# Apprendre à lire aux ordinateurs pour améliorer le blé

Hadi Quesneville

Journées Nationales de la Science Ouverte 6 Décembre 2018



Provide the research community with a *single* entry point of access to genetic, phenotypic and genomics resources.

Promote the development of services on top of current databases.

Authority to define guidelines for data curation, nomenclature, standards and integration.

Registry for bioinformatics tools.





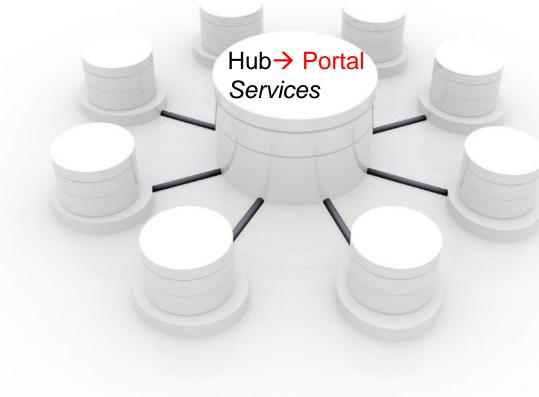
# WheatIS nodes (#12)





# **Distributed information system**

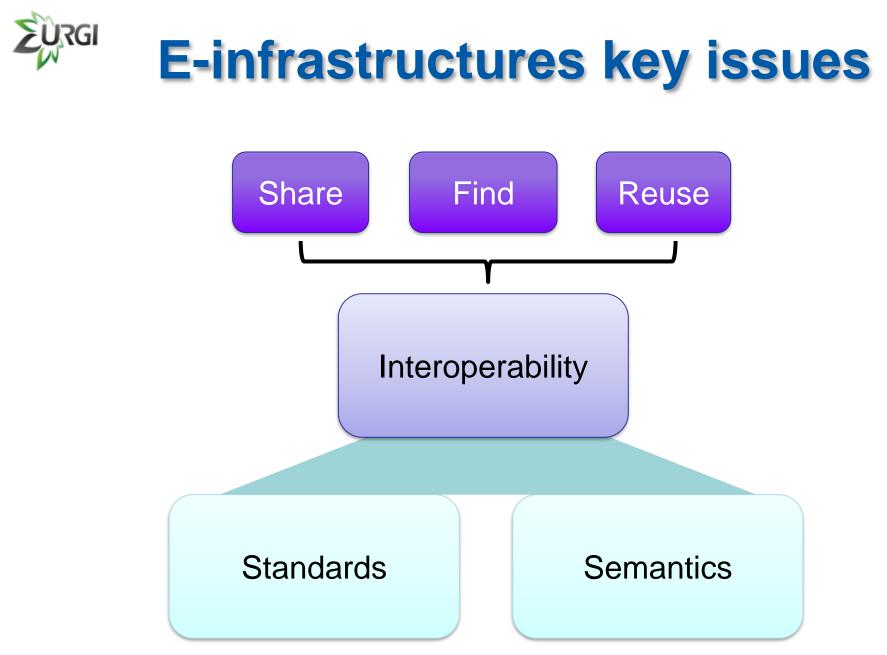
A network of bioinformatics platformes



Node (Platform) → resources

Computes / Storage Integrative database: genomic, genetic, and phenotypic information, comparative genomics, and functional genomics









### **FAIR principles**

### To be Findable:

- Persistent identifier (like a DOI or Handle)
- **Rich metadata** to describe the data (making sure it is findable through disciplinary discovery portals.)

### To be Accessible:

 Data open using a standardised protocol

Clarity and transparency around the conditions governing access and reuse.

### To be Interoperable:

- Use community agreed **formats**, **language** and **vocabularies**.
- **Contain links** to related information using identifiers.

### To be **R**e-usable:

- Maintain its **initial richness** (not diminished for explaining the findings in one publication).
- Clear machine readable licence a nd provenance inf ormation on how the data was formed.

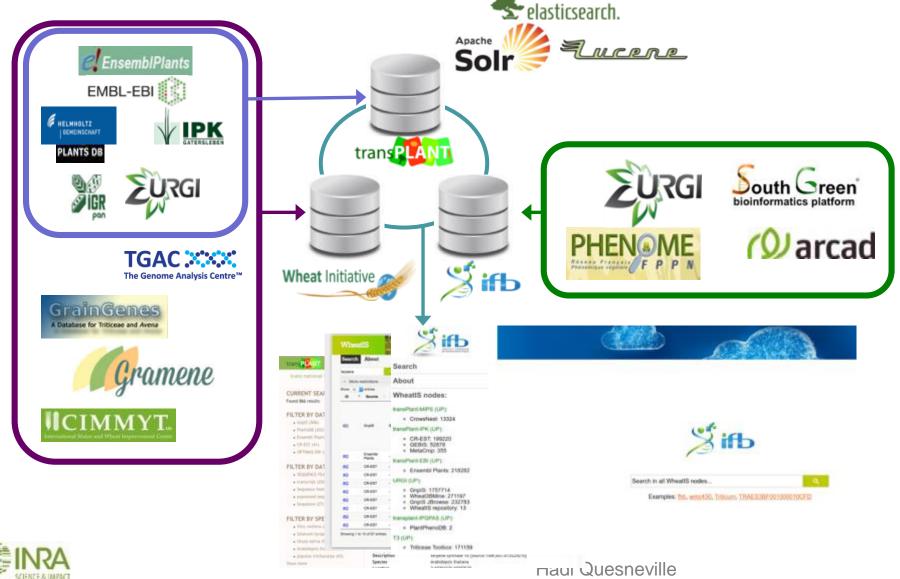




### FINDABLE: → DATA DISCOVERY



# Full text search of distributed databases

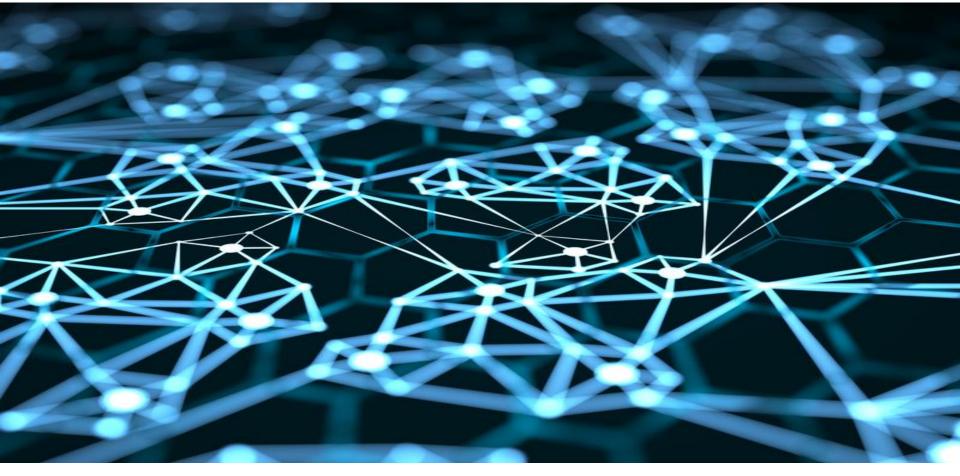




### wheatis.org

					wheatis.org			Ċ	
	Had auesneville - c	tlook Web App						About :: WheatIS	+
About Colla	borators Search	Data Standards	Sub	mit Dat	ta Tools	Links	W	neatIS Nodes	
WheatIS							P	bout	Help desk: If you have questions regarding this Wheat Information System project, please contact: wheatis-contact @ wheatis.org
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Sec. 1 and	Database	ID	Source	Туре	Taxon [	Description			
-AL 8 8	□ TRITICEAE TOOLBOX (64) □ CR-EST (7)	Traes_5DL_E12C501B4	Ensembl Plants	-				I Plants, Traes_5DL_E12C501B4, Traes_ /TrEMBL:Acc:A0FHB0], Triticum aestivun	5DL_E12C501B4, Multiple inositol polyphosphate phosphatase
	GNPIS (3)	HDP14M22T	CR-EST		Hordeum H	HDP14M22T, ex	pressed se		gi 26248924 ref NP_754964.1  Hypothetical protein yfhB [Escher
C NUR	GNPIS JBROWSE (1)	HDP20D01w	CR-EST		Hordeum H	HDP20D01w, ex	pressed se		gi 15604676 ref NP_221194.1  SFHB PROTEIN HOMOLOG (sfr
1 Alex	□PLANTPHENODB (1) <u>Type</u>	HDP20D01T	CR-EST		Hordeum	HDP20D01T, ex	pressed se		gi 15604676 ref NP_221194.1  SFHB PROTEIN HOMOLOG (sfh
CAN A.A.	ACCESSION (42)	HDP21C08T	CR-EST		Hordeum H	HDP21C08T, ex	pressed se		gi 15604676 ref NP_221194.1  SFHB PROTEIN HOMOLOG (sfr
Com Come	EXPERIMENT (9)	HDP31N10w	CR-EST		Hordeum H	HDP31N10w, ex	pressed se		gi 15604676 ref NP_221194.1  SFHB PROTEIN HOMOLOG (sfr
C S A	TAGS (7)	HDP35A10T	CR-EST		Hordeum H	HDP35A10T, ex	pressed se	quence tags, CR-EST, Hordeum vulgare,	gi 26248924 ref NP_754964.1  Hypothetical protein yfhB [Escher
12 90° 1	□PHENOTYPE (1) □QTL (1)	<u>TS034007u</u>	CR-EST		Triticum	TS034O07u, exp	pressed sec		Gi 15233419 ref NP_192328.1  hypothetical protein [Arabidopsis
att a the	SEQUENCE FEATURE (1)		Triticeae	Experiment	Tritioum			1820 hypo; Gi 15604676 ref NP_221194. ox, HWW FHB, phenotype experiment, Ir	1) SFHB PROTEIN HOMOLOG (st[] includes trials FHB_2014_Lincoln, HWWFHB_2014_Brookings,
	Species	HWW FHB	Toolbox	Experiment	aestivum I	HWWFHB_2014	_Fargo, Tri	ticum aestivum, phenotype	
	□ TRITICUM AESTIVUM (69) □ HORDEUM VULGARE (6)	URSN_2012_BrookingsSD	Triticeae Toolbox	Experiment				ox, URSN_2012_BrookingsSD, phenotyp ght disease index, visually scabby kernels	e trial, traits=Fusarium head blight incidence, Fusarium head blig ; URSN, descripti[]
- A Same	□ TRITICUM AESTIVUM L. (1) □ TRITICUM DURUM (1)								
	Search								
	About								
	WheatIS nodes:								
If we have missed a link	transPlant-MIPS (UP):								
The site is supported by	- CrowsNest: 13324								
	transPlant-IPK (UP):								
	- CR-EST: 199220 - GEBIS: 52878 - MetaCrop: 355								





### **ONTOLOGIES MAPPING**







### •WIPO:

- The Wheat INRA **Phenotypes** Ontology is developped in the frame of the BreedWheat project.
- Observations variables
- The WIPO v1.3 contains 262 variables.

### WTO:

- Wheat Trait Ontology
- General traits found in the literature: traits of resistance, development, nutritional, baking quality, etc.





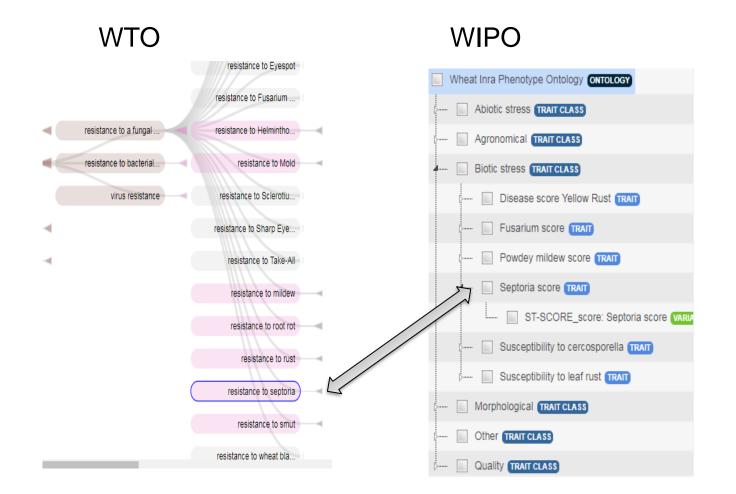


- 1. Link wheat phenotyping data to the literature
- 2. Semantic enrichment of the wheat phenotyping data
- Align the traits of agronomical interest (WTO) and experimental data (WIPO)
- ➔ finds correspondences between semantically related entities of the ontologies





# **Alignment example**







# **Alignment example**

	١	NIPO	WTO				
		/		(		(	
WIPO:0000101	Fusarium score, Susceptibility to fusarium head blight	FUS-SCORE_score	WIPO:Biotic stress/Fusarium score/Fusarium score, Susceptibility to fusarium head blight/FUS-SCORE_score	ID:0030905	resistance to Fusarium head blight	/FSOV Concept/plant property/response to environmental condition/response to biotic stress/pest resistance/pathogen resistance/resistance to a fungal pathogen/resistance to Fusarium head blight	
WIPO:0000105	Spikes with fusarium at 350DD post fusarium inoculation (INOC+350DD)	FUS-SPK.350DD_score	WIPO:Biotic stress/Spikes with fusarium post fusarium inoculation/Spikes with fusarium at 350DD post fusarium inoculation (INOC+350DD)/FUS-SPK.350DD_score	ID:0030905	resistance to Fusarium head blight	/FSOV Concept/plant property/response to environmental condition/response to biotic stress/pest resistance/pathogen resistance/resistance to a fungal pathogen/resistance to Fusarium head blight	
WIPO:0000106	Spikes with fusarium at 450DD post fusarium inoculation (INOC+450DD)	FUS-SPK.450DD_score	WIPO:Biotic stress/Spikes with fusarium post fusarium inoculation/Spikes with fusarium at 450DD post fusarium inoculation (INOC+450DD)/FUS-SPK.450DD_score	ID:0030905	resistance to Fusarium head blight	/FSOV Concept/plant property/response to environmental condition/response to biotic stress/pest resistance/pathogen resistance/resistance to a fungal pathogen/resistance to Fusarium head blight	
WIPO:0000113	Septoria tritici - Field Disease Index	ST-FDI	WIPO:Biotic stress/Septoria tritici - Field Disease Index/Septoria tritici - Field Disease Index/ST- FDI		resistance to Septoria Leaf Blotch	/FSOV Concept/plant property/response to environmental condition/response to biotic stress/pes resistance/pathogen resistance/resistance to a funga pathogen/resistance to septoria/resistance to Septori Leaf Blotch	
WIPO:0000114	Septoria score on leaf 1	ST-F1-SCORE score	WIPO:Biotic stress/Septoria score on leat/Septoria score on leaf 1/ST-F1- SCORE score	ID:0000107	resistance to Septoria Leaf Blotch	/FSOV Concept/plant property/response to environmental condition/response to biotic stress/pes resistance/pathogen resistance/resistance to a funga pathogen/resistance to septoria/resistance to Septori Leaf Blotch	
WIPO:0000115	Septoria score on leaf 2	ST-F2-SCORE score	WIPO:Biotic stress/Septoria score on leat/Septoria score on leaf 2/ST-F2- SCORE score		resistance to Septoria Leaf Blotch	/FSOV Concept/plant property/response to environmental condition/response to biotic stress/pest resistance/pathogen resistance/resistance to a fungal pathogen/resistance to septoria/resistance to Septoria Leaf Blotch	
WIPO:0000145	Powdey mildew score, Susceptibility to powdery mildew	PM-SCORE score	WIPO:Biotic stress/Powdey mildew score/Powdey mildew score, Susceptibility to powdery mildew/PM-SCORE score		resistance to Powdery Mildew	/FSOV Concept/plant property/response to environmental condition/response to biotic stress/pesi resistance/pathogen resistance/resistance to a fungal pathogen/resistance to mildew/resistance to Powdery Mildew	
WIPO:0000152	Brown rust score		WIPO:Biotic stress/Brown rust score/Brown rust score/BR-SCORE_1 to 9 score		resistance to Leaf Rust	//FSOV Concept/plant property/response to environmental condition/response to biotic stress/pes resistance/pathogen resistance/resistance to a funga pathogen/resistance to rust/resistance to Leaf Rust	
WIPO:0000162	Yellow rust score, Susceptibility to stripe rust	YR-SCORE_score	WIPO:Biotic stress/Disease score Yellow Rust/Yellow rust score, Susceptibility to stripe rust/YR-SCORE_score	ID:000089	resistance to Stripe Rust	/FSOV Concept/plant property/response to environmental condition/response to biotic stress/pes resistance/pathogen resistance/resistance to a fungal pathogen/resistance to rust/resistance to Stripe Rust	





# **Processing PubMed**

### Publication data from the European OpenMinTed project

### Processing PubMed collection Documents 3 881 10 254 Genes Taxa 14 853 Phenotypes 8792 Markers 1 941

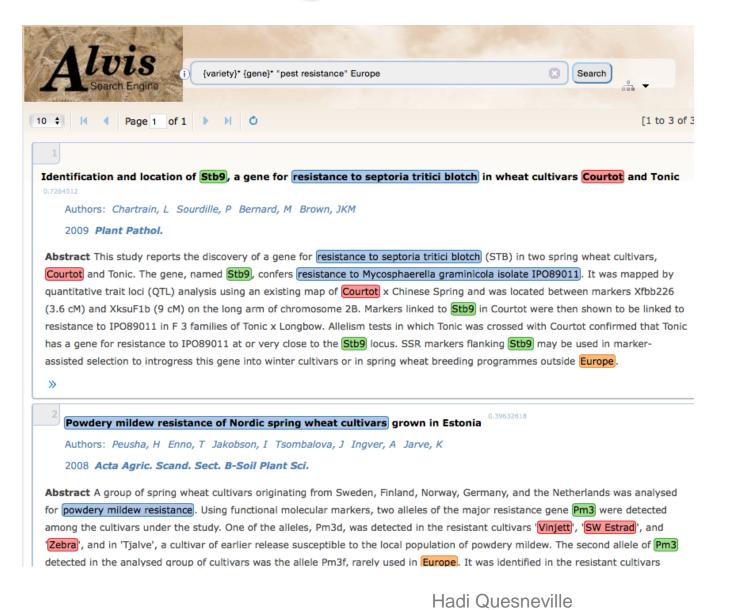
DOI 10.1007/s13353-014-0264-3		
PLANT GENETICS - SHORT COMMUNICATION Effective transfer of chromosomes carrying leaf rust resistance genes from <i>Aegilops tauschii</i> Coss. into hexaploid	Alvis Garch Engine (pmid=10.1007/s13353-014-0264-3 LR32 Search) 🚓 🗸	and the second
triticale ( <i>X Triticosecale</i> Witt.) using <i>Ae. tauschii</i> × <i>Secale cereale</i> amphiploid forms	10 V H 4 Page 1 of 1 > H 0 [1 to 1 of 1]	pmid=10.1007/s13353-014-02 (1)
Michal Kwiatek - Maciej Majka - Halina Wišniewska - Barbara Apolinarska - Jolanta Beiter	Effective transfer of chromosomes carrying leaf rust resistance genes from Aegilops tauschii Coss. Into hexaploid triticale (X Triticosecale Witt.) using Ae. tauschii x Secale cereale amphiploid forms	Lr32 (Gene) (7) ▶ Synonyms (1)
Received: 26 September 2014 / Revised: 23 November 2014 / Accepted: 2 December 2014 / Published online: 14 December 2014 © The Author(s) 2014. This article is published with open access at Springerlink.com	851413 2015 J. Appl. Genetics	
Abtried: This page shows the results of effective uses of a mander leaf rast resistance genes from Argelaps stander tittade (X. Triticosreale Witt,) was created using wide crosses to combine the valuable traits of wheat (Triticosreale Witt,) and tye (Scale cervale L) (Asse 1790); a conset to combine the valuable traits of wheat (Triticosreale Witt,) and tye (Scale cervale L) (Asse 1790); a conset to combine the valuable traits of wheat (Triticosreale Witt,) and tye (Scale cervale L) (Asse 1790); a conset to combine the valuable traits of wheat (Triticosreale Witt,) and tye (Scale cervale L) (Asse 1790); a conset to combine the valuable traits of wheat (Triticosreale Witt,) was conset to the service hard witt, but partice the Cl-F to the BC-F to the Scale conset of this opposed increasing regular bioleant formation of the side by bolds showed increasing regular bioleant formation of the side phole forms as by bayes the value of the side showed increasing regular bioleant formation of the side showed inc	Abstract This paper shows the results of effective uses of a molecular cytogenetics toolbox and molecular marker to transfer leaf rust resistance genes from Aegilops tauschi x Secale cereale (DDRR, 2n = 4x = 28) amphipioid forms to triticale cx. Bogo (ABBRR, 2n = 6x = 42). The molecular markers of resistance genes and in situ hybridization analysis of mitotic metaphase of root meristems confirmed the stable inheritance of chromosome 3D segments carrying Ir28 from the BC2F2 to the BC2F5 generation of (Ae. tauschi x 5. cereale) x thickale hybrids. The chromosome pairing analysis dimitotic of BC2F4 and BC2F5 hybrids showed increasing regular bivalent formation of 3D chromosome pairs and decreasing number of univalents in subsequent generations. The results indicate that using amphipioid forms as a bridge between wild and cultivated forms can be a successful technology to transfer the D-genome chromatin carrying leaf rust resistance genes into triticale.	



J Appl Genetics (2015) 56:163-168 DOI 10 1007/13351.014.0264.3



# **Parsing litterature**







# Integrating results

WheatIS

Filters	pathogen resistant	Q 📧	<ul> <li>1-20 of 139</li> </ul>	🕪 🕖 20 results per page 🔹 🧮				
Clear	ID	Source	Taxon	Description				
Database OPENMINTED (138) GRAMENE (1) Type	IPR002812	Gramene	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	InterPro Family, Gramene, IPR002812, DHQ_synth, 3-dehydroquinate synthase, 3-Dehydroquinate synthase () is an enzyme in the common pathway of aromatic amino acid biosynthesis that catalyses the conversion of 3-deoxy-D-[]				
BIBLIOGRAPHY (138)	10.1007/s00122-015-2514-0	<u>OpenMinTeD</u>	Triticum	Bibliography, OpenMinTeD, 10.1007/s00122-015-2514-0, Identification of a stem rust resistance locus effective against Ug99 on <mark>wheat</mark> chromos[]				
Species TRITICUM (138) AEGILOPS TAUSCHII (1) BRACHYPODIUM DISTACHYON (1) HORDEUM VULGARE SUBSP. VULGARE (1) TRITICUM AESTIVUM (1) TRITICUM URARTU (1)	<u>10.1016/j.fgb.2015.03.018</u>	<u>OpenMinTeD</u>	Triticum	Bibliography, OpenMinTeD, 10.1016/j.fgb.2015.03.018, A gene locus for targeted ectopic gene integration in Zymoseptoria tritici Understanding th cellular organization and biology of fungal pathogens requires accurate []				
	<u>10.1094/PHYTO-08-14-0224-</u> <u>R</u>	<u>OpenMinTeD</u>	Triticum	Bibliography, OpenMinTeD, 10.1094/PHYTO-08-14-0224-R, Resistance I Puccinia graminis f. sp avenae in Barley Is Associated with the Rpg5 L[				
	<u>10.1007/s00122-015-2460-x</u>	<u>OpenMinTeD</u>	Triticum	Bibliography, OpenMinTeD, 10.1007/s00122-015-2460-x, Fine mapping and characterization of <u>Sr21</u> , a temperature-sensitive diploid wheat resistanc[]				
Search	<u>10.1007/s13313-014-0339-y</u>	<u>OpenMinTeD</u>	Triticum	Bibliography, OpenMinTeD, 10.1007/s13313-014-0339-y, Races of Puccinia triticina detected on wheat in Zimbabwe, Zambia and Malawi ar regional ge[]				
About	<u>10.1007/s00122-014-2442-4</u>	<u>OpenMinTeD</u>	Triticum	Bibliography, OpenMinTeD, 10.1007/s00122-014-2442-4, Identification and mapping of Sr46 from Aegilops tauschii accession Clae 25 conferrin resist[]				
	<u>10.1007/s10658-014-0556-9</u>	<u>OpenMinTeD</u>	Triticum	Bibliography, OpenMinTeD, 10.1007/s10658-014-0556-9, Identification o new sources of adult plant resistance to Puccinia hordei in international []				
	<u>10.1007/s11032-015-0198-4</u>	<u>OpenMinTeD</u>	Triticum	Bibliography, OpenMinTeD, 10.1007/s11032-015-0198-4, Mapping of two loci conferring resistance to wheat stem rust pathogen races TTKSK (Ug99) and TRTTF in the elite hard red spring[]				
	<u>10.1094/PHYTO-12-13-0340-</u> R	<u>OpenMinTeD</u>	Triticum	Bibliography, OpenMinTeD, 10.1094/PHYTO-12-13-0340-R, Genetic Characterization of Resistance to Wheat Stem Rust Race TTKSK in Landrace and Wild Barley Accessions Identifies the rpg[]				
	10.1007/s10658-014-0509-3	<u>OpenMinTeD</u>	Triticum	Bibliography, OpenMinTeD, 10.1007/s10658-014-050-7, Population genetic structure of Microdochium majus and Microdochium nivale associated with Fusarium head blight of wheat in Hok[]				
	<u>10.1007/s10681-014-1157-6</u>	<u>OpenMinTeD</u>	Triticum	Bibliography, OpenMinTeD, 10.1007/s10681-014-1157-6, Genetic mapping of quantitative trait loci (OTL) for resistance to septoria tritici blotch in a winter multiregional adaptation to host partial resistance in a plant pathogenic comycete: Evidence from European pop[]				



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### **SEARCH EXAMPLES**





### **Exact match**

Filters	resistance		٩	🖲 🔹 1-10 of 5,673 🕟 👀	10 results per page
Clear Database	Link to source	Source	Туре	Taxon	Description
GRAMENE (1844)	<u>GO:0009862</u>	Gramene	GO process	Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare, GO process, Gramene, GO:0009862, systemic acquired resistance, salicylic acid mediated signaling pathway, The series of molec[]
OPENMINTED (1607)	<u>GO:0046686</u>	Gramene	GO process	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	response to cadmium, Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare, GO process, Gramene, GO:0046686, response to cadmium ion, Any process that results in[]
☐ TRITICEAE TOOLBOX (34) ☐ GNPIS (2) ☐ PLANTPHENODB (1)	<u>GO:0009816</u>	Gramene	GO process	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	Gramene, GO:0009816, defense response to bacterium, incompatible interaction, A response of an organism to a bacterium that prevents the occurrence or spread of disease., defence response to bacterium, incompatible int[]
<b>Type</b> □ GENE (1751) □ <u>SEQUENCE FEATURE</u> (1669)	<u>GO:1902479</u>	Gramene	GO process	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	positive regulation of response to pathogenic bacteria (incompatible interaction), positive regulation of response to pathogenic bacterium (incompatible interaction), up regulation of defence response to bacterium, inc[]
BIBLIOGRAPHY (1607)	<u>GO:1901672</u>	Gramene	GO process	Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	GO process, Gramene, GO:1901672, positive regulation of systemic acquired resistance, Any process that activates or increases the frequency, rate or extent of systemic acquired resistance., activation of salicylic acid[]
GENE ANNOTATION (73)	<u>GO:0009870</u>	Gramene	GO process	Triticum aestivum, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	defence response signalling pathway, resistance gene-dependent, defense response signalling pathway, resistance gene-dependent, Triticum aestivum, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulg[]
☐ INTERPRO FAMILY (29) ☐ GO PROCESS (27)	<u>GO:0007568</u>	Gramene	GO process	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	ageing, Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare, GO process, Gramene, GO:0007568, aging, A developmental process that is a deterioration and loss o[]
Species TRITICUM AESTIVUM (2582) TRITICUM (1607)	<u>GO:0009635</u>	Gramene	GO process	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare, GO process, Gramene, GO:0009635, response to herbicide, Any process that results in a change in state or activity of a cell o[]
AEGILOPS TAUSCHII (787) TRITICUM URARTU (631) HORDEUM VULGARE SUBSP.	<u>GO:0009817</u>	Gramene	GO process	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	GO process, Gramene, GO:0009817, defense response to fungus, incompatible interaction, A response of an organism to a fungus that prevents the occurrence or spread of disease., defence response to fungus, incompatible []
VULGARE (219) BRACHYPODIUM DISTACHYON (90) CEDITION	<u>GO:0009627</u>	Gramene	GO process	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	salicylic acid-dependent systemic resistance, Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare, GO process, Gramene, GO:0009627, systemic acquired resistanc[]
TRITICUM AESTIVUM L. (47)					



SPELTA (32)

**DURUM (14)** 

(1)

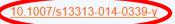
TRITICUM AESTIVUM; TRITICUM

TRITICUM AESTIVUM AESTIVUM

TRITICUM TURGIDUM SSP.



## **Access to bibliographie**



10.1007/s11032-015-0293-6

10.1007/s00122-014-2442-4

10.1007/s00122-014-2445-1



Australasian Plant Pathology

### Races of *Puccinia triticina* detected on wheat in Zimbabwe, Zambia and Malawi and regional germplasm responses

esence of gene

on

nce gene

/s13313-014-03

ce (1692)

Authors

### Authors and affiliations

Z. A. Pretorius 🖂 , B. Visser, T. Terefe, L. Herselman, R. Prins, T. Soko, J. Siwale, B. Mutari, T. I. Selinga, D. P. Hodson

Original Paper First Online: 11 December 2014

226	4
Downloads	Citations

### Abstract

To identify races of *Puccinia triticina* in southern Africa, samples of infected wheat leaves obtained from Zimbabwe, Zambia and Malawi were analysed at the University of the Free State, Bloemfontein and the Agricultural Research Council-Small Grain Institute, Bethlehem, South Africa (SA). Four races were identified from 63 isolates obtained during 2011–2013. Using the North American notation, these races coded to MCDS (74.6 %), TCPS (12.7 %), FBPT (6.3 %) and SCDS (6.3 %). MCDS and TCPS occurred in both Zimbabwe and Zambia whereas FBPT and SCDS were only detected in Zimbabwe and Malawi, respectively. Three of these races (MCDS, FPBT and SCDS) are also known in SA. SSR analysis of races detected in southern Africa suggested that MCDS and FPBT are more closely related to CCPS (3SA45), a race identified in





# **Semantic match**

Filters	pathogen		٩	📧 🖪 1-10 of 1,552 🕟 🚺	▶ 10 results per page ∨ Ξ ΞΞ
Clear	Link to source	Source	Туре	Taxon	Description
OPENMINTED (1160)  SPAMENE (331)  WHEAT PANGENOME (46)  IWGSC@GNPIS (7)	<u>GO:0010599</u>	Gramene	GO process	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	Aegilops tauschii, Hordeum vulgare subsp. vulgare, GO process, Gramene, GO:0010599, production of IsiRNA involved in RNA interference, Cleavage of double- stranded RNA to form IsiRNA (long small interfering RNA), a clas[]
GRAINGENES (6) PLANTPHENODB (1) TRITICEAE TOOLBOX (1) Type	<u>GO:0045087</u>	Gramene	GO process	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	Reactome:REACT_31297 "Innate Immune System, Xenopus tropicalis", Reactome:REACT_32992 "Innate Immune System, Gallus gallus", Reactome:REACT_6802 "Innate Immune System, Homo sapiens", Reactome:REACT_78575 "Innate Immune[]
☐ BIBLIOGRAPHY (1160) ☐ GENE (262) ☐ SEQUENCE FEATURE (46) ☐ INTERPRO DOMAIN (24)	<u>GO:0052169</u>	Gramene	GO process	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	Aegilops tauschii, Hordeum vulgare subsp. vulgare, GO process, Gramene, GO:0052169, pathogen-associated molecular pattern dependent modulation by symbiont of host innate immune response, Any process that involves recog[]
INTERPRO FAMILY (23) GO PROCESS (20) QTL (5) GENOME ANNOTATION (4)	<u>GO:0052308</u>	Gramene	GO process	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare, GO process, Gramene, GO:0052308, pathogen-associated molecular pattern dependent modulation by organism of innate immune response in other org[]
GENE ANNOTATION (3) EXPERIMENT (2) Species TRITICUM (1160)	<u>GO:0009405</u>	Gramene	GO process	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare, GO process, Gramene, GO:0009405, pathogenesis, The set of specific processes that generate the ability of an organism to induce an abnormal, g[]
□ TRITICUM AESTIVUM (174) □ AEGILOPS TAUSCHII (147) □ HORDEUM VULGARE SUBSP. VULGARE (130)	<u>GO:0009816</u>	Gramene	GO process	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	resistance response to pathogenic bacterium, response to pathogenic bacteria (incompatible interaction), response to pathogenic bacterium (incompatible interaction), Triticum aestivum, Triticum urartu, Brachypodium dis[]
□ TRITICUM URARTU (128) □ BRACHYPODIUM DISTACHYON (67) □ TRITICUM AESTIVUM L. (2)	<u>GO:1902479</u>	Gramene	GO process	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	activation of resistance response to pathogenic bacteria, activation of resistance response to pathogenic bacterium, activation of response to pathogenic bacteria (incompatible interaction), activation of response to p[]
Search	GO:0009817	Gramene	GO	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops	resistance response to pathogenic fungi, resistance response to pathogenic fungus, response to pathogenic fungi (incompatible interaction), response to pathogenic
How To Join	<u>30.0000011</u>	Gramene	process	tauschii, Hordeum vulgare subsp. vulgare	fungus (incompatible interaction), Triticum aestivum, T[]
About WheatIS nodes:	<u>GO:0052257</u>	Gramene	GO process	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vuloare	PAMP dependent induction of innate immunity of other organism, PAMP-dependent induction of innate immunity of other organism, pathogen-associated molecular pattern dependent induction by organism of innate immunity of []





# **Semantic match**

Filters	pathogen	ه ۱	1-10 of 1,16	60 🕟	▶ 🕨 10 results per page ~ Ξ
Clear	Link to source	Source	Туре	Taxon	Description
Detabase ✓ OPENMINTED (1160)	<u>10.1007/s10681-014-1343-6</u>	<u>OpenMinTeD</u>	Bibliography	Triticum	Silva, P et al. (2015). Effects and interactions of genes Lr34, Lr68 and Sr2 on wheat leaf rust adult plant resistance in Uruguay. Euphytica Effects and interactions of []
Турс — BIBLIOGRAPHY (1160)	<u>10.1007/s10681-014-1349-0</u>	<u>OpenMinTeD</u>	Bibliography	Triticum	Zhou, XL et al. (2015). Identification of QTL for adult plant resistance to stripe rust in Chinese wheat landrace Caoxuan 5. Euphytica Identification of QTL for a full of
Species	<u>10.1007/s00122-015-2532-y</u>	<u>OpenMinTeD</u>	Bibliography	Triticum	Suzuki, T et al. (2015). Resistance to wheat yellow mosaic virus in Madsen wheat is controlled by two major complementary QTLs. Theor. Appl. Genet. Resistance to wheat y[]
Search How To Join	<u>10.1007/s00122-015-2533-x</u>	<u>OpenMinTeD</u>	Bibliography	Triticum	Du, ZY et al. (2015). A QTL with major effect on reducing leaf rust severity on the short arm of chromosome 1A of wheat detected across different genetic backgrounds and diverse environments. Theor. Appl. Genet. []
About WheatIS nodes:	<u>10.1007/s00122-015-2536-7</u>	<u>OpenMinTeD</u>	Bibliography	Triticum	Liang, Y et al. (2015). Dynamic evolution of resistance gene analogs in the orthologous genomic regions of powdery mildew resistance gene MIIW170 in Triticum dicoccoides and Aegilops tauschii. Theor. Appl. Genet. []
UWA (UP):	10.1016/j.cropro.2015.04.006	<u>OpenMinTeD</u>	Bibliography	Triticum	Ma, DF et al. (2015). Inheritance and molecular mapping of stripe rust resistance genes in Chinese winter wheat Zhongliang 16. Crop Prot. Inheritance and molecular mappi[]
• Wheat Pangenome: 167167 GrainGenes (UP):	<u>10.1016/j.jcs.2015.04.005</u>	<u>OpenMinTeD</u>	Bibliography	Triticum	Kumar, A et al. (2015). Real-time quantitative PCR based method for the quantification of fungational to discriminate quantitative resistance in barley and wheat genotypes to fusarium head blight. Cereal Sci. []
<ul> <li>GrainGenes: 14968</li> <li>Gramene-WheatIS (UP):</li> </ul>	10.3835/plantgenome2014.08.0040	<u>OpenMinTeD</u>	Bibliography	Triticum	Harrison, NR et al. (2015). Y Using RNA Sequencing and In Silico Subtraction to Identify Resistance Gene Analog Markers for Lr16 in Wheat. Plant Genome Y Using RNA Seque[]
<ul> <li>Gramene: 229851</li> <li>transplant-IPGPAS (UP):</li> </ul>	10.3835/plantgenome2015.01.0002	<u>OpenMinTeD</u>	Bibliography	Triticum	Juliana, P et al. (2015). Genome-Wide Association Mapping for Leaf Tip Necrosis and Pseudo-black Chaff in Relation to Durable Rust Resistance in Wheat. Plant Genome Geno[]
<ul> <li>PlantPhenoDB: 2</li> <li>T3 (UP):</li> </ul>	<u>10.1007/s00122-015-2502-4</u>	<u>OpenMinTeD</u>	Bibliography	Triticum	Khanna, A et al. (2015). Development and evaluation of near-isogenic lines for major blast resistance gene(s) in Basmati rice. Theor. Appl. Genet. Development and evalua[]





## **TDM enrichment**

Filters	cold resistance	० । ।	1-10 of 3	,050 🕟 🗭 🕅	10 results per page $\lor$ $\equiv$ $\Xi$
Clear	ID	Source	Туре	Taxon	Description
Database □ OPENMINTED (1634) □ IWGSC@GNPIS (911) □ GNPIS (459) □ GRAMENE (46)	IPR026057	Gramene	InterPro Family	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	InterPro Family, Gramene, IPR026057, PC-Esterase, The PC-Esterase family [] is comprised of Cas1p, the Homo sapiens C7orf58, Arabidopsis thaliana PMR5 and a group of plant freezing resistance/cold acclimatization proteins typified by Arabidopsis thaliana ESKIMO1 [, ], animal FAM55D proteins, and animal FAM113 proteins []
<i>Type</i> □ BIBLIOGRAPHY (1634)	10.1017/S0021859614000409	<u>OpenMinTeD</u>	Bibliography	Triticum	Bibliography, OpenMinTeD, 10.1017/S0021859614000409, Wang, L et al []
GENOME ANNOTATION (836)	10.1080/13102818.2014.944401	<u>OpenMinTeD</u>	Bibliography	Triticum	Bibliography, OpenMinTeD, 10.1080/13102818.2014.944401, Todorovska, EG et al []
	10.1007/s00217-015-2630-8	<u>OpenMinTeD</u>	Bibliography	Triticum	Bibliography, OpenMinTeD, 10.1007/s00217-015-2630-8, Gawronska, K et al []
□ INTERPRO FAMILY (1) □ MARKER (1)	10.1038/srep28702	<u>OpenMinTeD</u>	Bibliography	Triticum	Bibliography, OpenMinTeD, 10.1038/srep28702, Kovi, MR et al []
PHENOTYPE (1)  Species	10.2135/cropsci2006.11.0712	<u>OpenMinTeD</u>	Bibliography	Triticum	Bibliography, OpenMinTeD, 10.2135/cropsci2006.11.0712, Al-Abed, D et al []
☐ TRITICUM (1634) □ TRITICUM AESTIVUM (865)	10.1094/PHYTO-97-9-1083	<u>OpenMinTeD</u>	Bibliography	Triticum	Bibliography, OpenMinTeD, 10.1094/PHYTO-97-9-1083, Hulbert, SH et al []
□ TRITICUM AESTIVUM AESTIVUM (458) □ TRITICUM AESTIVUM L. (48)	10.1007/s00122-005-0119-8	<u>OpenMinTeD</u>	Bibliography	Triticum	Bibliography, OpenMinTeD, 10.1007/s00122-005-0119-8, Shinozuka, H et al []
TRITICUM URARTU (22)	10.1139/gen-2015-0122	<u>OpenMinTeD</u>	Bibliography	Triticum	Bibliography, OpenMinTeD, 10.1139/gen-2015-0122, Upadhyaya, HD et al []
VULGARE (21)	<u>10.1104/pp.003046</u>	<u>OpenMinTeD</u>	Bibliography	Triticum	Bibliography, OpenMinTeD, 10.1104/pp.003046, Choi, DW et al []

BRACHYPODIUM DISTACHYON

(1)





### TDM enrichment Phenotypes

Filters	cold resistance	Back to Form						
Clear		Trial name	BTH_Chaux_des_F	Prés_2000_SetA				
	ID	Trial code	BTH_Chaux_des_F	Prés_2000_SetA				
Database	IRIAL BTH Chaux des Prés	Site name	Chaux des Prés					
Type	TRIAL_BTH_Chaux_des_Prés_	Trial date	from 1999/10/20 to	2000/07/31				
Species	TRIAL RTU Observates Refe	Project       INRA Wheat Breeding Network         BTH_Chaux_des_Prés       Phenotyping data         BTH_Chaux_des_Prés       Charger         Accession number       Accession name         Triticu         BTH_Chaux_des_Prés						
TRITICUM AESTIVUM AESTIVUM (457)	TRIAL_BIH_Chaux_des_Pres_	Project	INRA Wheat Breed	ing Network				
	TRIAL_BTH_Chaux_des_Prés_	Phenotyping data	Go to trial's phenoty	yping data				
Search	TRIAL BTH Chaux des Prés		Lot number	Accession number	Accession name	Тахо	n	
How To Join			Charger	CHARGER	CHARGER	Tritic	um aestivum aestivum	
About	ITRIAL_BTH_Chaux_des_Prés       Trial         NMENT (457)       TRIAL_BTH_Chaux_des_Prés       Phen         UM AESTIVUM AESTIVUM       TRIAL_BTH_Chaux_des_Prés       Phen         Join       TRIAL_BTH_Chaux_des_Prés       Phen         TRIAL_BTH_Chaux_des_Prés       TRIAL_BTH_Chaux_des_Prés       Phen         Join       TRIAL_BTH_Chaux_des_Prés       Phen         TRIAL_BTH_Chaux_des_Prés       TRIAL_BTH_Chaux_des_Prés       Frial         TRIAL_BTH_Chaux_des_Prés       TRIAL_BTH_Chaux_des_Prés       Gen         TRIAL_BTH_Chaux_des_Prés       TRIAL_BTH_Chaux_des_Prés       TRIAL_BTH_Chaux_des_Prés		Isengrain	ISENGRAIN	ISENGRAIN T		Triticum aestivum aestivum	
	TRIAL_BTH_Chaux_des_Prés_		Tremie	TREMIE	TREMIE	Tritic	um aestivum aestivum	
	TRIAL_BTH_Chaux_des_Prés_	Genotypes	AO00001	<u>AO00001</u>	AO00001	Tritic	um aestivum aestivum	
			Voltige	VOLTIGE	VOLTIGE	Tritic	um aestivum aestivum	
	TRIAL_BTH_Chaux_des_Prés_		CF9804	CF9804	CF9804	Tritic	um aestivum aestivum	
			CF9825	<u>CF9825</u>	CF9825 <u>Tr</u>		um aestivum aestivum	
				· · · · · · · · · · · · · · · · · · ·				
		Variables	Name	Notato	or Comments			
		Valiables	fr: Frost susceptib	ility	mark on a 1 to 9	9 increa	asing scale	
			Туре	Name	Email		Institution	
			Coordinator experiments Netw	of Gilles CHARMET	charmet at clermont.in	ra.fr	UMR INRA-UB Amilioration & Santi de Plantes	
		Contact	Coordinator experiments Netw	of Emmanuel rork HEUMEZ	emmanuel.heumez mons.inra.fr	at	Mons	
			Coordinator experiments Netw	of Francois-Xavier rork OURY	Francois-Xavier.OURY clermont.inra.fr	' at	INRA	
			Coordinator experiments Netw	of Bernard ROLLAND	bernard.rolland at inra.	fr	INRA	
				Δmaud				







- Text mining vocabulary closer to natural language
- Data findable by non-specialists of the data production
- Fill the gap between community







Tools are open access

www.weatis.org/search.php

openminted.eu

Ontologies

agroportal.lirmm.fr

www.weatis.org/DataStandards.php

fairsharing.org/collection/WheatDataInteroperability Guidelines





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OpenMIN7ED OpenMining Infrastructure for Text & Data

S. Aubin, C. Nedellec, *et al.* 



D. Edwards, G. Lazo, M. Caccamo, *et al.* 



E. Dzalé Yeumo Kadoré, R. Fulss, *et al.* 

