Genomics and Biomarkers of Lymphoma and Solid Tumours

RESEARCH AREAS & OBJECTIVES

Research areas
Genomic and transcriptomic of lymphomas

Objectives
The laboratory aims at establishing correlations between molecular data and phenotype / clinic of lymphomas: prognostic or theranostic value; setup of diagnostic assays; identification of the biological value of identified variants in tumor and plasma.

EXPERTISE

Biological targets and in vitro / in vivo / ex vivo models
Targets: molecular studies of genes coding for BCR component and particularly VH genes

Blood and tissue biomarkers
- Study of recurrent mutations and abnormal copy number of genes affecting prognostic
- Targeted transcriptomic studies and transfer in immunohistochemistry

Early pharmacodynamic signs of activity
Correlation between transcriptome/ genomics and PETScan imaging

Tools, processes and platforms in connection with clinical research
- Average throughput genotyping platform, multiplex PCR analysis, study of key gene methylation by pyrosequencing
- Tumor bank
- Conventional cytogenetics and FISH
- Clinical research unit including early phase trials

PLATFORMS & TECHNICAL RESOURCES

- Sequencing, (PGM) quantitative PCR (TaqMan) pyrosequencing
- Genotyping platform and transcriptomic analysis of average throughput (Illumina, BeadExpress)
- Flow cytometry
- Cell transfection (Amaxa), cloning, cell culture
- Tissue-microarray
- Conventional cytogenetics and FISH
- Bioinformatics

R&D OFFER

The laboratory offers collaborative projects on:
- targeted sequencing (tumor and plasmatic DNA) and molecular phenotyping (genetic expression profiles) in clinical assays
- quantification of recurrent mutations in plasmatic DNA
- correlation between anatomical-clinical / molecular and PET scan imaging
- bioinformatics tools for analysis of variants and their integration in routine diagnosis
- development of B and T-cell lymphomas phenotyping tools.

KEY WORDS
Genome, Genotyping, Transcriptome, Immunoglobulin genes, Transfer methylation