



Gene Ontology (GO) for Microbe-Host Interactions and its Use in Ongoing Annotation of 3 *Pseudomonas syringae* genomes via the Pseudomonas-Plant Interaction (PPI) Website



Candace W. Collmer^{1,2}, Magdalen Lindeberg¹ and Alan Collmer¹

¹Dept. of Plant Pathology, Cornell University, Ithaca NY, USA and ²Dept. of Biological and Chemical Sciences, Wells College, Aurora, NY, USA

Question: How to use full-genome analyses to learn about gene products important in pathogenesis?

- 1) Can use structural analysis tools such as Blast or the Artemis Comparison Tool (ACT) – see below – to see what genes are present in one species or in one pathovar, but disrupted or missing in another
- 2) Can search for the presence or absence of proteins with functions important in pathogenesis, if these gene products have been annotated with precisely defined terms that describe relevant biological processes – e.g. **all bacterial gene products delivered into a host cell that suppress plant defenses**

Sub-menus for each of the three sequenced *P. syringae* pathovars

***P. s. tomato* DC3000**

***P. s. syringae* B728a**

***P. s. phaseolicola* 1448A**

The **Gene Ontology (GO) Consortium** (<http://www.geneontology.org/>) has been developing a controlled vocabulary to systematically describe gene products in terms of their:

- Molecular function (what does it do?)
- Cellular component (where does it do it?)
- Biological process (why, or as part of what larger process?)

The **Plant-Associated Microbe Gene Ontology (PAMGO)** project has been developing Biological Process terms for GO that describe the biological processes involved in interactions between microbes and their hosts:

- during symbiosis (encompassing mutualism through parasitism)
- in plants or in animals
- in prokaryotic or eukaryotic microbes – bacteria, oomycetes, fungi, and nematodes

Newly developed Biological Process GO terms (shown in their "trees" of relationships) to describe gene products:

- GO:0051701 : interaction with host (279)**
- GO:0044002 : acquisition of nutrients from host (1)
 - GO:0044406 : adhesion to host (85)
 - GO:0044413 : avoidance of host defenses (22)
 - GO:0044415 : evasion of host defenses (21)
 - GO:0030682 : evasion of host defense response (10)
 - GO:0044414 : suppression of host defenses (0)
 - GO:0044007 : dissemination or transmission of organism from host (12)
 - GO:0044409 : entry into host (72)
 - GO:0044408 : growth on or near host surface (0)
 - GO:0044412 : growth within host (6)
 - GO:0044416 : induction of host defense response (23)
 - GO:0030581 : intracellular protein transport in host (2)
 - GO:0044003 : modification of host morphology or physiology (61)
 - GO:0044004 : disruption of host cells (57)
 - GO:0001907 : killing of host cells (57)
 - GO:0001897 : cytotoxicity of host cells
 - GO:0044005 : induction in host of tumor, nodule, or growth (0)
 - GO:0044000 : movement within host (3)
 - GO:0044405 : recognition of host (0)
 - GO:0044417 : translocation of molecules into host (0)

We are currently **continuing to develop "children terms"** of these "parent terms" that are more specific – e.g. "modification of host morphology or physiology via protein secreted by type III secretion system." These terms will then **be ready to be used to annotate genes** in *Pseudomonas syringae* pathovars, as well as genes in other bacteria, oomycetes, fungi, and nematodes that are pathogens of plants or of animals.

PPI Home Page

The PPI website features a "Hub" model for smaller scale genome biology websites that is:

- **current** - links out to primary databases and analytical programs instead of maintaining and updating them on-site
- **cost-effective** - by not duplicating pre-existing tools and databases, time and personnel power can focus on needs specific to the particular research community
- **responsive** - designed and maintained by personnel familiar with the biology of the organism and the needs of the research community
- **broad in scope** - resources and links to related topics added as needed

Tools for genome viewing and analysis

Artemis genome viewer

Artemis Comparison Tool (ACT) for alignment of similar sequences

Maintenance of existing annotation databases at TIGR and Genbank

- Annotation updates from literature and personal communication →
1. Forwarded to GenBank and TIGR
 2. Posted on the PPI website updates log