

Microbial biodiversity information for researchers and agrofood sector

Goal : a structured catalog of information on the way **microorganisms interact with their environment** for several domains (health, agriculture, environment)

Key achievements

- Ontology-based extraction and normalization of structured information on microorganism habitat and phenotypes
- From a large collection of PubMed papers.
- High quality extraction of taxa and habitats named entities, relations among them and assignment to very large taxonomy (NCBI) and ontology (OntoBiotope) measured on BioNLP-ST benchmark.
- Information available through three on-line public services at the MaIAGE **IFB bioinformatics infrastructure** (*French Bioinformatics Institute*).

Processing PubMed collection	
Documents	2,3 millions
Habitats	18,5 millions
Taxa	8,4 millions
Lives_in rel	7,2 millions
Phenotypes	1 millions
Expresses rel.	7,2 millions

On-line TDM services for microbial diversity study

Semantic relational search through all Pubmed references

Florilege: data integration on positive flora in food processing, preservation, nutrient

Alvis Search Engine

bacteria lives in "milk and milk product"

Page 2 of 772

11 **Genome sequence of *Corynebacterium casei* UCMA 3821, isolated from a smear-ripened cheese.**

Authors: *Christophe Monnet Valentin Loux Pascal Bento Jean-François Gibrat Cécile Straub Pascal Bonnarme Sophie Landaud Françoise Irlinger*

2012 *Journal of bacteriology*

Abstract *Corynebacterium casei* is one of the most prevalent species present on the surfaces of smear-ripened cheese where it contributes to the production of the desired organoleptic properties. Here, we report the draft genome sequence of *Corynebacterium casei* UCMA 3821 to provide insights into its physiology.

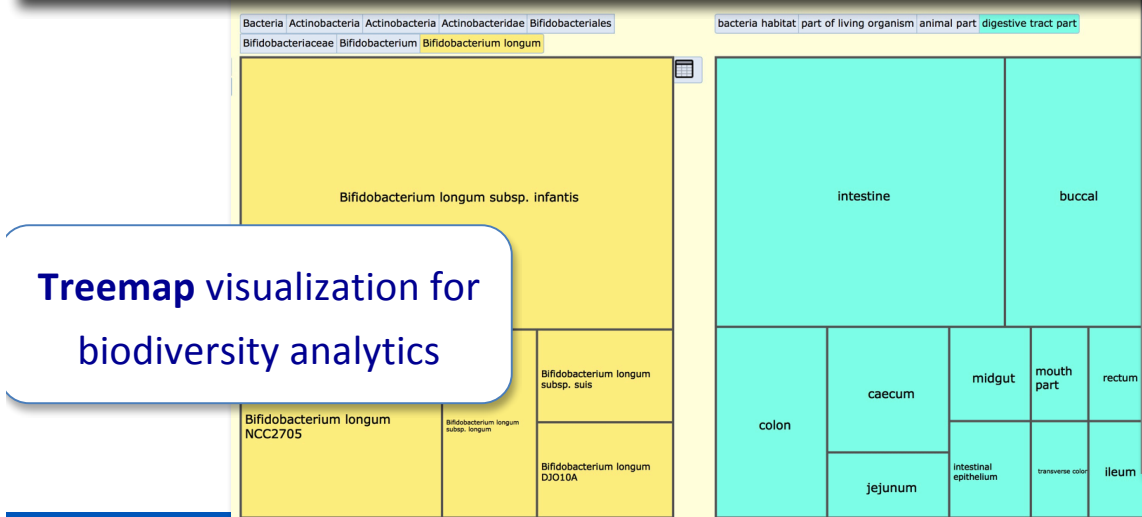
FLORILEGE

Search relations by taxon | Search relations by habitat | Search by phenotype

Search relations by taxon: CFU of *Listeria monocytogenes*

1014 relations for the taxon *Listeria monocytogenes*

SURFACE FORM OF <i>Listeria monocytogenes</i>	HABITAT	SURFACE FORM OF HABITAT
<i>Listeria monocytogenes</i>	wort	brewery wort
<i>Listeria monocytogenes</i> , <i>L. monocytogenes</i>	worm	Worms, adult worms, worm, worms
<i>Listeria monocytogenes</i> , <i>L. monocytogenes</i>	worker	laboratory workers, previous studies workers, workers, causal workers, slaughterhouse workers
<i>Listeria monocytogenes</i> , <i>L. monocytogenes</i>	wood	wood, wood surfaces, dry wood
<i>Listeria monocytogenes</i> , <i>L. monocytogenes</i>	woman	year-old woman, 69-year-old woman with bioprosthetic endocarditis, woman, young woman with immune thrombocytopenic purpura, year-old immunocompetent woman, non-pregnant women, women with abortive disease, woman with rheumatoid arthritis, elderly woman, diabetic woman, nonpregnant women, Hispanic women, women with listeriosis, year-old woman with Hodgkins disease, women
RS of <i>L. monocytogenes</i> , <i>Listeria monocytogenes</i> , <i>L. monocytogenes</i>	winter savory	savory, Satureja montana, winter savory, mountain savory, S. montana
<i>Listeria monocytogenes</i> , <i>L. monocytogenes</i>	wine	refined rice wine, wine, red wine, wines
<i>Listeria monocytogenes</i> , <i>L. monocytogenes</i>	wild animal	wild animals, wild-type animals, wild animal
<i>Listeria monocytogenes</i> , <i>L. monocytogenes</i>	whole egg	raw liquid whole egg, whole liquid egg, liquid whole egg samples, liquid whole egg, whole egg
<i>L. monocytogenes</i>	wheat flour	wheat flour



Treemap visualization for biodiversity analytics



Linking Wheat data with literature for researchers and breeders


Goal: Improve **wheat breeding** by collecting information on plant species, genes and traits of agronomic interest and link it to experimental data

Key achievements

- Public semantic search engine on Wheat phenotype information in PubMed Wheat scientific literature.
- Integration with phenotype data as a service in the international **Wheat Information System** search tool (*Wheat Initiative*), URGI IFB infrastructures.
- Based on the integration of two ontologies (WTO for general traits / WIPO observations)

Processing PubMed collection	
Documents	3 881
Genes	10 254
Taxa	14 853
Phenotypes	8 792
Markers	1 941

Wheat Data Search in WheatIS



WheatIS

Filters pathogen resistant 1-20 of 139 20 results per page

Clear

Database

- OPENMINTED (138)
- GRAMENE (1)

Type

- BIBLIOGRAPHY (138)
- INTERPRO FAMILY (1)

Species

- TRITICUM (138)
- AEGILOPS TAUSCHII (1)
- BRACHYPODIUM DISTACHYON (1)
- HORDEUM VULGARE SUBSP. VULGARE (1)
- TRITICUM AESTIVUM (1)
- TRITICUM URARTU (1)

ID	Source	Taxon	Description
IPR002812	Gramene	Triticum aestivum, Triticum urartu, Brachypodium distachyon, Aegilops tauschii, Hordeum vulgare subsp. vulgare	InterPro Family, Gramene, IPR002812, DHQ_synth, 3-dehydroquinase synthase, 3-Dehydroquinase synthase () is an enzyme in the common pathway of aromatic amino acid biosynthesis that catalyses the conversion of 3-deoxy-D-...
10.1007/s00122-015-2514-0	OpenMinTeD	Triticum	Bibliography, OpenMinTeD, 10.1007/s00122-015-2514-0, Identification of a stem rust resistance locus effective against Ug99 on wheat chromos[...]
10.1016/j.fgb.2015.03.018	OpenMinTeD	Triticum	Bibliography, OpenMinTeD, 10.1016/j.fgb.2015.03.018, A gene locus for targeted ectopic gene integration in Zymoseptoria tritici Understanding the cellular organization and biology of fungal pathogens requires accurate [...]
10.1094/PHYTO-08-14-0224-R	OpenMinTeD	Triticum	Bibliography, OpenMinTeD, 10.1094/PHYTO-08-14-0224-R, Resistance to Puccinia graminis f. sp. avenae in Barley Is Associated with the Ppg5 L[...]
10.1007/s00122-015-2460-x	OpenMinTeD	Triticum	Bibliography, OpenMinTeD, 10.1007/s00122-015-2460-x, Fine mapping and characterization of Sr21 , a temperature-sensitive diploid wheat resistanc[...]



Publication

PUBLICATION DETAILS

Title	The transcription factor BcLTF1 regulates virulence and light responses in the necrotrophic plant pathogen Botrytis cinerea
Authors	Schumacher J, Simon A, Cohrs KC, Viaud M, Tudzynski P
Journal	PLoS Genetics
Volume	10
Subvolume	1
Pages	e1004040
Year	2014

CROSS REFERENCES

Cross references : 1

Db name	Reference name	Reference value
PubMed	PMID	24415947

ASSOCIATED PROJECTS

Projects number: 1

Project name
BcLTF1

Alvis

Search Engine

[1 to 10 of 85]

Page 1 of 9

1 **Effects and interactions of genes [Lr34](#), [Lr68](#) and [Sr2](#) on **wheat leaf rust adult plant resistance** in Uruguay**

2.0

2015 *Euphytica*

Abstract Achieving **durable resistance to leaf rust** (LR), caused by Puccinia triticina, in wheat has been one of the main objectives of breeding programs. Durability of LR resistance is considered to be associated with adult plant resistance (APR) genes that are quantitatively inherited and whose expression is largely influenced by environment. Our objective was to study the effects and interactions of APR genes [Lr34](#), Lr68 and Sr2 on LR response in Uruguay using two BC1F6 populations ('LE2304*2/Parula' and 'ORL99192*2/Parula'). The experimental material was screened for LR in three artificially inoculated

pathogen resi (Phenotype)

- Synonyms (10)
- Sub-concepts (69)

Lr34 (Gene)

- Synonyms (1)

Information extraction of mechanisms involved in plant development for researchers and breeders

Goal Improving crop plant development by a better understanding of their biological mechanisms

Key achievement

- Extraction of several entities and relations involved in gene regulation mechanisms
- On-line relational semantic search engine on plant development on PubMed references
- Integration with genetic data of *Arabidopsis* plant model in the FlagDB++ information system (Institute for Plant Science, IPS2).

Processing PubMed collection	
Documents	2 046
Gene	9 490
Gene family	2
Protein	34 961
Protein family	916
RNA	56
Interaction	2 551

Plant functional analysis at FlagDB++



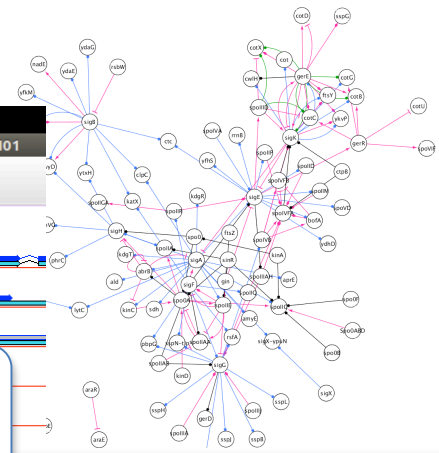
Activités net-sourceforge-jnlp-runtime-Boot mar. 15:34
 FLAGdb++ on Arabidopsis thaliana ATH01

File View Tools Gene Classification Help

Feature Manager Blast Search pattern Select region Change Species Clean Quit

3036224 3038224 3040224 3042224
 3046224 3048224 3050224 3052224
 3056224 3058224
 3066224 3068224
 3076224 3078224

genome browser



FLAGdb++

coding gene additional annotation tagged mutant
 curated annotation GST probes
 RNA gene gene family/GO repeat element
 MPS tag Affymetrix probes protein motif

Arabis thaliana
 Oryza sativa
 Populus trichocarpa
 Vitis vinifera

WEB LINKS TO...
 GENBANK, PDB, PFAM, MIPS, TAIR, ARAMEMNON, SWISSPROT, GENEVESTIGATOR, RAP-DB, eFP-BROWSER, CATdb, GENEFARM, KOG, ARABIDOPSIS-IT, JGI, INTERPRO, GENOSCOPE, ATOMEdb...

Retrieve sequences See the hits/ID outside genes Compare gene structures and promoters

Query	Relation	Target	Subcell. loc.	Function	Occurrence(s)/Nb article(s)	Inferred by
AT2G45640	INTERACTS_WITH	AT1G50640	mitochondria	ethylene responsive element binding factor 3	2/1	text mining
AT2G45640	INTERACTS_WITH	AT2G22540	nucleus	K-box region and MADS-box transcription factor family protein	1/1	text mining
AT2G45640	INTERACTS_WITH	AT3G15210	No targeting	ethylene responsive element binding factor 4	1/1	text mining
AT2G45640	BINDS_TO	AT3G57390	nucleus	AGAMOUS-like 18	1/1	text mining
AT2G45640	INTERACTS_WITH	AT4G24540	nucleus	AGAMOUS-like 24	1/1	text mining
AT2G45640	INTERACTS_WITH	AT5G63110	No targeting	histone deacetylase 6	1/1	text mining
AT2G45640	INTERACTS_WITH	AT5G13790	nucleus	AGAMOUS-like 15	none	prediction

Save Print Close

Semantic relational search

Alvis Search Engine

ABSTRACT

Postembryonic organ formation in higher plants relies on the activity of stem cell niches in shoot and root meristems, where differentiation of the resident cells is repressed by signals from surrounding cells. We searched for mutations affecting stem cell maintenance and isolated the semidominant *z28* mutant, which displays premature termination of the shoot meristem and differentiation of the stem cells. Allele competition experiments suggest that *z28* is a dominant-negative allele of the *APETALA2/AP2* gene, which previously has been implicated in floral patterning and seed development. Expression of both *WUSCHEL/WUS* and *CLAVATA3/CLV3* genes, which regulate stem cell maintenance in the wild type, were disrupted in *z28* shoot apices from early stages on. Unlike in floral patterning, *AP2* mRNA is active in the center of the shoot meristem and acts via a mechanism independent of *AGAMOUS* which is a repressor of *WUS* and stem cell maintenance in the floral meristem. Genetic analysis shows that termination of the primary shoot meristem in *z28* mutants requires an active *CLV* signaling pathway, indicating that *AP2* functions in stem cell maintenance by modifying the *WUS/CLV3* feedback loop.

Alvis AE (Alvis Annotation Editor) Demo