

Plant-Pathogen Interactions Ontology (PPIO)

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Abstract. Plant-pathogen interactions are an important knowledge domain within plant biology and biotechnology, both scientifically and in economic terms. Unlike other knowledge domains within life sciences, however, semantic technologies have not been used extensively to codify it; therefore, there is a lack of axiomatic models amenable to automated integration and inference. We present the Plant-Pathogen Interactions Ontology (PPIO), a first step towards the axiomatization of plant-pathogenic bacteria interactions knowledge domain.

Keywords: Plant pathogenic bacteria, Ontologies, Semantic Web, PPIO

1. Introduction

Plants can be susceptible to the attack of a multitude of different pathogenic bacterial genera [12], and if the different levels of the host plant defense barriers are overcome by the pathogen, the infection process can ultimately lead to the death of the plant. This phenomenon affects crop yield, which automatically will translate into considerable economic loss [13]. Therefore, being able to accurately explore and query biological data regarding plant-pathogenic bacteria interactions is a necessary step towards the improvement and protection of worldwide crops. This issue continues being subject of intensive research worldwide. Hundreds of articles that focus on the mechanisms of pathogenic bacteria interactions with their hosts reflect the biological significance of this area of research [6] [7].

The area of plant-pathogenic bacteria is an illustrious example of biodiversity richness [3]. Traditionally, *Agrobacterium*, *Erwinia*, *Pseudomonas* and *Xanthomonas* were considered the four main plant pathogenic genera some years ago. Nowadays, and thanks to the development of new research techniques, the number of known plant pathogenic bacteria genera has increased up to 30. One of the direct conse-

quences from these discoveries is the generation of vast amounts of unexplored biological data. The effectiveness of the use of Semantic technologies to manage with large sets of data has been already proved in other areas of life sciences, as discussed later. However, these tools that the Semantic Web offers have not been extensively applied to the knowledge domain of plant-pathogenic bacteria to date. Here we present the Plant Pathogen Interactions Ontology (PPIO), an ontology developed to semantically collect data in the context of the plant-pathogenic bacteria interactions. The main goal of PPIO is to ultimately serve as a reference ontology for plant pathologists, providing the knowledge necessary to assist in the interpretation of the phenotypic responses that result from the interaction established during the infection of the pathogenic bacteria and the potential host plants.

2. Modelling

The initial data necessary to start building PPIO was collected manually by accessing and consulting a number of different of expert web resources. The web page <http://pseudomonas-syringae.org/> was the starting point, containing diverse state-of-art datasets related with various *Pseudomonas syringae* pathogenic strains. This web page was a bridge to other web ser-

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vices where more datasets were collected¹. After an initial collection of data was gathered and revised, the modelling of these datasets was performed using the ontology editor Protégé.

2.1. Design principles

The main goal pursued during the modelling and designing process was to semantically capture as many biological data existing as possible, and special effort has been done in modelling the *disease triangle*². This term is one of the essentials milestones in the plant pathology ambit, and its principal statement asserts that three factors must be present for a disease to occur: a virulent pathogen, a susceptible host and a propitious environment for disease progression. Two classes have been successfully created to represent these three elements in a truthful and precise manner, the *Environmental parameter* and the *Organism* classes. This latter class contains two subclasses that semantically describe both plant and pathogenic bacteria; these subclasses are linked to the *NCBITaxon_1* class, which involves both bacterial and plant genera hierarchy with their corresponding taxa identifier. The connection between the three components of the disease triangle and the precise description of each one in the ontology is vital for accurately expressing this biological information into ontology language. To this end, terms such as 'Plant Pathogen', 'Host Plant' or 'Resistant plant' have been strongly axiomatically modelled to assure a trustworthy capture of the extracted biological data. By making a good use of the reasoning power this technology offers, which can generate new data based on the information already represented, the members of the *Host Plant* and *Resistant Plant* subclasses were properly inferred after the reasoning process took place using the FaCT++ and HermiT 1.3.8 reasoners.

Physiological state of plants can be inferred visually by observing different phenotypes. Thus, significant endeavour has also been done in modelling plant phenotypic representations in PPIO. Therefore, a number of classes have been specifically created to meticulously represent plant phenotypic traits. Specially important are the *Phenotype* and the 'Phenotypic process' classes. These two classes semantically illustrate the output of the interaction between the host and the bacteria, which is ultimately represented as a re-

sistance or a susceptibility phenotype expressed in the plant.

The *Trait* class contains various physiological, biochemical and molecular plant traits. To be able to work with the classes that contain these traits, the Plant Trait Ontology³ platform [10] has been imported and integrated into PPIO, converting this ontology into an archetype of the Semantic Web technologies capabilities for data integration. The traits described in the different PTO classes can be affected if a bacterial attack takes place, and this has also been semantically illustrated in PPIO by axiomatically relating the *Trait* class with both *Phenotype* and 'Phenotypic process' classes.

3. Creation methodology

3.1. URI design

The ontology URI (<http://purl.oclc.org/PPIO>) is HTTP resolvable and permanent (the PURL server redirects to our current server at biordf.org). The identifiers for entities (classes, individuals and object properties) are alphanumeric, with a URI of the type http://purl.oclc.org/PPIO#PPIO_NNNNNNNN, and every entity has an informative `rdfs:label` annotation. Currently hash URIs are used due to the small size of the ontology, but since URIs are generated programmatically⁴, when the ontology grows into a Knowledge Base or Linked Data dataset (see section 4) slash URIs can be generated.

3.2. Ontology production

The development of PPIO is automated as much as possible. Once the main structure is set, most of the remaining parts are produced programmatically using the Galaxy platform, a bioinformatics-oriented workflow environment [8]. By using Galaxy, the specific workflow we need is defined once and executed for each release; also, we can plug PPIO directly with other Bioinformatics tools.

The workflow adds the necessary entities and axioms⁵ (Figure 1):

³<http://www.gramene.org>

⁴<https://github.com/wilkinsonlab/>

OWLNumericIDGenerator

⁵The workflow can be reproduced at <http://biordf.org:8090/u/alejandroriglesias/w/ppio-taxa-punning>

¹<http://ncppb.fera.defra.gov.uk/>

²<http://www.apsnet.org/edcenter/instcomm/TeachingArticles/Pages/DiseaseTriangle.aspx>

1. The organism taxa hierarchy is produced by the tool NCBITaxonomy2OWL⁶: it gets the user-defined taxa from the NCBI taxonomy through a BioPortal Web Service [17] and injects them in PPIO, reproducing the original taxonomical hierarchy (representing each rank-subrank as a simple subsumption relation [14]) and adding each taxon with a resolvable OntoBee⁷ URI.
2. Since pathogens in PPIO are modelled as individuals, they cannot be directly related with class hierarchies like the NCBI taxonomy and the symptoms hierarchy. Therefore, PPIO exploits OWL punning⁸ and an individual with the same URI as each type class is generated programmatically (see below) for those hierarchies: the linking of pathogens to those hierarchies (e.g. NCBITaxon_552 types *Erwinia amylovora* NCBITaxon_552 causes Canker, NCBITaxon_552 causes Blight) is done manually. This is achieved by defining two Ontology Pre Processor Language (OPPL)⁹ scripts and executing them via OPPL-Galaxy [1]¹⁰:

```
?x:CLASS,
?y:INDIVIDUAL = create(?x.RENDERING)
SELECT ?x SubClassOf NCBITaxon_1
WHERE ?x != Nothing, ?x != Thing
BEGIN
ADD ?y Type ?x
END;

?x:CLASS,
?y:INDIVIDUAL = create(?x.RENDERING)
SELECT ?x SubClassOf PPIO_0000069
WHERE ?x != Nothing, ?x != Thing
BEGIN
ADD ?y Type ?x
END;
```

4. Discussion

Semantic-oriented platforms like the OBO foundry [15], which includes Gene Ontology (GO) [4], Bio2RDF

[2] or the W3C Semantic Web for Health Care and Life Sciences Interest Group¹¹ are excellent paradigms of the success in using semantics to assist in the integration of automated data. Nevertheless, taking a deep look at the study fields of plant biotechnology and phytopathology, it is surprising to notice that these technologies have been applied to a limited number of domain resources. There are some precedents prior to the ontology discussed here, such as the Plant Ontology¹², developed by the Plant Ontology Consortium, to describe plant anatomy, morphology and developmental stages [9]. The Plant Disease Ontology (IDOPlant) [16] [5], serves as a reference ontology and it has been built to contain plant infectious diseases. Finally, the GO extension for description of the Type III Effectors [11] is maybe the ontological contribution in the plant pathology and microbiology area more related to PPIO.

In a comparison between the IDOPlant and PPIO, a more generalistic approach of data modelling can be appreciated in the case of the first platform, which describes plant infectious diseases caused by either biotic or abiotic agents. The ontology reported here pursues a knowledge capture strategy focused on data that concerns plant-pathogenic bacteria interactions, in order to be able to exhaustively represent this area of knowledge. On the other hand, although the GO extension for the type III effectors is built for capturing processes in the host-pathogen level, effector proteins data capture is emphasized. So, the justification for building this ontology lies mainly in its coverage of a domain not fully represented by other resources. Of course, PPIO has been designed to complement these previous ontologies by introducing accurate and concrete biological information. It is our objective to continue the process of data integration not only importing related ontologies, but other resources such as the Darwin Core glossary of terms (DwC) [18]. The final goal of this initiative is to use this platform, combined with others, as a diagnosis/prevention/alert system. PPIO will make it possible for users to pose, and answer, questions like the following ones and obtain a meaningful answer:

1. Is *Solanum lycopersicum* susceptible to the attack of *Pseudomonas syringae* pv. *tomato* DC3000?
2. Does a high humidity favours the development of *Pectobacterium carotovorum* subsp. *carotovorum*?

⁶<https://github.com/wilkinsonlab/NCBITaxonomy2OWL>

⁷<http://www.ontobee.org/>

⁸<http://www.w3.org/TR/owl2-new-features/>
Punning

⁹<http://oppl.sf.net>

¹⁰Since we are using OPPL, any complex axiomatisation -not only punning- can be defined once and automatically applied -expanded to different parts of the ontology- every time the workflow is executed.

¹¹<http://www.w3.org/blog/hcls/>

¹²<http://www.plantontology.org/>

Fig. 1. Galaxy workflow for producing a release of PPIO. In the first step, NCBITaxonomy2OWL is executed; it gets the ontology and a flat file containing the NCBI taxonomy IDs, and it adds them to the ontology. Then two OPPL scripts are executed against the resulting ontology, adding axioms and entities to create

3. What is the phenotype of the disease produced by *Dickeya dadantii* in *Solanum tuberosum*?

Knowledge acquisition is based on the process of transcribing the knowledge from unstructured sources into a format that is machine-readable and useful. This approach can report a great benefit if big amounts of datasets are required in order to populate ontologies. One of the main ideas behind this is that the participation of field experts should ensure the fiability of the data content captured. At the moment, a knowledge capture project is now being developed in our laboratory, and it is our thought that it will aid in the process of collecting data that will ultimately populate PPIO with trustworthy and scientifically relevant information. All these steps will help to our objective of converting PPIO into a basic and essential bioinformatic tool for scientific community in the area plant pathogens.

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