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P800: Databases

Genome Annotation And Report System: An Integrated System For Structural And Functional Genome Annotation

[Joelle Amselem](#)¹ , [Michael Alaux](#)¹ , [Baptiste Brault](#)¹ , [Nicolas Lapalu](#)¹ , [Fabrice Legeai](#)² , [francoise Alfama](#)¹ , [Laetitia Brigitte](#)¹ , [Nathalie Choisne](#)¹ , [Aminah Keliet](#)¹ , [Erik Kimmel](#)¹ , [Jonathan Kreplak](#)¹ , [Isabelle Luyten](#)¹ , [Cyril Pommier](#)¹ , [Sebastien Reboux](#)¹ , [Stephanie SIDIBE BOCS](#)³ , [Delphine Steinbach](#)¹ , [Marc-Henri Lebrun](#)⁴ , [Hadi Quesneville](#)¹

¹ INRA - URGI, Bat 18, Route de Saint-Cyr, Versailles, 78026, France

² INRA/AGROCAMPUS OUEST/Université de Rennes 1 - UMR BIO3P, Domaine de la Motte, Le Rheu, 36653, France

³ CIRAD - UMR DAP, Campus de Lavalette, Av Agroplois, Montpellier, 34398, France

⁴ INRA - BIOGER, av Lucien Brétignières Thiverval Grignon, 78850, France

Nowadays with the development of NGS, more and more genomes are sequenced, producing very large amount of data. However, annotations can't keep pace, introducing a lack between genome data and annotation releases. To face this challenge, the URGI (<http://urgi.versailles.inra.fr>) platform aims at providing tools to annotate entirely sequenced genome comprising: pipelines, databases and user-friendly interfaces to browse and query the data. We will focus here on complementary systems developed in the frame of GnpIS and GnpAnnot project:

- The distributed annotation system allows the curation of gene structure. This system relies on the well known GMOD databases and interfaces (chado/GBrowse/Apollo). Curated data are available and shared by the consortium community as soon as they are committed in the database using the "pure JDBC" direct communication protocol between Apollo and Chado.

- The Genome Report System (GRS), written in Java, was developed to produce various and user-friendly Web reports. GRS uses structural and functional genomic data stored in Chado database in order to provide users with a comprehensive list of information including cross references related to a specific gene. GRS proposes also a Gene Ontology browser and an editing module (GRE) to allow manual functional annotation.

- Quick and advanced search are processed respectively through GnpIS QuickSearch (<http://urgi.versailles.inra.fr/gnpis>) and Biomart (GMOD).

We will present the integration of these tools in the frame of a fungal genome annotation.