



UMR 1313 GABI

Core facilities

INRA Jouy en Josas
Domaine de Vilvert
F-78350 Jouy en Josas
www.jouy.inra.fr/gabi



Objectives

The “Platform” team brings together the expertise and equipment of the core facilities supported by GABI that are open to external users: the @BRIDGE facility (animal Biological Resources for Integrated and Digital Genomics), the histology facility, and the transmission electron microscopy service of the MIMA2 multi-site facility.

The team aims at providing integrated services and equipment from the storage of biological samples to their analysis at the molecular, cellular or tissue level.

Its fields of activity are structural and functional genomics, microgenomics, morphological and ultrastructural analyses. The facilities have a Biological Resources Center with secured management, characterization and distribution of collections, coupled with support for experimental procedures and tools for data analysis.

The biobanking, genomic and transcriptomic facilities are part of the national CRB-Anim infrastructure for animal biobanks supported by the 2012-2019

Joint research unit

Animal Genetics and Integrative Biology (GABI)

Core facilities

Team leader

Michèle Tixier-Boichard (michele.boichard@jouy.inra.fr)

Co-leaders

Claudia Bevilacqua (claudia.bevilacqua@jouy.inra.fr): microgenomics, qPCR

Christine Longin (christine.longin@jouy.inra.fr): electron microscopy

Marco Moroldo (marco.moroldo@jouy.inra.fr): genomics, biobanking

Silvia Vincent-Naulleau (silvia.vincentn@cea.fr): histology

Technological offers and know-how

Biobanking services: biological samples of any kind, including tissue preparations, except for infectious material. The facility provides a service of DNA and RNA extraction, and quality control.

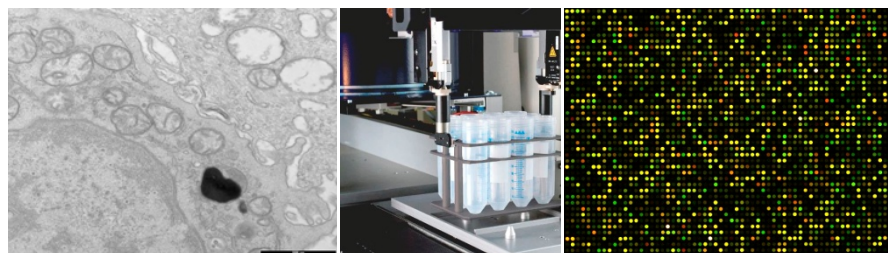
Structural genomics: BAC libraries and preparation of NGS libraries, capture of targeted genomic regions and whole genomes of pathogen agents that cannot be cultured.

Functional genomics: Agilent microarray workflow and qPCR with specialized software for data analysis (GeneSpring GX (Agilent) and Ingenuity Pathway Analysis (Ingenuity) for transcriptomic data analysis and GeneX (Multid) for qPCR analyses.

Functional and structural analysis at cell or tissue level

- Histology: tissue processing, sectioning and staining; in situ hybridization on tissue cryosections; digitalization of histological slides (brightfield);
- Laser capture microdissection: production and analysis of micro-quantities of material extracted from cells that are isolated from their tissue environment under morphological control
- Ultra-structural analysis of cell morphology with transmission electron microscopy

The main equipments include: 19 -80°C freezers, five instruments to measure nucleic acid quality and quantity, a DNA sonicator (Covaris), a liquid handler, a nucleic acid extractor (Chemagic STAR), an Agilent micro-array workflow, an ABI 7900HT qPCR system equipped with a TaqMan Array Card block and a QuantStudio (96-well plate) qPCR system, two laser capture microdissection systems (VERITAS and XT), two cryostats, a SnapFrost, a batch Stainer, a microtome, a tissue embedding facility and an automated vacuum tissue processor (LEICA), a brightfield and fluorescence virtual slide scanning system (09-2014), two ultramicrotomes (Reichert E – Leica UC6), a Zeiss EM902 EELS for





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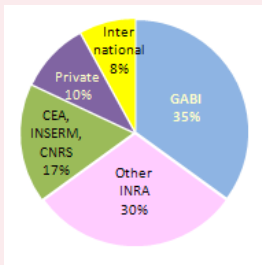
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Users

The total number of users per year ranges from 120 to 170.



Quality policy

Most activities of "Platform" team are ISO 9001:2008 certified.

In 2013, @BRIDGE was granted the national strategic label of INRA and MIMA2 the regional strategic label of INRA.

Platform network

The core facilities belong to the network of facilities of the Jouy-en-Josas Research center ARPEJ (www.jouy.inra.fr/Outils-et-Ressources/Plateformes)

Joint research unit

Animal Genetics and Integrative Biology (GABI)

Scientific production

On average, members of GABI's core facilities are co-authors of approximately 20 papers each year. Most of these papers have co-authors from other research units than GABI. Our objective is to trace and make an inventory of all publications referring to the facilities in the Material and Methods or in the Acknowledgements sections of the articles.

Recent publications

Brenaut P, Bangera R, Bevilacqua C, Rebours E, Cebo C, Martin P: Validation of RNA isolated from milk fat globules to profile mammary epithelial cell expression during lactation and transcriptional response to a bacterial infection. *J Dairy Sci* 2012, 95:6130-6144.

Degrelle SA, Jaffrezic F, Champion E, Le Cao KA, Le Bourhis D, Richard C, Rodde N, Fleurot R, Everts RE, Lecardonnel J, Heyman Y, Vignon X, Yang XZ, Tian XCC, Lewin HA, Renard JP, Hue I: Uncoupled embryonic and extra-embryonic tissues compromise blastocyst development after somatic cell nuclear transfer. *PLoS ONE* 2012, 7:e38309.

Diribarne M, Mata X, Rivière J, Bouet S, Vaiman A, Chapuis J, Reine F, Fleurot R, Auvinet G, Deretz S, Allain D, Schibler L, Cribiu E, Guerin G: LIPH expression in skin and hair follicles of normal coat and Rex rabbits. *PLoS ONE*, 2012, 7:e30073

Gao Y, Wahlberg P, Marthey S, Esquerré D, Jaffrézic F, Lecardonnel J, Hugot K, Rogel-Gaillard C: Analysis of porcine MHC using microarrays. *Vet Immunol Immunopathol* 2012, 148:78-84.

I Marangon, N Boggetto, C Menard-Moyon, E Venturelli, M-L Beoutis, C Pechoux, N Luciani, C Wilhelm, A Bianco, F Gazeau: Intercellular carbon nanotube translocation assessed by flow cytometry imaging. *Nano Lett* 2012, 12):4830-4837.

Aïoun J, Chat S, Bordat C, Péchoux C: Antigen recovery and preservation using the microwave irradiation of biological samples for transmission electron microscopy analysis. *Micron* 2013, 52-53:16-23.

Leymarie O, Jouvion G, Hervé PL, Chevalier C, Lorin V, Lecardonnel J, Da Costa B, Delmas B, Escriou N, Le Goffic R: Kinetic characterization of PB1-F2-mediated immunopathology during highly pathogenic avian H5N1 influenza virus infection. *PLoS ONE* 2013, 8:e57894.

Mach N, Gao Y, Lemonnier G, Lecardonnel J, Oswald I, Estellé J, Rogel-Gaillard C: The peripheral blood transcriptome reflects variations in immunity traits in swine: towards the identification of biomarkers. *BMC Genomics* 2013, 14:894.

Ruscanu S, Jouneau L, Urien C, Bourge M, Lecardonnel J, Moroldo M, Loup B, Dalod M, Elhmouzi-Younes J, Bevilacqua C, Hope J, Vitour D, Zientara S, Meyer G, Schwartz-Cornil I: Dendritic cell subtypes from lymph nodes and blood show contrasted gene expression programs upon bluetongue virus infection. *J Virol* 2013, 87:9333-9343.

A complete list of publications is available at: www.jouy.inra.fr/gabi

