



# **WheatIS DataDiscovery**



## **AgBioData**

Toward enhanced genomics, genetics, and breeding research outcomes through standardization of practices and protocols across agricultural databases

- V
- Please keep your microphone muted and your webcam off
- rec
- Notice that the webinar will be recorded
- 0
- Ask your questions in the chat
- **①**
- The presentation and the recorded video will be available





## **Outline**

- ☐ The WheatIS project
- ☐ WheatIS DataDiscovery: behind the scene
- □ Data providers & data exchange format
- ☐ WheatIS DataDiscovery web interface: live demo
- ☐ Beyond WheatIS: other species (FAIDARE)
- ☐ How to contribute
- Perspectives
- □ Q&A session





Created in 2011 following endorsement from the G20 Agriculture Ministries, the Wheat Initiative provides a framework to establish strategic research and organisation priorities for wheat research at the international level.



ABOUT EVENTS FUNDING INC NEWS PUBLICATIONS RESOURCES

WHEAT INFORMATION SYSTEM



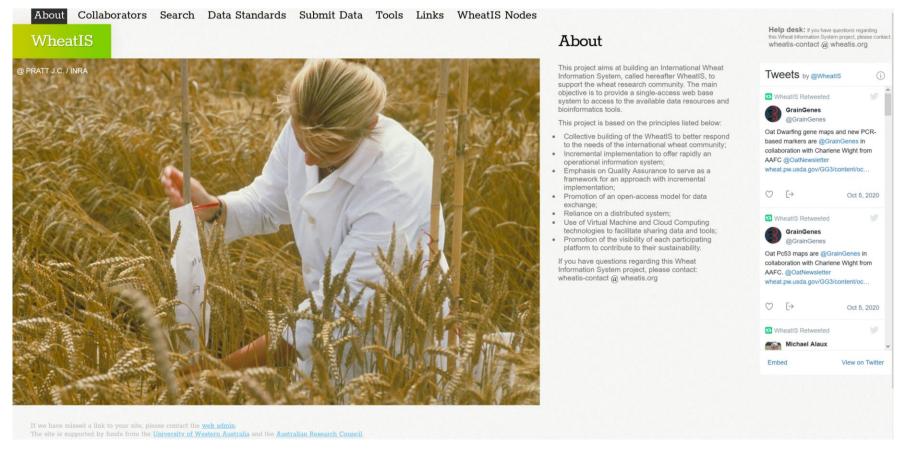
The Wheat Initiative endorsed the WheatIS Expert Working group in 2013.

Leadership team in 2020:

Chair: Taner Sen (USDA-ARS & Iowa State University)
Co-Chair: Hadi Quesneville (INRAE, FR), Mario
Caccamo (NIAB, UK), David Edwards (University of Western Australia)



The WheatIS project aims at building an International Wheat Information System to support the wheat research community.







In this paper, we present our experience, the challenges we faced, and the answer we brought for establishing an international research community to build an informational infrastructure. Our hope is that our experience with building wheatis.org will guide current and future research communities to facilitate institutional and international challenges to

Community paper published in 2020

### Keywords

WheatIS, community, data sharing, bioinformatics, wheat

create global tools and resources to help their respective scientific communities



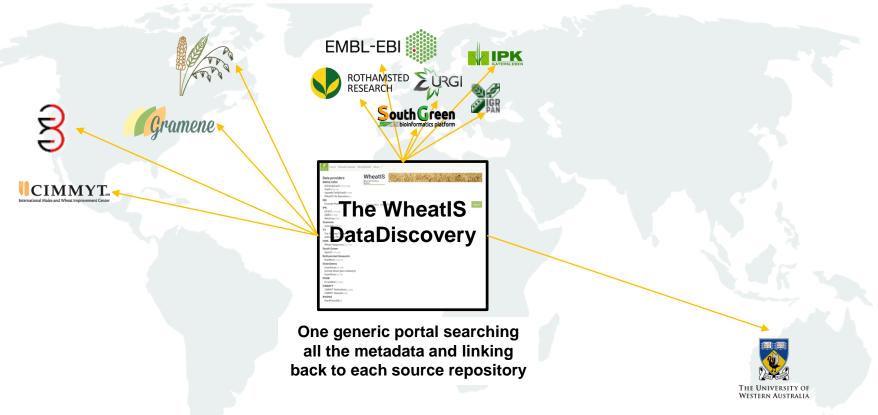
The main objective is to provide a single-access web based system to access to the available data resources and bioinformatics tools. A federated plant data portal is needed because plant data with valuable information are published in dispersed data repository.





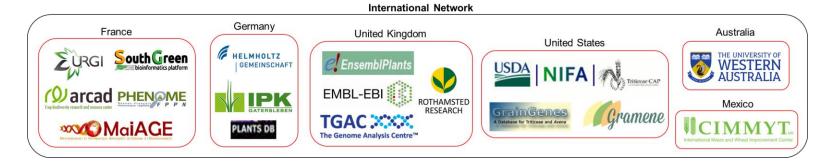


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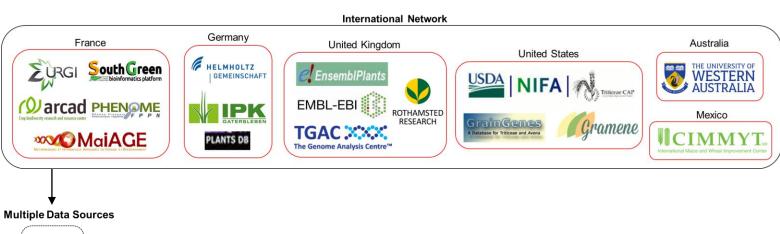








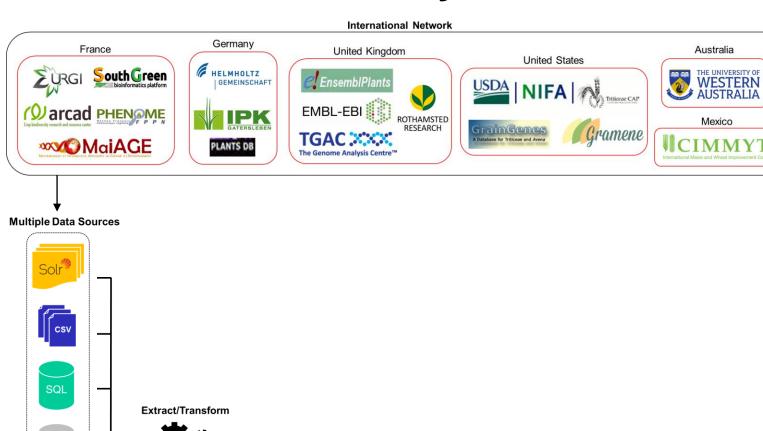








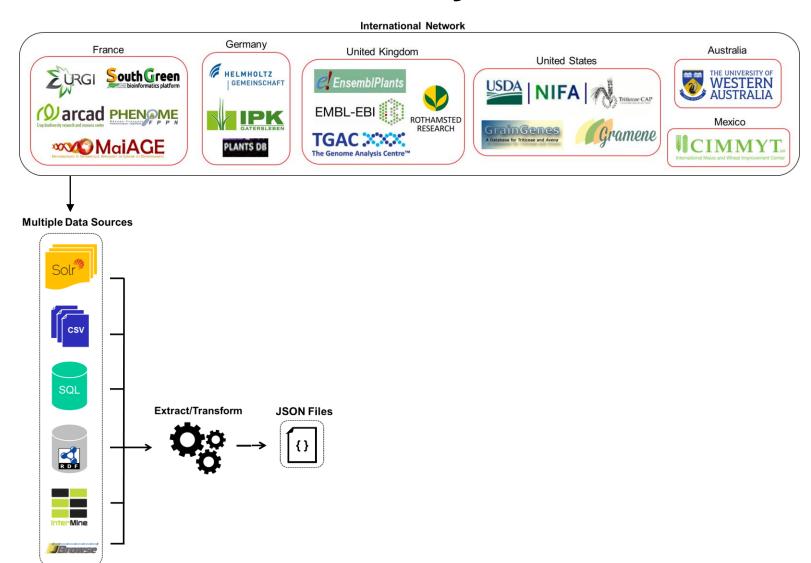
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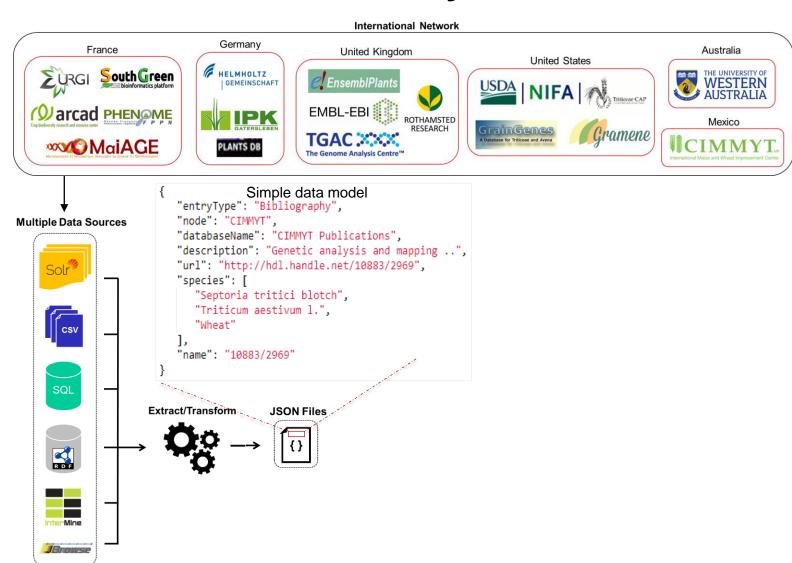


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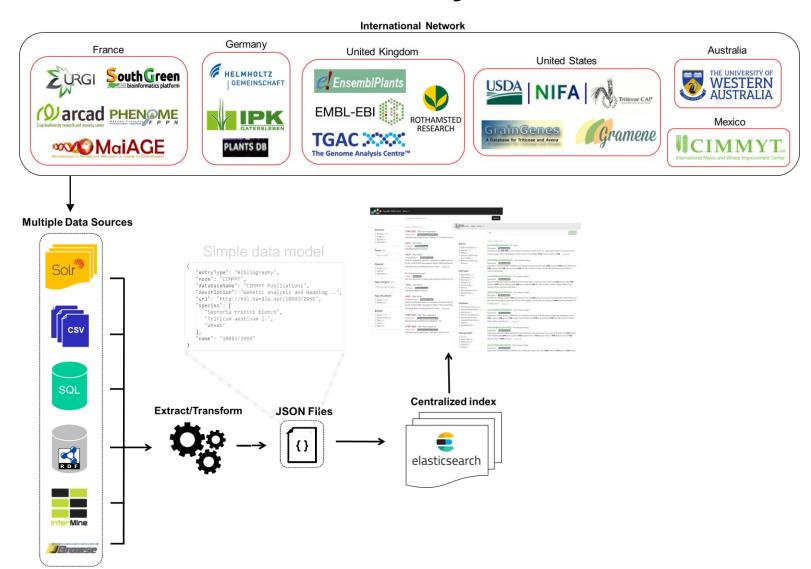
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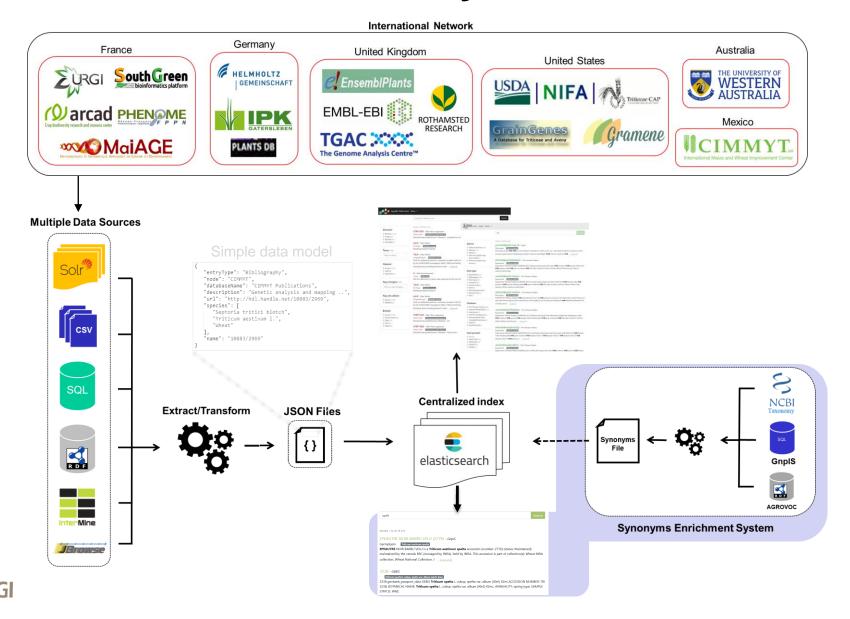


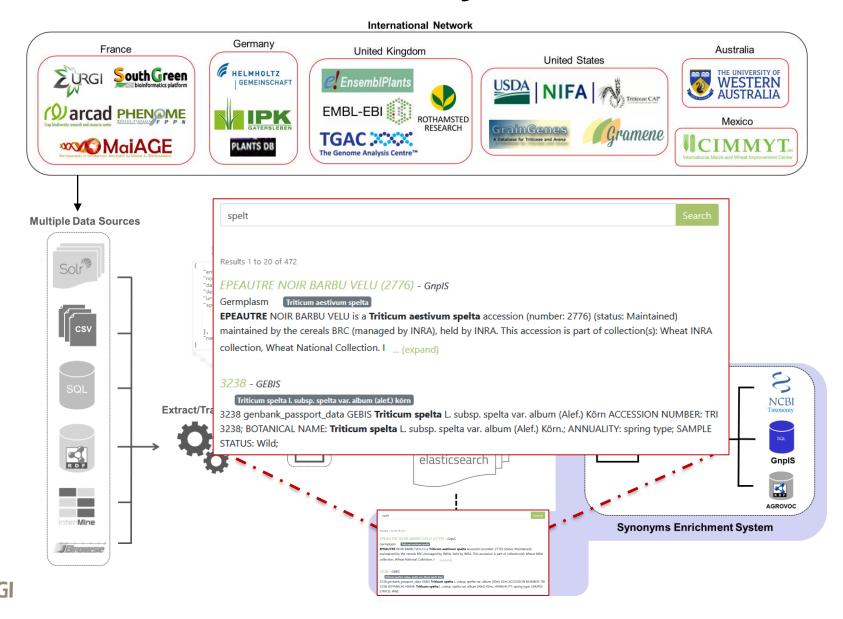


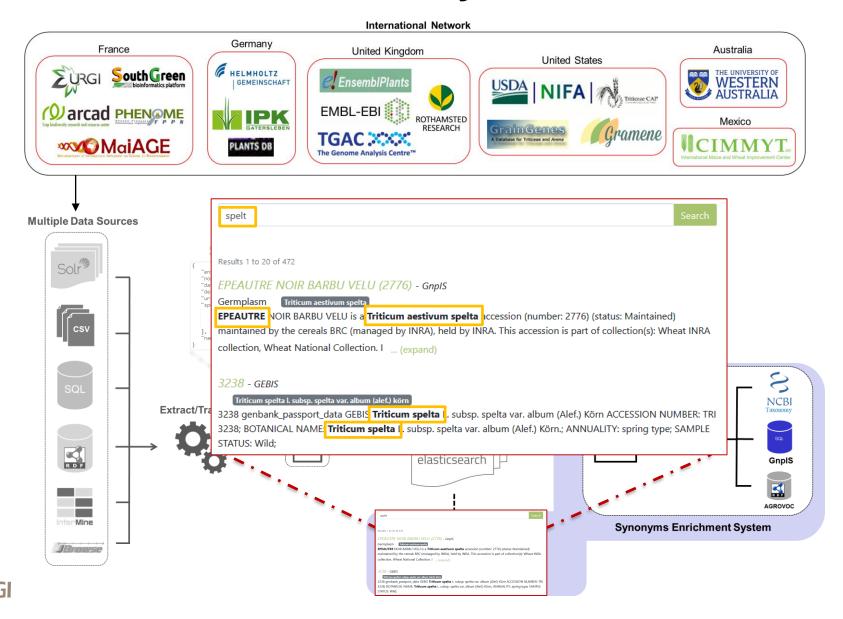












## Data providers

INRAF-URGI IWGSC@GnpIS [19 195 264] GnpIS [642 142] OpenMinTeD@GnpIS [1 589] WheatIS File Repository [6] FBI Ensembl Plants [1 168 762] IPK CR-EST [199 220] GEBIS [51302] MetaCrop [355] Gramene Gramene [229 851] T3 The Triticeae Toolbox [206 406] UniProt by T3 [16 607]

UWA Wheat Pangenome [167 167] South Green AgroLD [137 060] Rothamsted Research KnetMiner [108 474] GrainGenes GrainGenes [20 190] Komugi wheat gene catalog by GrainGenes [3 119] PGSB CrowsNest [13 324] CIMMYT CIMMYT Publications [1 605] CIMMYT Datasets [183] **IPGPAS** PlantPhenoDB [6]



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UniProt by T3 [16 607]

Genome annotation [14 176 618]

Gene annotation [3 170 532]

Physical map feature [2 157 405]

Marker [314390]

Germplasm [10448]

Repeat reference [6671]

Bibliography [1589]

Phenotyping study [821]

Other results are available. Refine your search **UWA** 

Wheat Pangenome [167 167]

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Data type

☐ Genome
annotation [1 168 762]

UWA Wheat Pangenome [167 167] South Green AgroLD [137 060] Rothamsted Research KnetMiner [108 474] GrainGenes GrainGenes [20 190] Komugi wheat gene catalog by GrainGenes [3 119] PGSB CrowsNest [13 324] CIMMYT CIMMYT Publications [1 605] CIMMYT Datasets [183] **IPGPAS** PlantPhenoDB [6]



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☐ Germplasm [556]
Gene [6]
☐ Genetic map [3]
☐ Bibliography [1]
☐ Interpro family [1]
☐ Repeat reference [1]

## UWA Wheat Pangenome [167 167] South Green AgroLD [137 060] Rothamsted Research KnetMiner [108 474] GrainGenes GrainGenes [20 190] Komugi wheat gene catalog by GrainGenes [3 119] PGSB CrowsNest [13 324] CIMMYT CIMMYT Publications [1 605] CIMMYT Datasets [183] **IPGPAS**



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Gene [215 134]

Go process [4287]

Interpro family [3 289]

Interpro domain [3 039]

Go function [2088]

Go component [723]

Reaction [502]

Interpro conserved\_site [357]

Other results are available. Refine your search. **UWA** 

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- ☐ Genetic map [147]
- ☐ Physical map [12]
- ☐ Bibliography [3]

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# Data exchange format

## Field

- name
- url
- description
- entryType
- species
- node
- databaseName

## Status

- mandatory

## Cardinality

- 1
- 1
- 1
- 1
- 1-\*
- 1
- 1

## Constraints

- unique
- none
- none
- cf. list in doc, recom.
- cf. Species list below
- same for all a dataset
- none
- WheatIS species list: Aegilops\*, Hordeum\*, Triticum\*, Wheat\*
- Format: JSON or TSV, as you wish!
- Web server: HTTP of FTP, as you wish!
- The up-to-date format is always available at <a href="https://urgi.versailles.inrae.fr/wheatis/join">https://urgi.versailles.inrae.fr/wheatis/join</a>



# https://urgi.versailles.inrae.fr/wheatis/



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IWGSC@GnpIS [19,195,264]

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OpenMinTeD@GnpIS [1,589]

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Examples: yield, fhb

Search

## Demo time!



## CFD2

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OpenMinTeD@GnpIS [1,589]

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Wheat Information System



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Wheat Information **S**ystem



Examples: yield, fhb

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# **WheatIS**

Wheat Information System



cfd

Searcl

cfd

cfd014

cfd046

**cfd**066

**cfd**069

cfd1

cfd1-2

cfd10

cfd101

cfd101\_5d



Species  ☐ Triticum aestivum [8] ☐ Aegilops tauschii [1] ☐ Triticum aestivum aestivum [1]
Data type  ☐ Gene annotation [4] ☐ Physical map feature [3] ☐ Marker [2] ☐ Genome annotation [1]
Ontology annotation  Aucun [10]  Expand search
Database  ☐ IWGSC@GnpIS [8]  ☐ GnpIS [2]
Data provider  ☐ INRAE-URGI [10]

Results 1 to 10 of 10

# cfd2 - IWGSC@GnpIS

Physical map feature Triticum aestivum

Physical map feature IWGSC@GnpIS **cfd2 cfd2** is a marker (type=marker, source=FPC) of Triticum aestivum located between positions 189601 and 189601 and which properties are Name=**cfd2**,Contig\_hit=ctg2725 - 2 (TaaCsp3DShA\_0070A24 TaaCsp3DShA\_0079J22) Triticum a ... (expand)

# JBrowse\_chr5D\_517967021\_517967269\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr5D\_517967021\_517967269\_CFD\_SSR\_TRIMMED Start = 517967021, End = 517967269, Strand = 0, Source = ePCR, Seq\_id = chr5D, Size = 247, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(9) Triticum aestivum similari ... (expand)

# JBrowse\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED Start = 7333656 , End = 7333940 , Strand = 0 , Source = ePCR , Seq\_id = chr4A , Size = 283 , Marker = **CFD2** , Id = **CFD2** , Type = similarity , Motif = ca(11) Triticum aestivum similarity chr4 \_\_\_ (expand)

# JBrowse\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED Start = 100120355, End = 100120651, Strand = 0, Source = ePCR, Seq\_id = chr2A, Size = 295, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(10) Triticum aestivum similar ... (expand)

# CFD2 - IWGSC@GnpIS

Genome annotation Triticum aestivum



Species  ☑ Triticum aestivum [8] ☐ Aegilops tauschii [1] ☐ Triticum aestivum aestivum [1]
Data type  ☐ Gene annotation [4] ☐ Physical map feature [3] ☐ Genome annotation [1]
Ontology annotation  Aucun [8] Expand search
Database  □ IWGSC@GnpIS [8]
Data provider

☐ INRAE-URGI [8]

Results 1 to 8 of 8

# cfd2 - IWGSC@GnpIS

Physical map feature Triticum aestivum

Physical map feature IWGSC@GnpIS **cfd2 cfd2** is a marker (type=marker, source=FPC) of Triticum aestivum located between positions 189601 and 189601 and which properties are Name=**cfd2**,Contig\_hit=ctg2725 - 2 (TaaCsp3DShA\_0070A24 TaaCsp3DShA\_0079J22) Triticum a ... (expand)

# JBrowse\_chr5D\_517967021\_517967269\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr5D\_517967021\_517967269\_CFD\_SSR\_TRIMMED Start = 517967021, End = 517967269, Strand = 0, Source = ePCR, Seq\_id = chr5D, Size = 247, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(9) Triticum aestivum similari ... (expand)

# JBrowse\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED Start = 7333656 , End = 7333940 , Strand = 0 , Source = ePCR , Seq\_id = chr4A , Size = 283 , Marker = **CFD2** , Id = **CFD2** , Type = similarity , Motif = ca(11) Triticum aestivum similarity chr4 ... (expand)

# JBrowse\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED Start = 100120355, End = 100120651, Strand = 0, Source = ePCR, Seq\_id = chr2A, Size = 295, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(10) Triticum aestivum similar ... (expand)

# CFD2 - IWGSC@GnpIS

Genome annotation Triticum aestivum



# Species

☑ Triticum aestivum [4]

# Data type

- ☑ Gene annotation [4]
- ☐ Physical map feature [3]
- ☐ Genome annotation [1]

# Ontology annotation

Aucun [4]

# Database

☐ IWGSC@GnpIS [4]

# Data provider

☐ INRAE-URGI [4]

### Results 1 to 4 of 4

# JBrowse chr5D 517967021 517967269 CFD SSR TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr5D\_517967021\_517967269\_CFD\_SSR\_TRIMMED Start = 517967021, End = 517967269, Strand = 0, Source = ePCR, Seq\_id = chr5D, Size = 247, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(9) Triticum aestivum similari ... (expand)

# JBrowse\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED Start = 7333656 , End = 7333940 , Strand = 0 , Source = ePCR , Seq\_id = chr4A , Size = 283 , Marker = CFD2 , Id = CFD2 , Type = similarity , Motif = ca(11) Triticum aestivum similarity chr4 ... (expand)

# JBrowse\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED Start = 100120355, End = 100120651, Strand = 0, Source = ePCR, Seq\_id = chr2A, Size = 295, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(10) Triticum aestivum similar ... (expand)

# JBrowse\_chr7D\_631739332\_631739579\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr7D\_631739332\_631739579\_CFD\_SSR\_TRIMMED Start = 631739332, End = 631739579, Strand = 0, Source = ePCR, Seq\_id = chr7D, Size = 246, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(19) Triticum aestivum similar ... (expand)



Species ☑ Triticum aestivum [4] Intersection (AND query) Data type ☑ Gene annotation [4] ☐ Physical map feature [3] ☐ Genome annotation [1] Ontology annotation Aucun [4] Database ☐ IWGSC@GnpIS [4] Data provider ☐ INRAE-URGI [4]

Results 1 to 4 of 4

# JBrowse chr5D 517967021 517967269 CFD SSR TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr5D\_517967021\_517967269\_CFD\_SSR\_TRIMMED Start = 517967021, End = 517967269, Strand = 0, Source = ePCR, Seq\_id = chr5D, Size = 247, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(9) Triticum aestivum similari ... (expand)

# JBrowse\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED Start = 7333656 , End = 7333940 , Strand = 0 , Source = ePCR , Seq\_id = chr4A , Size = 283 , Marker = CFD2 , Id = CFD2 , Type = similarity , Motif = ca(11) Triticum aestivum similarity chr4 ... (expand)

# JBrowse\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED Start = 100120355, End = 100120651, Strand = 0, Source = ePCR, Seq\_id = chr2A, Size = 295, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(10) Triticum aestivum similar ... (expand)

# JBrowse\_chr7D\_631739332\_631739579\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr7D\_631739332\_631739579\_CFD\_SSR\_TRIMMED Start = 631739332, End = 631739579, Strand = 0, Source = ePCR, Seq\_id = chr7D, Size = 246, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(19) Triticum aestivum similar ... (expand)



# CFD2

cfd2

# SELECT WHERE CONTAINS « cfd2 »

Search

AND species = « Triticum aestivum »
AND entryType = « Gene annotation »

Results 1 to 4 of 4

# JBrowse chr5D 517967021 517967269 CFD SSR TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr5D\_517967021\_517967269\_CFD\_SSR\_TRIMMED Start = 517967021, End = 517967269, Strand = 0, Source = ePCR, Seq\_id = chr5D, Size = 247, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(9) Triticum aestivum similari ... (expand)

# JBrowse\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED Start = 7333656 , End = 7333940 , Strand = 0 , Source = ePCR , Seq\_id = chr4A , Size = 283 , Marker = **CFD2** , Id = **CFD2** , Type = similarity , Motif = ca(11) Triticum aestivum similarity chr4 ... (expand)

# JBrowse\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED Start = 100120355, End = 100120651, Strand = 0, Source = ePCR, Seq\_id = chr2A, Size = 295, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(10) Triticum aestivum similar ... (expand)

# JBrowse chr7D 631739332 631739579 CFD SSR TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr7D\_631739332\_631739579\_CFD\_SSR\_TRIMMED Start = 631739332, End = 631739579, Strand = 0, Source = ePCR, Seq\_id = chr7D, Size = 246, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(19) Triticum aestivum similar ... (expand)

# Intersection (AND query) Data type ☐ Gene annotation [4] ☐ Physical map feature [3] ☐ Genome annotation [1]

# Ontology annotation

Aucun [4]

Species

# Database

☐ IWGSC@GnpIS [4]

# Data provider

☐ INRAE-URGI [4]



# Species

✓ Triticum aestivum [7]

# Data type

- ☐ Gene annotation [4]
- ☑ Physical map feature [3]
- ☐ Genome annotation [1]

# Ontology annotation

Aucun [7]

Expand search ?

# Database

☐ IWGSC@GnpIS [7]

# Data provider

☐ INRAE-URGI [7]

### Results 1 to 7 of 7

# cfd2 - IWGSC@GnpIS

Physical map feature Triticum aestivum

Physical map feature IWGSC@GnpIS **cfd2 cfd2** is a marker (type=marker, source=FPC) of Triticum aestivum located between positions 189601 and 189601 and which properties are Name=**cfd2**,Contig\_hit=ctg2725 - 2 (TaaCsp3DShA\_0070A24 TaaCsp3DShA\_0079J22) Triticum a ... (expand)

# JBrowse\_chr5D\_517967021\_517967269\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr5D\_517967021\_517967269\_CFD\_SSR\_TRIMMED Start = 517967021, End = 517967269, Strand = 0, Source = ePCR, Seq\_id = chr5D, Size = 247, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(9) Triticum aestivum similari ... (expand)

# JBrowse\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED Start = 7333656 , End = 7333940 , Strand = 0 , Source = ePCR , Seq\_id = chr4A , Size = 283 , Marker = **CFD2** , Id = **CFD2** , Type = similarity , Motif = ca(11) Triticum aestivum similarity chr4 \_\_\_ (expand)

# JBrowse\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED Start = 100120355, End = 100120651, Strand = 0, Source = ePCR, Seq\_id = chr2A, Size = 295, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(10) Triticum aestivum similar ... (expand)

# JBrowse\_chr7D\_631739332\_631739579\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr7D\_631739332\_631739579\_CFD\_SSR\_TRIMMED Start = 631739332, End = 631739579, Strand = 0, Source = ePCR, Seq\_id = chr7D, Size = 246, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(19) Triticum aestivum similar ... (expand)



cfd2

Species ☑ Triticum aestivum [7] Data type ☐ Gene annotation [4] ☑ Physical map feature [3] (OR query) ☐ Genome annotation [1] Ontology annotation Aucun [7] Database ☐ IWGSC@GnpIS [7]

Data provider

☐ INRAE-URGI [7]

Results 1 to 7 of 7

# cfd2 - IWGSC@GnpIS

Physical map feature Triticum aestivum

Physical map feature IWGSC@GnpIS cfd2 cfd2 is a marker (type=marker, source=FPC) of Triticum aestivum located between positions 189601 and 189601 and which properties are Name=cfd2, Contig\_hit=ctg2725 - 2 (TaaCsp3DShA\_0070A24 TaaCsp3DShA\_0079J22) Triticum a ... (expand)

# JBrowse chr5D 517967021 517967269 CFD SSR TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr5D\_517967021\_517967269\_CFD\_SSR\_TRIMMED Start = 517967021, End = 517967269, Strand = 0, Source = ePCR, Seq\_id = chr5D, Size = 247, Marker = CFD2, Id = CFD2, Type = similarity , Motif = gt(9) Triticum aestivum similari ... (expand)

# JBrowse chr4A 7333656 7333940 CFD SSR TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED Start = 7333656, End = 7333940 , Strand = 0 , Source = ePCR , Seq\_id = chr4A , Size = 283 , Marker = CFD2 , Id = CFD2 , Type = similarity , Motif = ca(11) Triticum aestivum similarity chr4 ... (expand)

# JBrowse\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS chr2A 100120355 100120651 CFD SSR TRIMMED Start = 100120355 , End = 100120651, Strand = 0, Source = ePCR, Seq\_id = chr2A, Size = 295, Marker = CFD2, Id = CFD2, Type = similarity , Motif = gt(10) Triticum aestivum similar ... (expand)

# JBrowse\_chr7D\_631739332\_631739579\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr7D\_631739332\_631739579\_CFD\_SSR\_TRIMMED Start = 631739332, End = 631739579, Strand = 0, Source = ePCR, Seq\_id = chr7D, Size = 246, Marker = CFD2, Id = CFD2, Type = similarity , Motif = gt(19) Triticum aestivum similar ... (expand)



Union

cfd2

# SELECT WHERE CONTAINS « cfd2 »

Search

Results 1 to 7 of 7

AND species = « Triticum aestivum »

AND (entryType = « Gene annotation »

OR entryType = « Phhysical map feature »)

results i to i oi i

cfd2 - IWGSC@GnpIS

Physical map feature Triticum aestivum

Physical map feature IWGSC@GnpIS **cfd2 cfd2** is a marker (type=marker, source=FPC) of Triticum aestivum located between positions 189601 and 189601 and which properties are Name=**cfd2**,Contig\_hit=ctg2725 - 2 (TaaCsp3DShA\_0070A24 TaaCsp3DShA\_0079J22) Triticum a ... (expand)

JBrowse chr5D 517967021 517967269 CFD SSR TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr5D\_517967021\_517967269\_CFD\_SSR\_TRIMMED Start = 517967021, End = 517967269, Strand = 0, Source = ePCR, Seq\_id = chr5D, Size = 247, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(9) Triticum aestivum similari ... (expand)

JBrowse\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED Start = 7333656 , End = 7333940 , Strand = 0 , Source = ePCR , Seq\_id = chr4A , Size = 283 , Marker = **CFD2** , Id = **CFD2** , Type = similarity , Motif = ca(11) Triticum aestivum similarity chr4 ... (expand)

JBrowse\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

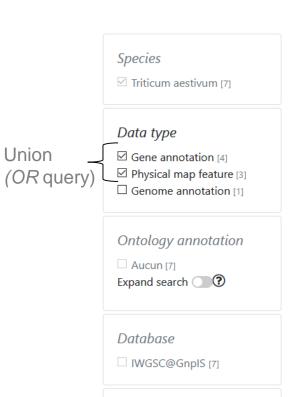
Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED Start = 100120355, End = 100120651, Strand = 0, Source = ePCR, Seq\_id = chr2A, Size = 295, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(10) Triticum aestivum similar ... (expand)

JBrowse\_chr7D\_631739332\_631739579\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr7D\_631739332\_631739579\_CFD\_SSR\_TRIMMED Start = 631739332, End = 631739579, Strand = 0, Source = ePCR, Seq\_id = chr7D, Size = 246, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = qt(19) Triticum aestivum similar ... (expand)



Data provider

☐ INRAE-URGI [7]



Species  ☐ Triticum aestivum [8] ☐ Aegilops tauschii [1] ☐ Triticum aestivum aestivum [1]
Data type  ☐ Gene annotation [4] ☐ Physical map feature [3] ☐ Marker [2] ☐ Genome annotation [1]
Ontology annotation  Aucun [10]  Expand search
Database  ☐ IWGSC@GnpIS [8]  ☐ GnpIS [2]
Data provider  ☐ INRAE-URGI [10]

Results 1 to 10 of 10

# cfd2 - IWGSC@GnpIS

Physical map feature Triticum aestivum

Physical map feature IWGSC@GnpIS **cfd2 cfd2** is a marker (type=marker, source=FPC) of Triticum aestivum located between positions 189601 and 189601 and which properties are Name=**cfd2**,Contig\_hit=ctg2725 - 2

(TaaCsp3DShA\_0070A24 TaaCsp3DShA\_0079J22) Triticum a ... (expand)

# JBrowse\_chr5D\_517967021\_517967269\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr5D\_517967021\_517967269\_CFD\_SSR\_TRIMMED Start = 517967021, End = 517967269, Strand = 0, Source = ePCR, Seq\_id = chr5D, Size = 247, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(9) Triticum aestivum similari ... (expand)

# JBrowse\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED - **IWGSC@GnpIS**

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED Start = 7333656 , End = 7333940 , Strand = 0 , Source = ePCR , Seq\_id = chr4A , Size = 283 , Marker = **CFD2** , Id = **CFD2** , Type = similarity , Motif = ca(11) Triticum aestivum similarity chr4 ... (expand)

# JBrowse chr2A 100120355 100120651 CFD SSR TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED Start = 100120355, End = 100120651, Strand = 0, Source = ePCR, Seq\_id = chr2A, Size = 295, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(10) Triticum aestivum similar ... (expand)

# CFD2 - IWGSC@GnpIS

Genome annotation Triticum aestivum



Species
☐ Triticum aestivum [8]
☐ Aegilops tauschii [1]
☐ Triticum aestivum
aestivum [1]
Data type
☐ Gene annotation [4]
☐ Physical map feature [3]
☐ Marker [2]
☐ Genome annotation [1]
Ontology annotation
☐ Aucun [10]
Expand search
Expand search
Database
☐ IWGSC@GnpIS [8]
☐ GnpIS [2]
Data provider
☐ INRAE-URGI [10]

Results 1 to 10 of 10

# cfd2 - IWGSC@GnpIS

Physical map feature Triticum aestivum

Physical map feature IWGSC@GnpIS **cfd2 cfd2** is a marker (type=marker, source=FPC) of Triticum aestivum located between positions 189601 and 189601 and which properties are Name=**cfd2**,Contig\_hit=ctg2725 - 2

(TaaCsp3DShA\_0070A24 TaaCsp3DShA\_0079J22) Triticum a ... (expand)

# JBrowse\_chr5D\_517967021\_517967269\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr5D\_517967021\_517967269\_CFD\_SSR\_TRIMMED Start = 517967021, End = 517967269, Strand = 0, Source = ePCR, Seq\_id = chr5D, Size = 247, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(9) Triticum aestivum similari ... (expand)

# JBrowse\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr4A\_7333656\_7333940\_CFD\_SSR\_TRIMMED Start = 7333656 , End = 7333940 , Strand = 0 , Source = ePCR , Seq\_id = chr4A , Size = 283 , Marker = **CFD2** , Id = **CFD2** , Type = similarity , Motif = ca(11) Triticum aestivum similarity chr4 ... (expand)

# 

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED Start = 100120355, End = 100120651, Strand = 0, Source = ePCR, Seq\_id = chr2A, Size = 295, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(10) Triticum aestivum similar ... (expand)

# CFD2 - IWGSC@GnpIS

Genome annotation Triticum aestivum



# Species

☐ Triticum aestivum [8]

☐ Aegilops tauschii [1]

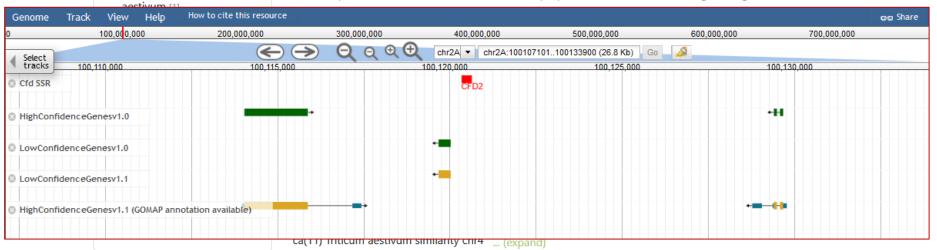
☐ Triticum aestivum

Results 1 to 10 of 10

# cfd2 - IWGSC@GnpIS

Physical map feature Triticum aestivum

Physical map feature IWGSC@GnpIS **cfd2 cfd2** is a marker (type=marker, source=FPC) of Triticum aestivum located between positions 189601 and 189601 and which properties are Name=**cfd2**,Contig\_hit=ctg2725 - 2



# Database

☐ IWGSC@GnpIS [8]

GnpIS [2]

# Data provider

☐ INRAE-URGI [10]

# JBrowse\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

Gene annotation Triticum aestivum

SEQUENCE FEATURE IWGSC@GnpIS\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED Start = 100120355, End = 100120651, Strand = 0, Source = ePCR, Seq\_id = chr2A, Size = 295, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(10) Triticum aestivum similar ... (expand)

# CFD2 - IWGSC@GnpIS

Genome annotation Triticum aestivum



# **Species**

☐ Triticum aestivum [8]

☐ Aegilops tauschii [1]

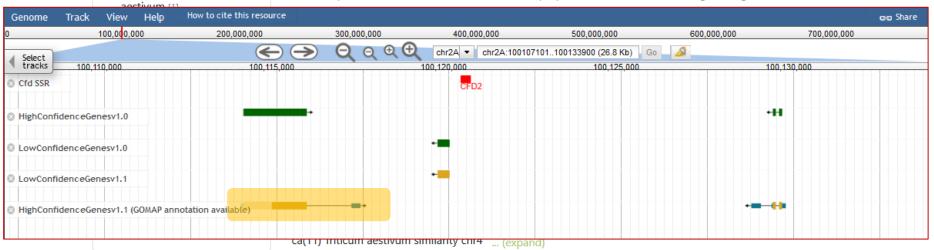
☐ Triticum aestivum

Results 1 to 10 of 10

# cfd2 - IWGSC@GnpIS

Physical map feature Triticum aestivum

Physical map feature IWGSC@GnpIS **cfd2 cfd2** is a marker (type=marker, source=FPC) of Triticum aestivum located between positions 189601 and 189601 and which properties are Name=**cfd2**,Contig\_hit=ctg2725 - 2



# Database

☐ IWGSC@GnpIS [8]

☐ GnpIS [2]

# Data provider

☐ INRAE-URGI [10]

# JBrowse\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED - IWGSC@GnpIS

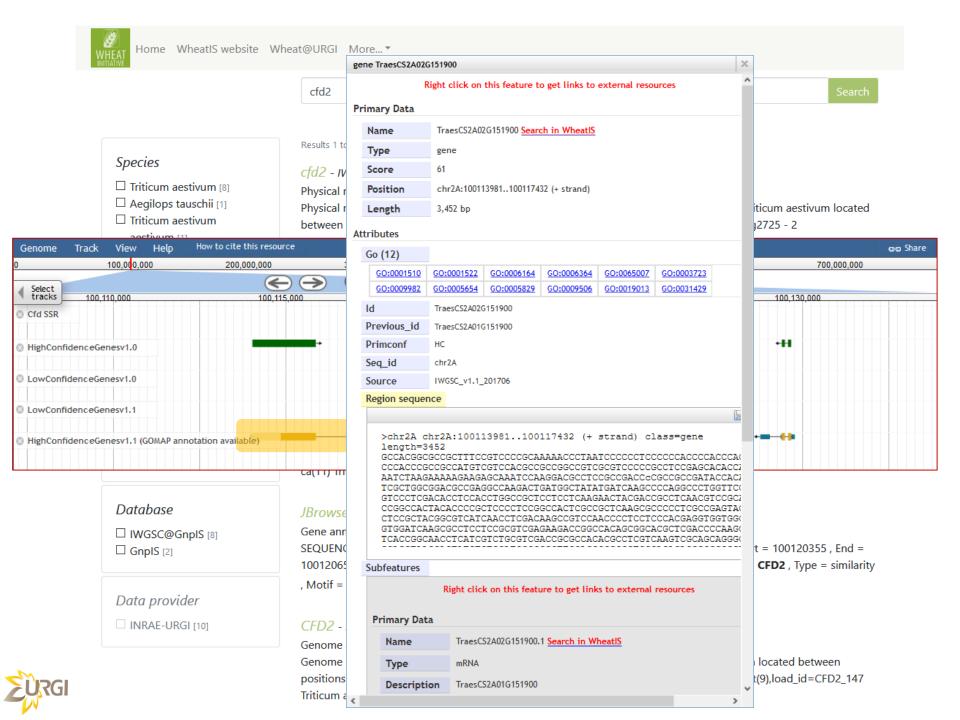
Gene annotation Triticum aestivum

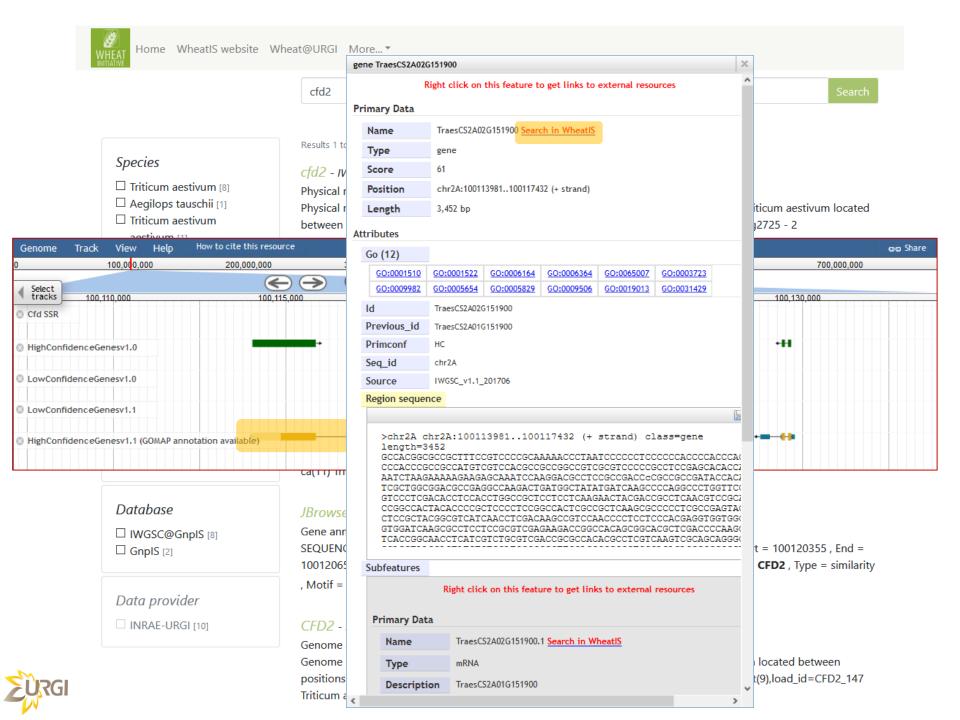
SEQUENCE FEATURE IWGSC@GnpIS\_chr2A\_100120355\_100120651\_CFD\_SSR\_TRIMMED Start = 100120355, End = 100120651, Strand = 0, Source = ePCR, Seq\_id = chr2A, Size = 295, Marker = **CFD2**, Id = **CFD2**, Type = similarity, Motif = gt(10) Triticum aestivum similar ... (expand)

# CFD2 - IWGSC@GnpIS

Genome annotation Triticum aestivum







TraesCS2A02G151900 Search

Species  ☐ Triticum aestivum [3]
Data type  ☐ Genome annotation [2] ☐ Gene annotation [1]
Ontology annotation  Aucun [3] Expand search
Database  ☐ Ensembl Plants [1] ☐ IWGSC@GnpIS [1] ☐ KnetMiner [1]
Data provider  ☐ EBI [1] ☐ INRAE-URGI [1] ☐ Rothamsted Research [1]

Results 1 to 3 of 3

chr2A:100113980..100117432 - IWGSC@GnpIS

Genome annotation Triticum aestivum

Genome annotation IWGSC@GnpIS chr2A:100113980..100117432 Start = 100113980, End = 100117432, Strand = 1, Source = IWGSC\_v1.1\_201706, Previous\_id = TraesCS2A01G151900, Seq\_id = chr2A, Name =

TraesCS2A02G151900 , Score = 61 , Primconf = HC , Type = gen ... (expand)

wheatknet:TRAESCS2A02G151900 - KnetMiner

Gene annotation Triticum aestivum

Gene ID **TRAESCS2A02G151900** has alternative name(s): **TRAESCS2A02G151900**, Start position 100113981 and End position 100117432 on Chromosome 2A, The species is 'Triticum aestivum' (https://eutils.ncbi.nlm.nih.gov/entrez/eutils/esummary.fcgi?db=taxonomy&id=456 ... (expand)

TraesCS2A02G151900 - Ensembl Plants

Genome annotation Triticum aestivum

Uncharacterized protein At3g57150 (Fragment) [Source:Projected from Arabidopsis thaliana (AT3G57150)

UniProtKB/TrEMBL;Acc:COSVF3] feature type = protein\_coding



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TraesCS2A02G151900 - Ensembl Plants

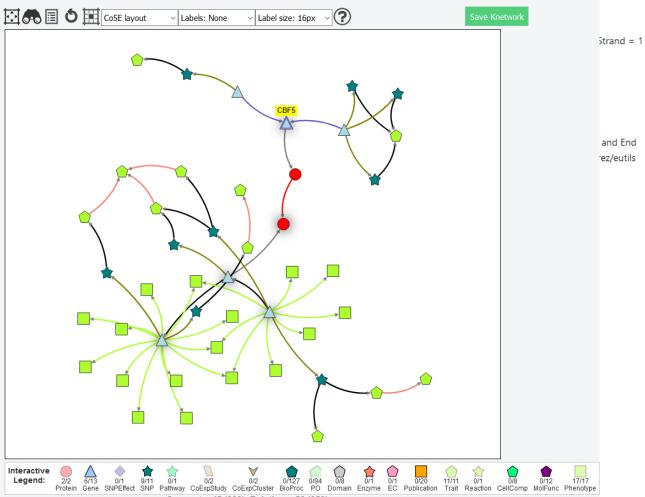
Genome annotation Triticum aestivum

Uncharacterized protein At3g57150 (Fragment) [Source:Projected from Arabidopsis thaliana (AT3G57150) UniProtKB/TrEMBL;Acc:COSVF3] feature type = protein\_coding



Discover the KnetMiner knowledge network for gene(s): TRAESCS2A02G151900 (blue triangles with yellow label) and potential links to any phenotype/trait (green rectangles and pentagons). Tip: Right-click-hold on nodes to add labels or to show their properties. Use the Interactive Legend to add (single-click) or hide (double-click) other types of information to/from the network.

and End





TraesCS2A02G151900 Search

Species  ☐ Triticum aestivum [3]
Data type  ☐ Genome annotation [2] ☐ Gene annotation [1]
Ontology annotation  Aucun [3] Expand search
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TraesCS2A02G151900 - Ensembl Plants

Genome annotation Triticum aestivum

Uncharacterized protein At3g57150 (Fragment) [Source:Projected from Arabidopsis thaliana (AT3G57150)

UniProtKB/TrEMBL;Acc:COSVF3] feature type = protein\_coding



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Genome annotation IWGSC@GnpIS chr2A:100113980..100117432 Start = 100113980, End = 100117432, Strand = 1, Source = IWGSC\_v1.1\_201706, Previous\_id = TraesCS2A01G151900, Seq\_id = chr2A, Name =

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TraesCS2A02G151900 - Ensembl Plants

Genome annotation Triticum aestivum

Uncharacterized protein At3g57150 (Fragment) [Source:Projected from Arabidopsis thaliana (AT3G57150) UniProtKB/TrEMBL:Acc:COSVF3] feature type = protein\_coding



# Triticum aestivum (IWGSC) ▼

Location: 2A:100.113.981-100.117.432

Gene: TraesCS2A02G151900 Trans: TraesCS2A02G151900.1

### Gene-based displays

# 

 Splice variants Transcript comparison

☐ Gene alleles

☐ Secondary Structure

Gene families

Literature

□ Plant Compara

Genomic alignments

- Gene tree

- Gene gain/loss tree

 Orthologues Paralogues

Homoeologues Pan-taxonomic Compara

- Gene Tree

Orthologues

 GO: Biological process - GO: Cellular component

☐ GO: Molecular function

Phenotypes

⊟ Genetic Variation

Variant table

Variant image

└─ Structural variants

Gene expression

Pathway

Regulation

External references

Supporting evidence

☐ Gene history

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Ensembl Plants is produced in collaboration with Gramene

# Gene: TraesCS2A02G151900

Description Uncharacterized protein At3g57150 (Fragment) [Source: Projected from Arabidopsis thaliana (AT3G57150)

UniProtKB/TrEMBL;Acc:C0SVF3]

Location Chromosome 2A: 100,113,981-100,117,432 forward strand.

This gene has 1 transcript (splice variant) and 144 orthologues. About this gene

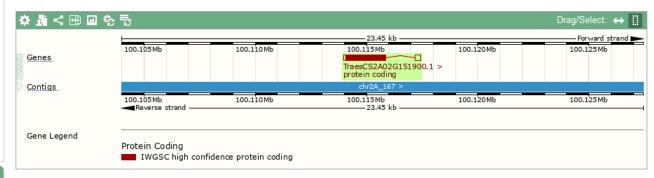
**Transcripts** 

# Summary @

Gene type Protein coding

Annotation method Genes annotated with high confidence by IWGSC

Go to Region in Detail for more tracks and navigation options (e.g. zooming)



# **1** Configuring the display

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Tip: use the "Configure this page" link on the left to show additional data in this region.

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TraesCS2A02G151900 Search

Species  Triticum aestivum [3]
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### wheatknet:TRAESCS2A02G151900 - KnetMiner

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### TraesCS2A02G151900 - Ensembl Plants

Genome annotation Triticum aestivum

Uncharacterized protein At3g57150 (Fragment) [Source:Projected from Arabidopsis thaliana (AT3G57150) UniProtKB/TrEMBL:Acc:COSVF3] feature type = protein\_coding



# **Ontology annotation**

- Objective: link literature with experimental data (genotyping, phenotyping...) using ontology annotation
- Corpus of ~1600 wheat open access publications:

Title = (Gene Marker AND (Triticum aestivum OR wheat))
OR

abstract = (Gene Marker AND (Triticum aestivum OR wheat))

- Text mining ontology: Wheat Trait Ontology <a href="http://wheat.agroportal.lirmm.fr/ontologies/WHEATPHENOTYPE">http://wheat.agroportal.lirmm.fr/ontologies/WHEATPHENOTYPE</a>
- Semantic facet filtering:
  - document annotation using 2 fields
  - generic enough for any ontology
  - tested with GO and WTO
  - search optionaly on ontology subtree



soft red winter wheat grain yield Results 1 to 20 of 20,200,398 (limited to 10,000) Species (978) 10.1186/s12863-019-0785-1 - OpenMinTeD@GnpIS Filter on Species... Bibliography Triticum Accuracy of genomic selection for grain yield and agronomic traits in soft red winter wheat. 2019 Accuracy of genomic selection for grain yield and agronomic traits in soft red winter wheat Background Genomic selection has the potential to increase genetic ... (expand) Data type (34) Filter on Data type... 2014 SRWW YNVP - The Triticeae Toolbox Genotyping Experiment Triticum 2014\_SRWW\_YNVP Yield Validation Panel, used to verify results of 2012\_ElitePanel. Soft Red Winter Wheat, cut with Ontology annotation Pstl. (66)SG-1550 - GrainGenes Filter on Ontology annotati Germplasm Triticum aestivum ssp. aestivum Germplasm GrainGenes SG-1550 Cultivar. The Ohio Grain Company, Marysville, OH. USA-Ohio. USDA/FGIS Soft Red Expand search ( ? Winter Wheat. Winter growth habit. Triticum aestivum ssp. aestivum ... (expand) Database (19) USSRWWN 2016 Champaign - The Triticeae Toolbox Filter on Database... Phenotyping Experiment Triticum USSRWWN 2016\_Champaign Uniform Southern Soft Red Winter Wheat Nursery, USSRWWN, Despite high yield levels, results were affected by winterkill and stripe rust. Fertilizer: 70 + 40 N. Data provider UESRWWN\_2014\_Urbana - The Triticeae Toolbox ■ INRAE-URGI [19,577,154] ☐ UWA [167,167] Phenotyping Experiment Triticum Gramene [127,291] UESRWWN\_2014\_Urbana Uniform Eastern Soft Red Winter Wheat Nursery, UESRWWN Coop. test of elite SRWW lines, Rothamsted wet winter and early spring. FHB data are from irrigated and grain spawn inoculated nursery using single row plots. Research [108,474] South Green [103,639] 10.1371/journal.pone.0208217 - OpenMinTeD@GnpIS IPK [60,170] Bibliography Arabidopsis thaliana Triticum Triticum aestivum T3 [33,452] Genome-wide association studies for yield-related traits in soft red winter wheat grown in Virginia. 2019 Genome-GrainGenes [21,241] wide association studies for yield-related traits in soft red winter wheat grown in Virginia Grain yield is a trait of ☐ CIMMYT [1,758] paramount importance in ... (expand) EBI [47]

10883/3464 - CIMMYT Publications

Bibliography Winter wheat



☐ IPGPAS [5]

Home WheatIS website Wheat@URGI More... ▼

soft red winter wheat grain yield

### Species (978)

Filter on Species...

# Data type (34)

Filter on Data type...

# Ontology annotation

(66)

Filter on Ontology annotati

# Expand search ( ?

Database (19)

Filter on Database...

# Data provider

- INRAE-URGI [19,577,154]
- ☐ UWA [167,167]
- Gramene [127,291]
- Rothamsted
  - Research [108,474]
- South Green [103,639]
- IPK [60,170]
- T3 [33,452]
- GrainGenes [21,241]
- ☐ CIMMYT [1,758]
- EBI [47]
- ☐ IPGPAS [5]

Results 1 to 20 of 20,200,398 (limited to 10,000)

10.1186/s12863-019-0785-1 - OpenMinTeD@GnpIS

Bibliography Triticum

Accuracy of genomic selection for grain yield and agronomic traits in soft red winter wheat. 2019 Accuracy of genomic selection for grain yield and agronomic traits in soft red winter wheat Background Genomic selection has

the potential to increase genetic

# 2014 SRWW YNVP - The Triticeae Toolbox

Genotyping Experiment



2014\_SRWW\_YNVP Yield Validation Panel, used to verify results of 2012\_ElitePanel. Soft Red Winter Wheat, cut with Pstl.

### SG-1550 - GrainGenes

Germplasm Triticum aestivum ssp. aestivum

Germplasm GrainGenes SG-1550 Cultivar. The Ohio Grain Company, Marysville, OH. USA-Ohio. USDA/FGIS Soft Red

Winter Wheat. Winter growth habit. Triticum aestivum ssp. aestivum ... (expand)

# USSRWWN 2016 Champaign - The Triticeae Toolbox

Phenotyping Experiment



USSRWWN\_2016\_Champaign Uniform Southern Soft Red Winter Wheat Nursery, USSRWWN, Despite high yield levels, results were affected by winterkill and stripe rust. Fertilizer: 70 + 40 N.

# UESRWWN\_2014\_Urbana - The Triticeae Toolbox

Phenotyping Experiment Triticum



UESRWWN\_2014\_Urbana Uniform Eastern Soft Red Winter Wheat Nursery, UESRWWN Coop. test of elite SRWW lines, wet winter and early spring. FHB data are from irrigated and grain spawn inoculated nursery using single row plots.

# 10.1371/journal.pone.0208217 - OpenMinTeD@GnpIS

Bibliography Arabidopsis thaliana Triticum Triticum aestivum

Genome-wide association studies for yield-related traits in soft red winter wheat grown in Virginia. 2019 Genomewide association studies for yield-related traits in soft red winter wheat grown in Virginia Grain yield is a trait of paramount importance in ... (expand)

# 10883/3464 - CIMMYT Publications

Bibliography Winter wheat



soft red winter wheat grain yield

Species (978)

Filter on Species...

Data type (34)

Filter on Data type...

Ontology annotation (66)

Filter on Ontology annotati

Database (19)

Filter on Database...

# Data provider

- INRAE-URGI [19,577,154]
- ☐ UWA [167,167]
- Gramene [127,291]
- Rothamsted
- Research [108,474]
- South Green [103,639]
- IPK [60,170]
- T3 [33,452]
- GrainGenes [21,241]
- ☐ CIMMYT [1,758]
- EBI [47]
- ☐ IPGPAS [5]

Results 1 to 20 of 20,200,398 (limited to 10,000)

10.1186/s12863-019-0785-1 - OpenMinTeD@GnpIS

Bibliography

Triticum

Accuracy of genomic selection for grain yield and agronomic traits in soft red winter wheat. 2019 Accuracy of genomic selection for grain yield and agronomic traits in soft red winter wheat Background Genomic selection has the potential to increase genetic gains by using molecular markers as predictors of breeding values of individuals. This study evaluated the accuracy of predictions for grain yield, heading date, plant height, and yield components in soft red winter wheat under different prediction scenarios. Response to selection for grain yield was also compared across different selection strategies- phenotypic, marker-based, genomic, combination of phenotypic and genomic, and random selections. Results Genomic selection was implemented through a ridge regression best linear unbiased prediction model in two scenarios- cross-validations and independent predictions. Accuracy for cross-validations was assessed using a diverse panel under different marker number, training population size, relatedness between training and validation populations, and inclusion of fixed effect in the model. The population in the first scenario was then trained and used to predict grain yield of biparental populations for independent validations. Using subsets of significant markers from association mapping increased accuracy by 64-70% for grain yield but resulted in lower accuracy for traits with high heritability such as plant height. Increasing size of training population resulted in an increase in accuracy, with maximum values reached when 60% of the lines were used as a training panel. Predictions using related subpopulations also resulted in higher accuracies. Inclusion of major growth habit genes as fixed effect in the model caused increase in grain yield accuracy under a cross-validation procedure. Independent predictions resulted in accuracy ranging between - 0.14 and 0.43, dependent on the grouping of site-year data for the training and validation populations. Genomic selection was %22superior%22 to marker-based selection in terms of response to selection for yield. Supplementing phenotypic with genomic selection resulted in approximately 10% gain in response compared to using phenotypic selection alone. Conclusions Our results showed the effects of different factors on accuracy for yield and agronomic traits. Among the factors studied, training population size and relatedness between training and validation population had the greatest impact on accuracy. Ultimately, combining phenotypic with genomic selection would be relevant for accelerating genetic gains for yield in winter wheat. Lozada, DN et al. BMC GENETICS Hide

2014 SRWW YNVP - The Triticeae Toolbox

Genotyping Experiment Triticum

2014\_SRWW\_YNVP Yield Validation Panel, used to verify results of 2012\_ElitePanel. Soft Red Winter Wheat, cut with Pstl.

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☐ IPGPAS [5]

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☐ IPGPAS [5]

Bibliography Winter wheat

10883/3464 - CIMMYT Publications

Genotyping Data Project Details

About



# Genotyping Data Project: 2014\_SRWW\_YNVP



Genotyping Data Project Name	2014_SRWW_YNVP				
Breeding Program	Kansas State University				
Trial Location	[No Location]				
Year	2014				
Description	Yield Validation Panel, used to verify results of 2012_ElitePanel. Soft Red Winter Wheat, cut with PstI.				
Genotyping Facility	Kansas State Genotyping Lab				



View basic information about the genotyping data project.

2014\_SRWW\_YNVP SGN8146



**⊕** Genotyping Protocols

View basic information about the genotyping protocols used in this genotyping data project.

SHIRLEY, id =



⊖ Genotyping Data

site, KSG

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Protocol	Sample Name	Sample Type	Accession Name	Synonyms	Description	Number of Marker Scores	IGD Number	Download
GBS restriction site, KSG	KY07C- 1249-148-3-1	accession	KY07C- 1249-148-3-1		SNP genotypes for stock (name = KY07C- 1249-148-3-1, id = 219126)	112307		Download
GBS restriction site, KSG	OH11-204-61	accession	OH11-204-61		SNP genotypes for stock (name = OH11-204-61, id = 219175)	112307		Download
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### Species (978)

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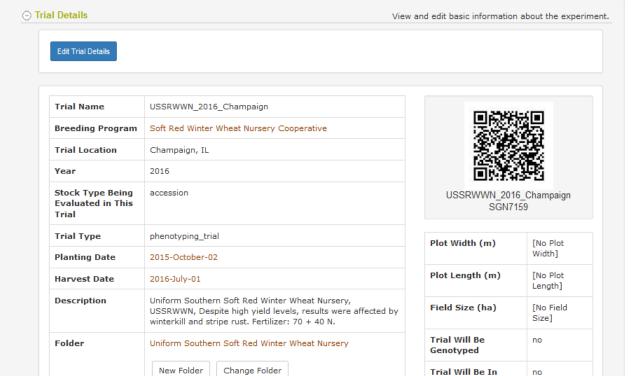


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# T3/Wheat

# Trial detail for USSRWWN 2016 Champaign







Generate barcode labels for plots or plants or accessions in this trial.



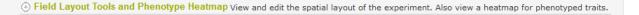


Directly record phenotypes to database for this trial.

Crosses







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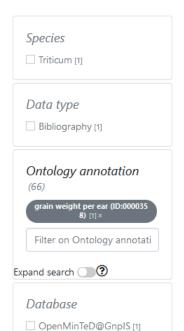


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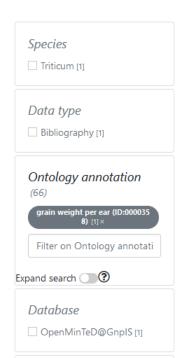
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Quantitative trait loci for leaf chlorophyll fluorescence parameters, chlorophyll and carotenoid contents in relation to biomass and yield in bread wheat and their chromosome deletion bin assignments, 2013 Quantitative trait loci for leaf chlorophyll fluorescence parameters, chlorophyll and carotenoid contents in relation to biomass and yield in bread wheat and their chromosome deletion bin assignments Relatively little is known of the genetic control of chlorophyll fluorescence (CF) and pigment traits important in determining efficiency of photosynthesis in wheat and its association with biomass productivity. A doubled haploid population of 94 lines from the wheat cross Chinese Spring x SQ1 was trialled under optimum glasshouse conditions for 4 years to identify quantitative trait loci (QTL) for CF traits including, for the first time in wheat, JIP-test parameters per excited cross section (CSm): ABS/CSm, DIo/CSm, TRo/CSm, RC/CSm and ETo/CSm, key parameters determining efficiency of the photosynthetic apparatus, as well as chlorophyll and carotenoid contents to establish associations with biomass and grain yield. The existing genetic map was extended to 920 loci by adding Diversity Arrays Technology markers. Markers and selected genes for photosynthetic light reactions, pigment metabolism and biomass accumulation were located to chromosome deletion bins. Across all CF traits and years, 116 QTL for CF were located on all chromosomes except 7B, and 39 QTL were identified for pigments on the majority of chromosomes, excluding 1A, 2A, 4A, 3B, 5B, 1D, 2D, 5D, 6D and 7D. Thirty QTL for plant productivity traits were mapped on chromosomes 3A, 5A, 6A, 7A, 1B, 2B, 4B, 6B, 7B, 3D and 4D. A region on chromosome 6B was identified where 14 QTL for CF parameters coincided with QTL for chlorophyll content and grain weight per ear. Thirtyfive QTL regions were coincident with candidate genes. The environment was shown to dominate in determining expression of genes for those traits. Czyczylo-Mysza, I et al. MOLECULAR BREEDING Hide



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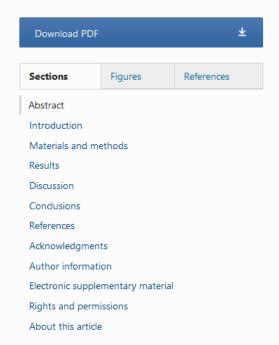
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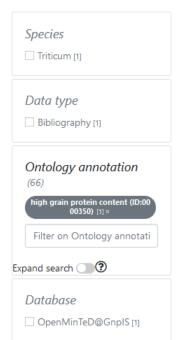
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Results 1 to 20 of 20,200,398 (limited to 10,000) Species (978) 10.1186/s12863-019-0785-1 - OpenMinTeD@GnpIS Bibliography Triticum Filter on Species... Accuracy of genomic selection for grain yield and agronomic traits in soft red winter wheat. 2019 Accuracy of genomic selection for grain yield and agronomic traits in soft red winter wheat Background Genomic selection has the potential to increase genetic ... (expand) Data type (34) Filter on Data type... 2014 SRWW YNVP - The Triticeae Toolbox Genotyping Experiment Triticum 2014\_SRWW\_YNVP Yield Validation Panel, used to verify results of 2012\_ElitePanel. Soft Red Winter Wheat, cut with Ontology annotation Pstl. (66)SG-1550 - GrainGenes grain Triticum aestivum ssp. aestivum GrainGenes SG-1550 Cultivar. The Ohio Grain Company, Marysville, OH. USA-Ohio. USDA/FGIS Soft Red grain hardness (ID:0000096) [12] eat. Winter growth habit. Triticum aestivum ssp. aestivum ... (expand) grain weight per ear (ID:0000358) [1] high grain protein content (ID:0000350) [1] N\_2016\_Champaign - The Triticeae Toolbox soft **grain** texture (ID:00000063) [1] 3 Experiment Triticum USSRWWN 2016\_Champaign Uniform Southern Soft Red Winter Wheat Nursery, USSRWWN, Despite high yield levels, results were affected by winterkill and stripe rust. Fertilizer: 70 + 40 N. Data provider UESRWWN\_2014\_Urbana - The Triticeae Toolbox ■ INRAE-URGI [19,577,154] ☐ UWA [167,167] Phenotyping Experiment Triticum Gramene [127,291] UESRWWN\_2014\_Urbana Uniform Eastern Soft Red Winter Wheat Nursery, UESRWWN Coop. test of elite SRWW lines, Rothamsted wet winter and early spring. FHB data are from irrigated and grain spawn inoculated nursery using single row plots. Research [108,474] South Green [103,639] 10.1371/journal.pone.0208217 - OpenMinTeD@GnpIS IPK [60,170] Arabidopsis thaliana Triticum Triticum aestivum Bibliography T3 [33,452] Genome-wide association studies for yield-related traits in soft red winter wheat grown in Virginia. 2019 Genome-GrainGenes [21,241] wide association studies for yield-related traits in soft red winter wheat grown in Virginia Grain yield is a trait of ☐ CIMMYT [1,758] paramount importance in ... (expand) EBI [47] ☐ IPGPAS [5] 10883/3464 - CIMMYT Publications

CIMMYT Dspace Winter wheat Publication 10883/3464 10883/3464 Effect of climate change and variety on long-term



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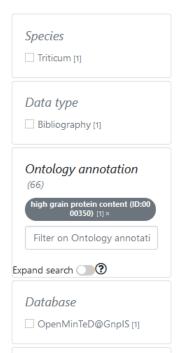
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Introgression of a major gene for high **grain** protein content in some Indian **bread wheat** cultivars. 2011 Introgression of a major gene for high **grain** protein content in some Indian **bread wheat** cultivars In **bread wheat**, high **grain** protein content (GPC) determines nutritional value, processing properties and quality of the end-product. In view of this, marker-assisted selection (MAS) was performed for introgression of a major gene for high GPC (Gpc-B1) into 10 **wheat** genotypes. As a result, 124 BC(3)F(5)/F(6) progenies with Gpc-B1 were developed and evaluated in multi-location field trials. Significant interaction of Gpc-B1 with the recipient parent genotypes and the environment was noticed. However, a total of seven MAS-derived progenies with significantly higher GPC (14.83-17.85%) than their recipient parental genotypes and having no **yield** penalty were obtained. In these selected progenies, no significant negative correlation of **grain yield** with GPC (%) or protein **yield** was observed suggesting that GPC could be improved without **yield** penalty. This study thus suggested that MAS in combination with phenotypic selection is a useful strategy for development of **wheat** genotypes with high GPC associated with no loss in **yield**. (c) 2011 Elsevier B.V. All rights reserved. Kumar, J et al. FIELD CROPS RESEARCH Hide

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☐ INRAE-URGI [1]

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Introgression of a major gene for high **grain** protein content in some Indian **bread wheat** cultivars. 2011 Introgression of a major gene for high **grain** protein content in some Indian **bread wheat** cultivars In **bread wheat**, high **grain** protein content (GPC) determines nutritional value, processing properties and quality of the end-product. In view of this, marker-assisted selection (MAS) was performed for introgression of a major gene for high GPC (Gpc-B1) into 10 **wheat** genotypes. As a result, 124 BC(3)F(5)/F(6) progenies with Gpc-B1 were developed and evaluated in multi-location field trials. Significant interaction of Gpc-B1 with the recipient parent genotypes and the environment was noticed. However, a total of seven MAS-derived progenies with significantly higher GPC (14.83-17.85%) than their recipient parental genotypes and having no **yield** penalty were obtained. In these selected progenies, no significant negative correlation of **grain yield** with GPC (%) or protein **yield** was observed suggesting that GPC could be improved without **yield** penalty. This study thus suggested that MAS in combination with phenotypic selection is a useful strategy for development of **wheat** genotypes with high GPC associated with no loss in **yield**. (c) 2011 Elsevier B.V. All rights reserved. Kumar, J et al. FIELD CROPS RESEARCH Hide





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## Introgression of a major gene for high grain protein content in some Indian bread wheat cultivars

J. Kumar <sup>a, c, 1</sup>, V. Jaiswal <sup>a, 1</sup>, A. Kumar <sup>a</sup>, N. Kumar <sup>a</sup>, R.R. Mir <sup>a, d</sup>, S. Kumar <sup>a</sup>, R. Dhariwal <sup>a</sup>, S. Tyagi <sup>a</sup>, M. Khandelwal <sup>a</sup>, K.V. Prabhu <sup>b</sup>, R. Prasad <sup>a</sup>, H.S. Balyan <sup>a</sup>, P.K. Gupta <sup>a</sup> A. ⊠

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## Abstract

In bread wheat, high grain protein content (GPC) determines nutritional value, processing properties and quality of the end-product. In view of this, marker-assisted selection (MAS) was performed for introgression of a major gene for high GPC (*Gpc-B1*) into 10 wheat genotypes. As a result, 124 BC<sub>3</sub>F<sub>5</sub>/F<sub>6</sub> progenies with *Gpc-B1* were developed and evaluated in multilocation field trials. Significant interaction of *Gpc-B1* with the recipient parent genotypes and the environment was noticed. However, a total of seven MAS-derived progenies with significantly higher GPC (14.83–17.85%) than their recipient parental genotypes and having no yield penalty were obtained. In these selected progenies, no significant negative correlation of grain yield with GPC (%) or protein yield was observed suggesting that GPC could be improved without yield penalty. This study thus suggested that MAS in combination with phenotypic selection is a useful strategy for development of wheat genotypes with high GPC associated with no loss in yield.



--- 4 31 4

# **URL** dereferencing

All search parameters and filters are available in the URL for later direct reference, ie.:

https://urgi.versailles.inra.fr/wheatis/search?query=yield&node=Gramene&entry=Gene&species=Triticum%20urartu



# Beyond WheatIS: other species/communities

FAIDARE

- ELIXIR: European Infrastructure for life science
- ELIXIR Plant Data Search Service: FAIDARE
- Data repositories federation extends WheatIS
- FAIDARE is global, beyond Elixir
  - open to US (eg. TERRA-REF) and other!
- BreedingAPI (<a href="http://brapi.org">http://brapi.org</a>): International collaboration
  - Standard Open Web Service REST API
  - Information Exchange, Main target: Breeding
  - Excellence in Breeding platform (CGIAR, Peter Selby)
  - MIAPPE compliant (<a href="http://www.miappe.org">http://www.miappe.org</a>): Minimum Information about Plant Phenotyping Experiment
  - More: MIAPPE Webinar 11th December 2020 (stay tuned)

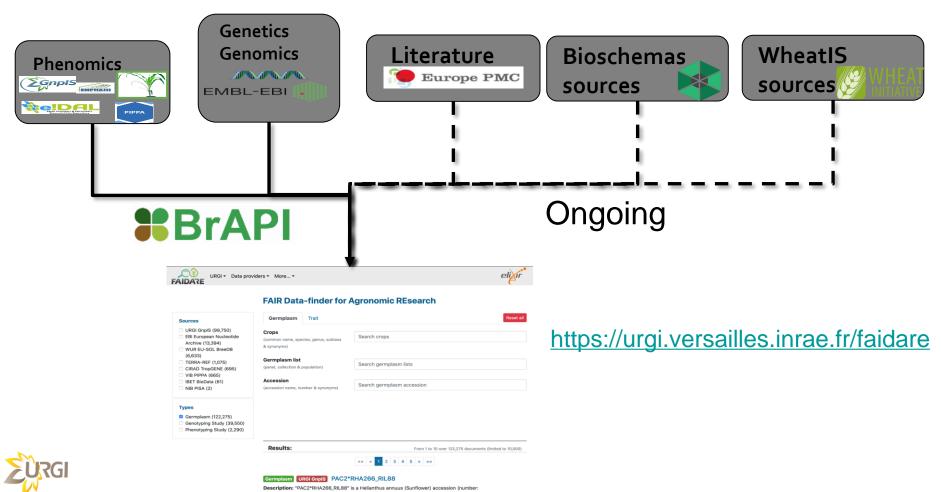


# Beyond WheatIS: other species/communities



**ELIXIR Plant Data Search Service:** 





# **Perspectives**

- ☐ IWGSC RefSeq v2
- ☐ What about your data?
- ☐ Automatic data updates on a regular basis
- ☐ Ontology annotation extended to GO, TO, CO\_321...
- ☐ Ontology alignment (ie. WTO with CO\_321)



# How to contribute/join

# Data

- □ Documentation on How to join the WheatIS federation https://urgi.versailles.inrae.fr/wheatis/join
- ☐ We offer support, contact us at <u>urgi-contact@inrae.fr</u>

# Code

- ☐ Open source under BSD3 License
- □ Available on our Gitlab instance <a href="https://forgemia.inra.fr/urgi-is/data-discovery">https://forgemia.inra.fr/urgi-is/data-discovery</a>
- ☐ Have a look at the <u>readme</u> to install and run locally
- ☐ Contributions (any) are very welcome! Follow the guidelines



# Take home message

WheatIS

- □ A federation of wheat data repositories for public data discovery
- □ Simple and generic data model
- ☐ Open source state-of-the-art web interfaces
- ☐ Easy to join: provide TSV or JSON files and ping us!



# **Acknowledgements**



Raphaël Flores **Cyril Pommier** Bilal El-Houdaigui Maud Marty Célia Michotey Erik Kimmel Dorothée Charruaud Nacer Mohellibi Nicolas Francillonne A.F. Adam-Blondon Hadi Quesneville Michael Alaux







## Data providers:

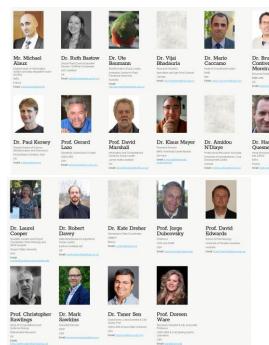
Kate Dreher (CIMMYT) Jesus Herrera de la Cruz (CIMMYT) Dave Edwards (UWA) Philipp Bayer (UWA) Clayton L. Birkett (T3) Marc Chakiachvili (EBI) Bruno Contreras Moreira (EBI) Dan Bolser (EBI) Paul Kersey (EBI) Victoria Blake (GrainGenes) Margaret Woodhouse (GrainGenes) Steve Michel (GrainGenes) Uwe Scholz (IPK) Matthias Lange (IPK) Daniel Arend (IPK) Andrew Olson (Gramene)

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Claire Nedellec (INRAE)



## The WheatIS EWG



Publication on WheatIS DataDiscovery under writing Since then, please cite:

Alaux et al., Genome Biology 2018 https://doi.org/10.1186/s13059-018-1491-4

Community paper: Sen et al., F1000

https://f1000research.com/articles/9-536





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