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WheatIS EWG annual meeting 2023

Michael Alaux

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Submitted on 8 Apr 2024

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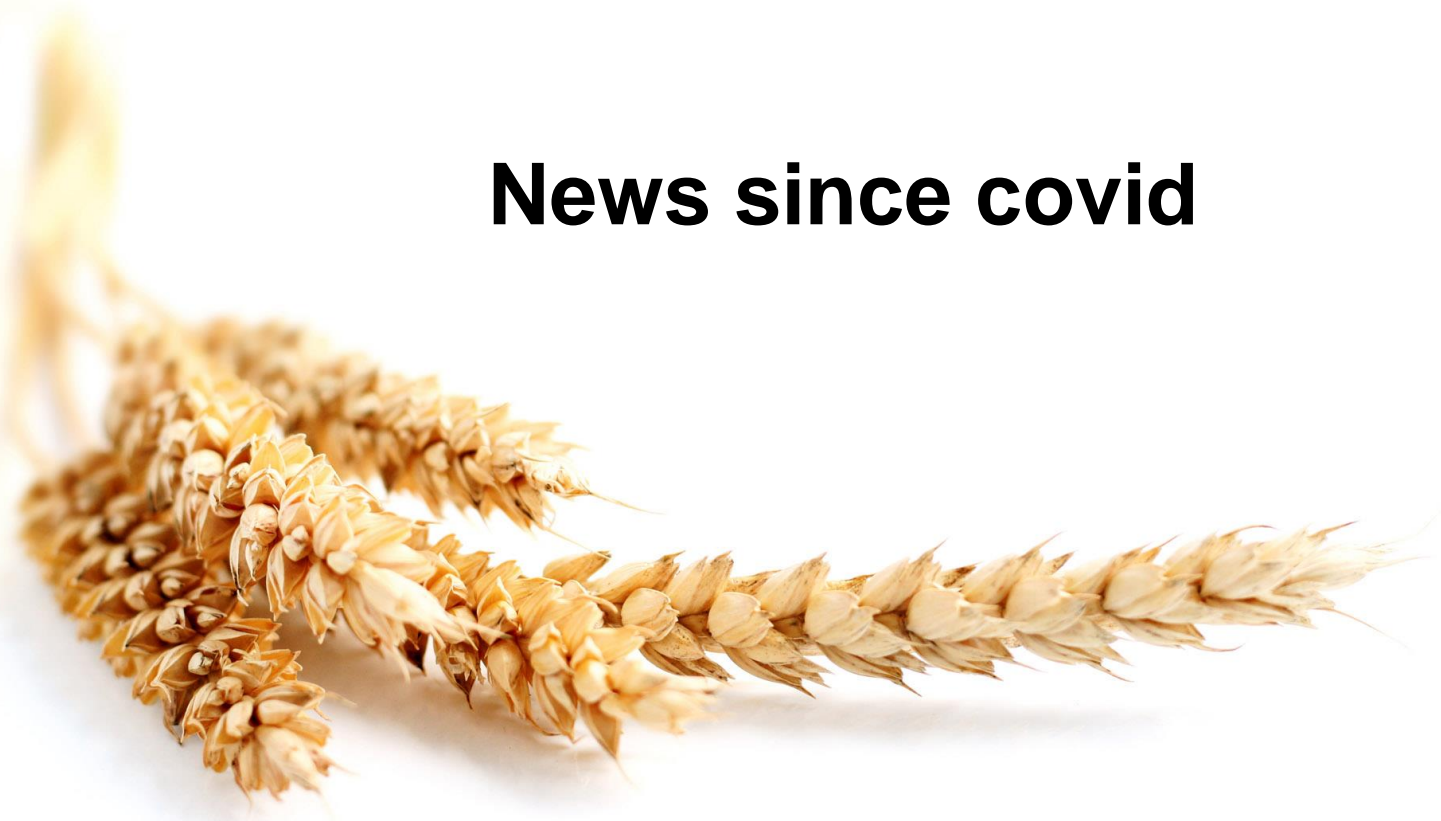
WheatIS EWG annual meeting



Agenda

- ❑ WheatIS EWG news since covid (Michael Alaux, 10 min)
- ❑ WheatIS data discovery tool (Cyril Pommier & Michael Alaux, 40 min presentation + 20 min questions)
- ❑ What future for the WheatIS data repository ? (Michael Alaux, 10 min)
- ❑ Database spotlight: GrainGenes (Taner Sen, 20 min presentation + 10 min questions)
- ❑ Discussion and budget request for 2023 (Michael Alaux, 10 min)

News since covid



EWG chair and co-chairs

- ❑ Taner Sen rotates from chair to co-chair
- ❑ Thanks to Hadi Quesneville for his effort and achievements as former chair and co-chair
- ❑ Since 2022:
 - ❑ Chair: Michael Alaux (INRAE-URGI)
 - ❑ Co-chairs:
 - ❑ Taner Sen (USDA-ARS)
 - ❑ Mario Caccamo (NIAB)
 - ❑ Dave Edwards (University of Western Australia)

New EWG members

- ❑ Welcome to 2 Early Career Researchers:
 - ❑ Sherry Sun (University of British Columbia)
 - ❑ Saloni Sharma (National Agri-Food Biotechnology Institute, India)

New logo

❑ New logo designed by

Delphine Laurenchet

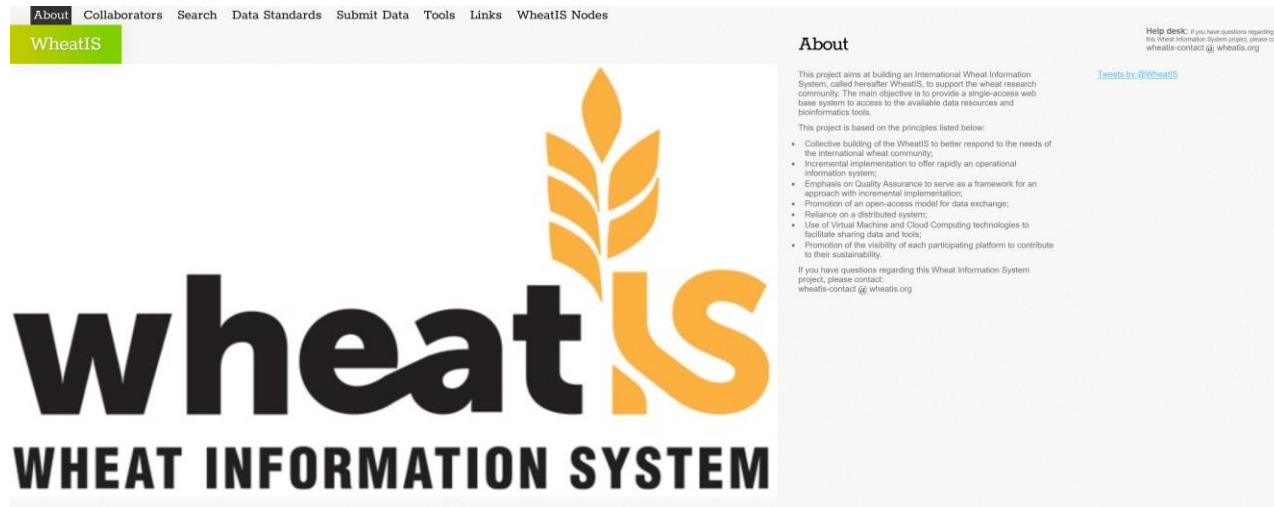
Graphiste | Directrice artistique free lance

delphine@delphine-laurenchet.fr

Port. +33 (0)6 67 32 17 67

www.delphine-laurenchet.fr

❑ Added to the WheatIS website: <http://www.wheatis.org/>



The screenshot shows the WheatIS website interface. At the top, there is a navigation menu with links: About, Collaborators, Search, Data Standards, Submit Data, Tools, Links, and WheatIS Nodes. The 'WheatIS' link is highlighted in a green box. Below the navigation menu is the new logo, which features a stylized orange wheat stalk above the text 'wheatIS' in a bold, sans-serif font. The 'IS' part of 'wheatIS' is in orange, while 'wheat' is in black. Below the logo, the text 'WHEAT INFORMATION SYSTEM' is written in a smaller, all-caps, bold font. To the right of the logo, there is an 'About' section with a heading 'About' and a paragraph of text. Below the paragraph is a list of bullet points. To the right of the 'About' section, there is a 'Help desk' section with a heading 'Help desk: if you have questions regarding the Wheat Information System project, please contact wheatis-contact@wheatis.org' and a link 'Tweets by @WheatIS'.

WheatIS

About Collaborators Search Data Standards Submit Data Tools Links WheatIS Nodes

wheatIS
WHEAT INFORMATION SYSTEM

About

This project aims at building an International Wheat Information System, called hereafter WheatIS, to support the wheat research community. The main objective is to provide a single-access web base system to access to the available data resources and bioinformatics tools.

This project is based on the principles listed below:

- Collective building of the WheatIS to better respond to the needs of the international wheat community;
- Incremental implementation to offer rapidly an operational information system;
- Emphasis on Quality Assurance to serve as a framework for an approach with incremental implementation;
- Promotion of an open-access model for data exchange;
- Reliance on a distributed system;
- Use of Virtual Machine and Cloud Computing technologies to facilitate sharing data and tools;
- Promotion of the visibility of each participating platform to contribute to their sustainability.

If you have questions regarding this Wheat Information System project, please contact: wheatis-contact@wheatis.org

Help desk: if you have questions regarding the Wheat Information System project, please contact wheatis-contact@wheatis.org

[Tweets by @WheatIS](#)

Tools

❑ New version of the WheatIS data discovery tool

Dissemination

Two webinars presented the WheatIS DataDiscovery tool:

1. On [2020 February the 25th](#) (with a [replay available](#)) under the umbrella of the WheatInitiative.
2. On [2020 October the 7th](#) (with a [replay available](#)) for the AgBioData community.

Data updates

2020-2021

Ensembl Plants

Ensembl Genomes Plants has been updated up to release 51.

GrainGenes

GrainGenes data has been updated with 3407 new QTL, and 58 genetic maps.

TheTriticeaeToolbox & Gramene (USDA)

T3 data as well as Gramene got updated with respective latest releases.

New features

2022

Add BrAPI data sources

Resources and databases that offers a [Breeding API](#) end point are currently indexable in [FAIDARE](#), the Elixir plant data lookup service. The WheatIS data discovery and FAIDARE codebase have been unified to ease the management of data sources, to bring Breeding API indexation to WheatIS and to ease development and maintenance.

Look and feel

Addition of the WheatIS logo and usage of the WheatIS theme colors.

2020-2021

Ontologies

Searching resources annotated with [Gene Ontology](#) terms is now offered through a dedicated facet. So far, only resources from Wheat literature are annotated, but we plan to extend this soon.



















Search by synonyms

Search by taxon now uses synonyms from 2 data sources: [NCBI](#) and [GnplIS](#). Any search term matching a known taxon name also searches its synonyms. Matching synonyms are highlighted in the results to inform the user of the process.

Usage metrics

□ Number of WheatIS data discovery searches

2018	2019	2020	2021	2022
3790	4639	7421	7814	8477

Countries			Unique visitors
	China	cn	(23.0%)
	United States	us	(14.6%)
	Japan	jp	(12.8%)
	Australia	au	(6.6%)
	India	in	(4.8%)
	Republic of Serbia	rs	(4.5%)
	France	fr	(4.3%)
	Germany	de	(4.0%)
	Spain	es	(2.7%)
	Canada	ca	(2.9%)
	Morocco	ma	(2.4%)
	Russian Federation	ru	(1.9%)
	Great Britain	gb	(1.4%)
	Indonesia	id	(1.3%)
	Croatia	hr	(1.2%)
	Argentina	ar	(1.0%)
	Sweden	se	(1.0%)
	Pakistan	pk	(0.9%)

News from the Wheat Initiative

❑ Jamboree in Carlow 2022

❑ SRA publication 2022



Open Access Feature Paper Review

Meeting the Challenges Facing Wheat Production: The Strategic Research Agenda of the Global Wheat Initiative

by Peter Langridge ^{1,2,*} Michael Alaux ³, Nuno Felipe Almeida ⁴ Karim Ammar ⁵, Michael Baum ⁶, Faouzi Bekkaoui ⁷, Alison R. Bentley ⁵ Brian L. Beres ⁸ Bettina Berger ⁹ Hans-Joachim Braun ⁵, Gina Brown-Guedira ¹⁰ Christopher James Burt ¹¹, Mario Jose Caccamo ¹² Luigi Cattivelli ¹³ Gilles Charmet ¹⁴, Peter Civián ¹⁴, Sylvie Cloutier ¹⁵ Jean-Pierre Cohan ¹⁶, Pierre J. Devaux ¹⁷ Fiona M. Doohan ¹⁸, + Show full author list

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⁷ INRA (National Institute for Agricultural Research), Rabat 10090, Morocco

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⁹ Australian Plant Phenomics Facility, School of Agriculture, Food and Wine, University of Adelaide, Urrbrae, SA 5064, Australia

¹⁰ USDA-ARS (United States Department of Agriculture—Agricultural Research Service), Plant Science Research, Raleigh, NC 27695, USA

+ Show full affiliation list

* Author to whom correspondence should be addressed.

Agronomy **2022**, *12*(11), 2767; <https://doi.org/10.3390/agronomy12112767>

Received: 26 September 2022 / Revised: 28 October 2022 / Accepted: 29 October 2022 /

Published: 7 November 2022

<https://doi.org/10.3390/agronomy12112767>

WheatIS data discovery tool

Presentation by Cyril Pommier

Short demo

Questions

- About
- Join us
- Terms of use
- Help
- News/Perspectives



Data providers

INRAE-URGI

- IWGSC@GnplS [19,195,264]
- GnplS [631,498]
- brapi@INRAE-URGI [15,949]
- OpenMinTeD@GnplS [1,692]
- WheatIS File Repository [6]

EBI

- Ensembl Plants [3,071,189]

IPK

- CR-EST [199,220]
- GEBIS [51,820]
- MetaCrop [355]

Gramene

- Gramene [229,851]

T3

- The Triticeae Toolbox [206,406]
- UniProt by T3 [16,607]

UWA

- Wheat Pangenome [167,167]

Rothamsted Research

- KnetMiner [108,474]

GrainGenes

- GrainGenes [20,190]
- Komugi wheat gene catalog by GrainGenes [3,119]

PGSB

- CrowsNest [13,324]

CIMMYT

- CIMMYT Publications [1,600]
- CIMMYT Datasets [183]

EVA

- brapi@EVA [710]

TERRA-REF

- brapi@TERRA-REF [284]

IPGPAS

- PlantPhenoDB [6]

cf

Search

- cf
- cf-1
- cf014
- cf046
- cf066
- cf069
- cf1
- cf1-2
- cf10
- cf101

CFD2



cfid2

Search

Species

Triticum [1]

Data type

Bibliography [1]

Database

IWGSC@GnpIS [4]

OpenMinTeD@GnpIS [1]

Data provider

INRAE-URGI [1]

Results 1 to 1 from 1

[10.1007/s00122-012-1838-2](#) - OpenMinTeD@GnpIS

Bibliography **Triticum**

Bibliography OpenMinTeD 10.1007/s00122-012-1838-2 Mapping QTL for resistance to eyespot of <span class='openminted_taxon' [...] 415, and **cfid2** are tightly linked to Q.<span class='ope ... (Expand)

[JDIOWSE_C1114A_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)

[10.1007/s00122-012-1838-2](#) - OpenMinTeD@GnpIS

Bibliography **Triticum**

Bibliography OpenMinTeD 10.1007/s00122-012-1838-2 Mapping QTL for resistance to eyespot of <span class='openminted_taxon' [...] 415, and **cfid2** are tightly linked to Q.<span class='ope ... (Expand)

Intersection
(AND query)



Triticum aestivum (IWGSC)

Location: 2A:100,113,981-100,117,432

Gene: [TraesCS2A02G151900](#)

Trans: [TraesCS2A02G151900.1](#)

Gene-based displays

- Summary
 - Splice variants
 - Transcript comparison
 - Gene alleles
- Sequence
 - Secondary Structure
- Gene families
- Literature
- Plant Comparison
 - Genomic alignments
 - Gene tree
 - Gene gain/loss tree
 - Orthologues
 - Paralogues
 - Homoeologues
- Pan-taxonomic Comparison
 - Gene Tree
 - Orthologues
- Ontologies
 - 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
- ID History
 - Gene history

- Configure this page
- Custom tracks
- Export data
- Share this page
- Bookmark this page

[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.

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

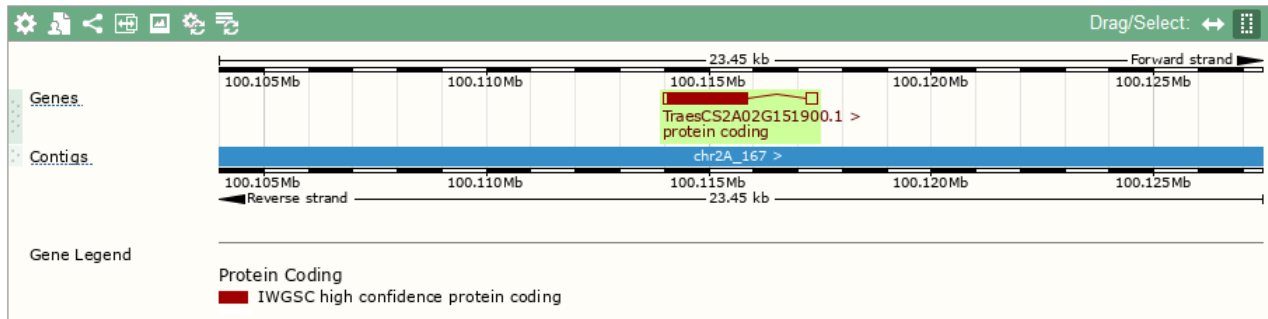
Transcripts [Show transcript table](#)

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)



Ensembl Plants release 48 - August 2020 © [EMBL-EBI](#)

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CFD2



Home WheatIS website Wheat@URGI More... ▾

cfid2

Search

Species

Triticum [1]

Results 1 to 1 from 1

[10.1007/s00122-012-1838-2](#) - OpenMinTeD@GnpIS

Bibliography **Triticum**

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Original Paper | Published: 11 March 2012

Mapping QTL for resistance to eyespot of wheat in *Aegilops longissima*

Hongyan Sheng, Deven R. See & Timothy D. Murray

[Theoretical and Applied Genetics](#) **125**, 355–366(2012) | [Cite this article](#)

402 Accesses | 14 Citations

Abstract

Eyespot is an economically important disease of wheat caused by the soilborne fungi *Oculimacula yallundae* and *O. acuformis*. These pathogens infect and colonize the stem base, which results in lodging of diseased plants and reduced grain yield. Disease resistant cultivars are the most desirable control method, but resistance genes are limited in the wheat gene pool. Some accessions of the wheat wild relative *Aegilops longissima* are resistant to eyespot, but nothing is known about the genetic control of resistance. A recombinant inbred line population was developed from the cross PI 542196 (R) × PI 330486 (S) to map the resistance genes and better understand resistance in *Ae. longissima*. A genetic linkage map of the S¹ genome was constructed with 169 wheat microsatellite markers covering 1261.3 cM in 7 groups. F₅ lines (189) were tested for reaction to *O. yallundae* and four QTL were detected in chromosomes 1S¹, 3S¹, 5S¹, and 7S¹. These QTL explained 44 % of the total phenotypic variation in reaction to eyespot based on GUS scores and 63 % for visual disease ratings. These results demonstrate that genetic control of *O. yallundae* resistance in *Ae. longissima* is polygenic. This is the first report of multiple QTL conferring resistance to eyespot in *Ae. longissima*. Markers *cfid6*, *wmc607*, *wmc415*, and *cfid2* are tightly linked to *O. Pch.wheat-1S¹*

CFD2 - IWGSC@GnpIS

Genome annotation **Triticum aestivum**

Genome annotation IWGSC@GnpIS **CFD2 CFD2** is a similarity:ePCR_cfd of Triticum aestivum located between positions 14028 and 14311 on 4AS_v2_5981297 and which properties are Size=283,Motif=gt(9),load_id=CFD2_147 Triticum aestivum similarity

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Sections

Figures

References

Abstract

References

Yield



New T3/Wh

Species

- Hordeum vulgare
- Triticum aestivum
- Triticum durum
- Brachypodium distachyon
- Aegilops tauschii

Data

- Interactome
- Genes
- Genomes
- Gene Ontology
- Interactions
- Gene Ontology
- Interactions

Data

- Gramene

Data

- INRA
- CIMMYT
- Gramene
- Rothamsted
- GrassGen
- T3/Wh
- Southern Cross
- IPK
- IPGRI

TRIUR3_07354 *Triticum urartu*

Putative deoxyribonuclease TATDN1

Location Homology X-refs

Compara Gene Tree

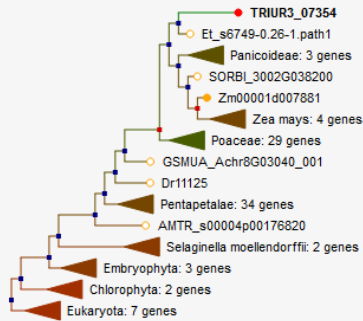


Search for genes, species, pathways, ontology terms, domains...



1 genes in 1 genomes

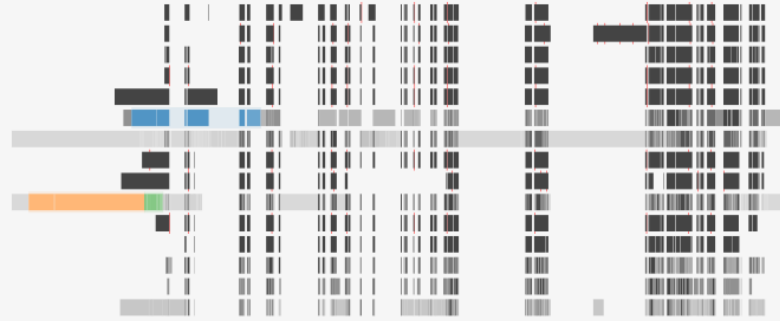
Gene | TRIUR3_07354



Search Gramene

Show All Homologs 91

Show Orthologs 89



Links to other resources

Ensembl Gene Tree view

Model Species Homolog
Zm00001d007881 *Zea mays*
TatD related DNase

Login

Release Notes (62) About Cite Feedback Privacy

Gramene is a collaborative effort among Cold Spring Harbor Laboratory, Oregon State University, and EMBL-EBL.

Funding is provided by the NSF and USDA ARS.

Application Info


- Data Release 62
- Gramene Search UI LOCAL DEVELOPMENT BUILD
- Built on January 14th 2020 at 1:01:57 pm

Actions

Reset Gramene Search

Open Access | Published: 10 April 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

[I. Czyczyło-Mysza](#) , [M. Tyrka](#), [I. Marcińska](#), [E. Skrzypek](#), [M. Karbarz](#), [M. Dziurka](#), [T. Hura](#), [K. Dziurka](#) & [S. A. Quarrie](#)

Molecular Breeding **32**, 189–210(2013) | [Cite this article](#)

3466 Accesses | 39 Citations | [Metrics](#)

Abstract

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 × 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 (CS_m): ABS/CS_m , DI_0/CS_m , TR_0/CS_m , RC/CS_m and ET_0/CS_m , 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. Thirty-five QTL regions were coincident with candidate genes. The environment was shown to dominate in determining expression of genes for those traits.

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Sections

Figures

References

Abstract

Introduction

Materials and methods

Results

Discussion

Conclusions

References

Acknowledgments

Author information

Electronic supplementary material

Rights and permissions

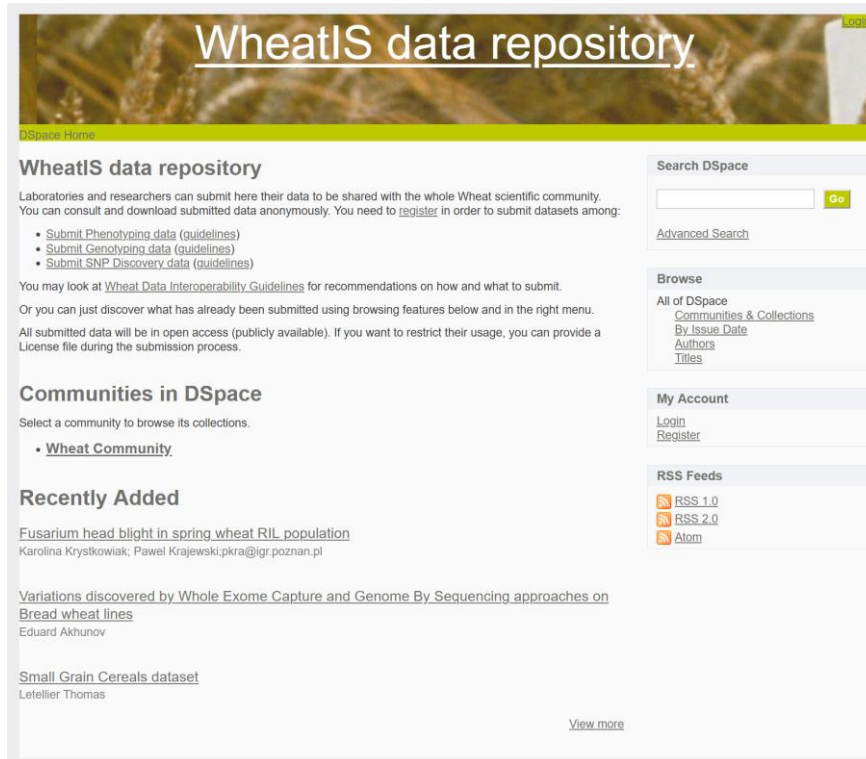
About this article

WheatIS data repository



Historic

❑ DSpace created in 2016



❑ very little usage since then

Now

- All the submitted files are already in other repositories
 - IWGSC Data Repository
 - GnpIS
 - PlantPhenoDB
- There are alternatives widely used by the community
 - Zenodo
 - FAIRDOM
 - Dataverse

Futur

- ❑ We propose to shutdown this service
- ❑ Focus on providing recommendations, documents and support on how to submit FAIR data in repositories

Database spotlight: GrainGenes

Discussion and budget request for 2023



Budget for workshops

- Annual meeting of next year at PAG
- Gene nomenclature:
 - There is a publication coming soon about wheat gene nomenclature led by Scott Boden.
 - Workshop could be focused on supporting the use of the nomenclature and guidelines.
- Other meetings ?

Budget for workshops

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 - Workshop could be focused on supporting the use of the nomenclature and guidelines.
- Other meetings ?

Acknowledgements

WheatIS Expert Working Group



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USDA ARS & Cold Spring Harbor Laboratory
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Data providers



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