





# Genomic, genetic and phenomic plant data at the INRA URGI: GnpIS.

Training on Triticeae







- GnpIS presentation
- Part I, Wheat Genomic resources
  - Quick tour of private sections
- Part II, Genetic resources and Phenotyping
- Part 3: Data set building with Biomarts





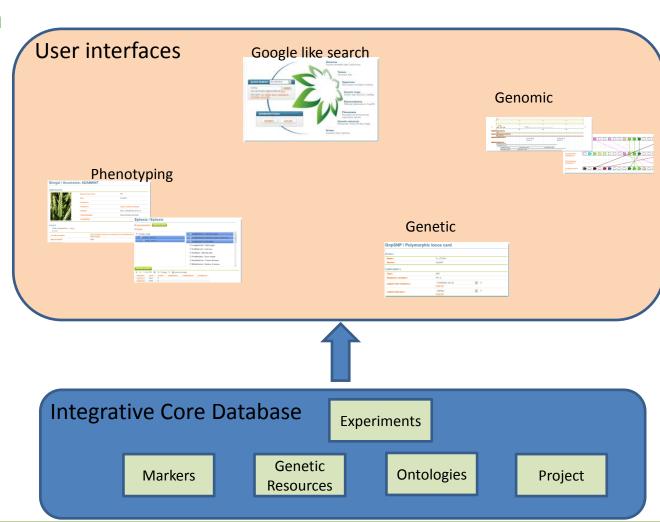
#### **GNPIS PRESENTATION**





## **GnpIS, URGI's Information system**

- Information system
  - Integrative
  - Multi thematic
    - Genetic
    - Genomic
    - Phenotyping
  - Multispecies





#### **User interfaces**

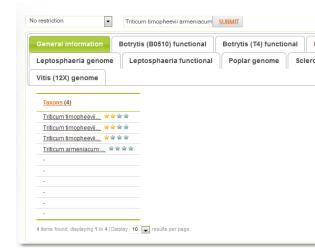
- Query, navigate, export data
  - Integrative/transversal tools
  - Thematic tools.





# User interfaces Integrative and transversal tool

- Quick search interface
  - URGI development
    - Apache Lucene : full text search
  - Google like search on GnpIS
  - Entry point for thematic tools
  - Wheat portal http://wheat-urgi.versailles.inra.fr/
- Advanced search : Biomart
  - Datamart
    - Aggregation/Computation of GnpIS core database
    - Designed for a specific questioning: fact with attributes with dimension for filtering.
  - Multicriterion based dataset building
  - Available data marts
    - Genetic maps (markers, Qtls), Polymorphisms (snps, genes), Genetic and Phenotype resources with Genes annotations
    - Grapevine stuctural and functional annotation with Genetic maps (genetic markers)
    - Wheat, stuctural annotation with Genetic maps (genetic markers..) and Polymorphisms (snps)
    - Genes functional annotation
      - Arabidopsis Thaliana TAIRV10, Zea mays ZmB73, Populus trichocarpa, Botrytis cinerea T4, Botrytis cinerea B0510, Sclerotinia sclerotiorum, Leptosphaeria maculans
- Advanced Search and pipeline: Galaxy





## Dedicated thematic interfaces Genetic

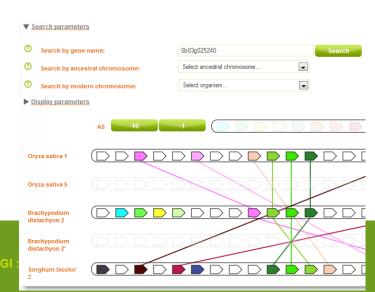
- Gene expression
- Genetic maps, markers and QTLs
  - MetaQTL
- Sequence
  - DNA Polymorphisms
  - Genotyping
  - NGS Sequence
- Phenotyping
  - Genetic ressources, passports
    - Primary phenotypes
  - Phenotyping experiment (G\*E)





## Dedicated thematic interfaces Genomic

- Gbrowse
  - Genome with annotations (partners, consortium, public)
  - Markers, SNP (URGI)
    - SNP Clustering and mapping via MapHits (URGI)
  - Transposable elements (URGI)
- Sequence Retrieval System (SRS) or Mobyle
  - Blast or Blat against URGI databanks.
- Genome Report System (GRS)
  - Gene annotation integration interface.
- Synteny viewer (URGI, GDEC J. Salse)







#### WHEAT GENOMIC RESOURCES





#### Exercise 1.1

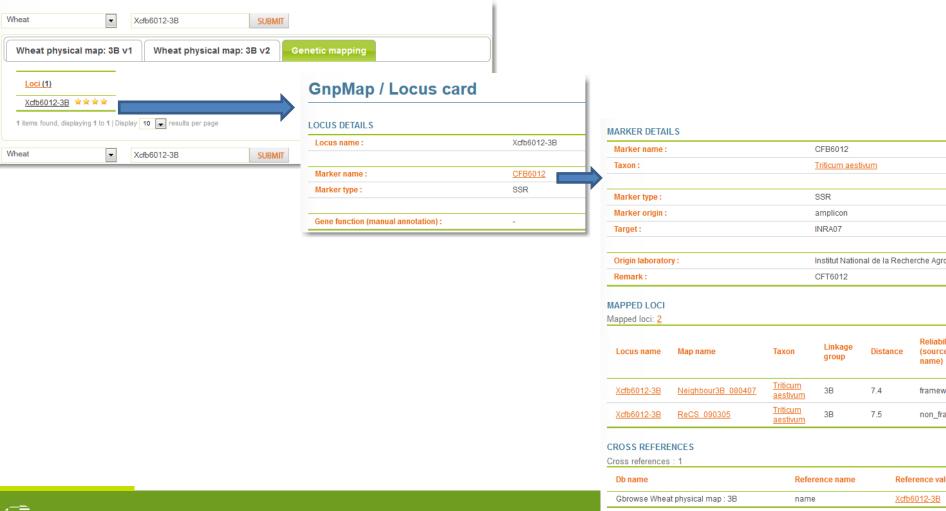
- Entry point <a href="http://wheat-urgi.versailles.inra.fr">http://wheat-urgi.versailles.inra.fr</a>
- I want all information on loci Xcfb6012-3B
  - Any marker ? If yes :
    - Type, name
    - What are the positions on the Genetic Maps?





## **Exercise 1.1, solution**

Loci Xcfb6012-3B





#### Exercise 1.2

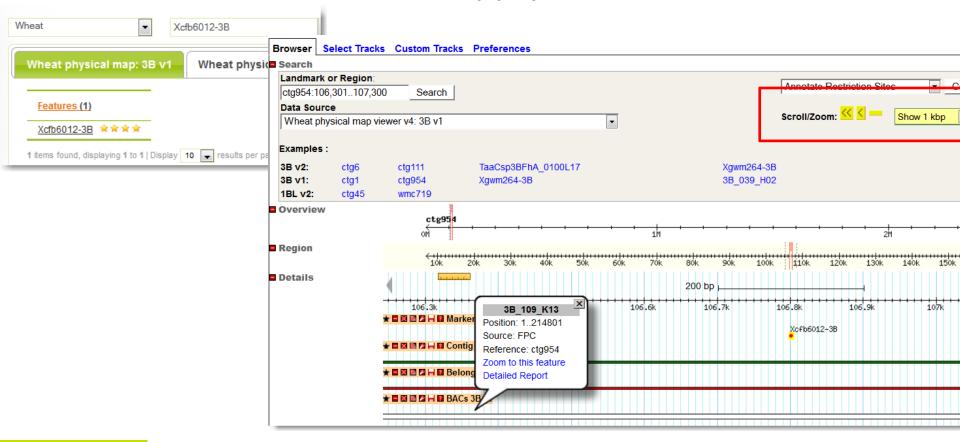
- Display loci Xcfb6012-3B 's region on 3B V1 physical Map
- Is Xcfb6012-3B 's located on any physical BAC, is there any nearby annotation?
  - Find Xcfb6012-3B contigs and deletion bin
  - Identify the First physical BAC
  - On Annotation Browser (Wheat annotation viewer v2), find one mRNA colocalised with this physical BAC and display the sequence
  - What QTL is colocalised on this BAC. What is the associated Trait?





## **Exercise 1.2, solution**

- Display loci Xcfb6012-3B 's region on 3B V1 physical Map
- Is Xcfb6012-3B 's located on any physical BAC?







Exe

Overview

Region

Details

Search

Landmark or Region:

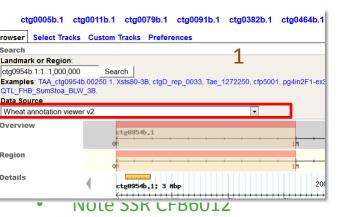
QTL\_FHB\_SumStoa\_BLW\_3B.

ctg0954b.1:2,865,343..3,097,( Search

Select Tracks Custom Tracks Preferences

Examples: TAA ctg0954b.00250.1, Xsts80-3B, ctgD rep 0033, Tae 1272250, cfp5001, pg4in2F1-ex3R1, cfb6001,

- Is Xcfb6012-3B 's located on any physical BAC, is there any nearby annotation?
- Copy / paste3B\_109\_K13 in Landmark



previously colocalised with Xcfb6012-3B

QTL name	4 QTL_FHB_Su	QTL_FHB_SumStoa_BLW_3B		
QTL detection	composite int	erval mapping		
Measure	FHB SumSto	a BLW		
Experimentation	SumStoa BL\	<u>V</u>		
Trait name	<u>FHB</u>			



**Data Source** Wheat annotation viewer v2 Overview ctg0954b.1 Region Details k 2860k 2870k 2880k 2890k 2900k 2910k 2920k 2930k 2940k 2950k 2950k 2970k 2980k 2990k 3000k 3010k ★ ■ 🖾 🖾 🗷 🛏 🔟 DIP allele tower (GnpSNP) ★■図園□H□ SNP (GnpSNP) ★■■ □ H ■ SNP allele tower (GnpSNP) ★ ■ 🖾 🖾 🗗 🗷 DIP (GnpSNP) \* E M M Z H M BAC TAA\_ctg0954b.00470.1 is a mRNA spanning from 2931924 to 2935328. Click for more details ★ ■ 🛛 🖾 🗷 🛏 🖪 Contig ★ ■ 🖾 🖾 🗗 🗎 mRNA ★ ■ 図 図 図 H 図 ISBP cfp5071 cfp5072 \* E M M Z H M SSR cfb6013 cfb6009 cfb6007 cfb6018 3062 cfb6010 cfb6012 ctg0954b.1 ★ ■ 🛛 🗗 🗗 QTL ★ ■ M M DIP allele tower (GnpSNP) ★■図図□H■ SNP (GnpSNP) QTL\_FHB\_SumStoa\_BLW 3B ★ ■ 🛮 🗗 🗗 SNP allele\_tower (GnpSNP) Positions: 2108439 .. 3109940 ★ ■ 🖾 🖾 🗗 🖊 DIP (GnpSNP) Length: 1001502 Zoom to this feature ★ ■ 図 図 図 H 図 BAC **Detailed Report** 3B\_109\_K13 Link to GnpMap ★ 🖿 🖾 🖾 🗷 🛏 🔟 Contig

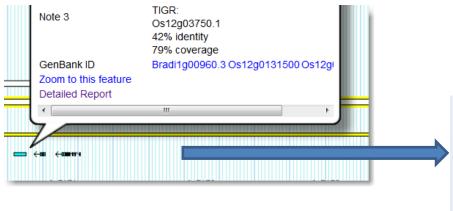
Download Decorated FA

Cyril Pommier / Genomic, genetic a



#### **Private**

- Consortium private area
- Free registration from wheat web site
  - http://wheat-urgi.versailles.inra.fr/Register
- Blast : SRS
- A quick tour
  - Sytneny viewer
  - Wheat dedicated portal



```
● Paste/Create your own sequence(s) or type in the sequence ID(s):

TCAGCTTACC AGTATAATTA CAGATTCAAG CTTGTTAAGT
AGAAATTCTT TTCTCCCCTC AGTGCAAGTT ATTGAAATCG
CCCATATAGA GGACCATTAT TTTACCCCAG AGCAGGAGGA
ATGGTTTGAA CAACTAACCT CTGTCGAAAA AATTGTGTTT
GATAATTGTT ATTTCTTGA ACGACTCCCT TCTACACTAG
GCAGACTCGC CTCCTTAAAG GTACTTCATA TCATGACAAA
ACCAGTGGCC CTCCTTAAAG GTACTTCATA TCATGACAAA
ACCAGTGGCC CCGAGAGAAA ATTTTCCACA GAAACTCCAA
GAATTTATTA TGCATGGATT TCCAGTTGAG GCAGAAAATG
ATTTCAAACC TGGAGGATCA GCTTGGATAA ACCATTCTCA
TGTTCCATAC ATCCGTCTTA ATGGGAAGAC GATCCAAAAT
CCGACAAATGG ATGCTGCCTC ATCGTCTTCA AACCAACAAA TTTGA

Save my sequence in USERDNA
```



#### PART II, GENETIC RESOURCES AND PHENOTYPING



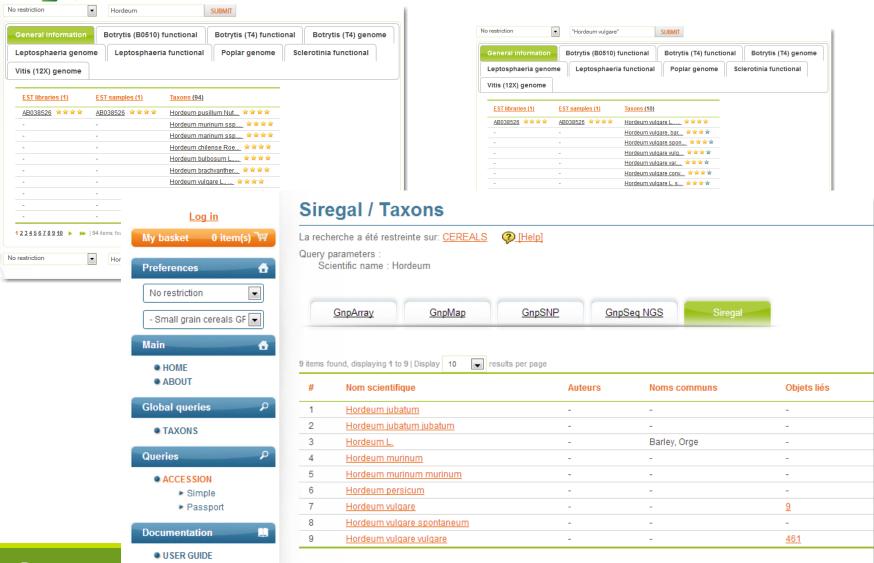


#### Exercise 2.1

- Important: be careful not to accidently order semences on Siregal interfaces.
- I want to study Hordeum vulgare.
  - What are the available resources on Hordeum genus?
  - What are the available subspecies (Siregal thematic interface recommended)



## Exercise 2,1, solution





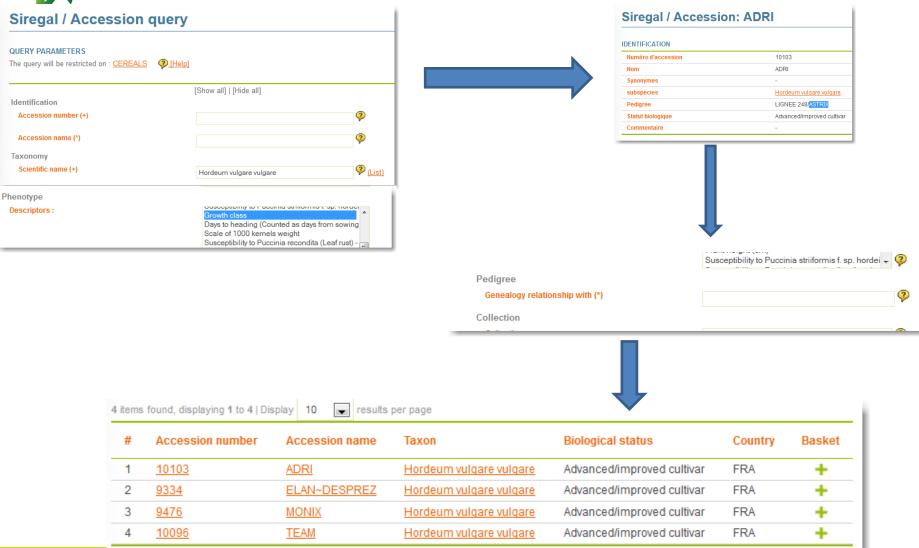
#### Exercise 2.2

- Is there any winter cultivar for Hordeum vulgare vulgare?
  - What is Adri cultivar pedigre/genealogy?
  - What are the Accessions related to Astrix ?





## Exercise 2.2, solution







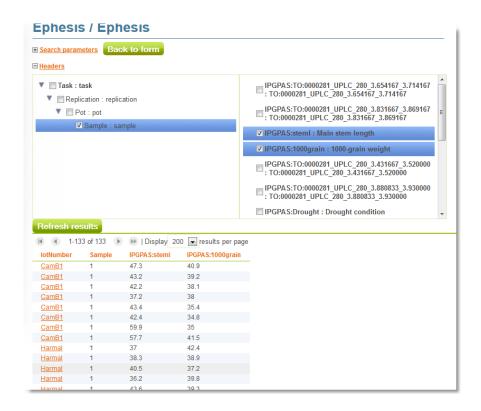
#### **Exercise 2.3**

- Find Hordeum related experimental data.
  - Ephesis thematic interface recomended
- Export sample ID, steml and 1000grain data for Harmal and CamB1





#### **Exercise 2.3 solution**





#### **PART 3: DATA SET BUILDING WITH BIOMARTS**





#### Exercise 3.1

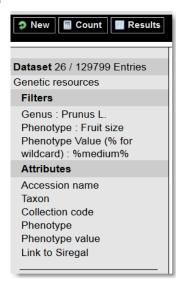
- Siregal thematic interface limitation
  - Growth class annotated data filter only.
  - To add value filter
    - Biomart now
    - Planned devlopment for siregal thematic interface
- Go to Biomart
  - http://urgi.versailles.inra.fr/biomart/martview/300678dcd6dcb13b10e1d c6b318d6a84
  - Choose genetic resources dataset
- I want all Spring accession of genus triticum
  - Growth class = %Spring%





#### **Exercise 3.3**

- Genetic resources dataset Phenotypes are Primary phenotypes
  - Constant for all individuals
  - Assumed more or less independant from the environment
  - Fruit size, fruit color, Mean LAI, etc...
- I want to study the variability of Primary phenotypes in experiments.
  - Prunus has a lot of public data
  - Exercise 3.2: I want all prunus with medium fruit size.
  - Exercise 3.3: Get all experiment data







### **Exercise 3.3 solution**

New Count Results								<b>☆</b> URL	
ataset 26 / 129799 Entries	Export all results to		File ▼ XLS ▼ ☑ Unique results only ② Go						
enetic resources	Email notification to								
Genus : Prunus L. Phenotype : Fruit size Phenotype Value (% for wildcard) : %medium%	View		150 rows as HTML -	Unique res	sults only				
	Accession name	Taxon	Collection code	Phenotype	Phenotype value	Link to Siregal	Phenotype	Phenoty value	
Attributes	Madame Guttin	Prunus domestica L.	PLUM_NATIONAL_COLLECTION	Fruit size	medium   moyen	13891	Fruit flesh color, L* value		
Accession name Taxon	Madame Guttin	Prunus domestica L.	PLUM_NATIONAL_COLLECTION	Fruit size	medium   moyen	13891	Fruit width		
Collection code	Quetsche verte	Prunus domestica L.	PLUM_NATIONAL_COLLECTION	Fruit size	medium   moyen	13944	Fruit weight		
Phenotype Phenotype value Link to Siregal	Quetsche verte	Prunus domestica L.	PLUM_NATIONAL_COLLECTION	Fruit size	medium   moyen	13944	Fruit width	33.9915	
	Ovale jaune	Prunus domestica L.	PLUM_NATIONAL_COLLECTION	Fruit size	medium   moyen	13947	Fruit flesh color, b* value		
ntaset 1101 / 20584 Entries nenotype ressources Filters Taxons : Prunus domestica,Prunus insititia L.	Ovale jaune	Prunus domestica L.	PLUM_NATIONAL_COLLECTION	Fruit size	medium   moyen	13947	Fruit cracking percentage	0.05	
	Ovale jaune	Prunus domestica L.	PLUM_NATIONAL_COLLECTION	Fruit size	medium   moyen	13947	Fruit flesh color, a* value	6.5137315	
	Verdanne	Prunus domestica L.	PLUM_NATIONAL_COLLECTION	Fruit size	medium   moyen	<u>13905</u>	Fruit weight	34.425	
	Verdanne	Prunus domestica L.	PLUM_NATIONAL_COLLECTION	Fruit size	medium   moyen	<u>13905</u>	Fruit weight		
Phenotype Name : Fruit cracking percentage,Fruit flesh	Verdanne	Prunus domestica L.	PLUM_NATIONAL_COLLECTION	Fruit size	medium   moyen	<u>13905</u>	Fruit weight	25.975	
color, L* value,Fruit flesh color, a* value,Fruit flesh color, b*	Verdanne	Prunus domestica L.	PLUM_NATIONAL_COLLECTION	Fruit size	medium   moyen	<u>13905</u>	Fruit flesh color, b* value		
value,Fruit height,Fruit weight,Fruit width	Verdanne	Prunus domestica L.	PLUM_NATIONAL_COLLECTION	Fruit size	medium   moyen	<u>13905</u>	Fruit height	40.082	
Attributes	Verdanne	Prunus domestica L.	PLUM_NATIONAL_COLLECTION	Fruit size	medium   moyen	<u>13905</u>	Fruit cracking percentage	0	
Phenotype Phenotype value Scientific name	Berudge	Prunus domestica L.	PLUM_NATIONAL_COLLECTION	Fruit size	medium   moyen	13917	Fruit weight	28.818182	
	Reine-Claude Davion	Prunus domestica	PLUM_NATIONAL_COLLECTION	Fruit size	medium   moyen	<u>13895</u>	Fruit weight	23.3	





## **GnpIS Perspectives**

- Data
  - 8 years of Triticea French phenotyping experiments (novembre)
  - Private data for national projects.
  - Wheat for all thematics
- Development
  - Improved searching capabilities
    - Project driven (10 national projects)
    - Thematic
    - Transversal entry point
  - Association genetic
  - Integration with Distributed search systems: Transplant.
  - Integration with Phenome, Ephesis as an integrative portal for FPPN.

