

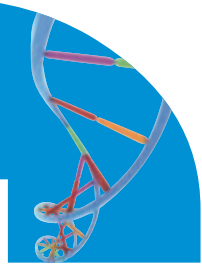


Genopole®

RESEARCH

Séquençage complet d'Arabidopsis thaliana \ Mise en place du programme d'épigénomique \ Séquençage du génome de la bactérie Rickettsia felis \ Identification du gène responsable de l'ichtyose Lamellaire de type 3 \ Création du Consortium biopuces \ Découverte d'un gène associé à l'autisme \ Identification du mécanisme cellulaire responsable du syndrome de Clouston \ Séquençage complet d'Arabidopsis thaliana \ Mise en place du programme d'épigénomique \ Séquençage du génome de la bactérie Rickettsia felis \ Identification du gène responsable de l'ichtyose Lamellaire de type 3 \ Création du Consortium biopuces \ Découverte d'un gène associé à l'autisme \ Identification du mécanisme cellulaire responsable du syndrome de Clouston \ Création d'une banque d'échantillons d'ADN \ Découverte des propriétés biologiques des nanodiamants \ Séquençage complet d'Arabidopsis thaliana \ Mise en place du programme d'épigénomique \ Séquençage du génome de la bactérie Rickettsia felis \ Identification du gène responsable de l'ichtyose Lamellaire de type 3 \ Création du Consortium biopuces \ Découverte d'un gène associé à l'autisme \

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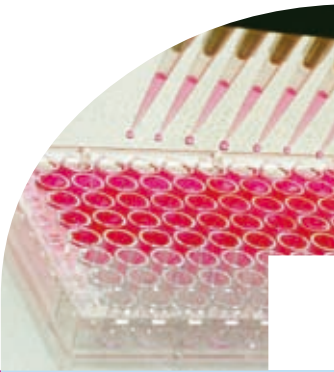


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Center for Mechanical Engineering and Automation Studies and Research [CERMA]



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MAIN TOPIC

- Engineering Sciences

FIELD OF ACTIVITY

- Development of new production methods, feasibility studies and specifications for products and machines requiring a multi- disciplinary approach. Applications in manufacturing, research and biology. The CERMA has been awarded «Technical Resource Center» status by the French Ministry of Research.

KEYWORDS

- Mechanical engineering, robotics, automation, instrumentation

RESEARCH THEMES

The CERMA stands out by its ability to provide total management of complex projects (from initial specification to commissioning) in the fields including mechanical engineering, electronics, special sensors and industrial IT. As a University of Evry Technology Transfer Center, it designs, builds and implements innovative machines, products and automated processes for a range of industrial sectors (notably in the field of biology).

The CERMA has particularly focused its work on the high-throughput automation of electrophoretic analysis and related techniques: sample preparation, dilution, PCR, UV luminescence imaging, etc. The CERMA collaborates with other public - and private-sector establishments: CNS, Généthon, University of Evry (the

CEMIF lab), University of Paris 7, University of Paris 11, the Gustave Roussy Institute, INRETS (LIVIC), Danone Research, etc. Since its creation, the CERMA has handled more than 250 projects in a variety of sectors: automated workstations in genetics, crash test beds in the automotive industry, industrial inkjet printers, medical electronics, etc.



Epigenomics Program



Supervisory bodies\ GENOPOLE/UNIVERSITÉ D'EVRY-VAL D'ESSONNE/CNRS Director\ François KÉPÈS

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MAIN TOPIC

- Synthetic systems biology and bioinformatics

FIELD OF ACTIVITY

- Modeling and simulation of biological processes in a (post)genomics context. Epi-organization of genomes

KEYWORDS

- Modeling, simulation, experimental validation of mathematical models, macromolecular networks, epigenesis

RESEARCH THEMES

The Genopole Epigenomics Program (founded in 2002 and whose slogan is «model to understand») aims first and foremost to be a forum for dialogue in order to catalyze research on complex biological problems via contributions from a range of disciplines: biology, computing, mathematics, theoretical physics, artificial chemistry and so on.

The Program simultaneously serves as :

- a vector for training researchers in disciplines other than their own.
- a visiting researcher program (one of whose missions is to attract world-renowned scientists to Evry.
- a mainly French-speaking, multidisciplinary research network with regular meetings.

- a hotbed of pioneering science (stimulating the invention of new research subjects and supporting them through targeted, thematic activities).

- a joint service which centralizes Evry-based research efforts on modeling in biology.

Researchers can meet at the center via four operating modes: regularly-convened working groups, the incubation of new research groups, targeted, thematic activities and national/international conventions.

All the activities funded by the Epigenomics Program are highly thematically targeted and are based around a small number of leading researchers.

HOLDER OF A GENOPOLE RESEARCH GROUP ESTABLISHMENT («ATIGE») GRANT

- «*Metamorphosys: studying metamorphosis with systems approaches*» Leader: Nicolas POLLET
- «*Towards a Reliable Synthetic Biology*» Leader: Alfonso JARAMILLO



Euroas Genomic Bank



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MAIN TOPIC

- Genomics/Postgenomics

FIELD OF ACTIVITY

- Constitution of DNA banks and clinical/immunological data-bases; physiopathology of spondylarthropathies, characterization of genetic factors other than HLA B27, function of HLA B27, clinical epidemiology.

KEYWORDS

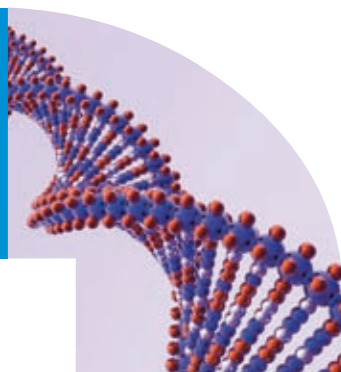
- Genetics, immunology, ankylosing spondylitis, spondylarthropathies

RESEARCH THEMES

Ankylosing spondylitis (AS) represents the archetypal and the most frequently encountered form of spondylarthropathy (SPA). The primary goal of the European EUROAS Consortium (which federates 10 research laboratories and clinical rheumatology centres from 9 European countries) is to build a European genomic bank encompassing the genetic & clinical characteristics of people suffering from AS (or other SPAs) and their families (the «EUROAS Genomic Bank» (EGB) program). The 5278 samples already collected from 830 families should enable the project to identify disease susceptibility and/or severity genes

involved in the genesis of SA and SPAs, elucidate the fundamental molecular mechanisms and open up development routes for new diagnostic techniques and new treatments (including cell and gene therapies). Thanks to the EGB a large cohort has been included MS and high-throughput MHC and whole genome scans studies.

European Research Laboratory for Rheumatoid Arthritis - GenHotel EA 3886



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MAIN TOPIC

- Genomics/Postgenomics

FIELD OF ACTIVITY

- Research on the genetic susceptibility to rheumatoid arthritis and on the pharmacogenetics of the disease

KEYWORDS

- Rheumatoid arthritis, auto-immunity, multifactorial diseases, pharmacogenetics

RESEARCH THEMES

Rheumatoid arthritis (RA, the most common auto-immune disease) is a very painful chronic disease which leads to progressive joint destruction. It is a multifactorial disease and probably involves a large number of genetic factors. New biotherapies have improved the treatment outcomes for RA.

GenHotel-EA3886 searches for disease-specific or -related genetic factors, with the goal of developing a definitive cure.

With its biobank of more than 6,000 DNA samples from families affected by RA and its detailed genome scan using more than 1,000 highly informative markers, GenHotel-EA3886 is focusing on candidate genes likely to play a role in RA and in the response to biotherapies.

At Genopole, GenHotel-EA3886 collaborates with the "Statistics and Genome" Laboratory headed by Professor Bernard Prum and the Genoscope headed by Professor Jean Weissenbach. Thanks to direct links with the Medical Center in Evry-Corbeil and the Lariboisière Hospital in Paris, GenHotel is developing the pharmacogenetics of RA biotherapies. With funding from the *Association Française des Polyarthritiques*, GenHotel-EA3886 is sharing its innovative science & resources by hosting researchers at its «science hotel», publishing its results on the Internet at www.GenHoTelcom and contributing its skills to complementary projects.

In 2006, GenHotel-EA3886 validated an innovative model of the first genetic factor linked to RA (*HLA-DRB1*) and then confirmed the second factor (*PTPN22*) in 2007 and the third (*C5-TRAF1*) in 2008, thanks to its "science hotel".

GenHotel-EA3886 contributes to the search for new leads towards a definitive cure for RA.



Genethon Department of Exploratory Research

CNRS FRE 3087 et Inserm U790

Inserm

Institut national
de la santé et de la recherche médicale



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MAIN TOPIC

- Genomics/Postgenomics

FIELD OF ACTIVITY

- Vectorology, gene transfer, gene therapy, immunology

KEYWORDS

- Cell biology, transfer of genes, gene therapy, stem cells, genetic diseases, limb-girdle dystrophies, lentiviral vectors, synthetic vectors, the hematopoietic system

RESEARCH THEMES

- Research on viral gene transfer vectors, adeno-associated vectors, synthetic vectors, physical administration techniques.
- Targeting, expression systems.
- Immunology and gene transfer.
- Limb-girdle dystrophies.
- Genetic diseases of the immune system.
- Immunity of gene transfer.



Genomics Research Unit - Info



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MAIN TOPIC

- Bioinformatics

FIELD OF ACTIVITY

- Genomics, computing, pests and pathogens in plant biology

KEYWORDS

- Bioinformatics applied to plant genomics, pests and pathogens

RESEARCH THEMES

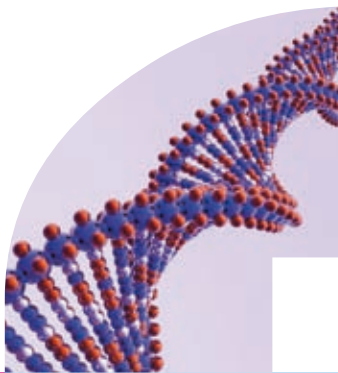
The Genomics Research Unit - Info is an INRA bioinformatics platform. Its primary missions are as follows:

- implementation of plant genomics information systems, notably in collaboration with partners laboratories as national (Genoplante) and international collaborative projects.
- data integration (sequences, cartography, transcriptomics, proteomics, sequence polymorphism) provided to researchers.

- development of analytical tools and interfaces for value-added exploitation of genomic data.
- specification and implementation of high-throughput analyses.



Genoscope CEA/Genomics Institute



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MAIN TOPIC

- Genomics/ Postgenomics

FIELD OF ACTIVITY

- High-throughput production of DNA sequences
- Genome analysis
- Functional genomics
- Applications (research on biological solutions for the replacement of chemical synthesis)

KEYWORDS

- Sequencing, genomics, biochemistry, metabolism, bioconversion, comparative genomics

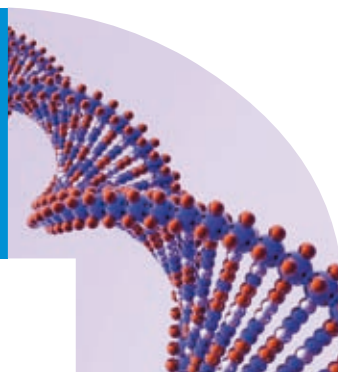
RESEARCH THEMES

Since 1998, Genoscope has been responding to the high-throughput sequencing needs of the French scientific community (~30,000 sequences per day). Genoscope has also participated in international collaborative sequencing efforts such as the Human Genome Project (chromosome 14), plant genome projects (*Arabidopsis*, *grapevine*, *rice*, etc.) and animal genome projects (*Tetraodon*, *Anopheles*, etc.), and has sequenced more than fifty prokaryotic genomes. Genoscope maintains state-of-the-art technology in the fields of sequencing and sequence analysis. The new sequencing technologies (Gsflex and Illumina) are partially operational and are currently undergoing

evaluation. For its in-house research projects, Genoscope is focusing on the genomics of micro-organisms and their environment. The exploitation of sequence data (now extended to the identification of biological functions, notably in the biocatalysis field) is opening up new perspectives for developments in industrial biotechnology. In the field of sustainable development, Genoscope is searching for biological solutions in synthetic chemistry, in order to reduce pollution and energy & fossil fuel consumption.

Immunochemistry of Cell Regulation and Viral Interactions

Inserm U672 [ex 354]



Inserm

Institut national
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MAIN TOPIC

- Genomics/Postgenomics

FIELD OF ACTIVITY

- The cancer/immune system interface.
- analysis of signal transduction mechanisms during human B lymphoma proliferation.
- analysis of the control mechanisms in human cell death: the role of the novel RB18A gene (discovered in Unit 354).
- inhibition of tumor and metastasis development in human melanomas.

KEYWORDS

- Signaling, proliferation, differentiation, lymphomas, melanomas, tumors, metastases

RESEARCH THEMES

A: Regulation of the proliferation and differentiation of human B lymphomas.

1\ Identification and analysis of signal transduction pathways specifically recruited during cell surface activation of the Epstein-Barr virus (EBV, a transforming virus) receptor and the C3d growth factor (EBV/C3dR, gp140, CR2, CD21).

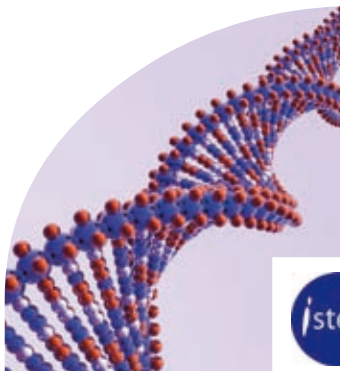
2\ Analysis of the role of RB18A, a transcription cofactor which regulates the functions of the p53 oncoprotein.

B: Inhibition of the tumorigenic and metastatic power of human melanomas.

Development of a new gene therapy approach: use of an anti-cathepsin-L ScFv.

Institute for Stem Cells in the Treatment and Study of Monogenic Diseases [I-STEM]

Inserm U861



Supervisory bodies \ AFM, INSERM, UNIVERSITÉ D'EVRY-VAL-D'ESSONNE Director \ Marc PESCHANSKI

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MAIN TOPIC

- Postgenomics/Cell therapy of monogenic diseases

FIELD OF ACTIVITY

- Evaluation of the full therapeutic potential of all types of human stem cells in the treatment of monogenic diseases. Set against this background, the group is particularly exploring substitutive cell therapies for degenerative diseases on one hand and the use of stem cell lines carrying pathological mutations as drug screening targets on the other

KEYWORDS

- Cell therapy - disease modelling - stem cells - monogenic diseases

RESEARCH THEMES

The I-STEM group is currently focusing on human embryonic stem cells (hESCs) and six major interconnected themes:

1 - A technology development program aimed at obtaining cells of interest.

It comprises two parts: mass stem cell production and automated long-term culture for guided stem cell differentiation.

2 - Use of the cardiomyocyte progeny of native hESCs in regenerative medicine for patients suffering from Duchenne muscular dystrophy.

3 - The ability of native hESC-derived GABAergic striatal neurons to replace the fetal neural tissue currently used in the intracerebral graft treatment of patients suffering from Huntington's disease.

4 - The immunosuppression conditions specifically required by this type of stem cell transfer in various tissues.

5 - The modelling of monogenic diseases in hESC lines derived from embryos rejected following pre-implantation genetic diagnosis. The first line carries the DM1 mutation which causes myotonic dystrophy. We are seeking mutation-linked biomarkers in the progeny of these cell lines for use in studying the disease mechanisms and screening for drug candidates.

6 - The development of the functional genomics tools required for gene overexpression or extinction under high-throughout screening conditions.

HOLDER OF A GENOPOLE RESEARCH GROUP ESTABLISHMENT («ATIGE») GRANT

- «Genetic mechanisms underlying the cardiac specification of embryonic stem cells» Leader: Michel PUCEAT.
- «Pathological modelling of motoneuron affection using human embryonic stem cells» Leader: Cécile MARTINAT.
- «Cell and protein therapy for cerebrovascular diseases» Leader: Brigitte ONTENIENTE.



IT for Integrated Biology and Complex Systems [IBISC]

FRE 2873



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MAIN TOPIC

- Computing, bioinformatics, ICST, engineering, biology

FIELD OF ACTIVITY

- Bioinformatics; analysis, modeling, identification and simulation of biological processes; software engineering; operational research; communication & transport networks; agent-based & communicative systems; biomedicine & healthcare (signals, machine-assisted medical procedures, assistive technology in handicap), biometrics, multimodal man-machine interfacing, road safety; biology of the cellular micro-environment; modeling in physiology

KEYWORDS

- Bioinformatics, postgenomics, data integration and advanced databases; formal methods; algorithmics, optimization, learning; complexity sciences; data, signal and image processing; virtual reality, augmented reality, haptics; intelligent vehicles; cell migration; the physiome

RESEARCH THEMES

The group's scientific activity is organized into three themes: biological systems, assistance robotics and interacting systems. Within Genopole@ , IBISC's specificity involves studying potential applications of computing science and automation to genomics and systems biology. Research in this area covers three main themes:

- the representation, analysis and comparison of DNA, RNA and protein sequences; the determination of functional motifs, annotation, etc.
- the organization and analysis of transcriptomic, proteomic and metabolomic data, together with statistical learning based on these data with a view to the development of systems biology tools.
- the representation, modeling, simulation and identification of biological processes, with a focus on the simulation of cellular and tissue processes (renal physiology, development); regulatory networks and cell/micro-environment interactions during metastatic spreading.



Laboratory for Analysis and Modeling in Biology and the Environment [LAMBE] CNRS UMR 8587



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MAIN TOPIC

- Physics/Chemistry

FIELD OF ACTIVITY

- Study of the cationization process in organic molecules, mass spectrometry proteomics, structural analysis of biologically relevant macromolecular systems.
- In silico modeling of the physical chemistry of proteins, nucleic acids, membranes and the interactions between these species. Vibrational spectroscopy of biological macromolecules.
 - Study and modeling of processes involved in the environmental containment of toxic or radioactive elements.
 - Electrochemistry and reactivity of materials at interfaces in contained milieus

KEYWORDS

- Mass spectrometry, modeling, proteomics analysis, radionuclide reactivity and thermochemistry, redox reactions of the actinides, solution chemistry, electrochemistry, biomolecular modeling and simulation

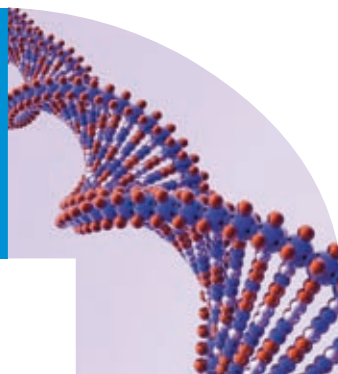
RESEARCH THEMES

- Prediction and modeling of the long-term behavior of final electronuclear waste.
- Study of the role of metal cations in the catalysis and activation of model biological compounds (amino acids, nucleotides, saccharides, etc) in the gaseous phase.
- Mass spec structural analysis of biomolecules (post-translational modifications, non-covalent binding, etc.) using MALDI/TOF, electrospray/QTOF and capillary electrophoresis/ion trap spectrometers.

- Multiscale molecular modeling and simulation of the structure and function of biological assemblies.



Laboratory for Functional Exploration of Genomes



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MAIN TOPIC

- Functional genomics/Postgenomics

FIELD OF ACTIVITY

- Carcinogenesis, RNA interference, radiobiology

KEYWORDS

- Bioinformatics, carcinogenesis, cell microarrays, differentiation, H2AX, ID2, irradiation, stem cells

RESEARCH THEMES

The missions of the CEA's Laboratory for Functional Exploration of the Genomes in Evry are as follows:

- the development of a DNA microarray production facility.
- the development of new chip concepts and, in particular, cell microarrays for functional genome exploration.

The Laboratory relies on these technological developments to characterize:

- 1 - genetic networks in differentiation: by comparing the expression profiles of differentiated cells (keratinocytes, hematopoietic cells) to those of progenitor and stem cells, the laboratory seeks to

identify the molecular signatures of each stage of differentiation and characterize the genetic networks which regulate transitions between these stages. We are currently focusing on the ID2 network.

- 2 - the response to genotoxic stresses. Using the technological and theoretical tools that we have developed, we are analyzing the signaling network that, in response to irradiation, leads to phosphorylation of histone H2AX.

In all of its activities, the laboratory relies on an expert bioinformatics team which develops the algorithms required for microarray production & analysis and the deduction of genetic networks.



Laboratory for the Genomics and Radiobiology of Hematopoiesis



Supervisory Body \ CEA Director \ Diana LE ROUX

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MAIN TOPIC

- Genomics/Postgenomics

FIELD OF ACTIVITY

- Analysis of the molecular response of hematopoietic stem cells to ionizing radiation

KEYWORDS

- Hematopoietic stem cells, transcriptome, DNA chips, ionizing radiation

RESEARCH THEMES

The laboratory's work seeks to (i) identify the genetic networks involved in the differentiation of hematopoietic stem cells and (ii) determine the molecular changes which appear in response to ionizing radiation. This analysis has mainly been based on the production of transgenic mice and the use of DNA chip technology developed in our lab. In fact, over the last few years, the research group has designed and produced DNA chips comprising up to 22,000 mouse genes.

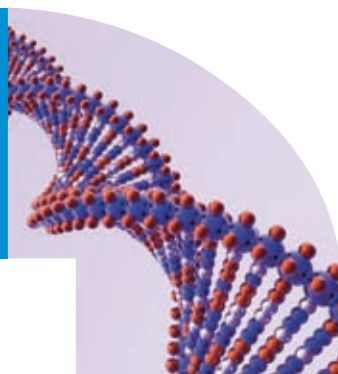
We produce 2 transgenic mouse models: transgenic mice defective in the alpha sub-unit of integrin $\text{I}\beta\text{-3}$ (Tronik-Le Roux *et al.*, *Blood* 2000) and the $\text{I}\beta\text{tk}$ mouse, which expresses a suicide gene for the reversible elimination of mature hematopoietic cells and enables

bone marrow reconstitution to be monitored while maintaining a healthy environment (Tronik-Le Roux *et al.*, *J.Exp.Med.* 1995; Tropel *et al.*, *Blood* 1997).

More recently, we have analyzed the response of hematopoietic cells to ionizing radiation *in vivo* and especially the latter's effect on stem cells and bone marrow reconstitution. Greater insight into the molecular mechanisms involved will enable us to deepen our knowledge of cellular radiosensitivity and, in the longer term, identify new diagnostic markers and novel drug targets.



Laboratory for the Genomics and Radiobiology of Keratinopoeisis



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MAIN TOPIC

- Stem cells of the human epidermis

FIELD OF ACTIVITY

- Cell biology, tissue engineering, genomics, cell signaling, radiobiology

KEYWORDS

- Stem cells, human skin, skin organogenesis, regenerative medicine, genomics, transcription factors, radiobiology, radiopathology

RESEARCH THEMES

Homeostasis, regenerative potential and radiosensitivity of human epidermal stem cells.



Laboratory for Polymeric Materials at Interfaces [MPI]

CNRS UMR 7581



Supervisory bodies \ CNRS/UNIVERSITÉ D'EVRY-VAL-D'ESSONNE Director \ Loïc AUVRAY

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MAIN TOPIC

- Physics/Chemistry/Biology

FIELD OF ACTIVITY

- Biophysics, macromolecular synthesis, electrophysiology, radiation scattering

KEYWORDS

- Polymers, nanopores, bionanotechnology, vectors

RESEARCH THEMES

The Laboratory for Polymeric Materials at Interfaces (MPI) has changed significantly since its creation ten or so years ago, when the University of Evry's «materials» focus and the «polymer» activities of its founders gave rise to the lab's title. The MPI lab is now a multidisciplinary laboratory where chemists and physicists work together on subjects at the interface between polymer chemistry, physics and biology, with a particular focus on biomimetic systems or those of therapeutic interest.

The lab members have acknowledged skills in macromolecular synthesis, supramolecular chemistry, the synthesis and study of polymers at interfaces,

the physics of polymers, colloids and biological membranes and radiation scattering. Over the last three years, our work has been structured into two main themes, linking chemists and physicists:

- study of the transport (translocation) of single macromolecules through natural (protein) and artificial (nanolithographic) nanometer-scale pores, with applications in the analysis and micromanipulation of biological macromolecules.
- synthesis of polymer vectors for gene therapy and study of their structure and function *in vitro* and *in vivo*.

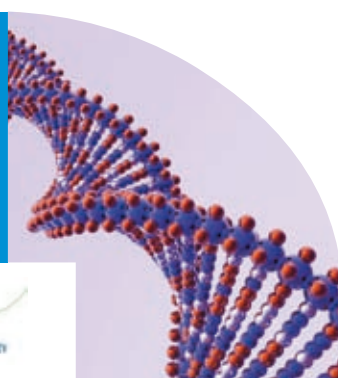
HOLDER OF A GENOPOLE RESEARCH GROUP ESTABLISHMENT («ATIGE») GRANT

- «Protein translocation and refolding on exiting nanopores: a comparison between natural and biomimetic systems. Applications.» Leader: Juan PELTA.



Metabolic Genomics

CNRS UMR 8030



Supervisory Bodies \ CNRS, GENOSCOPE, UNIVERSITÉ D'EVRY-VAL-D'ESSONNE **Director** \ Jean WEISSENBACH

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MAIN TOPIC

- Environmental genomics

FIELD OF ACTIVITY

- Analysis of eukaryotic and prokaryotic genomes, metagenome analysis, metabolic biochemistry, metabolic networks and modeling

KEYWORDS

- Sequencing, biochemistry, metabolism, metabolomics, comparative genomics, functional genomics

RESEARCH THEMES

The unit's themes are as follows:

- sequence analysis of eukaryotic and prokaryotic genomes
- metabolic and microbial biodiversity of wastewater treatment plants
- metabolic networks (modeling, reconstruction and analysis)
- the metabolic thesaurus (reconstruction of metabolic pathways and systematic functional analysis of the genes of *Acinetobacter baylyi*)
- new enzymatic functions of central and intermediary metabolism.

The Metabolic Genomics Group (UMR 8030) is the basic research structure of Genoscope-National Sequencing Center. Historically, the principal theme of the unit was tightly linked to Genoscope's sequencing and sequence analysis activities (eukaryotic and prokaryotic genomes).

The sequence analysis activities are still ongoing but have been extended by the functional identification of as yet unknown metabolic enzymes. The search for new enzyme activities fits into a larger framework with two central objectives: (1) obtaining an integrated vision of the metabolism of a bacterium and (2) completing the construction of bacterial metabolic pathways which are as yet unknown (or about which very little is known) and the anaerobic pathways in particular.

These two objectives mainly depend not only on knowledge of the complete sequences but also on sequence analysis using metagenomic approaches. To address these questions, we use two genomic resources which have been developed over a number of years:

- a pangenomic collection of *Acinetobacter baylyi* mutants.
 - a large collection of metagenomic sequences of prokaryotic flora from wastewater treatment plants.
- Critical examination of these resources constitutes the starting point for a whole series of questions which will then be addressed by either experimental or bioinformatics approaches or a combination of the two.





Molecular, Cellular and Tissue Biophysics Laboratory [BioMoCeTi]

CNRS UMR 7033

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MAIN TOPIC

- Physics/Chemistry

FIELD OF ACTIVITY

- From an experimental standpoint, the laboratory's activities are essentially based on optical methods: UV-vis absorption, circular dichroism, Raman spectroscopy, fluorescence spectroscopy, microspectrofluorimetry, phase-modulated time-resolved fluorescence spectroscopy, flow cytometry, fluorescence imaging, laser flash photolysis, stopped-flow, photochemistry, and so on

KEYWORDS

- Nucleic acids, targeting, membrane transport, molecular biophotonics

RESEARCH THEMES

1- Nucleic acids: structure, dynamics and interactions with:

- modified synthetic oligonucleotides.
- amphipathic, cationic peptides.
- proteins, notably transcription regulators.


This work relies on modeling the electronic properties (quantum calculation), dynamic properties (in the explicit presence of solvent and counter-ions) and folding properties of single-stranded RNA and DNA - the BCE (Biopolymer Chain Elasticity) approach.

2 - Drug targeting systems for use in gene therapy:

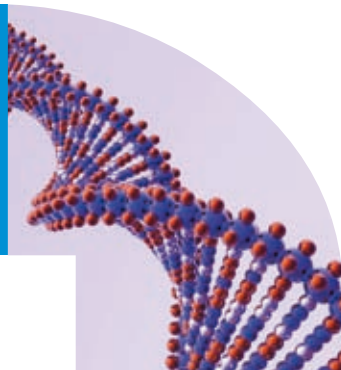
- the development of synthetic nucleic acid transfer systems (non-viral targeting of antisense oligonucleotides or siRNA) based on minimal-length cationic peptides or derived from antifungal compounds.
- targeting systems for molecules of therapeutic interest (photosensitizers and natural & synthetic oligonucleotides) using exosome-like vesicles secreted by a eukaryotic micro-organism (*Dictyostelium discoideum*).

3 - Molecular biophotonics and biomedical applications:

- study of the mechanisms of action of photoactivatable molecules (photosensitizers) of biological and therapeutic interest.
- development of diagnostic tools based on fluorescence spectroscopy and elastic & non-elastic light scattering for single cell-resolution analysis of biological tissues.



The National Genotyping Center [CNG] CEA/Genomics Institute





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MAIN TOPIC

- Genomics/Postgenomics

FIELD OF ACTIVITY

- The CNG is primarily devoted to the discovery and characterization of genes involved in human disease.

KEYWORDS

- Genotyping and related genomics technologies

RESEARCH THEMES

Since its creation, the CNG has maintained its international competitiveness by incorporating the many technological developments produced worldwide in the field of genotyping. It has set up a whole range of integrated platforms for studying the genes responsible for diseases or other traits (cardiovascular, auto-immune, neurological, psychiatric, dermatological and infectious diseases, diabetes, etc.):

- a biological resource laboratory, a genotyping platform (microsatellites), multiplex SNP genotyping platforms with 1534 markers (Illumina) or 48 markers (SNPlex), on an individual basis (MALDI-TOF, Amplifluor, Taqman) or by direct sequencing; Illumina and Affymetrix platforms for performing pan genomic linkage studies (SNPs); SNP discovery & mutation detection platforms;
- an epigenetic laboratory
- an animal model genomics laboratory;

- a molecular phenotyping laboratory
- a bioinformatics & computational biology laboratory.

The CNG participates in major European programs on both technological development and disease research. It is involved in a major «Genomics and Cancer» national program in collaboration with other programs funded by the French National Cancer Institute. The CNG's production infrastructure is widely used by the French and European scientific communities. Following scientific review, CNG groups have performed over 200 research projects submitted by scientists from across France and Europe. Between 1999 and 2006, the CNG's integrated infrastructure for genetic studies has enabled implementation of collaborative projects from around 300 French labs and 60 labs from outside France. The CNG's activity as a whole has helped generate more than 250 publications. The Center also hosts training fellowships (with over 110 researchers since 1999) and student projects (with over 100 interns and 70 students since 1999). It provides mid-term hosting for INRA and INSERM research groups involved in collaborative projects and runs international exchange programs with Japan, Russia and Thailand.



Plant Genomics Research Unit [URGV]

CNRS UMR 8114 et Inra UMR 1165



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MAIN TOPIC

- Genomics/Postgenomics

FIELD OF ACTIVITY

- Genomics and computing resources in plant biology

KEYWORDS

- Plant genomics

RESEARCH THEMES

The URGV's goals are to develop plant genome analysis tools and use them to identify genes which impact on agriculture (crop growth), the environment (disease resistance genes) and/or the agrifood industry (genes influencing the quality of crop-derived products).

The unit's research themes fall into three main categories:

a) functional analysis of the *Arabidopsis* model genome

- development of transcriptome analysis tools and of tiling arrays for ChIP/Chip analysis.
- analysis of the *Arabidopsis* ORFeome.
- development of gene inactivation techniques.
- analysis of the PPR (pentatricopeptide repeat) family involved in organelle function.
- analysis of MAP kinases and their role in adaptation to biotic and abiotic stress.

b) analysis of crop genomes

- comparative analysis of plant genome structure (wheat, canola and the grapevine in particular).

- positional cloning of agriculturally important genes.
- development of reverse genetics tools (gene tilling).
- grapevine genome transcript analysis.

c) bioinformatics

- development of a database (FLAGdb) on the *Arabidopsis* model genome and bioinformatics tools for managing and analyzing the data outputs.
- creation of new analysis tools for facilitating genome synteny conservation studies and work on plant improvement. Development of analytical tools for gene regulation sequences.
- collaboration with the Genoscope and URGI on the annotation of the grapevine genome.



Statistics and the Genome

CNRS UMR 8071



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MAIN TOPIC

- Mathematics/Biomathematics/Bioinformatics

FIELD OF ACTIVITY

- Development of mathematical tools for the analysis of biological sequence data, Markov chains, hidden Markov chains and genomic networks. Analysis of expression and SNP data. Biomolecular genetics.

KEYWORDS

- Biomathematics, modeling, statistical analyses, sequence evolution, large-scale comparisons. Biomolecular genetics

RESEARCH THEMES

- Design of statistical methods for the analysis of DNA/protein sequence & expression data.
- Making these methods available to the biology community via computer networks.

Our research axes notably include:

- Sequence analysis using Markov chains or hidden Markov chains
- Statistical inference of biological networks (interaction, regulation, metabolic pathways from statistical or dynamical data.

- Analysis of genomic data for the identification of genes involved in the etiology of diseases (SNP analysis); time-domain analysis of gene expression mechanisms (Markovian modeling or otherwise).
- Study of inter-gene relationships, support for automatic annotation via large-scale sequence comparisons. Transposable elements.
- Study of protein sequence evolution.
- Analysis of transcriptome/proteome data.



Structure and Activity of Normal and Pathological Biomolecules

Inserm U829



Inserm

Institut national
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MAIN TOPIC

- Tubulin dynamics

FIELD OF ACTIVITY

- Cell biology, cancer, neuroscience, medicine, drug design

KEYWORDS

- Structure, NMR, AFM, tubulin, cancers, nervous system, mutations, myopathies, AIDS

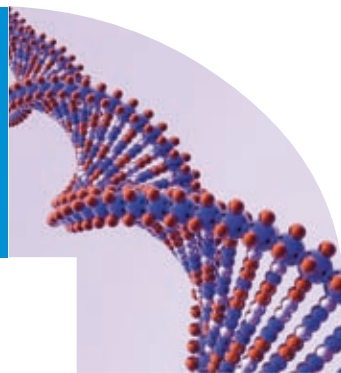
RESEARCH THEMES

- Physiopathology of the microtubule cytoskeleton and implications for the cell cycle and neuronal function.
- Functional genomics of the centriole.
- The structure, folding, stability & dynamics of proteins in solution

- Protein/protein, ligand/protein and protein/nucleic acid interactions
- Development of a multifunctional biomolecule vector based on nanodiamonds.

Unit for Integrated Biology in Adaptations to Exercise [UBIAE]

UEVE EA 3872/Inserm U902



Inserm

Institut national
de la santé et de la recherche médicale



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MAIN TOPIC

- Physiology/Genomics/Postgenomics

FIELD OF ACTIVITY

- Genomics and bioenergetics of muscle activity in healthy subjects and patients. Analysis of the physiological responses to acute and chronic exercise (training) in the mammal (the human, the mouse and the horse in particular)

KEYWORDS

- Motor performance, mitochondrion, heart, muscle, exercise, physiological responses

RESEARCH THEMES

The laboratory's work is set against a public health context, with the objective of optimizing motor performance. Our group analyzes the bioenergetic responses to muscle exercise (from physiology to molecular biology) in humans and animals (with murine and equine models). Our expertise in the field of effort training and re-training enables improvements in motor performance in both patients and experienced athletes. In fact, we develop physical training methods which are specifically adapted to an individual's physiological profile, in order to reconcile performance and health.

The LEPHE studies the molecular adaptations associated with the exercise and has developed a molecular approach for detecting transcriptome modifications induced by endurance exercise in horses participating in long-distance (140 km) events.

In collaboration with Xavier Gidrol (Director of the CEA Laboratory for Functional Exploration of Genomes), we have validated horse DNA chips by starting from murine and human DNA chips. The laboratory remains at the cutting edge of new technological developments for analyzing the bioenergetic responses to exercise (from physiology to molecular biology in humans and in animals (murine and equine models)). The laboratory advises top-level sportspeople (such as the best Kenyan distance runners) and also young sportspeople. By comparing humans with animals and physiological data with genetic data, the laboratory has adopted a truly novel approach here on the Genopole® campus.