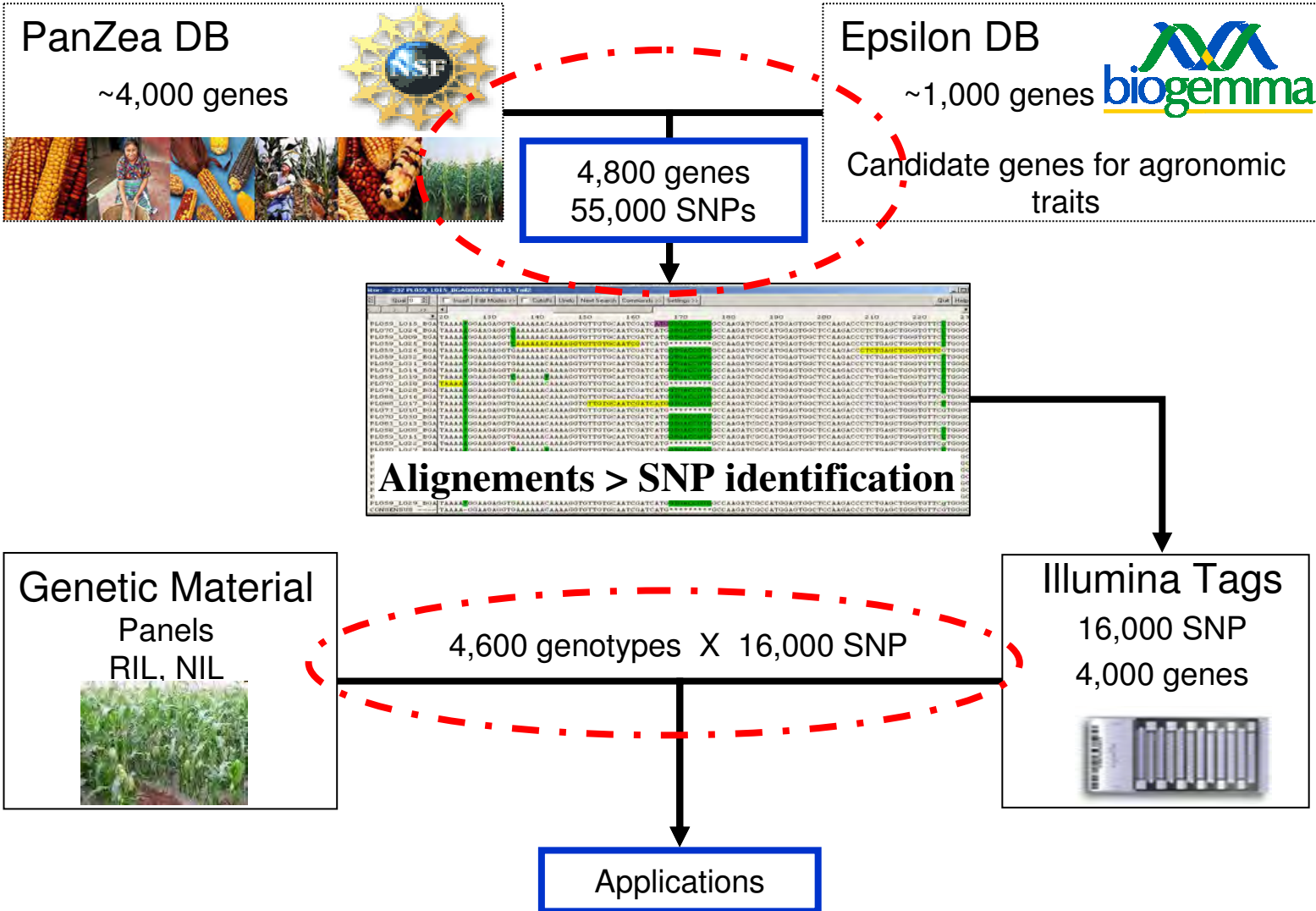
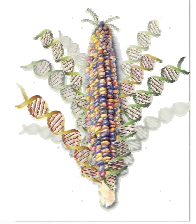
INTEGRAGEN

ILLUMINA chip: 16K

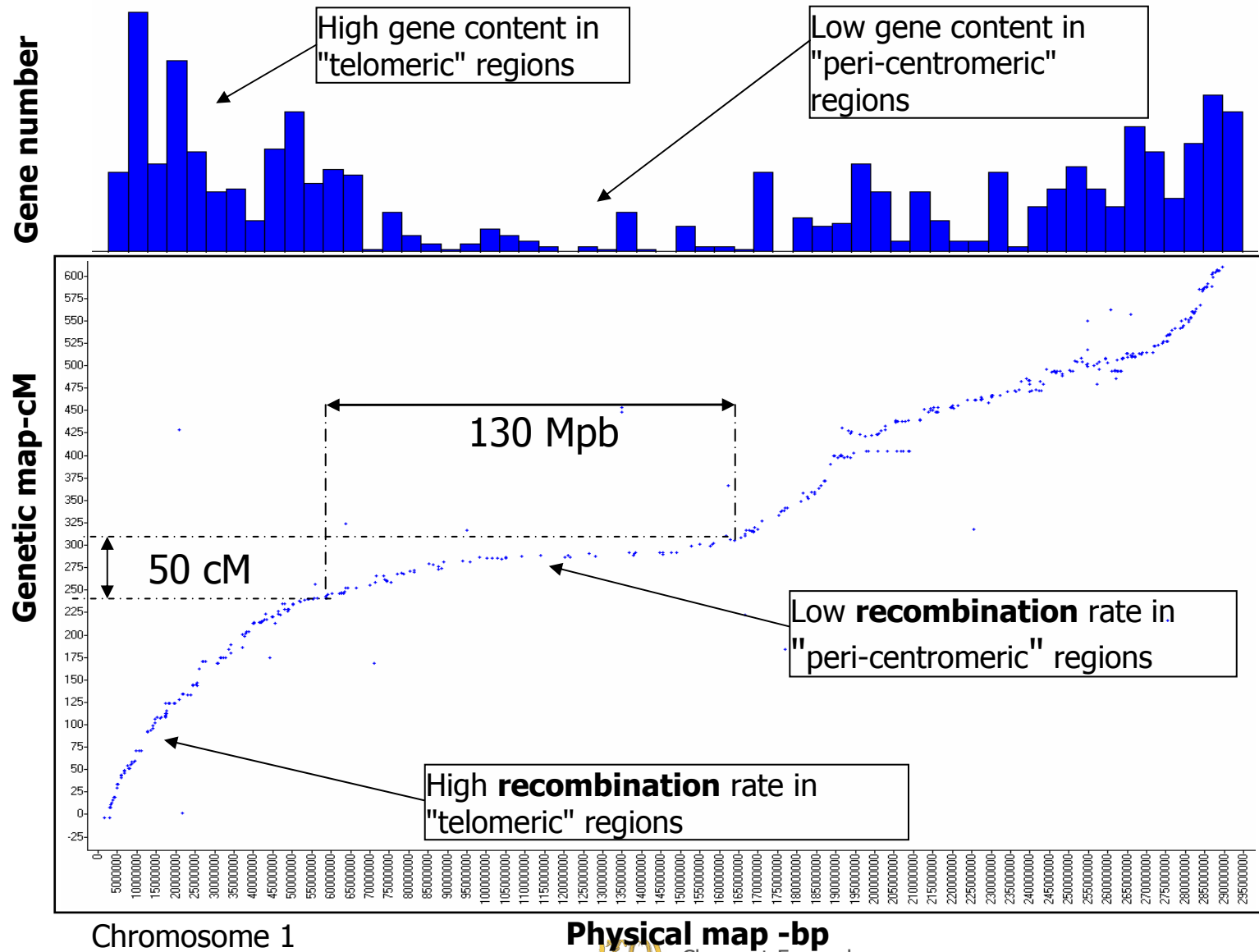
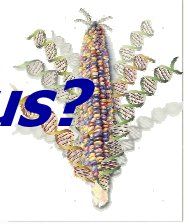


2008

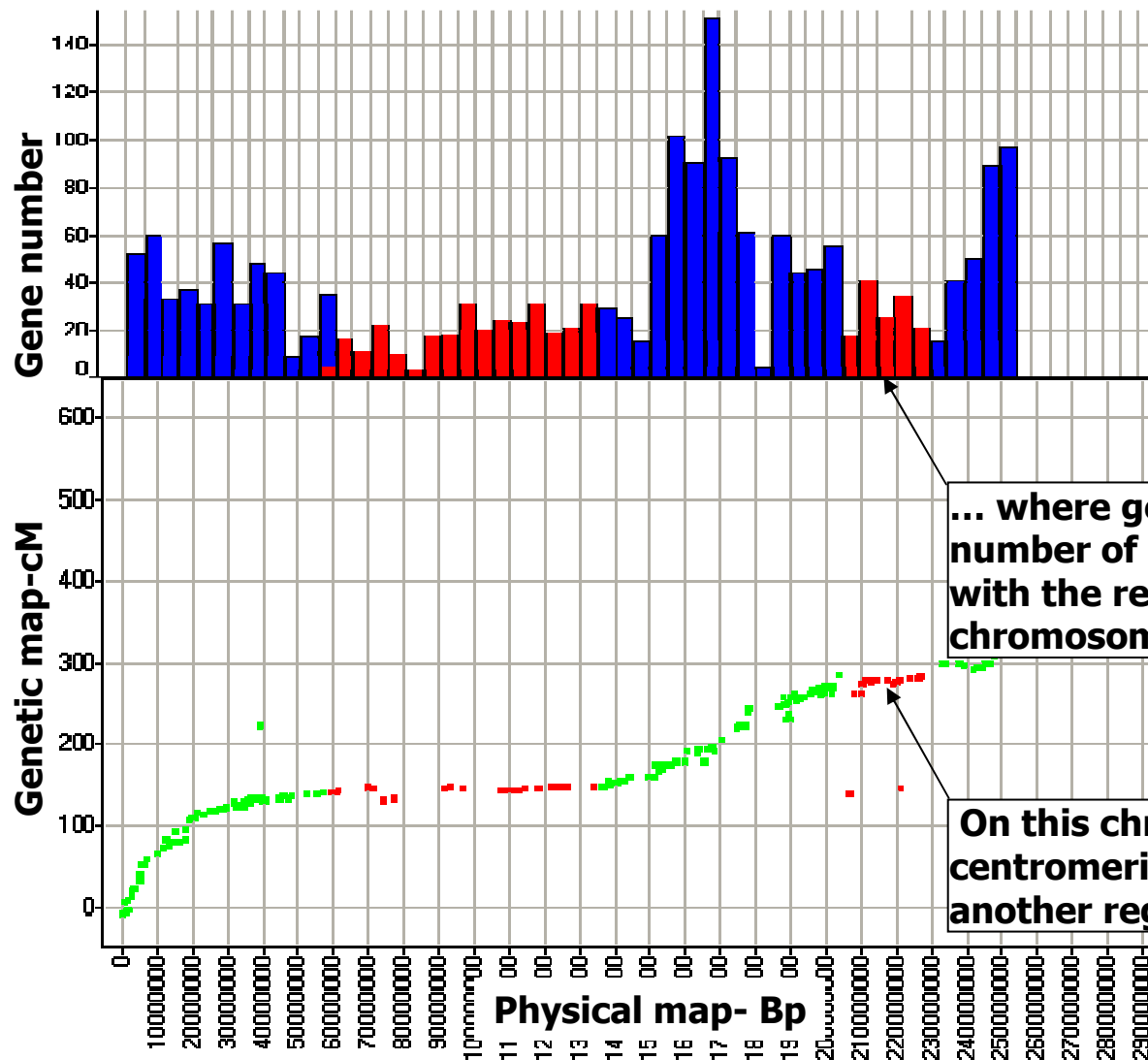
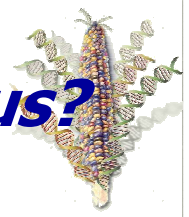
Genotype surveys with gene markers genome scanning



What do the genetic and genomic results teach us?



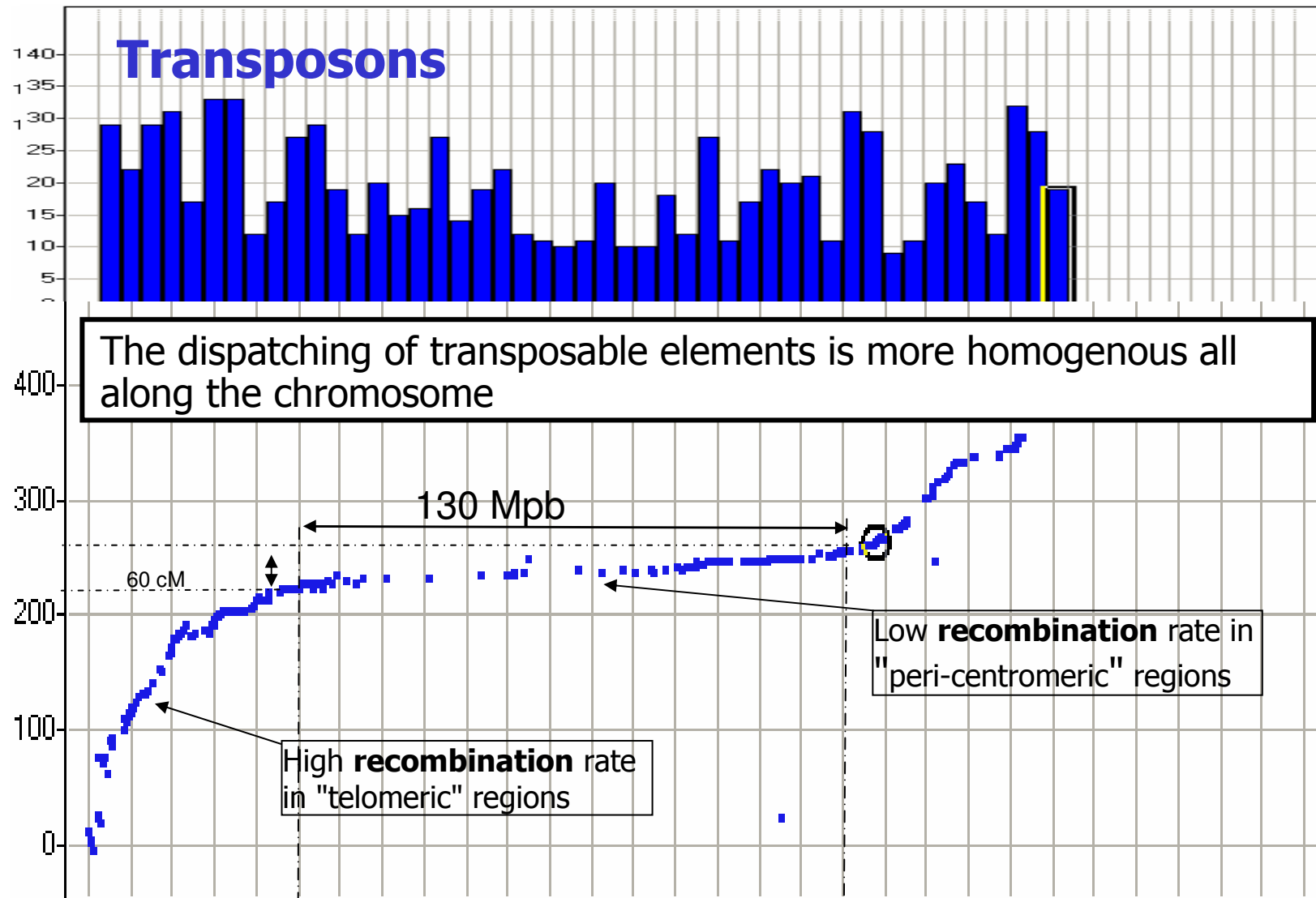
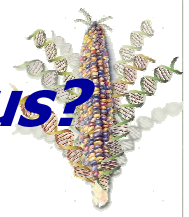
What do the genetic and genomic results teach us?



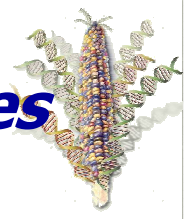
... where genes are less abundant. The number of genes seems to be correlated with the recombination rate at the chromosome scale!!

On this chromosome, in addition to the centromeric region the curve levels off in another region...

What do the genetic and genomic results teach us?



Integration of Genomic data to identify key genes

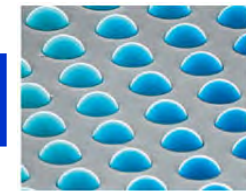


The assembled genome sequence provides a good basis for developing and precisely locating **a large number of markers in candidate genes** or within gene-rich regions that can, in a second time, be used in genetic studies.



INTEGRAGEN

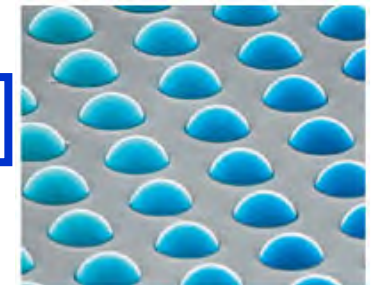
ILLUMINA chip: 16K



2008



ILLUMINA chip: 60K

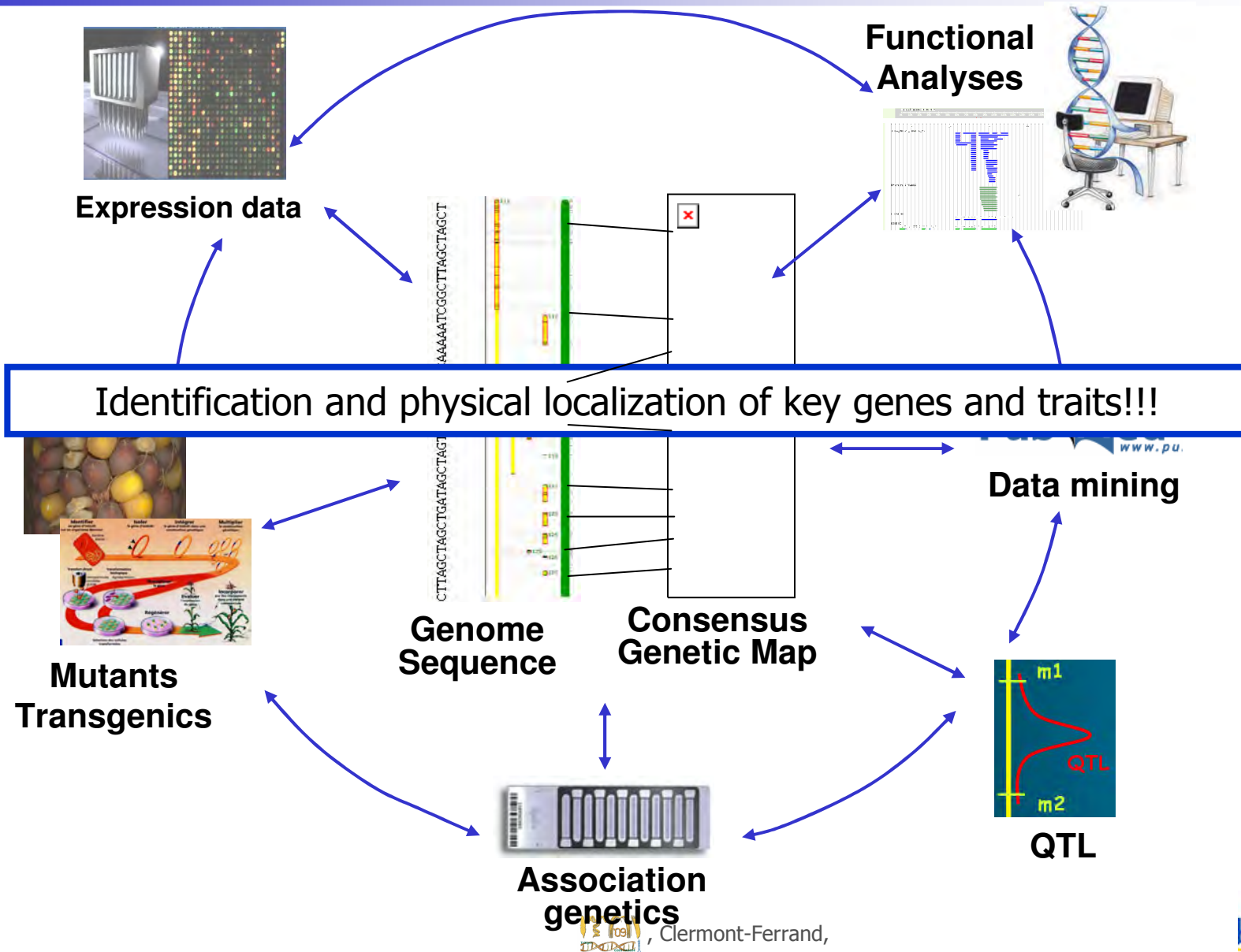
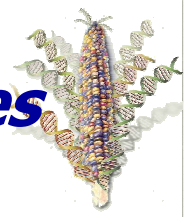


2010

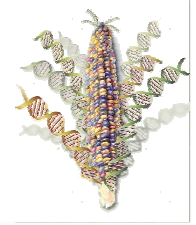
The number of links will drastically increase!!!



Integration of genomic data to identify key genes



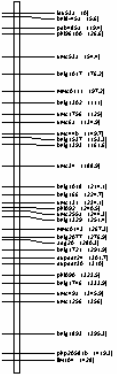
Localization of mQTL



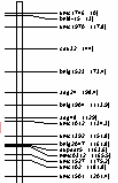
chr1



chr2



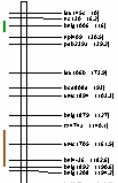
chr3



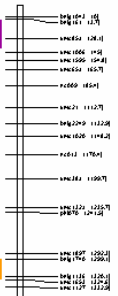
chr4



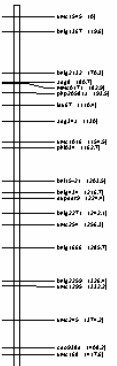
chr5



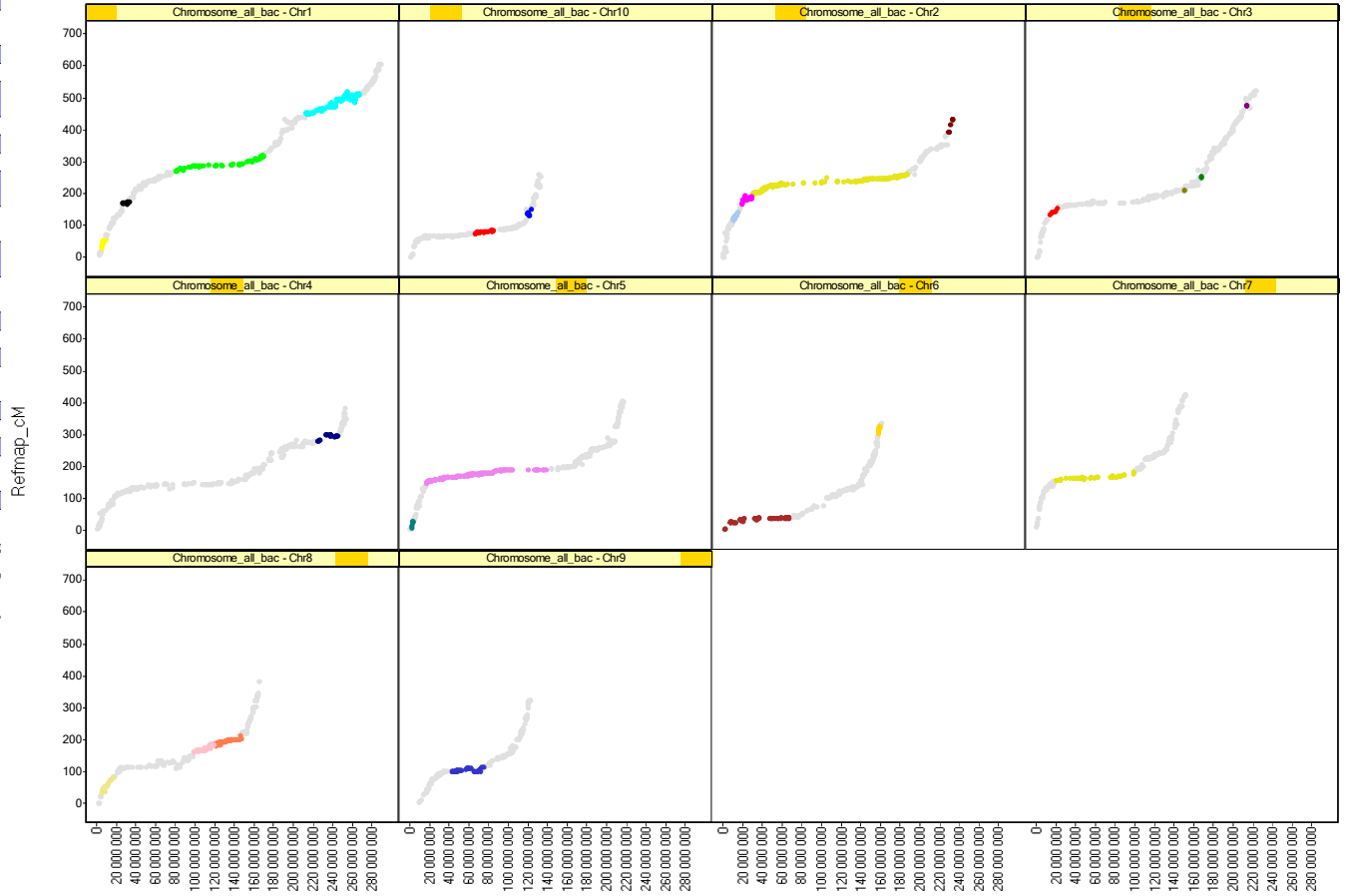
chr6



chr7

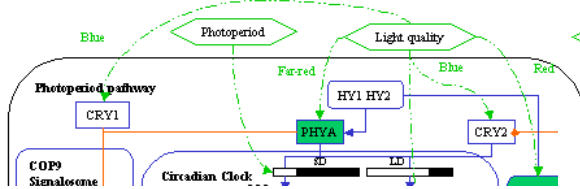
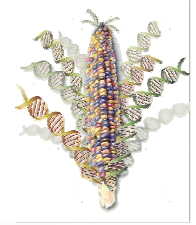


MetaQTL name	Chromosome	Debut	Fin	Debut FPC	Fin FPC	Zone couverte en cM par zone physique	Raisons du choix
QTL1a	1	30	55	4 973 500	8 491 700	29.8-55.05	stable sur la population
QTL1b	1	155	175	26 126 800	33 163 200	161.7-174.5	stable sur la population et/ou présent sur plusieurs populations
QTL1c	1	270	325	80 271 800	170 088 800	269.8-319.8	présent sur plusieurs populations
QTL1d	1						
QTL2a	2						
QTL2b	2						
QTL2c	2						
QTL2d	2						
QTL3a	3						
QTL3b	3						
QTL3c	3						
QTL3d	3						
QTL4a	4						
QTL5a	5						
QTL5b	5						
QTL5c	5						
QTL6a	6						
QTL6b	6						
QTL7a	7						
QTL8a	8						
QTL8b	8						
QTL8c	8						
QTL9a	9						
QTL10a	10						
QTL10b	10						



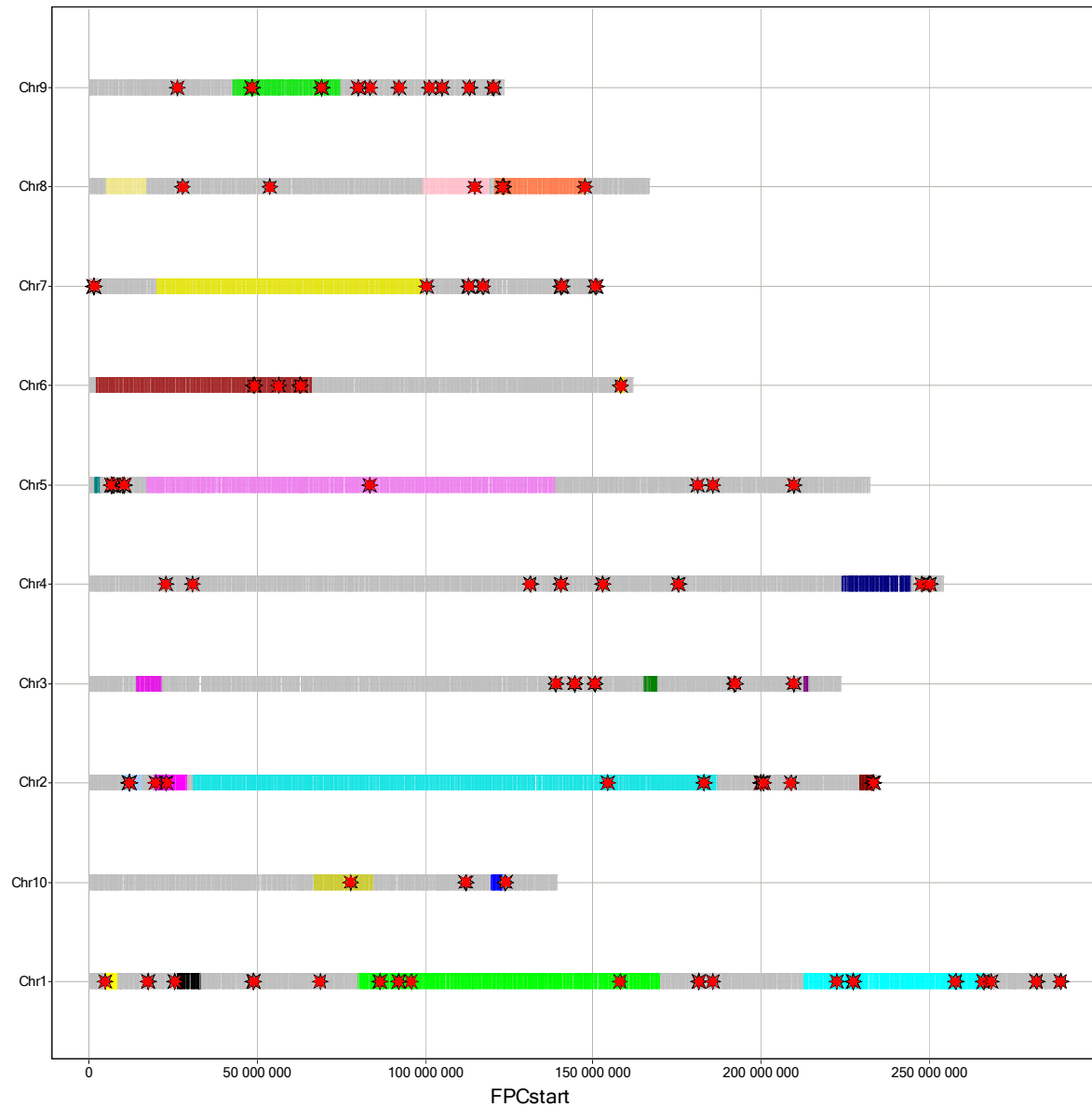
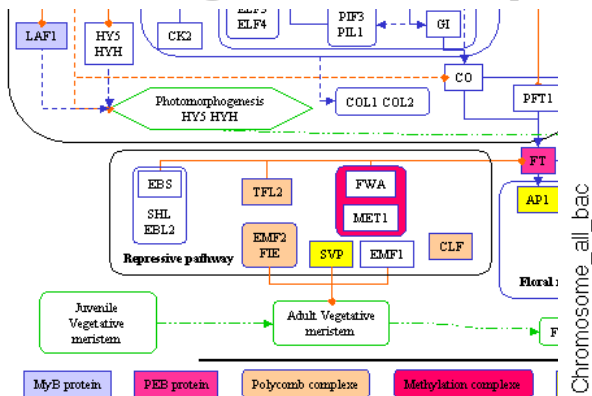
Localization of candidate genes

Document réalisé par F. Chardon, le 17 mars 2004

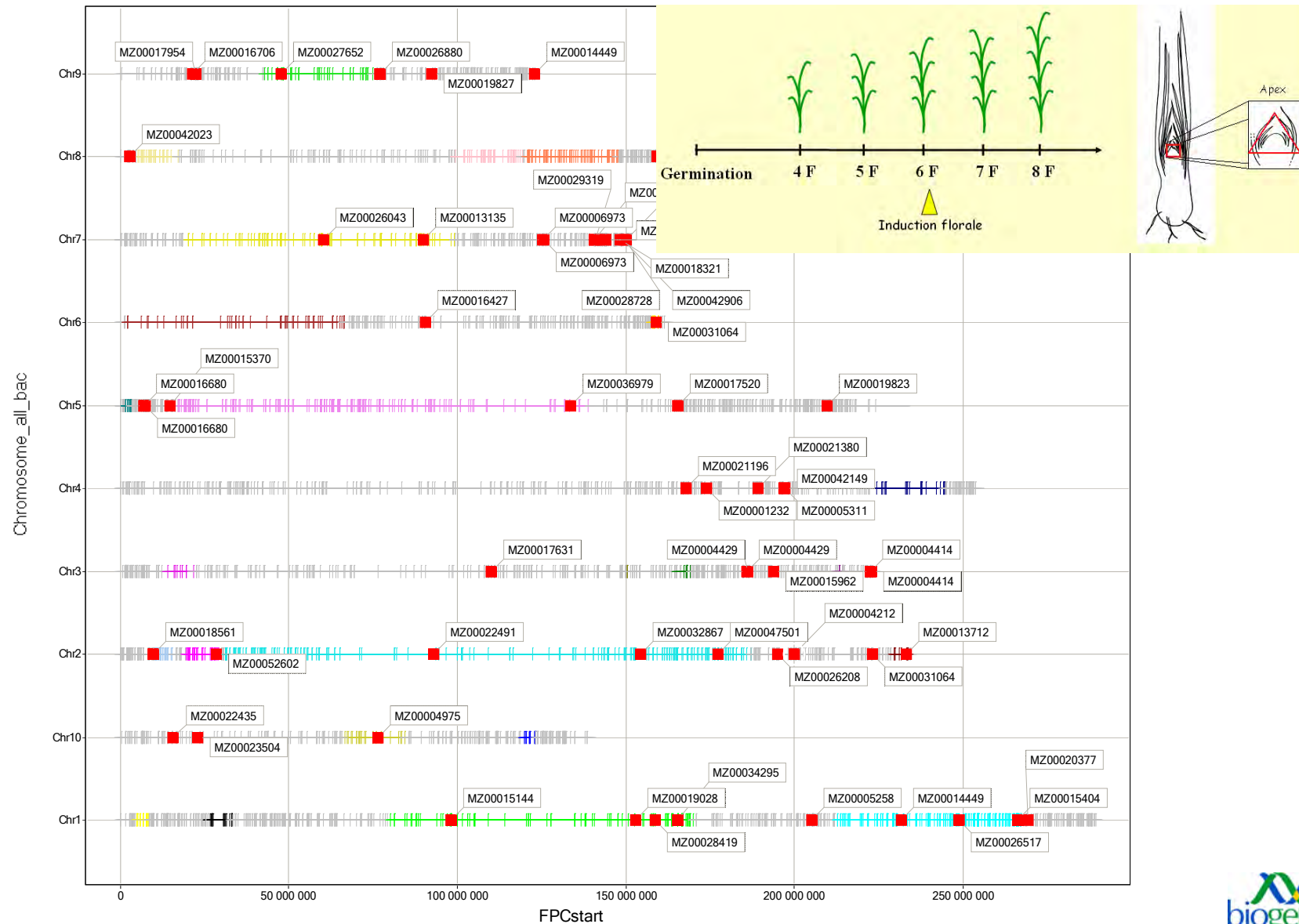
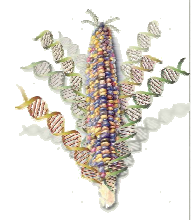


Research of the maize for important genes (A)

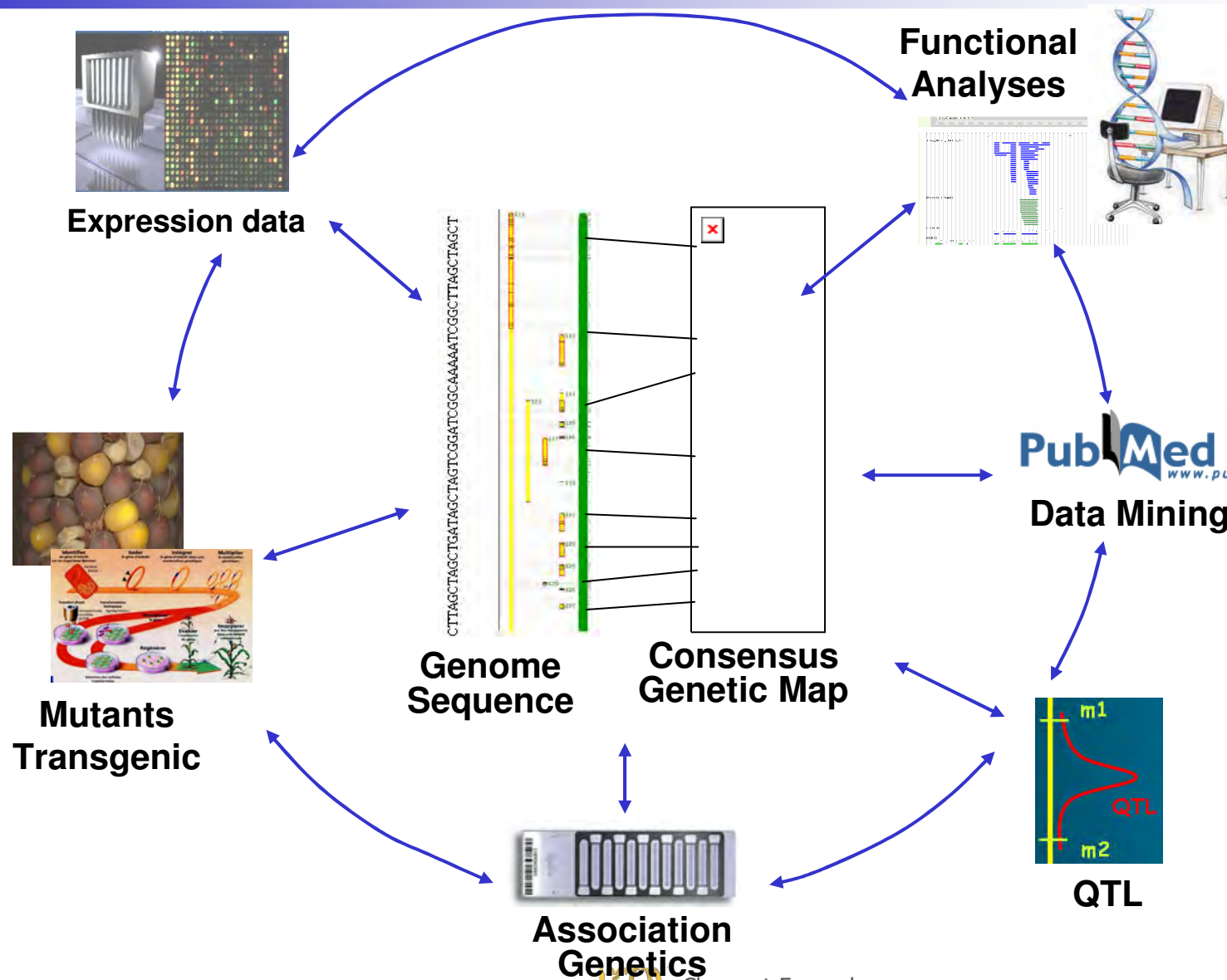
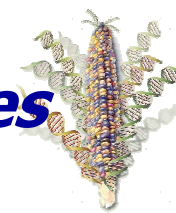
Assignment to a pl



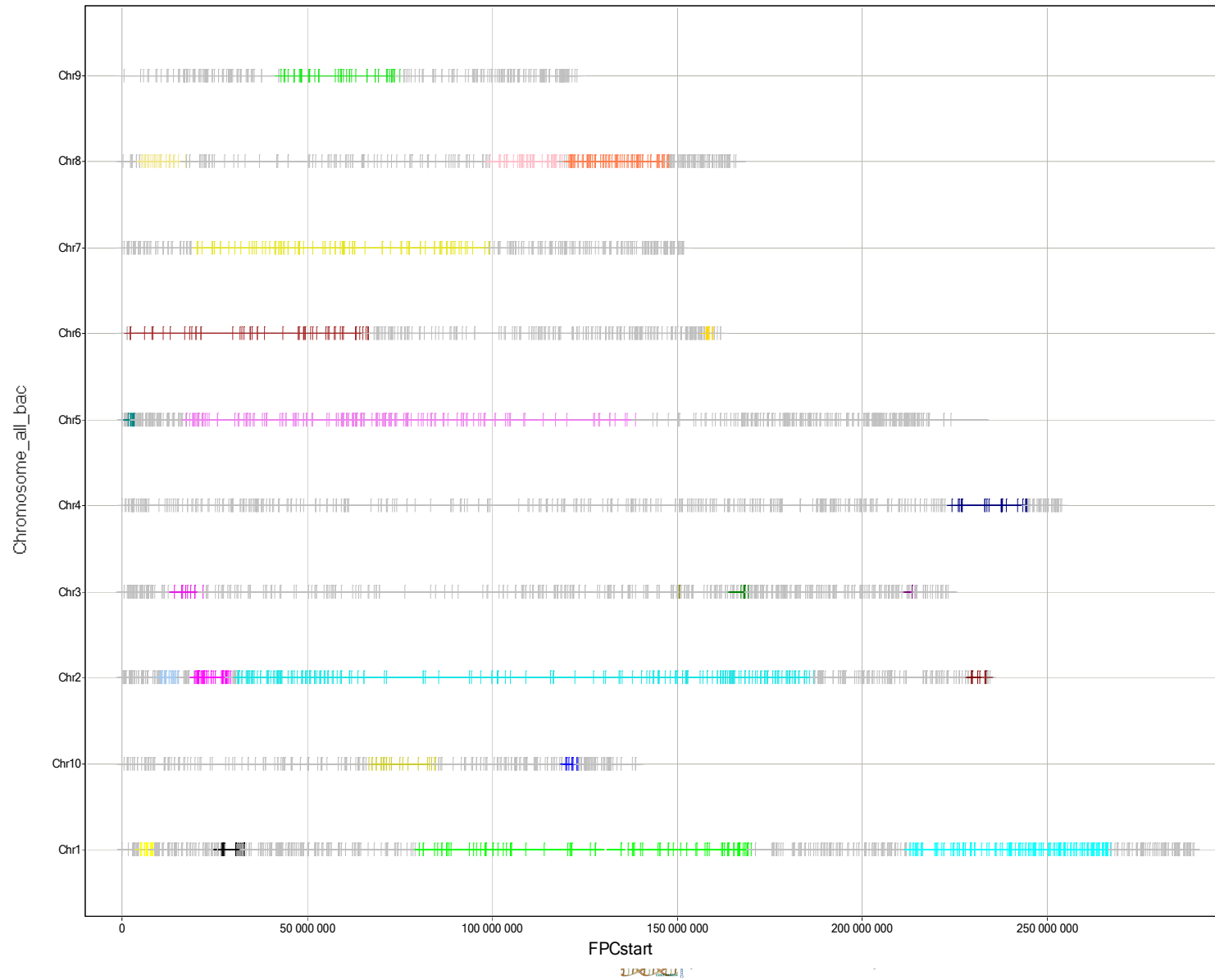
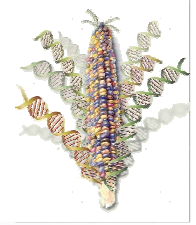
Localization of Transcriptomic data



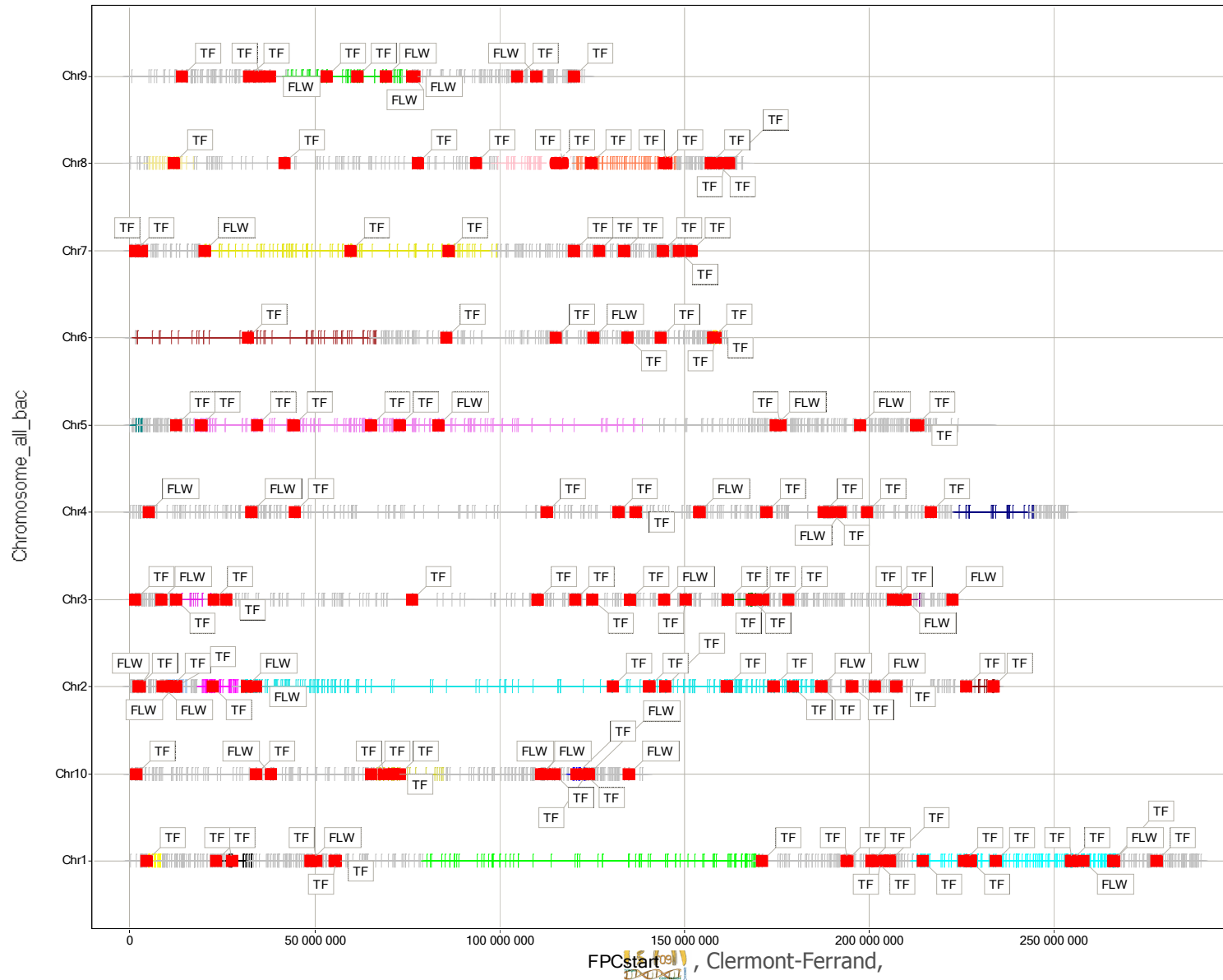
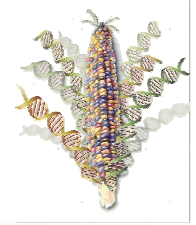
Integration of genomic data to identify key genes



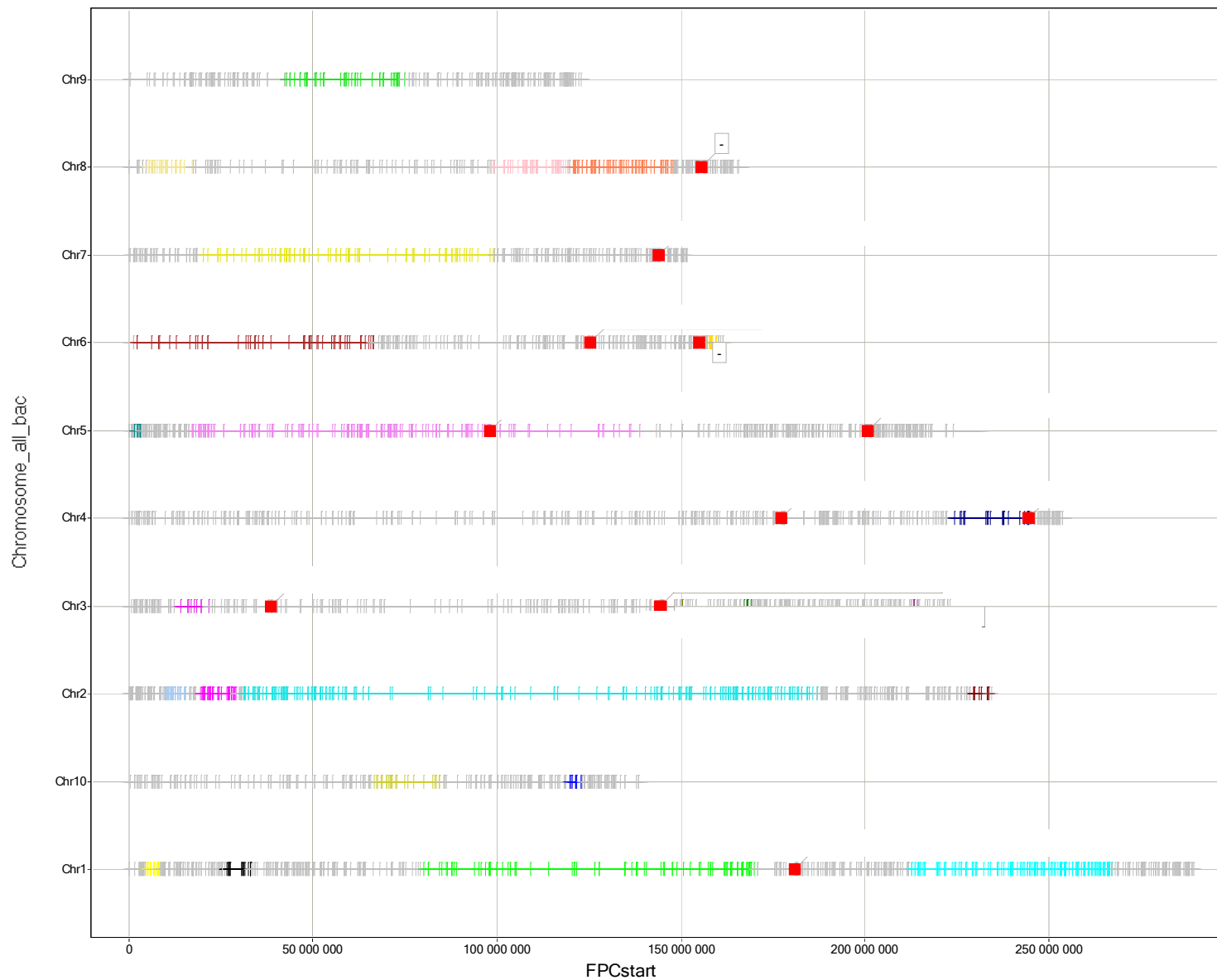
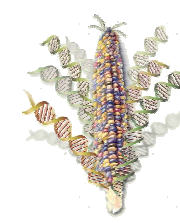
Anchoring of SNP



Annotation of the SNP



Results of the association



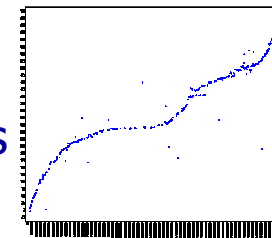
Outlines



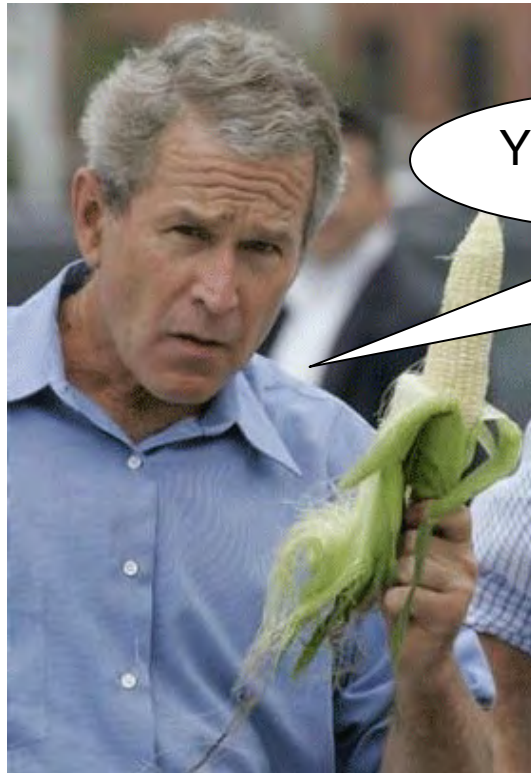
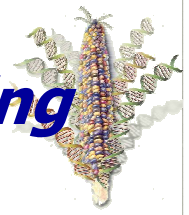
- The Maize Genome in Biogemma Bioinformatics Portal



- How can genomic information be used in genetic programs



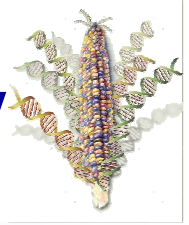
How can Genomic information be used in Breeding Programs?



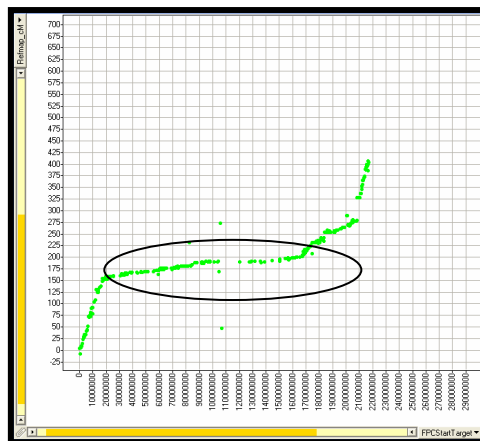
Yes, we corn!



Refinements and Changes in Molecular Breeding Programs



Knowledge about the recombination rate along the maize chromosomes is a useful information to choose germplasm and calibrate the experiments:

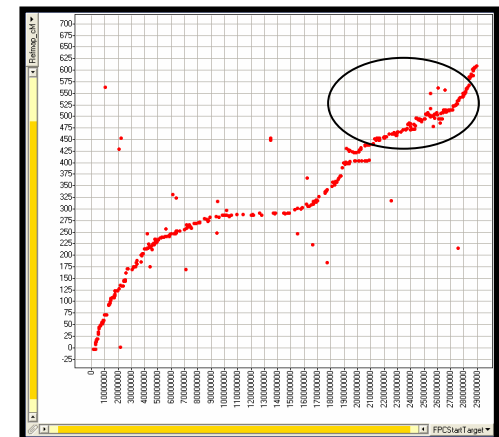


More difficult to eliminate alleles with negative effect

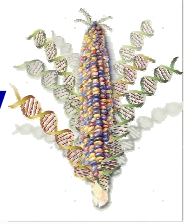
- better estimate the number of individuals to be used to identify recombinants in these regions
- use panel of lines from a broad genetic basis (low LD)

Easier to eliminate alleles with negative effect

- use less individuals to identify recombinants in these regions is sufficient
- use of panel of lines from a narrow genetic basis (moderate LD), NIL



Refinements and Changes in Molecular Breeding Programs

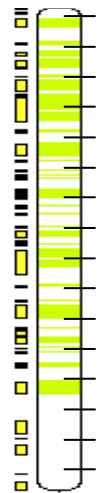


Choice of a « non-redundant and well-distributed marker sets»

Integration in a hapmap

What for?

Low density



Genetic mapping

GWAM (strong LD)

MARS

1

High density



NAM

GWAM (weak LD)

1

Targeted High density



Fine mapping

Backcrosses

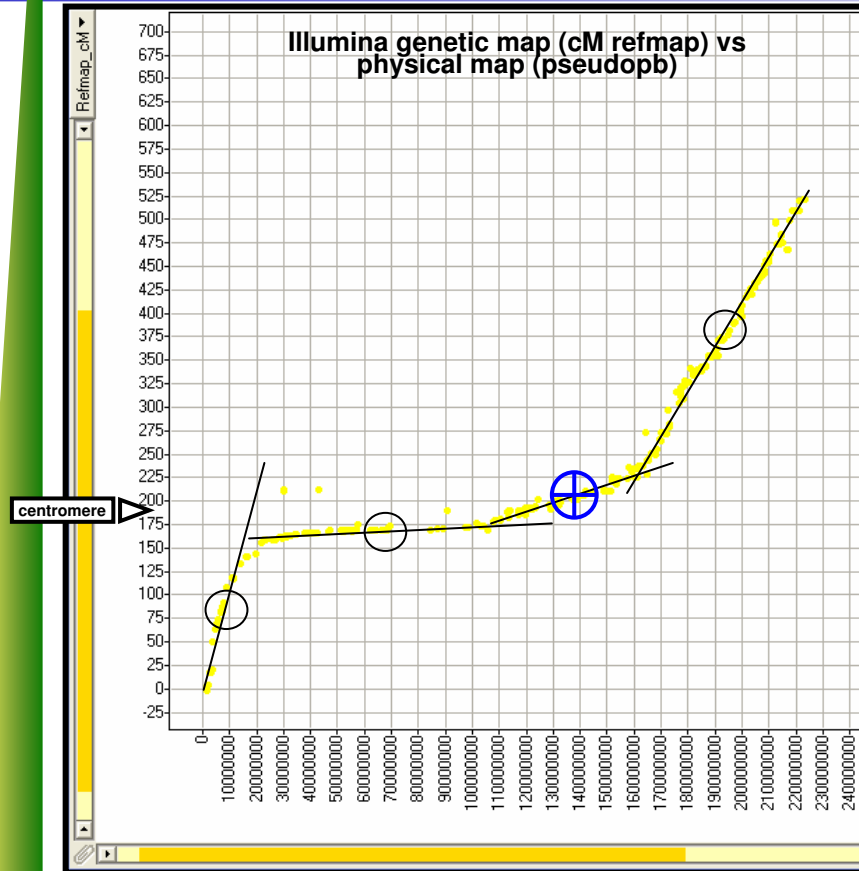
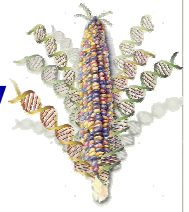
pyramiding

1

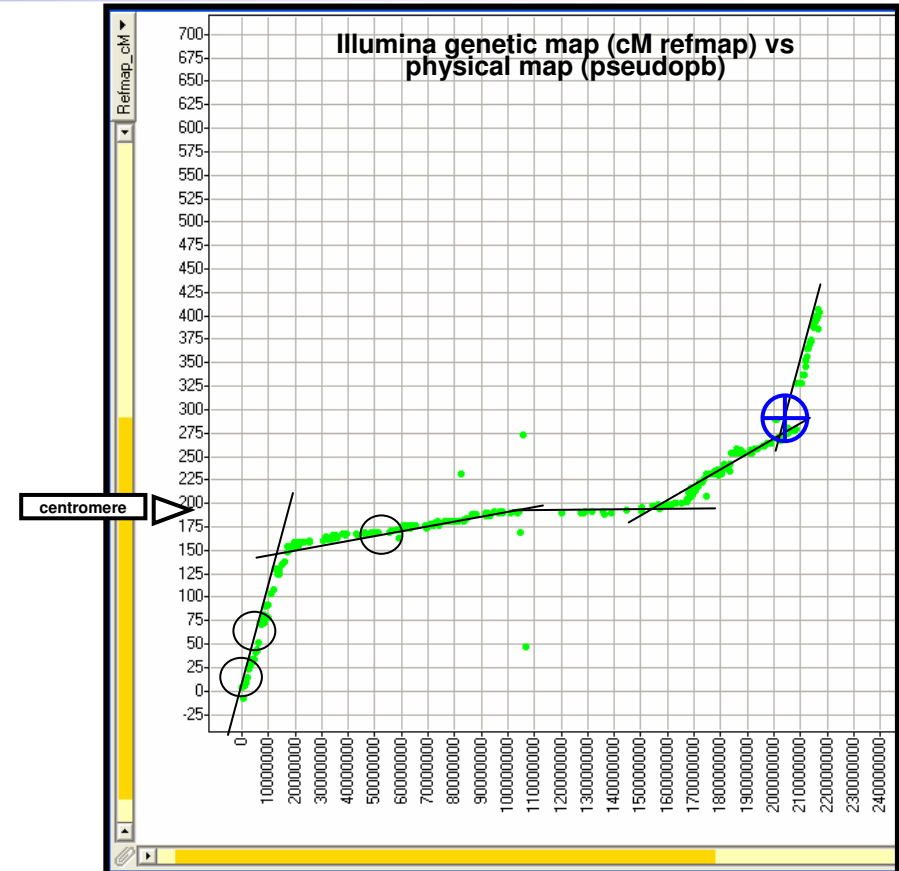
The location of the genes involved in agronomic traits can be identified using markers, and so bred directly. Ongoing in Biogemma and shareholders

Benefits to Breeding

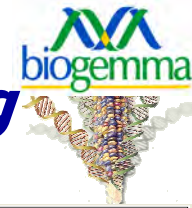
Refinements and Changes in Molecular Breeding Programs



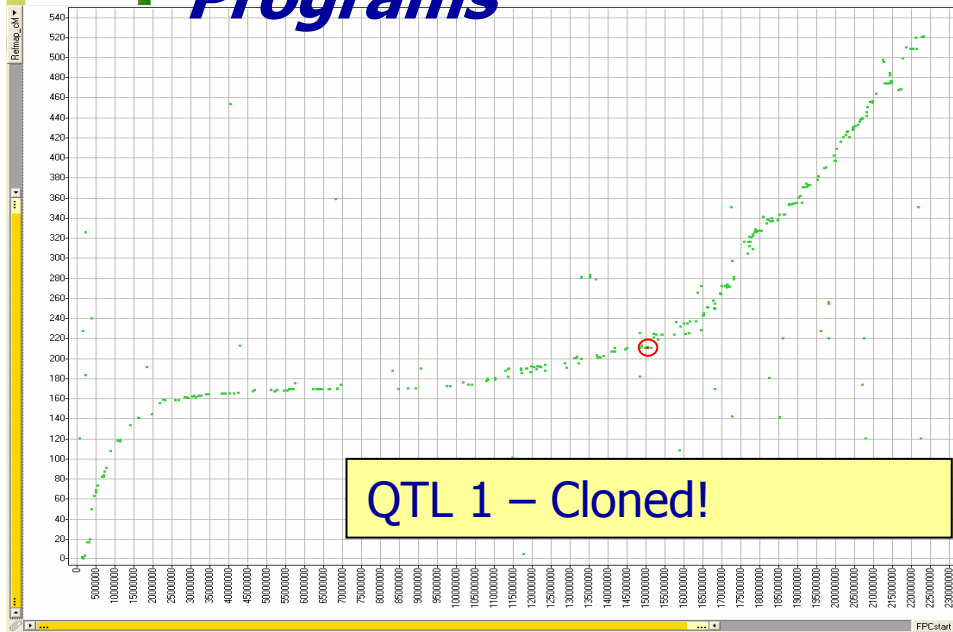
Low-recombination region
 → the responsible SNP could be quite close or not.



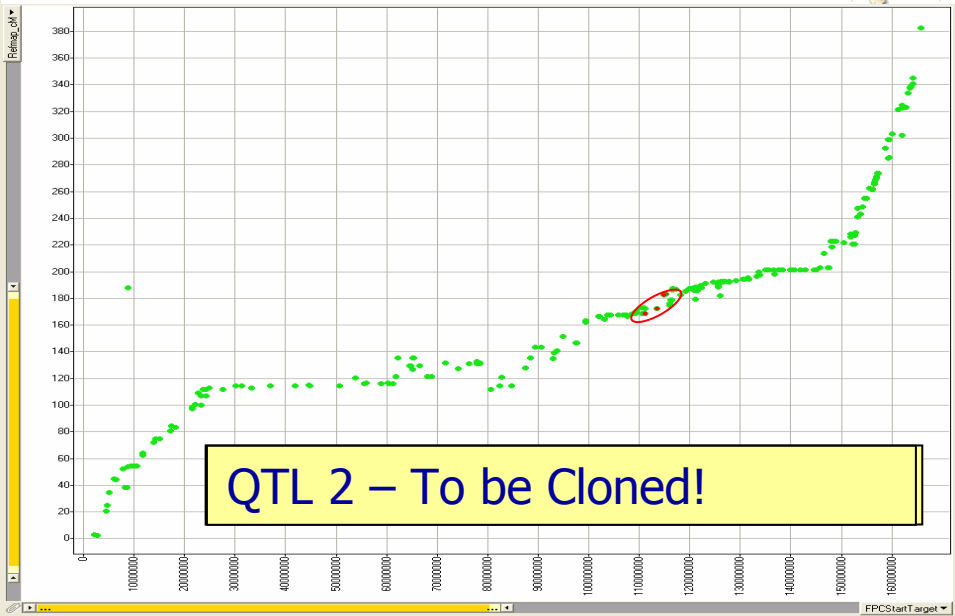
Highly recombinant region
 → the responsible SNP may be very close
 → **Prioritization for cloning**



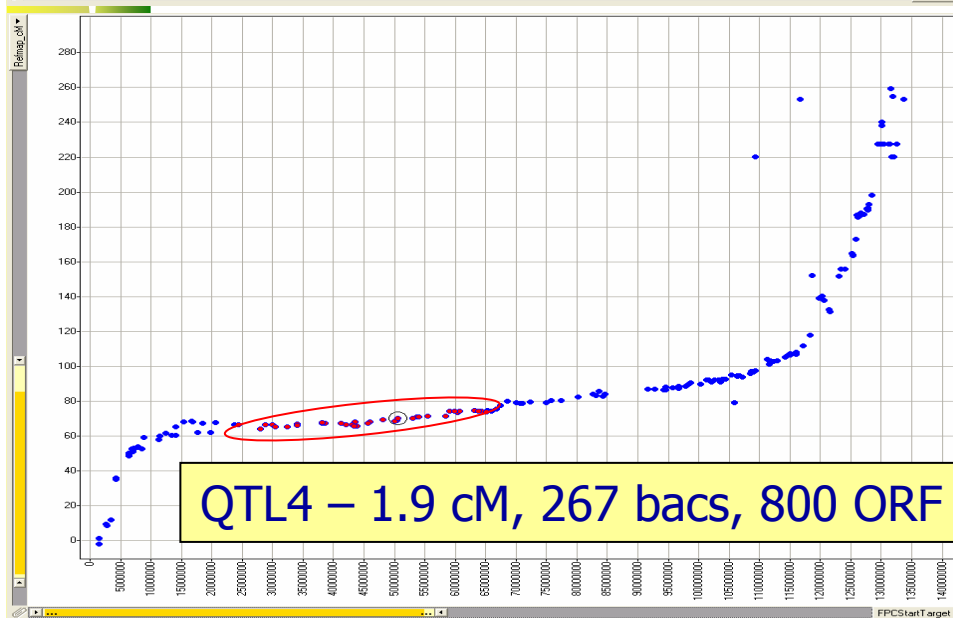
Refinements and Changes in Molecular Breeding Programs



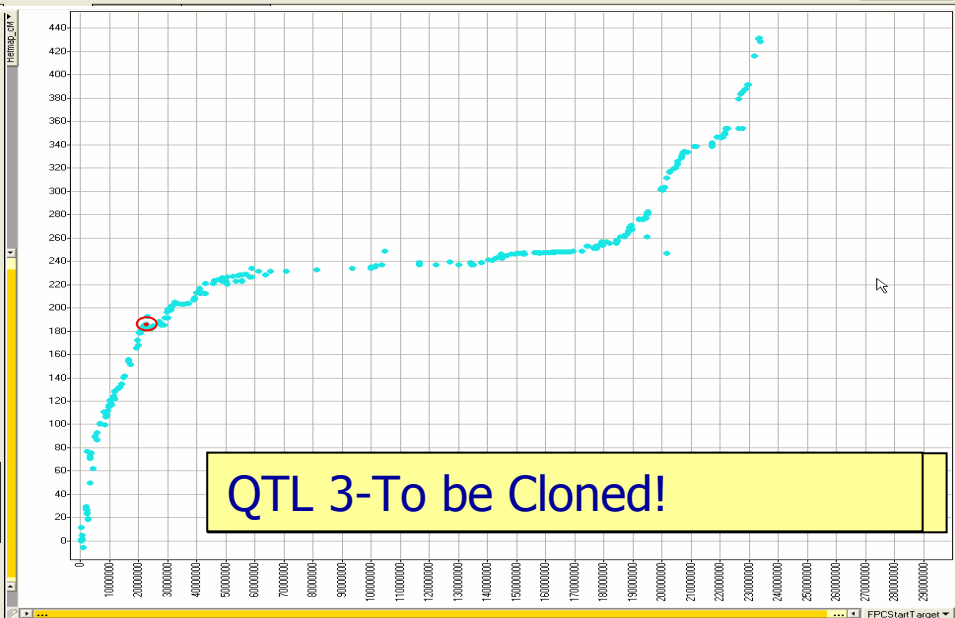
QTL 1 – Cloned!



QTL 2 – To be Cloned!

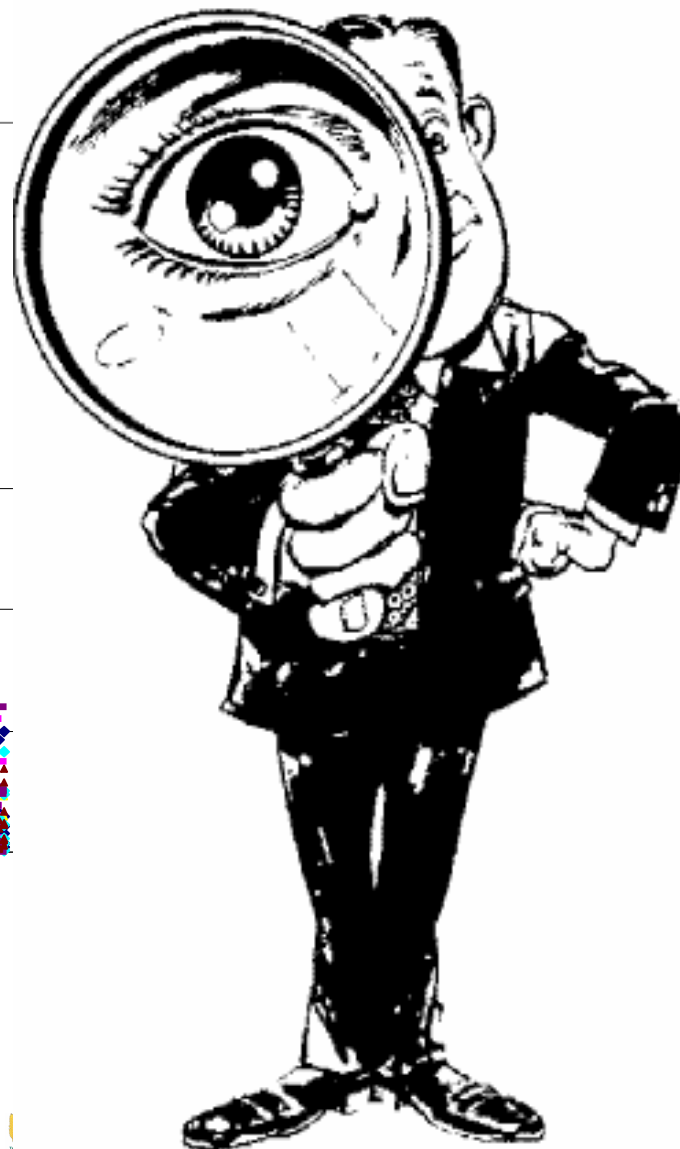
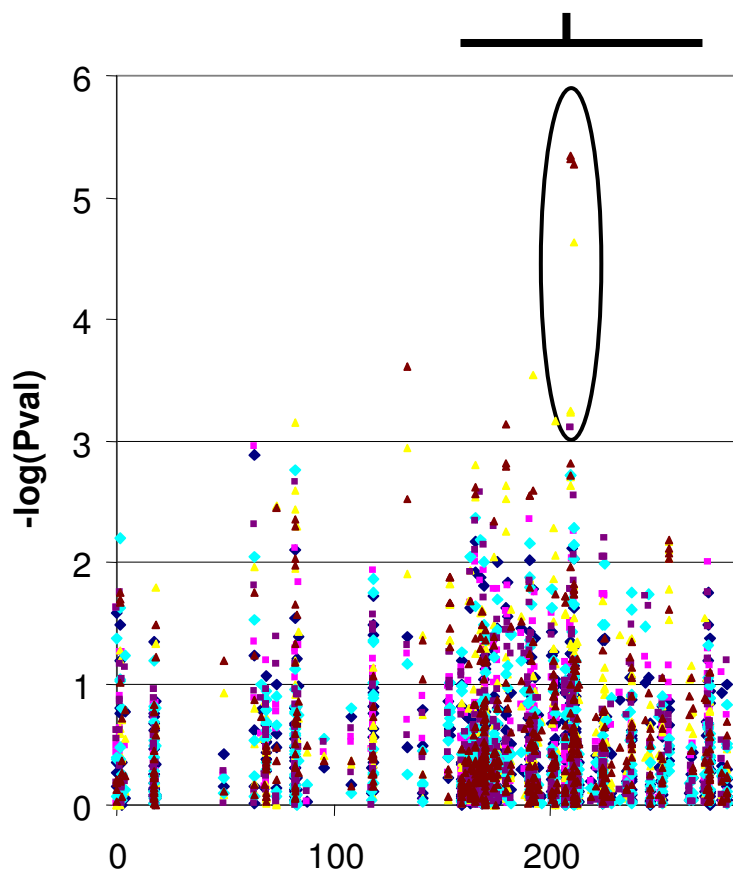
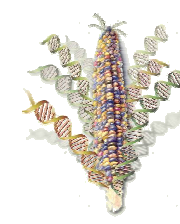


QTL4 – 1.9 cM, 267 bacs, 800 ORF



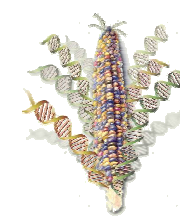
QTL 3 - To be Cloned!

Whole genome approach: studies on a major agronomical trait (1)

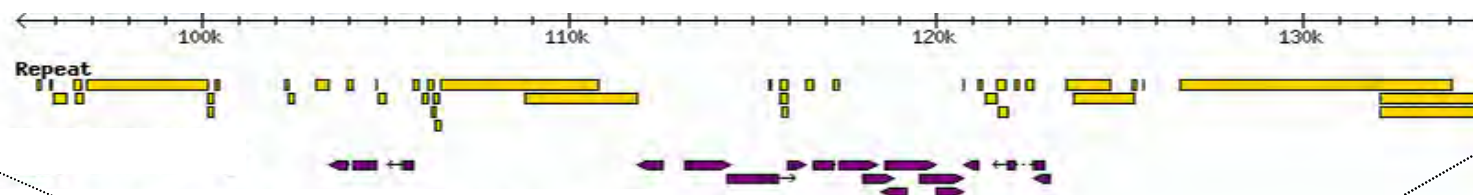


stability
analysis

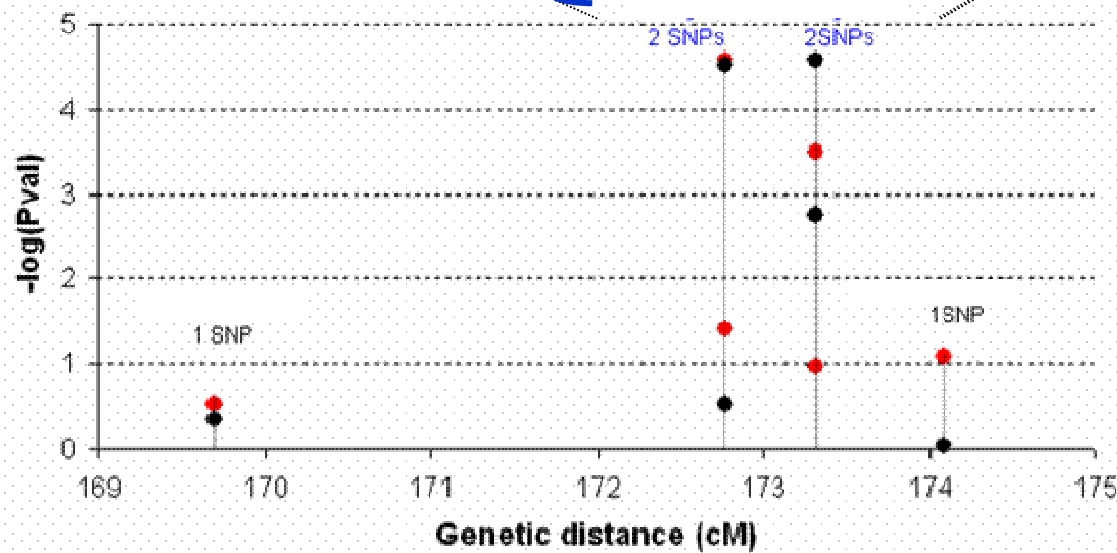
Whole genome approach: studies on a major agronomical trait (2)



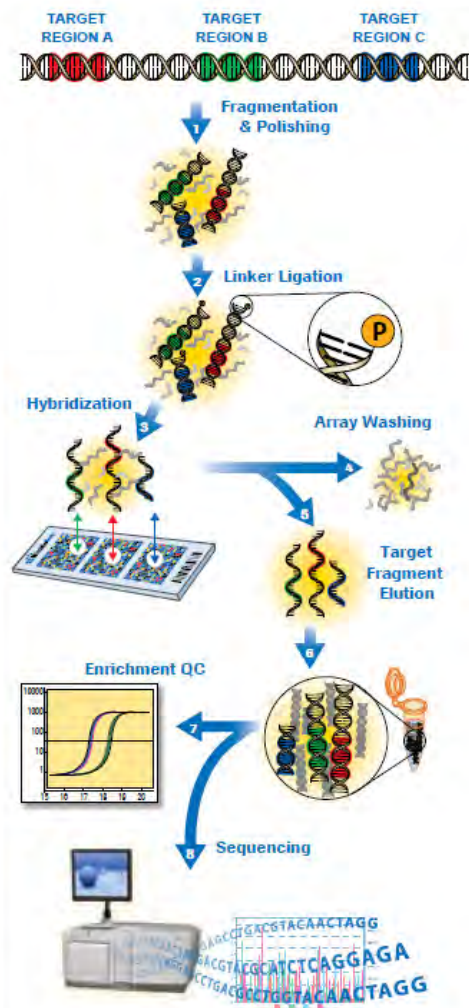
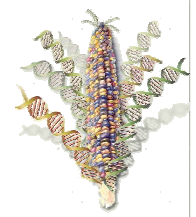
Physical distance (kb)



Two potential Genes



Further development: resequencing efforts



To clone QTL using positional information it is desirable to have available large numbers of genetic markers in the vicinity of the target QTL.



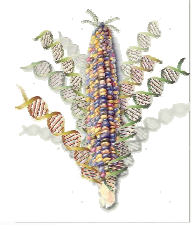
NimbleGen Sequence Capture technology offers the possibility to **conduct resequencing efforts** on targeted portions of complex genomes, thereby enabling the identification of region-specific SNPs.



**A strategic partnership with Biogemma:
wheat**

The marker densification is **becoming easier and cheaper!**

Take home messages (1)



Main message:

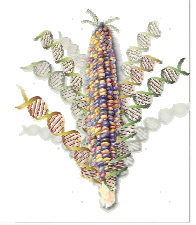


The genome provides a framework for who wants to understand how **genetic variation** influences **agronomic traits** by allowing the traits to be mapped back to **precise genomic locations and genes**.

This will be helpful to:

- increase and facilitate the cloning of QTLs: go directly from a trait to a gene
- develop a large number of “perfect” markers that can be used in genetic studies, useful for molecular breeding.
- characterize alleles and eliminates those with negative effects

Take home messages (2)



-Private companies need to encourage and push the initiatives and projects dedicated to **sequencing** the genome of our species:

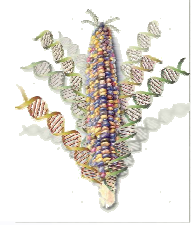
-European wheat initiative coordinated by Catherine Feuillet,
international initiative by Kellye Eversole,
Barley Initiative by Nils Stein



-To be ready when the genome will be available

Challenges: Material + Precise Phenotyping

Thanks



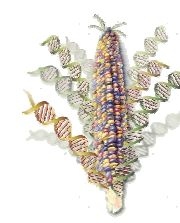
- Upstream Genomics: Olivier Dugas, Frédéric Sapet, Jorge Duarte
Genetics & Genomics in Maize: Christophe Tatout, Pierre Dubreuil, Sofiane Mezouk, Jérémy Derory, Laurent Decousset, Marie-Hélène Tixier, Nicolas Ribière, Christophe Thomas, Grégory Desmaizières, Johan Robin, Mickaël Bosio, Morgan Renault, Sébastien Praud, Alain Murigneux, Pascual Perez



- INRA Le Moulon:
Alain Charcosset,
Laurence Moreau



Thanks for your attention!



Merci!

ありがとう

謝謝

Спасибо



شكرا

شكرا

Grazie!

Danke!

תודה

Gracias!