



METHADA

TRAINING SCHOOL IN
& DATA ANALYSIS
TRANSCRIPTOMIC
METADATA HANDLING

TRAINERS

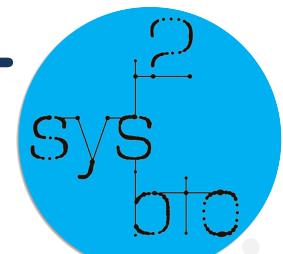


ORGANIZERS



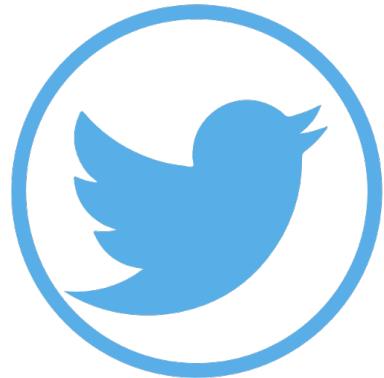
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EUROPEAN COOPERATION
IN SCIENCE AND TECHNOLOGY



CSIC - UNIVERSIDAD DE VALENCIA
VENUE



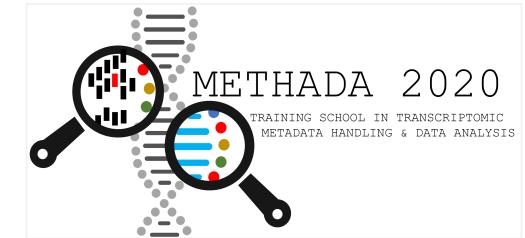


TWITTER

INTEGRAPE
@I17111

@i2sysbio

#METHADA2020



Program

Day 1 (5th Feb, 9:00-18:00)

- 9:00 Welcome from I2SysBio Director/Vice-director and COST Action MC Chair (Mario Pezzotti).
Presentation of the Training School (Jerome Grimpel, Tomás Matus).
- 9:30 Introduction and setting up of the Jupyter Notebook working environment (Marco Moretto).
- 10:30 Coffee
- 11:00 Metadata handling (Marco Moretto).
-Background. General standards: ISA tab tools, MIAMI protocol.
-Recurrent pitfalls in metadata submission. The NCBI-SRA case.
- 13:00 Lunch
- 14:30 Metadata handling (Continue, Marco Moretto and Tomas Matus).
-European metadata cases: upload from excel using ABI (Application Binary Interface).
-Relation between experimental designs and metadata annotation. Complex versus complicated designs.
- 15:45 Coffee
- 16:00 Best practices and useful tips for the analysis of gene expression data (Paolo Sonego).
-How to take decisions regarding: type of sequencing, number of replicates, depth, where to map reads (genome vs transcriptome, genome accessions) and annotations.





Day 2 (6th Feb, 9:00-18:00)

- 9:00 Transcriptomics data analysis (Paolo Sonego)
-Practical session with a typical workflow on grapevine real data downloaded from GEO/SRA. DE Analysis, EDA and visualization of transcriptomics data using R/Bioconductor (Paolo Sonego).
- 10:30 Coffee
- 11:00 Transcriptomics data analysis (Continue)
- 12:00 Tools available at Galaxy for transcriptomic analysis (Jerome Grimplet).
- 13:00 Lunch
- 14:30 Resources: The TomExpress RNA-Seq platform, what can we learn from the tomato community regarding public RNA-Seq data handling, visualization and mining? (Elie Maza)
- 16:30 Coffee
- 16:45 Grape-specific platforms (first part):
-GREAT (video-remote lecture: Camille Rustenholz, Amandine Velt, INRAE COLMAR).
-VitisNet/eFP-Browser Corvina (Jerome Grimplet).
- 21:00 Gala Dinner



Day 3 (7th Feb, 9:00-16:00)

- 9:00 Grape-specific platforms Marco Moretto)
-Tutorial and Outputs from the VESPUCCI platform.
- 10:30 Coffee
- 11:00 Access to Phyton/R packages in Jupyter to see how VESPUCCI is built.
- 12:00 Metadata annotation in VESPUCCI as a case of study.
- 14:00 Lunch
- 15:30 Discussion and roundup of Training school (Mario Pezzotti).



SELECTION OF ATTENDEES



Early career researchers (PhD, Postdocs, Early stage PIs)

From COST member countries or MC Observers from Near-neighbouring countries.

Evaluation criteria:

Knowledge in transcriptomics, genomics, and computational biology-related aspects of grapevine, with high motivation in spreading good metadata handling practices learned during the training school, directed to computational biologists or biologists/biotechnologists with bioinformatics skills:

Basic knowledge of bioinformatics and computational biology theory

Basic programming in R and/or Python.

Submitted data:

Reason for participating

Curriculum vitae

Recommendation letter (in case of PhD students and Postdocs)

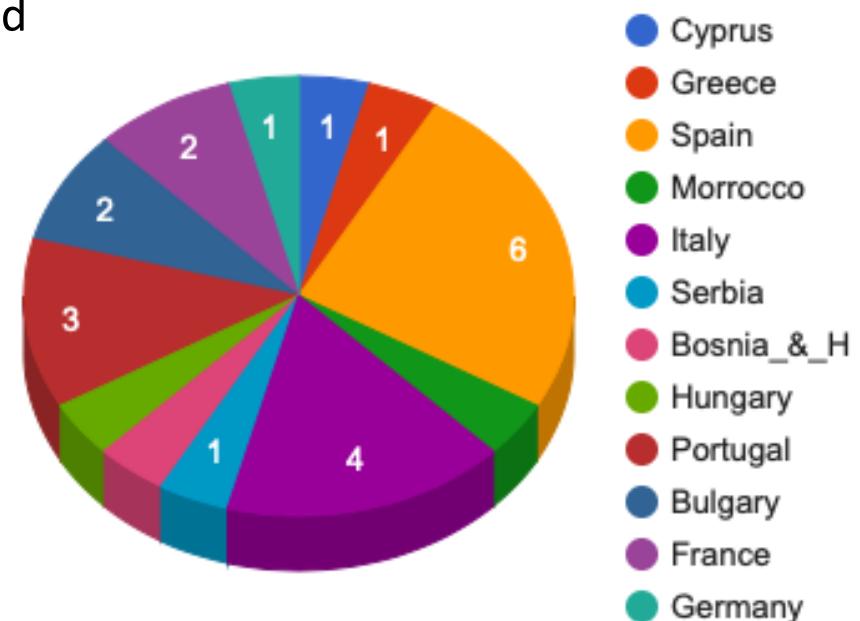
TRAINERS SELECTED



20 GRANTS AWARDED

24 TOTAL ATENDEES

- Gender Balance 12/12
- Inclusiveness Target Countries (ITC) included Institutes (not nationality)
- PhDs: 10
- Postdoc: 9
- PIs: 5





The *Vitis* phenotyping vocabulary

Éric Duchêne, SVQV, INRAE Colmar, France

É.Duchêne - COST IntegrApe January 2020



How to describe phenotypic data ?

- Describe the experiment,
- Describe the plant material,
- Describe the data and how they were obtained,



Objectives for the COST integrape projects

- Unique identifier for an accession?
- Controlled vocabulary for the organs,
- Guidelines for describing the developmental stages,
- An ontology for variables,
- A vocabulary for treatments?

How to describe the treatments?



- Fertilizers
- Water supply (method, date, dose,...)
- Heat treatment,...
- Use of phytochemicals (method, product, date, dose)
- Technical operation (trellising? hedging? pruning?,...)
-

->rely on ELIXIR?

Adapt/modify for grapevine?

How to describe phenotypic data ?



- Use data standards

- Semantic
 - Description of the data **key concepts** (the description of the data itself is more **in the metadata**)
 - Controlled vocabularies: term name and definitions
 - Ontologies: semantic links between terms
 - *Biologist* driven
- Reuse
 - Formatting and Organizing the data
 - **Format Standards** : CSV, VCF, GFF,
 - **Metadata Standards** (about their production): MIAPPE (www.miappe.org) , etc...
 - *Biologist & Computer scientist* driven
- Technical **infrastructure**
 - Data integration and sharing
 - Interoperability : tools and databases (GA4GH, Breeding API www.brapi.org)
 - *Computer scientist* driven

Describing the experiment



- Who was in charge of the experiment?
- What were the objectives?
- What were the objects to compare ? What kind of treatments were applied ?
- What was the statistical design?



Describing the experiment: the MIAPPE project

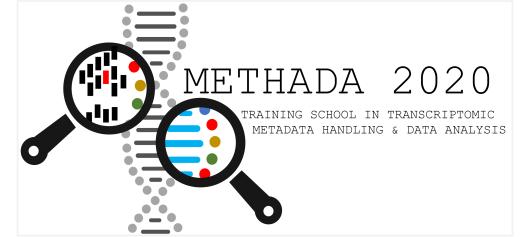


MIAPPE

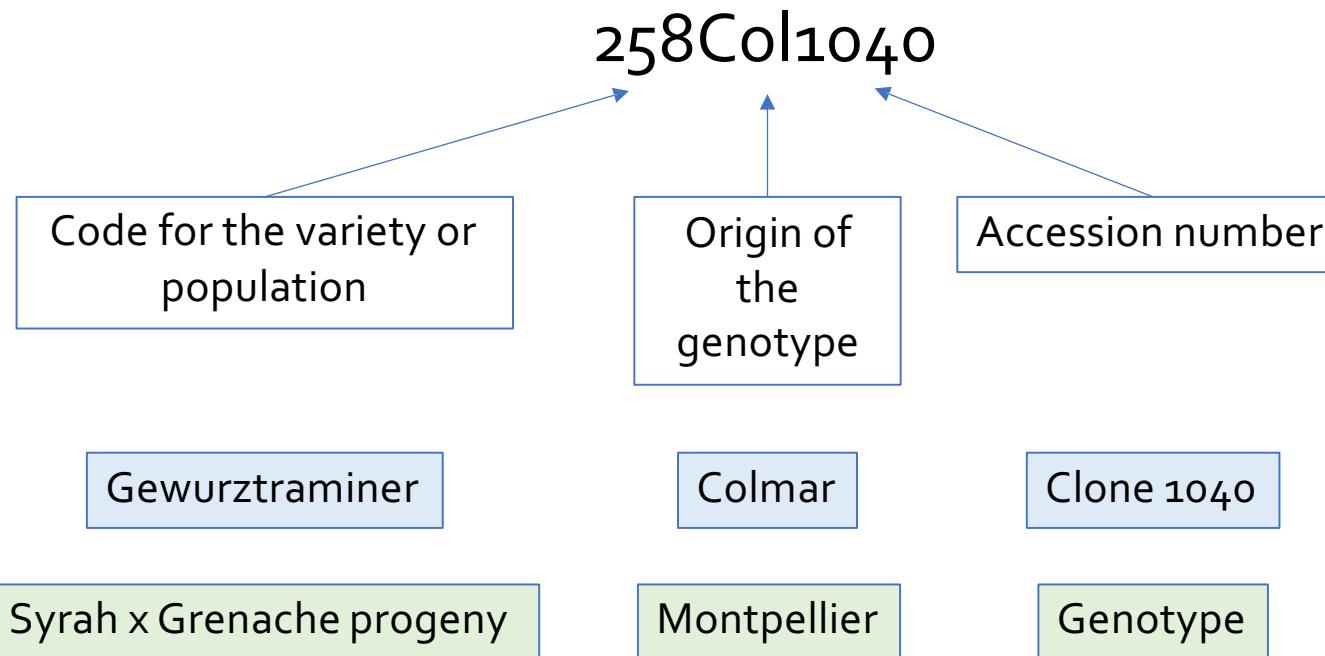
Minimum Information About a Plant Phenotyping Experiment

<https://www.miappe.org>

« Defines a list of attributes that might be necessary to fully describe a phenotyping experiment, following the model originally established for microarray data »



Describing the plant material: example for the grapevine accession number in France



Describing the plant material: VIVC database for varieties



Vitis International Variety Catalogue VIVC

Home Home / Cultivar name EXCEL Document

Cultivar name

Cultivar name (search includes both, prime names and synonyms)
 Prime name
 Synonym

merlot i

Definition of the term prime name

Search Reset

Showing 1-17 of 17 items.

Cultivar name	Prime name	Variety number VIVC	Species	Color of berry skin	Country or region of origin of the variety
MERLOT	MERLOT NOIR	7657	VITIS VINIFERA LINNÉ SUBSP. VINIFERA	NOIR	FRANCE
MERLOT BIANCO	MERLOT BLANC	7655	VITIS VINIFERA LINNÉ SUBSP. VINIFERA	BLANC	FRANCE
MERLOT BLACK	MERLOT NOIR	7657	VITIS VINIFERA LINNÉ SUBSP. VINIFERA	NOIR	FRANCE
MERLOT BLANC	MERLOT BLANC	7655	VITIS VINIFERA LINNÉ SUBSP. VINIFERA	BLANC	FRANCE

<http://www.vivc.de>

Describing the plant material: The European Vitis database for accession



Public access | Catalogue of autochthonous varieties

Search criterion : riesling
Search result : 13 (1 -- 13)

[Back to search form](#) [Previous page](#)

| [First](#) | [Last](#) |

Accession name	Color of berry skin	Variety name	Holding institution	Accession number (access to variety description pdf format)	Species	Subtaxa	Subtaxa authority	Country of origin of the variety	Year of description
Riesling			ESP074	P04#41043	VITIS VINIFERA LINNÉ	SUBSP. VINIFERA		SPAIN	2001
RIESLING		RIESLING	ITA368	ITA368-2448	VITIS VINIFERA LINNÉ	SUBSP. VINIFERA		GERMANY	2007
Riesling clone 1090		Riesling	FRA274	FRA274-274E5				FRANCE	
Riesling bleu		Riesling bleu (Collection Oberlin)	FRA139	FRA139-0Mtp964	VITIS VINIFERA LINNÉ	SUBSP. VINIFERA		FRANCE	2001
Riesling E15		Riesling	FRA274	FRA274-240300151				FRANCE	2008
Riesling E16		Riesling	FRA274	FRA274-240300161				FRANCE	2008
Riesling E20		Riesling	FRA274	FRA274-240300201				FRANCE	2008
Riesling E21		Riesling	FRA274	FRA274-240300211				FRANCE	2008
Riesling heiligenstein		Riesling Heiligenstein (Collection Oberlin)	FRA139	FRA139-0Mtp965	VITIS VINIFERA LINNÉ	SUBSP. VINIFERA		FRANCE	2001
Riesling musqué		Riesling musqué (Collection Rodrian)	FRA139	FRA139-0Mtp966	VITIS VINIFERA LINNÉ	SUBSP. VINIFERA		GERMANY	2001
Riesling Renano			ITA362	ITA362-1679	VITIS VINIFERA LINNÉ	SUBSP. VINIFERA		GERMANY	2008
RIESLING ROT			AUT024	AUT024-316					2001
RIESLING ROT		RIESLING ROT	DEU098	DEU098-1998-129	VITIS VINIFERA LINNÉ	SUBSP. VINIFERA		GERMANY	

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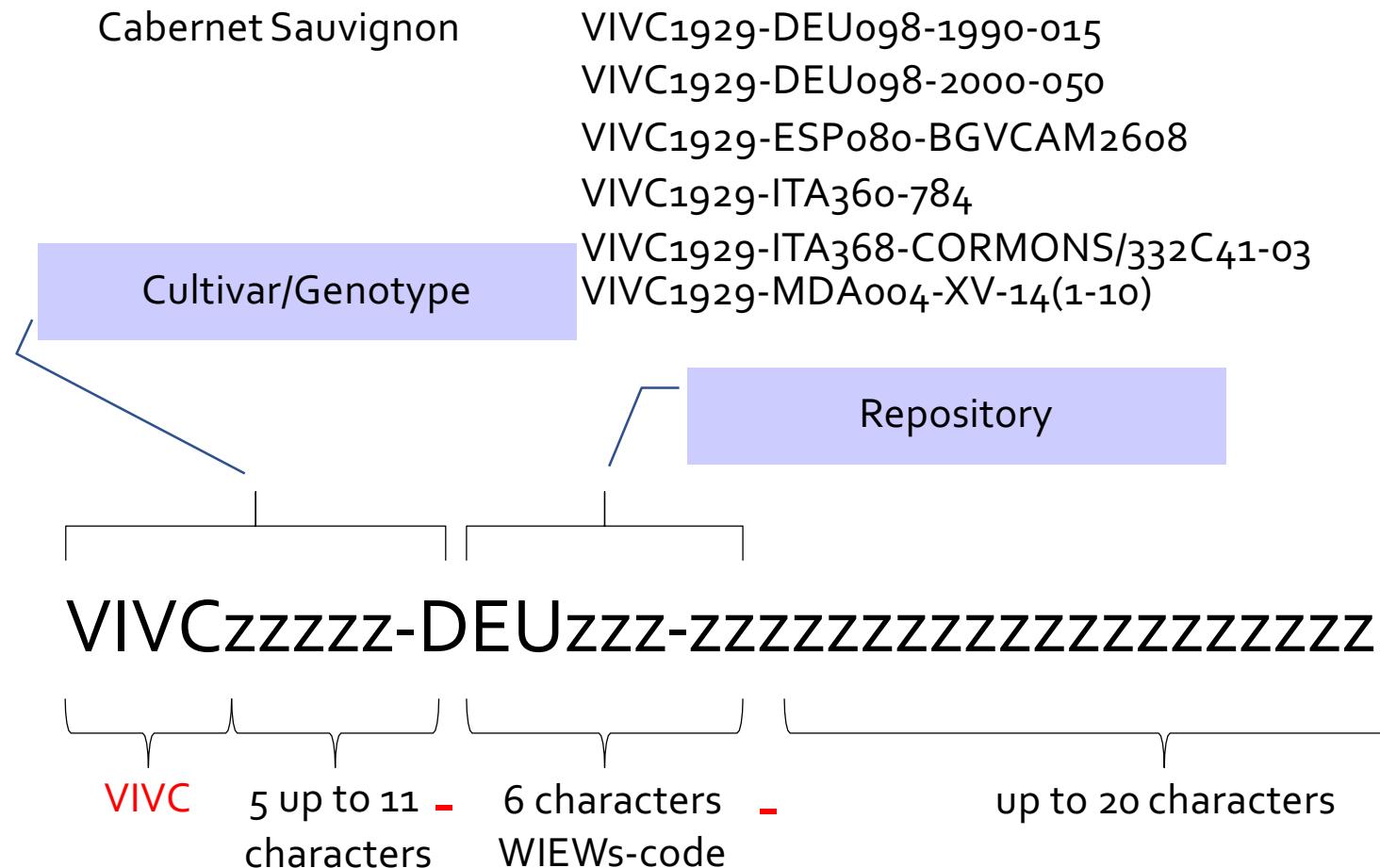
| [First](#) | [Last](#) |

EU.Vitis - Copyright JKI © 2007

<http://www.eu-vitis.de/index.php>

Developing a unique Identifier for an Accession

Reinhard Töpfer, JKI



Describing the organs: a proposal



Category	Organ	Synonym
Perennial organs	cane	
Perennial organs	grafting point	
Perennial organs	node	
Perennial organs	old wood	
Perennial organs	root	
Perennial organs	rootstock	
Perennial organs	scion	
Perennial organs	spur	
Perennial organs	trunk	
Perennial organs	wood	
Reproductive organs	berry	
Reproductive organs	berry flesh	berry pulp
Reproductive organs	berry skin	
Reproductive organs	cluster	bunch
Reproductive organs	flower	
Reproductive organs	green berry	
Reproductive organs	inflorescence	
Reproductive organs	ripening berry	maturing berry
Reproductive organs	seed	



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Describing the organs: a proposal



Category	Organ	Synonym
Vegetative organs	blade	
Vegetative organs	bud	
Vegetative organs	internode	
Vegetative organs	lateral branch	axillary shoot
Vegetative organs	leaf	
Vegetative organs	mature leaf	
Vegetative organs	petiole	
Vegetative organs	primary shoot	
Vegetative organs	secondary shoot	
Vegetative organs	shoot	
Vegetative organs	shoot tip	
Vegetative organs	sucker	water shoot
Vegetative organs	tendril	
Vegetative organs	young leaf	
Vegetative organs	young shoot	

Describing the organs: a proposal



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Describing the developmental stages

Descriptors from 950 RNA-seq datasets

103 days after anthesis (ripening, 22.4 °Brix)	6
121 days after anthesis (late ripening, 25.3 °Brix)	6
20 °Brix	5
20 Brix	23
22 °Brix	5
22 Brix	19
24 °Brix	5
24 Brix	21
26 °Brix	5
26 Brix	21
28 days after mid-veraison (v+28) mid-ripening	12
35 days after mid-veraison (v+35) ripeness	12
68 days after anthesis	6
7 weeks post-flowering	5
74 days after anthesis (early ripening, 17.5 °Brix)	6
93 days after anthesis	6
at 65 DAF (veraison)	1
at 90 DAF (ripe stage)	1
Berries beginning to color and enlarge (E-L stage 35)	2
Berries ripe for harvest (Bbch 89)	27
Berries with intermediate Brix values (E-L stage 36) ~	4

Describing the developmental stages



Organ	Green berries
41 days after anthesis	6
47 days after anthesis (before ripening, 4.9 °Brix)	6
5 weeks post-flowering	3
at 40 DAF (green stage)	1
Berries beginning to touch : Bbch 77 (just prior veraison)	15
Berries beginning to touch (Bbch77)	12
E-L 31 (pea-size berries)	2
E-L 33	3
E-L 34	3
EL-33/34 (green hard berry, just pre-veraison)	6
EL-33/34 (green hard berry, just pre-veraison) - 20 hours post treatment	3
EL-33/34 (green hard berry, just pre-veraison) - 24 hours post treatment	3
Green	7
Green berries	6
Green berries the day of veraison	6
Pea-size berries (E-L stage 31)	3
Pea-sized berries : Bbch 75 (almost 20 days after flowering)	15
Pea-sized berries (Bbch 75)	14
Post fruit set (35 DAF ; E-L 32)	3
Post-fruit set (5 weeks post flowering)	2
Post-veraison	1
Pre-veraison	1
Pre-veraison (5-6 weeks post-anthesis)	2
Pre-veraison (5-6 weeks post-anthesis) ; 1 hour post-treatment	2
Pre-veraison (E-L 34)	12
Pre-veraison, majority of berries touching, BBCH79	36
Veraison (10 weeks post flowering)	2
Young	1

Describing the developmental stages



Organ	Inflorescence
Immature, stage 1	2
Immature, stage 2	2
Immature, stage 3	2

Organ	Flower buds
Preatthesis early H stage (aprox. three weeks before flowering)	6
Stage B - BBCH 05	6
Stage D - BBCH 11	6
Stage G - BBCH 55	6
Stage H - BBCH 57	5

Describing the developmental stages



A working group in France proposed a protocol

<https://doi.org/10.15454/1.5514275483910464e12>

Under translation in several languages

3 Véraison / BBCH 85 - Stade M

Stade 50% de baies en véraison

La véraison marque le début du processus de maturation des raisins, qui se terminera à la vendange.

- Ne prendre en compte pour les notations que les souches formées de manière définitive et en production.
- On considère qu'une baie est verrée si elle est molle. Ce critère permet une comparaison sans biais des variétés blanches ou rouges. Faire les notations toujours à la même heure, de préférence le matin. Le stade retenu correspond au moment où 50% des baies sont molles.
- Comment évaluer le taux de baies verryées ? Deux méthodes sont possibles :
 - par palpation d'au moins 100 baies *in situ*, ou au laboratoire (ex. 20 baies sur 5 ceps). Pour certaines variétés il n'est en effet pas possible de faire des prélèvements ponctuels des baies car les grappes sont trop compactes. Il est donc nécessaire de faire l'évaluation *in situ* sans prélèvement destructif.
 - l'utilisation de l'apparition de la couleur est acceptable pour les comparaisons interannuelles d'un même cépage sur un même site. Dans ce cas, une estimation visuelle du pourcentage de baies colorées sur l'ensemble des grappes du pied doit être effectuée.
- Il est nécessaire de faire les observations sur un minimum de 5 souches par zone homogène.
- Fréquence de passage : à partir du moment où l'on observe au minimum 5% de baies molles, faire au moins un passage supplémentaire avec au maximum une semaine d'intervalle de manière à avoir une observation après 50% de baies molles.
- La date "50% de baies verryées" est obtenue par interpolation entre les valeurs observées avant et après 50%.

Auteurs:

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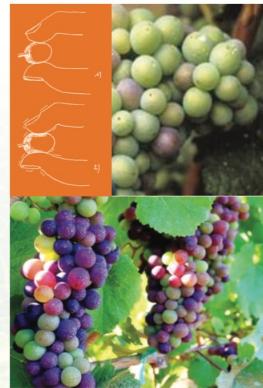
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Phénologie de la vigne
Quels stades observer et comment ?

PERPHECLIM

INRA
SCIENCE & IMPACT



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Describing the developmental stages

Organ	Leaves
oh	1
1 DPI with Erysiphe necator c-strain - fully expanded leaves	23
1 DPI with mock inoculation - fully expanded leaves	24
1 year with 6 mature leaves	3
10 minutes post inoculation with <i>Neofusicoccum parvum</i>	6
10 minutes post inoculation with sterile Potato Dextrose Broth	6
12 hours post inoculation - Fully expanded leaf	3
24 hours after inoculation - 2 year old plant	12
24 hours after <i>Plasmopara viticola</i> inoculation	1
24 hours after punching	1
24 hours after treatment with adapted spider mite herbivory- Plantlet (plant with 1–2 leaves)	4
24 hours after treatment with non-adapted spider mite herbivory- Plantlet (plant with 1–2 leaves)	4
24 hours after UV treatment	1
24 hours post inoculation - Fully expanded leaf	3
2h after heat stress - 1 year with 6 mature leaves	9
3 days post inoculation - Fully expanded leaf	3
3 months	3
40 days of illumination - Seedling	8
48 hours after <i>Plasmopara viticola</i> inoculation	1
48 hours after punching	1
48 hours after UV treatment	1
5 DPI with Erysiphe necator c-strain - fully expanded leaves	25
5 DPI with mock inoculation - fully expanded leaves	24
6 days post inoculation - Fully expanded leaf	3
7 days after bud break	6
before inoculation - 2 year old plant	12
Immature, stages 1, 2, 3	2
mix of 0.5 - 1 - 1.5 months post inoculation with <i>Neofusicoccum parvum</i>	6

Describing the developmental stages

A proposal for the berries:

- Clearly make the difference between green and ripening berries
- For green berries: days after flowering?
- For ripening berries, by priority:
 1. Days after véraison,
 2. °Brix
 3. Heat sums (base 10°C) after véraison,
 4. pH
 5.

A proposal for the leaves:

- Age (nb from the apex)
- Position (from the base of the shoot)
- (Total number of leaves on the shoot)
- Type of shoot (primary, secondary, lateral)

Describing a variable: a general approach

Principles for the « crop ontology »

<http://www.cropontology.org>

1 variable = {1 trait, 1 method, 1 scale}

The essence of the CO model is to decompose a variable recorded by the breeders into:

- A **trait**: “what is observed”
- A **method**: “how the observation is made”
- A **scale**: “how the observation is expressed”

In other words, **a variable is the combination of 1 trait, 1 method and 1 scale**. To illustrate this, the Table 2 shows the breakdown of the PH, GCOL and GY examples.

Table 2: Breakdown of PH, GCOL and GY into trait, method and scale

Variable	Trait	Method	Scale
PH	The distance from the ground to the top of the canopy	Measured with a ruler	cm
GCOL	Color of the grain	Visually assessed	5-category color scale
GY	Yield of dehulled grain	Divide harvested grain weight by plot surface	g/m ²

Describing a variable: for the grapevine

http://www.cropontology.org/ontology/CO_356/Vitis

- **a trait**, like pruning weight or flowering date,
- **a method** that describes how the trait was measured, *i.e.* with a scale or computed through image analysis,
- **a scale/unit** : *i.e.* . International system units like centimeter or meter, or notation scale like late, early, etc...
 - Built with scientist from INRA in France
 - 273 variables available

The *Vitis* Ontology: use-case

The screenshot shows the GnpIS interface with the following details:

- Header:** EURGI logo, GnpIS GENETIC AND GENOMIC INFORMATION SYSTEM, English/French flags, FEEDBACK link.
- Left Sidebar:**
 - Log in link.
 - Preferences: All species dropdown.
 - Main: HOME, NEWS, ABOUT.
 - GnpIS:
 - GNPIS PORTAL
 - PHENOTYPES
 - Experimental data
 - Phenotyping
 - Ontologies
 - Data submission
 - GENETIC RESOURCES
 - GRC COLLECTIONS
 - GENOMES
 - SEQUENCES
 - GENETIC MAPS
 - POLYMORPHISMS
 - ASSOCIATION
 - PLANT SYNTENY
 - TRANSCRIPTOMIC
- Middle Content:**
 - Traits, methods and scales** search bar: Search terms...
Results:
 - Biotic stress TRAIT CLASS
 - Morphological TRAIT CLASS
 - Phenological TRAIT CLASS
 - Budbreak TRAIT
 - Flowering TRAIT
 - DOY_FLO: Day of Year Flowering (50%)
 - FLO_50: Flowering date (50%) VARIABLE
 - FLO_END: Flowering end VARIABLE
 - FLO_OIV: OIV: Time of full bloom VARIABLE
 - FLO_START: Flowering start VARIABLE**
 - HS_Tmax_B10_BudFlo: Heat sums with
 - MI-FLO-relatif: Flowering date (50%) rel
 - Maturity TRAIT
 - Number of leaves TRAIT
 - Number of sprouted buds TRAIT
 - FLO_START: Flowering start VARIABLE** details:
 - Ontology name: Vitis inra ontology
 - Identifier: CO_356:1000083
 - Name: FLO_START
 - Synonyms: Flowering start
 - Institution: INRA
 - Scientist: Eric Duchene
 - Crop: VITIS
 - Flowering TRAIT** details:
 - Identifier: CO_356:2000001
 - Name: Flowering
 - Entity: Plant
 - Attribute: Flowering
 - Class: Phenological
 - FLO_START Method METHOD** details:
 - Identifier: CO_356:3000169
 - Name: FLO_START Method
 - Class: Estimation
 - Calendar date SCALE** details:
 - Identifier: CO_356:4000003
 - Name: Calendar date
 - Data type: Time

The *Vitis* Ontology: use-case

The screenshot shows the GnpIS interface with the following details:

- Header:** INRA-URGI logo, GnpIS GENETIC AND GENOMIC INFORMATION SYSTEM, English language selection, and a Feedback link.
- Left Sidebar:**
 - Log in** button.
 - Preferences** dropdown set to "All species".
 - Main** menu with links to HOME, NEWS, and ABOUT.
 - GnpIS** menu with links to GNPIIS PORTAL, PHENOTYPES (Experimental data, Phenotyping, Ontologies, Data submission), GENETIC RESOURCES (GRC COLLECTIONS, GENOMES, SEQUENCES, GENETIC MAPS, POLYMORPHISMS, ASSOCIATION, PLANT SYNTENY, TRANSCRIPTOMIC).
- Central Content:**
 - Traits, methods and scales** search bar and dropdown set to English.
 - BERRY_TA: Berry Titratable acidity VARIABLE** entry highlighted in the list.
 - Ontology name:** Vitis inra ontology
 - Identifier:** CO_356:1000231
 - Name:** BERRY_TA
 - Synonyms:** Berry Titratable acidity
 - Institution:** INRA
 - Scientist:** Eric Duchene
 - Crop:** VITIS
 - Titratable acidity TRAIT** entry with details:
 - Identifier:** CO_356:2000157
 - Name:** Titratable acidity
 - Description:** Necessary complement:Sampling date
 - Entity:** Berry
 - Attribute:** Acidity
 - Class:** Biochemical
 - BERRY_TA Method METHOD** entry with details:
 - Identifier:** CO_356:3000153
 - Name:** BERRY_TA Method
 - Class:** Measurement
 - meq/l SCALE** entry with details:
 - Identifier:** CO_356:4000012
 - Name:** meq/l
 - Data type:** Numerical

The woody plant ontology: an example to follow

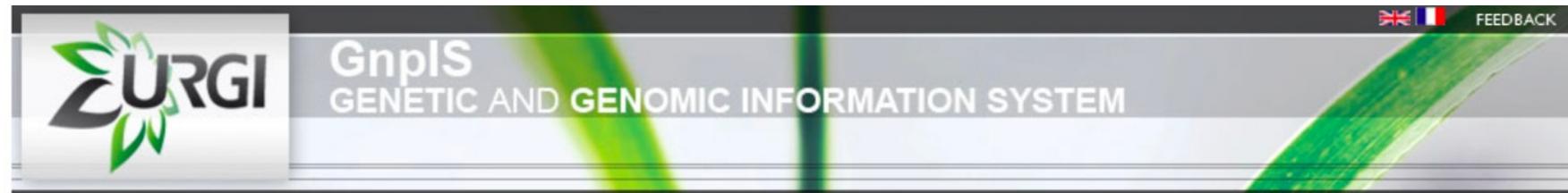
The screenshot shows the GnpIS interface with the following details:

- Header:** EURGI logo, GnpIS GENETIC AND GENOMIC INFORMATION SYSTEM, English language selection, and FEEDBACK link.
- Left Sidebar:**
 - Log In** button.
 - Preferences** dropdown set to "All species".
 - Main** menu with links to HOME, NEWS, ABOUT.
 - GnpIS** menu with sections:
 - GNPIS PORTAL
 - PHENOTYPES
 - Experimental data
 - Phenotyping
 - Ontologies
 - Data submission
 - GENETIC RESOURCES
 - GRC COLLECTIONS
 - GENOMES
 - SEQUENCES
 - GENETIC MAPS
 - POLYMORPHISMS
 - ASSOCIATION
 - PLANT SYNTENY
 - TRANSCRIPTOMIC
- Central Content:**
 - Ontologies** heading.
 - Traits, methods and scales** search bar and dropdown set to English.
 - LCC: Leaf chlorophyll content VARIABLE** entry highlighted in blue.
 - Search terms...** input field.
 - Trait List:** A tree view of traits under "LCC: Leaf chlorophyll content VARIABLE".
 - Content of Saccharose in the leaf (TRAIT)
 - Delta cadidene content (TRAIT)
 - Enzymatic activity of Glutamine (TRAIT)
 - Enzymatic activity of glycolate oxydase (TRAIT)
 - Enzymatic activity of hydroxypyruvate reducta
 - Enzymatic activity of phosphoenolpyruvate ca
 - Gamma cadidene content (TRAIT)
 - Germacrene content (TRAIT)
 - Hemicellulose wood composition (TRAIT)
 - Hydroxyphenylaldehyde/Syringaldehyde/Coni
 - Leaf chlorophyll content (TRAIT)
 - LCC: Leaf chlorophyll content VARIABLE (highlighted)
 - Limonene content (TRAIT)
 - Polyphenols cork composition (TRAIT)
 - Polysaccharide cork composition (TRAIT)
 - Detail View:** Information for "LCC: Leaf chlorophyll content VARIABLE".

Ontology name	Woody Plant Ontology
Identifier	CO_357:0000248
Name	LCC
Synonyms	Leaf chlorophyll content LCC[Adonis]
Context of use	QTL analysis
Status	Standard for INRA
Institution	INRA
Scientist	Célia Michotey
Date	20/02/2018
Crop	WoodyPlant

Leaf chlorophyll content (TRAIT)
Identifier: CO_357:1000207
Name: Leaf chlorophyll content
Description: Leaf chlorophyll content
Main abbreviation: LCC
Entity: leaf
Attribute: chlorophyll content
Status: Standard for INRA
Class: Biochemical

Leaf chlorophyll content protocol (METHOD)
Identifier: CO_357:2000096
Name: Leaf chlorophyll content protocol
Description: Chlorophyll content was measured twice a week from 6 days before water-logging to 47 days of treatment. Measurements were made on 3 fully developed leaves of the last growth flush before water-logging on each tree using a chlorophyll content



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Ontologies

Traits, methods and scales

English

Search terms...

```
graph TD; Root["Single berry weight TRAIT"] --- Sbw["Single berry weight TRAIT"]; Root --- Scw["Single cluster weight TRAIT"]; Root --- Ssw["Single seed weight TRAIT"]; Root --- Tnif["Total number of inflorescences/number of primary shoots TRAIT"]; Root --- Tns["Total number of shoots TRAIT"]; Root --- Vsg["Vigor of shoot growth TRAIT"]; Root --- Yld["Yield TRAIT"]; Root --- Bio["Biochemical TRAIT CLASS"]; Root --- Bst["Biotic stress TRAIT CLASS"]; Root --- Mph["Morphological TRAIT CLASS"]; Root --- Pnl["Phenological TRAIT CLASS"]; Root --- Tech["Technological TRAIT CLASS"]; Root --- Wto["Walnut Trait Ontology ONTOLOGY"]; Root --- Wlpo["Wheat Inra Phenotype Ontology ONTOLOGY"];
```

The diagram shows a hierarchical tree of traits and ontologies. At the top level are "Single berry weight", "Single cluster weight", "Single seed weight", and "Total number of inflorescences/number of primary shoots". Below "Total number of inflorescences/number of primary shoots" are "Total number of shoots" and "Vigor of shoot growth". Below "Yield" is "Biochemical". Below "Biotic stress" are "Morphological", "Phenological", and "Technological". At the bottom level are "Walnut Trait Ontology" and "Wheat Inra Phenotype Ontology". Each node is labeled with its name and a color-coded category: TRAIT, TRAIT CLASS, or ONTOLOGY.

FERT_PRIM: Total number of inflorescences/number of primary shoots VARIABLE

Ontology name	Vitis inra ontology
Identifier	CO_356:1000267
Name	FERT_PRIM
Synonyms	Total number of inflorescences/number of primary shoots
Institution	INRA
Scientist	Eric Duchene
Crop	VITIS

Total number of inflorescences/number of primary shoots TRAIT

Identifier	CO_356:2000228
Name	Total number of inflorescences/number of primary shoots
Description	Total number of inflorescences/number of primary shoots
Entity	Inflorescence
Attribute	Number
Class	Agronomical

FERT_PRIM Method METHOD

Identifier	CO_356:3000163
Name	FERT_PRIM Method
Class	Measurement

To conclude

- There are existing standards for describing an experiment and the plant material,
- For the grapevine, the *Vitis ontology* is ready to be used by the international scientific community,
- A draft for an ontology for organs,
- A draft for guidelines for developmental stages,
- How to finish and validate the drafts?
- Where to store the information/the guidelines?