

# IDODEN: An Ontology for Dengue

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## ABSTRACT

Dengue is an infectious disease caused by any of the four serotypes of the Dengue virus (DENV-1 to 4). This RNA virus is a member of the *Flaviviridae* family, genus *Flavivirus* (Gould & Solomon, 2008). Responsible for the transmission of the disease are female mosquitoes of the genus *Aedes* (WHO, 2009). Infection with one serotype does provide lifelong immunity for that serotype but not against the remaining three. In fact, several studies have shown that a subsequent infection with a different serotype leads to a higher probability of developing the severe manifestations of Dengue Hemorrhagic Fever (Guzman *et al.*, 2002 & 2010).

The number of studies and vaccine trials regarding Dengue has increased over the last years, as has the amount of data. The need for interoperability, a “common language”, knowledge management, decision support and reasoning has become clear. Under the framework of the Infectious Disease Ontology (IDO) project (Cowell & Smith, 2010), we are developing the Dengue Ontology (IDODEN) to fulfill the needs of the community. The decision to develop IDODEN as an extension of the basic IDO-core was made to ensure interoperability with already existing infectious disease ontologies, such as the Malaria Ontology IDOMAL (Topalis *et al.*, 2010). Furthermore, with the cooperation of partner NIAID Bioinformatics Resource Centers (BRC) this will ensure that it is compatible with existing databases and schemas used throughout the community, e.g. VectorBase (Lawson *et al.*, 2009) and ViPR (Pickett *et al.*, 2012).

The ontology is being built according to the guidelines of the OBO Foundry (Smith *et al.*, 2007) and is based on the Basic Formal Ontology (BFO) (Grenon *et al.*, 2004). IDODEN contains ontological descriptions covering a wide spectrum ranging from those that deal with the disease itself, to vector biology, to virus biology and to epidemiology. This complexity is due to the three different organisms involved in the disease (vectors, viruses and human hosts), as well as to the fact that mostly populations are involved, rather than individuals. According to the OBO Foundry rules, IDODEN imports terms from existing ontologies such as IDOMAL instead of creating duplicates of terms in other ontologies. All of the unique terms are subclasses of already existing higher level ontology terms.

Our aim is to develop an ontology that will help the Dengue and the infectious disease community in general, in the fight against the disease. This is only the first working version of IDODEN, as it will continue to expand and change to encompass new scientific developments. We are aiming for the first version to be available at the end of the year.

## ACKNOWLEDGEMENTS

The work was funded by contract HHSN266200400039C from the National Institute of Allergy and Infectious Diseases (NIAID) in the frame of the VectorBase project.

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