Abstract
The French National Institute for Agricultural Research (INRA) manages genetic resource collections [1] for more than 50 species (model species and crops). These genetic resources are regularly used for research programs of INRA or its partners, and are also widely distributed to the scientific community. The objectives of the Genetic Resources Centers (GRC) are to gather, conserve, and provide high quality materials for the scientific community. In order to do that, the GRCs have to be able to trace their actions and to ensure the community of a high degree of quality.

URGI (Unité de Recherche Génomique-Info) is an INRA bioinformatics lab dedicated to plant and pest genomics. It hosts a bioinformatics platform included in the French ReNaildi bioinformatics platform network and certified Bisa in 2009. One of the missions of the platform is to develop and maintain a genomic and genetic information system called GnpIS, for plants of agronomic interest and their bio-aggressors. Siregal, the INRA Plant Genetic Resources Information System, fulfills the essential need to manage the collections and associated data following the recommendations of the Biological Resource Centers (OECD). Siregal is suitable for all plant species and is used by INRA staff and its partners. It respects community standards, and it makes the integration of existing and future genetic data possible. Siregal is one of the GnpIS applications.

GnpIS
GnpIS, the URG1 Information System [2] is a web-based system composed of several applications built above a single database that includes integrated schemes as shown.

Data
Grapevine
Vitis genus
4,453 taxa and cultivars
7,862 accessions
51,558 phenotypes
Cherry
Prunus genus
115 taxa
178 accessions
Chestnut
Castanea genus
29 taxa
150 accessions
Bread wheat
Triticum genus
32 taxa
1,744 accessions
16,201 phenotypes
Pea
Pisum genus
17 taxa
240 accessions
TOTAL
4,644 taxa and cultivars
10,049 accessions
67,919 phenotypes

Aster
Aster is the key and central module of GnpIS. It allows the interoperability between the modules. It owns the common entities, allowing data links and the construction of powerful queries to bridge genomics and genetics.

Data analysis

International databases

Statistical analysis

Population genetics

Quantitative genetics

References
http://urgi.versailles.inra.fr/gnpiseweb/software.html

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