

Developing and sharing ontologies: a key step towards efficient genetic and breeding strategies, a sorghum case study

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Talk's Outline

My expectations, to reach my objectives, in relation with the description of phenotypic data ?

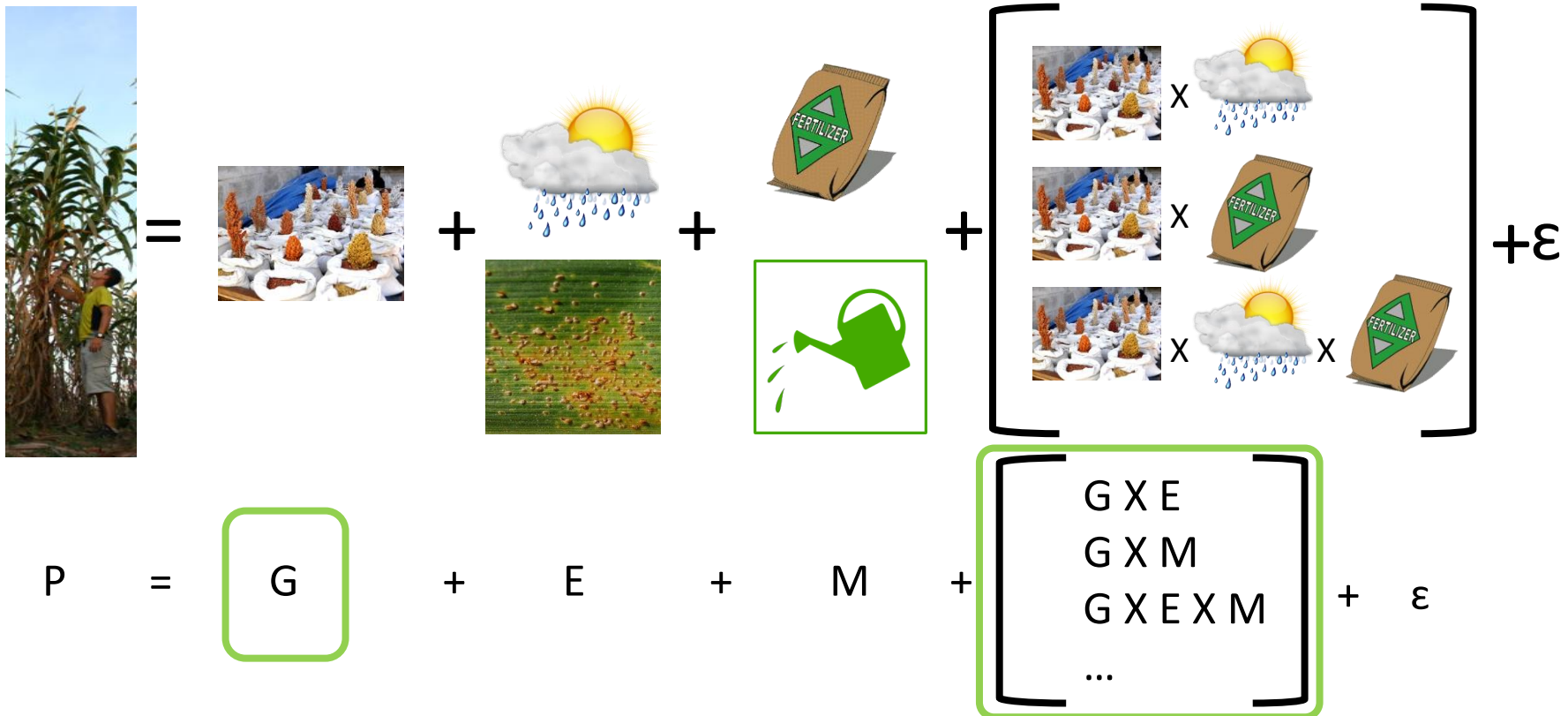
What do I need to efficiently describe traits and make them useful for me and the communities ?

How to optimize the development of controlled vocabularies and extend their uses ?

What are my expectations, in relation to phenotypic data,
to reach my objectives?

As a geneticist involved in a breeding programme, my objectives are:

- To develop varieties (growers and end-users)
- To predict their phenotype(s) in different contexts



- Estimating G...(on available trials) and predicting P (in non tested environments for tested and non tested genotypes)

Estimating G and GxN to predict P, Dissecting G components

$$P = G + E + M + \begin{bmatrix} G \times E \\ G \times M \\ G \times E \times M \\ \dots \end{bmatrix} + \varepsilon$$

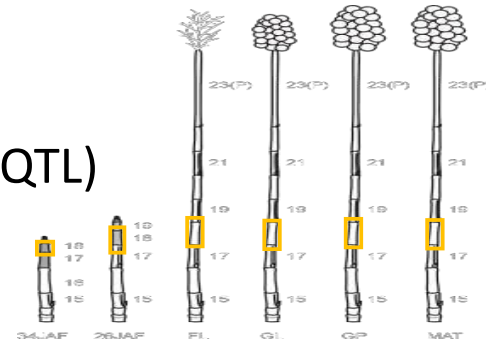
Arrows from the G box and the interaction matrix box point to two boxes below:

$G = \Sigma (QTL + QTN + E-QTL + QTL * QTL \dots)$

$G = f(\text{developmental stage})$

- **I want to:**

- Identify genomic locations (QTL, QTN, e-QTL)
- Highlight gene expression networks
- Estimate breeding values
- Predict phenotypes



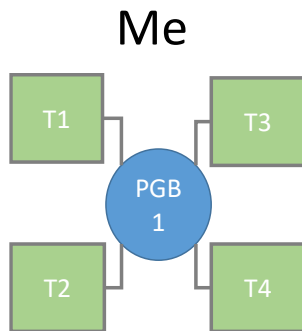
- **I need take to advantage of multi-environment trials and datasets from others**

Improving estimation and prediction accuracies of G, GXE, GXEXM

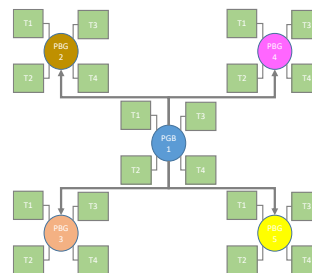
Requires aggregating trials and studies

$$P = \boxed{G} + E + M + \boxed{\begin{bmatrix} GXE \\ GXM \\ GXEXM \\ \dots \end{bmatrix}} + \varepsilon$$

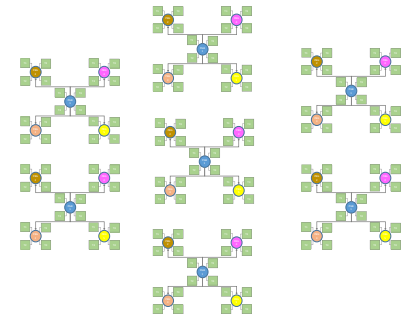
- 1 trial : merging G with E and M, not efficient to estimate G
- 2 trials : « starting » to better estimate G effect
- n trials : much more confidence on G and G X n estimates



My Network



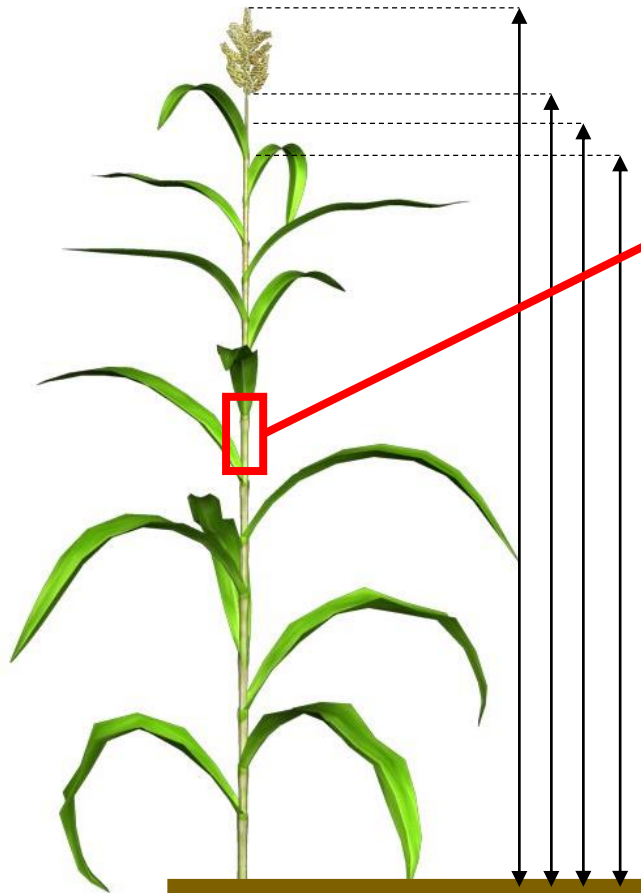
My species



- I need to have accurate « machine readable » trait descriptions
=> controlled vocabularies

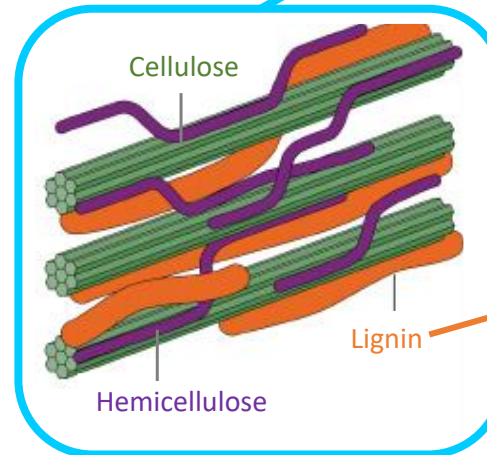
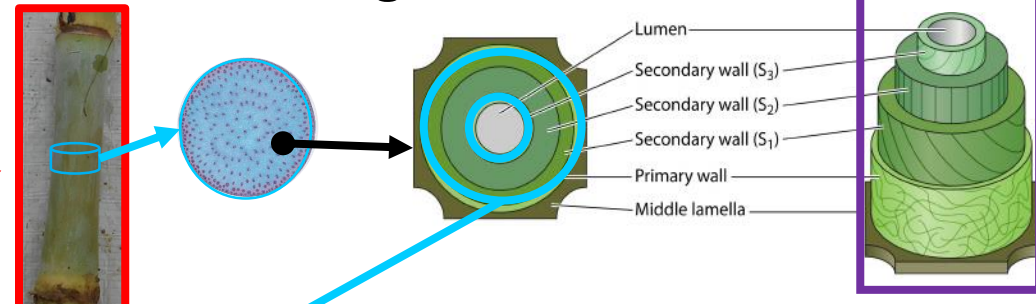
Trait description accuracy: Current publications

Plant Height



=> One trait = 4 traits...

Lignin content



[Lignin] expressed in
g/kg of DM g/kg of CW

	IVDMD	IVNDFD
ADL	0.79	0.40
KL	0.14	0.28
ABL	0.86	0.87

Adapted from Rytioja et al 2014 and Fukushima et al 2015



=> One trait = 6 traits...

Trait description accuracy: Identifying genomic regions of interest (QTL/ QTN)



<https://aussorgm.org.au/sorghum-qlt-atlas/> Mace, 2018

150 "QTL and GWAS" studies

191 traits

≈6000 QTL / QTN

- Lignin content
 - Trait Subcategory : "Stem composition"
 - Trait Description : "Lignin «
 - =>8 genomic regions (QTL / QTN)

General Information

Population	BTx623/Rio
Significance Value	6.39
Significance Measure	LOD
Additive effect	-0.22
Publication	Murray et al 2008b
Published Symbol/Identifier	not named
QTL/GWAS/Major effect gene	QTL

Position

Physical Map

Chromosome	Start (bp)	End (bp)
7	61,245,796	61,778,003

QSLIG7.1

Trait

Category	Subcategory	Notes
Stem composition	Stem composition	Stem lignin, g kg ⁻¹

Method?

Not clear in the paper

Ontogenic stage?

Dough grain stage?

Unit?

Dry Matter of stem?

- Need a more accurate definition of the traits (machine readable)

What do I need to efficiently describe my traits
and make them useful for me and the community ?

The Crop ontology a relevant framework to describe « Variables »

Crop Ontology Curation Tool

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Sorghum Ontology

Ontology curators: Praveen Reddy, ICRISAT

Scientists: Ibrahim Sissoko, breeder, ICRISAT; Eva Weltzien, breeder, ICRISAT; Jean-François Rami, breeder, CIRAD; Niaba Temé, breeder, IER

Crop Lead Center: ICRISAT

Partners: cirad, INRA, CGIAR research program

http://www.croponontology.org/ontology/CO_324/Sorghum

CO_324

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Variable = **Trait** + Method + Scale

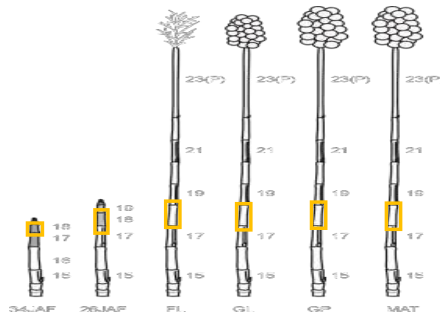
Entity + Attribute

Organ:

- Internode
- Stem
- Whole aboveground biomass
- Group of cells...

What we measure

- Length
- Height
- Weight
- Area...



The Crop ontology a relevant framework

That needs to take advantage of others Ontologies

Plant trait ontology (TO):

- Lignin
- 4 traits
- TO:0000731

Lignin content (ABL) of
IN18 120°C after
elongation start in mg/g
of cell wall residues



Units Ontology (UO):

- Milligram per g
- Not found
- UO:0000308 : mg per kg
- kg of what ?

Plant Anatomy ontology (PO):

- Internode
- 34 organs
- PO:0020142/PO:0005005

Plant Anatomy ontology (PO):

- Internode development stages
 - 18 « stages »
 - Number of IN (max=16)
 - Elongation start
 - Elongation stage
- No information on level
- No information on age

Environmental Ontology (ENVO):

- air temperature
- ENVO_09200001

• Method: no Ontology (?)

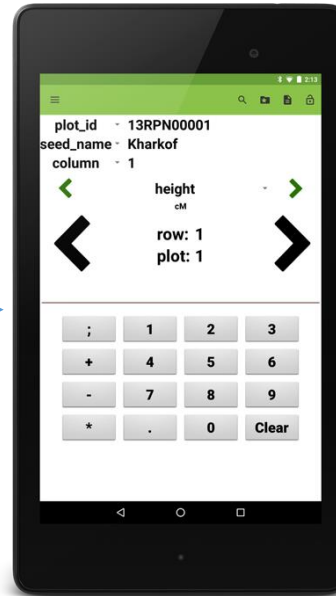
- ABL vs KL vs ADL
- Prediction vs reference values (where ?)
- Precision about unit (reference in proportion / ratio ?)

From the « CO » variables to the fields, databases, papers, and to aggregations

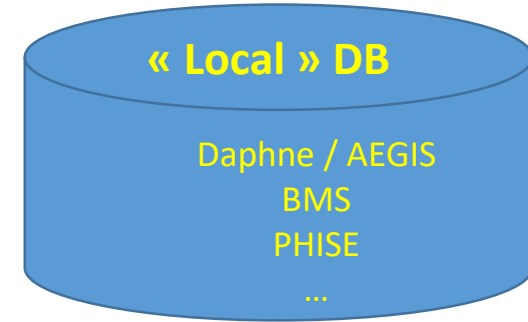


CO_324:0000623 :
PH_M_cm

Field book
alias
« Height »



<http://wheatgenetics.org/fieldbook>



Publication

Open data


- Data re-use
- Power and accuracy increases

We have the framework, We miss the « useful » content

Crop Ontology Curation Tool

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Sorghum Ontology




Ontology curators Scientists

- Praveen Reddy, ICRISAT
- Ibrahima Sissoko, breeder, ICRISAT
- Eva Weltzien, breeder, ICRISAT
- Jean-François Rami, breeder, CIRAD
- Niaba Temé, breeder, IER


Crop Lead Center



Partners



CGIAR research program



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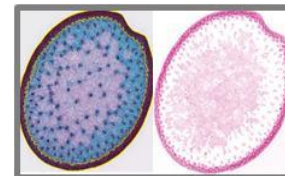
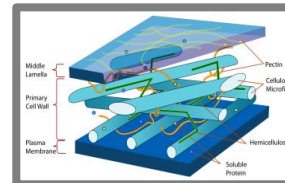
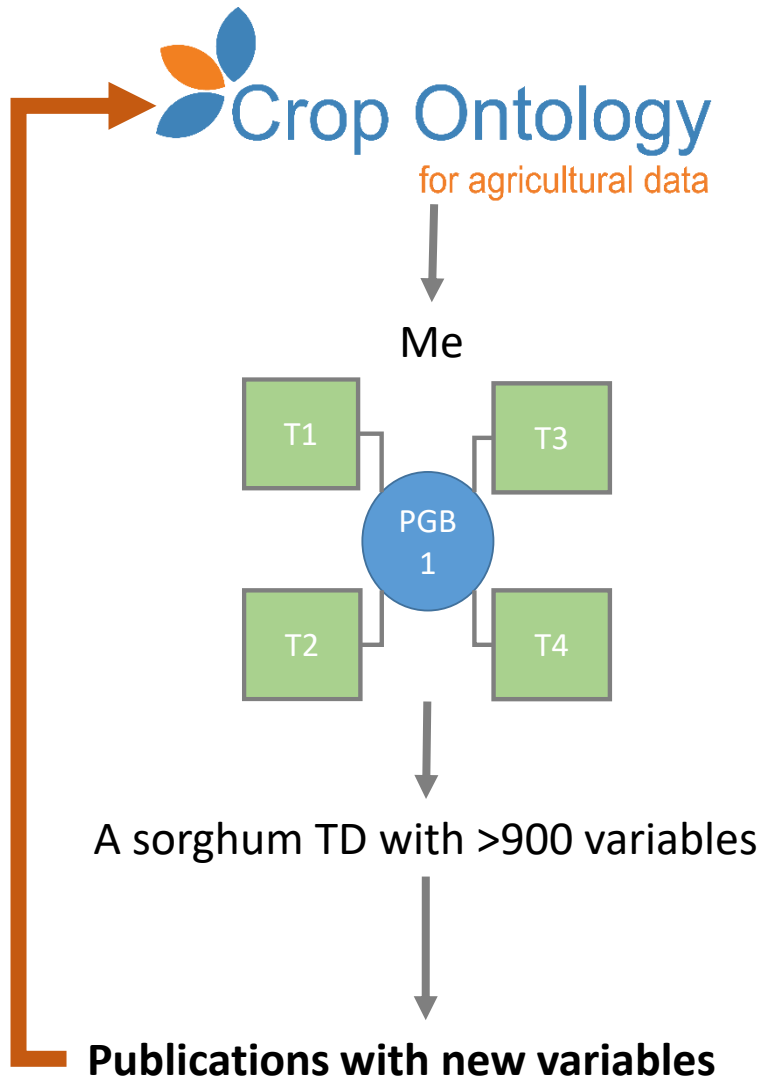
- Sorghum TDv5 - Jan 2018
- 174 variables

- 2017-2018 : >50 articles « Sorghum » « Genetics »
 - 1 article (Guitton et al 2018) with trait ontology information (4 traits)...
- Before 2017 : no paper with reference to CO_324
- **We need to improve the referencing of the published traits**

How to optimize the development of controlled vocabularies: 3 propositions

Feeding the Crop ontology

« Individual inputs »



Feeding the Crop ontology

Direct contributions of Communities of experts



- Setting up Sorghum multi-environments trials in West Africa (basic trials)
- 9 Breeders from 5 countries (some of them contributed to the previous CO_Sorghum version)
- 27 variables identified
 - 14 already in CO_324
 - 13 additional variables



=> It is only when people « get involved / are concerned / use the information » that it is efficient

Developping shared vocabularies

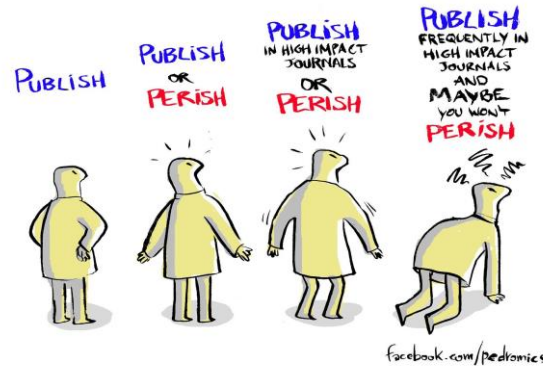
Requirements for interaction and decision tools

- A tool (website) to submit new variables to the crop ontology
- A Git like tool to « exchange » on the variables / methods / scales
 - Relevance of adding new traits / variables / methods / scales ?
 - Obtain information on already available traits
- A group of plant experts / curators (involved in the concerned species) validating / challenging the new inputs ?

Developping shared vocabularies

Editor's support

THE EVOLUTION OF ACADEMIA



- Science = papers....
- Science quality can be improved through the use of ontologies
- Providing ontologies for the variables in articles allows their re-uses, aggregations... Speed up research and allows reproducibility analyses
- Contacting editors to make relevant variable information compulsory !!

Developping shared vocabularies

A collaborative effort !



Jean-François Rami



Sandrine Auzoux



Lauriane Rouan



Elizabeth Arnaud



Marie-Angélique Laporte

