Update on an ontology for sweetpotato *(Ipomoea batatas)*

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Introduction

The sweetpotato ontology is part of a community effort to establish a set of related crop ontologies (www.cropontology.org). The crop ontologies provide a standard nomenclature to describe crop development and agronomic traits to facilitate the analyzing and sharing of phenotypic and genotypic information. An ontology consists of controlled, hierarchically-related phenotypic terms that enable large-scale computation among individuals, populations, and even multiple species (Hoehndorf *et. al* 2013). The International Potato Center (CIP) is currently pursuing the development of standards for sweetpotato phenotyping data, in collaboration with the crop ontology team.

Building on previous draft versions, here we focus on traits important to breeding: we have identified so far 109 descriptors. These include: morphological (28), agronomic performance (28), biochemical (23), reaction to biotic stress (7) and quality traits (23). We anticipate further refinements and cross-checks.

Materials and methods

Through collaborations with the 'crop ontology team' we aim at cross-crop compatibility of phenotypic data. The standard used in morphology according to Huaman (2001) (Figure1) and the evaluations were previously standardized (CIP 2009). Besides, ontology used descriptors published in the Catalogue of International Potato Center (Tumwegamire et al. 2014). We used the Crop Trait Dictionary Upload Template Version 4 to update the information on the web crop ontology.

Terms in an ontology are organized in the form of a tree: the nodes of the tree represent entities at greater or lesser levels of detail (Smith, 2004). The branches connecting the nodes represent the relation between two accession. For example the term Radicle Emergence Stage is a child of the parent term Germination Stage). Individual stages of a scale are then parts that can be related to the whole by their order of appearance during plant growth. Each term carries a unique identifier and strictly specified relationships between the terms allow systematic ordering of data within a database, this in turn improves input and retrieval of information (Bard and Rhee, 2004; Harris et al., 2004).

Figure1: Characteristics of a root of sweetpotato.

Results

The sweetpotato crop ontology currently describes over 109 traits representing important trait groups (agronomic, biotic stress, morphological, quality and biochemical traits). Agronomic, morphological, biochemical and quality characteristics traits are represented in equal proportions (see Table 1). Biotic stress terms constitute at present only a small portion.

These traits describe phenotypic variability for characteristics needed for crop improvement. The ontologies so far produced are largely managed in spreadsheets for ease of transfer from existing data dictionaries. The first version of sweetpotato Ontology (Fig.2 y 3) can be found online at

http://www.cropontology.org/ontology/CO_331/Sweetpotato

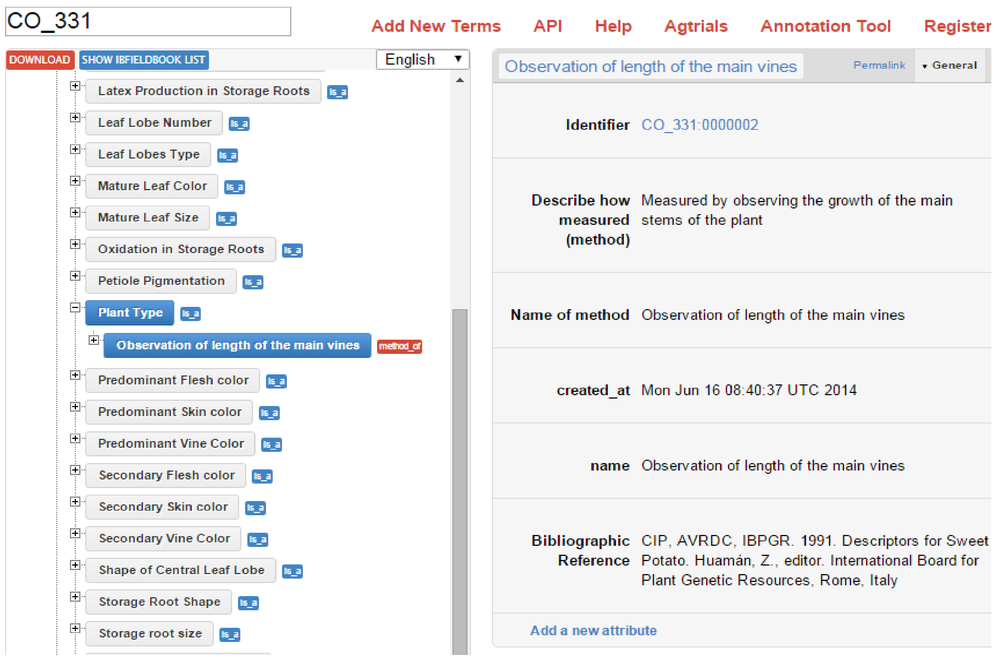

Figure2: Overview the sweetpotato ontology structure on the web crop ontology..

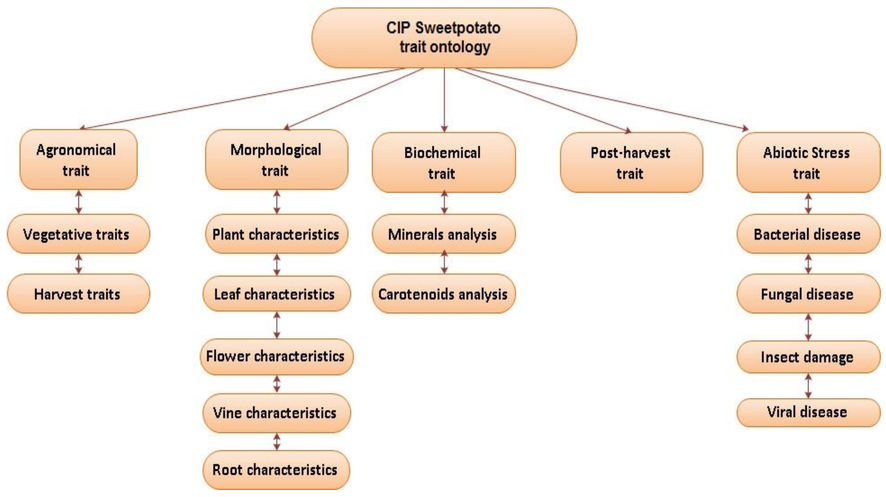

Figure3: Sweetpotato ontology structure trait group relationships.

Conclusions

- The definition of a set of common sweetpotato terms will help to develop shared databases.
- The use of ontological methods to organize biological knowledge is recommended for the creation of phenotypic databases.
- Crop ontologies will enhance future efforts to explore the relationships among phenotypic similarity, gene function, and sequence similarity in plants, and to make genotype-to-phenotype predictions relevant to plant biology, and crop improvement.

Variable	Frequency absolute	Percentage
Agronomic traits	28	26
Morphological traits	28	26
Biochemical traits	23	21
Quality traits	23	21
Biotic stress	7	6
Total	109	100

Table1. Frequency of characteristics on ontology

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Availability

The latest public version can be accessed through:

http://www.cropontology.org.

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