

## **The INRA (French National Institute for Agricultural Research) genomic program on Rainbow Trout: Trout-AGENAE**

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Rainbow trout, *Oncorhynchus mykiss*, is an important fish species for aquaculture and has been widely introduced around the world. It is also probably one of the most deeply studied fish species with a long history of research carried out in physiology, nutrition, ecology, genetics, pathology, carcinogenesis, toxicology. Its relatively large size compared to model fish like zebrafish or medaka, makes rainbow trout a particularly suited alternative model to carry out biochemical and molecular studies on specific tissues or cells that are impossible to decipher in small fish models. The genomic resources in rainbow trout are now being extensively developed and for instance a few high-throughput DNA sequencing programs of EST have been recently initiated.

AGENAE (Analyse du GENome des Animaux d'Elevage) is a project led by the French National Institute for Agricultural Research (INRA) that focuses on genomics of several livestock species (cattle, pig, chicken and rainbow trout). Objectives of this program are the identification and characterization of the expressed part of genomes, the mapping of entire genomes, and the study of genetic diversity in animal populations. This program was first started as a tool towards new integrative approaches for the study of physiological functions ; approaches combining cellular and molecular physiology, genetics, high throughput genomic tools, proteomics ... To this end we provided biological resources and tools to access knowledge like sequenced cDNA libraries, cDNA micro-arrays, genetic and physical maps, arrayed BAC library, ... and developed expertise on emerging genomics technologies including functional genomics, structure, proteomics, bio-informatics ...

### The AGENAE shared resources:

All AGENAE national projects rely on 2 main shared resources that are provided for all species studied within this program. All biological resources (cDNA, and BAC-YAC clones, DNA biochips on glass-slides or nylon surface) are provided by a core Biological Resources Centre (CRB-GADIE). This biological resources centre is in charge of various requests for general service activities i.e. conservation, management or delivery of cDNA and genomic libraries constructed at INRA, library screening, clones picking and spotting, high density membrane construction, specific cDNA chips printing. Basically, the aim is to provide a set of services, genomic tools and expertise to the scientific community. Besides, all bio-informatic resources are provided by a group of INRA bio-informaticians (SIGENAE Team) providing services to biologists working on various species. SIGENAE is also the name given to the Information System this team is developing and maintaining. The tools and services that SIGENAE provides include: ESTs sequence cleaning and clustering, library statistics including clone redundancy calculation, micro-array data storage and processing. In addition, computer programs have been developed for comparative genomic studies.

### The rainbow trout resources:

For the characterization of the expressed part of the trout genome, we constructed specific high quality cDNA libraries and initiated a high throughput ESTs sequencing project on these libraries. Right now more than 120 000 sequences have been performed by this program (5' or 5' and 3' sequences on more than 90 000 clones) and most of this information has been already released in international databanks (EMBL, GenBank). This information currently corresponds to roughly 50 % of the overall knowledge (240 000 EST sequences in GenBank in February 2006) in this species and brings rainbow trout as one of the major fish model in term of ESTs sequences just after Zebrafish, *Danio rerio*. Using these sequenced transcript collections and the related cDNA clones our bio-informatics and biological resources centres provided us with a DNA biochip on nylon surface (micro-arrays) corresponding to about 10 000 independent cDNA clones with corresponding functional annotations (more than 700 micro-arrays have been produced last year). Development on functional genomics will include the generation of a 15 000 full-length cDNA sequences collection and production of a new generation of trout micro-arrays.

For the improvement of the genetic map of rainbow trout we characterized 700 new microsatellites markers in ESTs, and investigated the development of some SNP markers in candidate genes. We tried to produce a Radiation Hybrid panel in trout without success and recently in collaboration with USDA we organized a rainbow trout BAC library for PCR superpools screening. Developments on structural genomics will include 70 000 BAC end sequencing and physical mapping of ESTs on the BAC library.

### The rainbow trout projects:

Projects using rainbow trout resources at INRA currently include: resistance to diseases, muscle growth and fat deposition, sex control, sexual maturation and gamete quality, optimal use of plant ingredients in fish diets and “welfare” indicators in farm animals. We also initiated some approaches in order to validate rainbow trout micro-arrays as a heterologous tool for other species like for instance the European seabass, *Dicentrarchus labrax*.

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Contacts:     AGENAE : Claude Chevalet ([claudc.chevalet@toulouse.inra.fr](mailto:claudc.chevalet@toulouse.inra.fr))  
                  Trout Resources Person : Yann Guiguen ([yann.guiguen@rennes.inra.fr](mailto:yann.guiguen@rennes.inra.fr))

Links:         AGENAE Website (in French): <http://www.inra.fr/agenae/>  
                  SIGENAE Bioinformatics Website: <http://www.sigena.org/>  
                  GADIE Resources Centre: <http://www-crb.jouy.inra.fr/BRC/index.htm>

