

Proceedings of TDWG, 2009

[HOME](#) [ABOUT](#) [LOG IN](#) [REGISTER](#) [SEARCH](#) [CURRENT](#) [ARCHIVES](#)

[Home](#) > [2009](#) > [Ruiz](#)

Semantic Standards for Genomic Analyses of the South and Mediterranean Plants: the Generation Challenge Program Use Case

Manuel Ruiz

Abstract

The Generation Challenge Programme (GCP) platform was developed to meet the challenges of data acquisition, computational resources, and software interoperability and integration across a globally distributed consortium of partners. This platform includes: (i) shared, public platform-independent domain models, ontology and data formats (ii) web service and registry technologies (iii) platform-specific middleware implementations of the domain model integrating a suite of public databases and software tools into a workbench to facilitate biodiversity analysis, including the comparative analysis of crop genomic data.

The cornerstone of the GCP platform is the development of common standards for GCP data. Major concepts in the domain of crop research - for example, concepts like "germplasm" and "genotype" - can be expressed in terms of a general blue print of such concepts-as-entities and of their relationships to one another, within a so-called domain model. The GCP development team has specified such a domain model to drive development of a "model driven architecture" within which tools and data sources may be efficiently connected to one another.

The GCP domain model is not a complete embodiment of semantics in GCP software systems since specifying such a complete model would not be practically feasible. Therefore, in addition to the GCP domain model, the GCP development team has also specified a formal framework to manage a GCP ontology that complements the semantics of the domain model.

Several applications and integrating tools have been developed, such as a GCP web query and display application ("Zeus"), a GCP Ontology browser, and the stand-alone molecular breeding components MBDT (Molecular Breeding Design Tool) and MOSEL (Molecular Selection Tool). Our team was particularly involved in the development of GenDiversity, a query and analysis Web application combining genotyping data from diverse data sources, developed in support of diversity studies. Furthermore, GCP components can also be used by non GCP projects. Indeed, we present Orylink, a personalized integrated system for rice functional genomic analysis.

The infrastructure of the platform is complex, and it still may discourage developers from using it. Therefore, we need to establish better training and documentation for users of the platform.