TAGC - Technologies avancées pour la génomique et la clinique

Rapport Hcéres

HCERES

High Council for the Evaluation of Research and Higher Education

Department of Research Evaluation

report on the research unit:

Theory and Approaches of Genomics Complexity

TAGC

under the supervision of the following institutions and research bodies:

Aix-Marseille Université

Institut National de la Santé Et de la Recherche Médicale - INSERM

Evaluation Campaign 2016-2017 (Group C)

HCERES

High Council for the Evaluation of Research and Higher Education

Department of Research Evaluation

In the name of HCERES,[1]

Michel Cosnard, president

In the name of the experts committee,[2]

Didier Auboeuf, chairman of the committee

Under the decree N°.2014-1365 dated 14 november 2014,

[1] The president of HCERES "countersigns the evaluation reports set up by the experts committees and signed by their chairman." (Article 8, paragraph 5)

[2] The evaluation reports "are signed by the chairman of the expert committee". (Article 11, paragraph 2)

Evaluation report

This report is the sole result of evaluation by the expert committee, the composition of which is specified below.

The assessments contained herein are the expression of an independent and collegial reviewing by the committee.

Unit name:	Theory and Approaches of Genomic Complexity
Unit acronym:	TAGC
Label requested:	UMR
Current number:	U1090
Name of Director (2016-2017):	Ms Catherine NGUYEN
Name of Project Leader (2018-2022):	Mr Pascal RIHET

Expert committee members

Chair: Mr Didier AUBOEUF, École Normale Supérieure, Lyon

Experts:

Mr Frédéric DELBAC, Université Clermont Auvergne, Aubière (representative of CNU)

Mr Hidde DE JONG, INRIA, Grenoble

Ms Isabelle DUROUX-RICHARD, CHU Saint-Éloi, Montpellier (representative of supporting personnel)

Ms Claire VANDIEDONCK, Université Paris-Diderot, Paris (representative of the INSERM - CSS)

Scientific delegate representing the HCERES:

Mr Pierre COUBLE

Representatives of supervising institutions and bodies:

Ms Chantal LASSERRE, INSERM

Mr Marc SENTIS, Aix-Marseille Université

Head of Doctoral School:

Mr Philippe NAQUET, Doctoral School n°62, “Life Sciences end Health”

1 • Introduction

History and geographical location of the unit

The unit "TAGC, Advanced Technologies for Genomics and Clinics" at the luminy campus (Faculty of Sciences, Marseille) was born in the center of immunology as a genomics team involved in the development of high-throughput technologies (1997-2001), and then established in 2002 as a research unit of technological and methodological innovation (ERIT-M). Research was centered on genome biology and clinical applications. During the 2004 quadrennial assessment, the unit was renewed and transformed into the ERM206 INSERM group. New resources were granted (premises, equipment, etc.). In 2008, the unit was transformed into a joint INSERM-university research unit UMR_S 928. The research unit was then renewed (UMR_S 1090) in 2012 to continue and amplify research aiming at deciphering complex biological networks in development or diseases.

Management team

The director of the unit is Ms Catherine NGUYEN and the deputy director is Mr Pascal RIHET. For the coming five-year period, Mr Pascal RIHET will be the director and Ms Catherine NGUYEN the deputy director.

HCERES nomenclature

Main scientific area: SVE2, cellular biology, imagery, molecular biology, biochemistry, genomics, systems biology, development, structural biology.

Secondary scientific areas: SVE3 microbiology, immunology, SVE5 physiology, physiopathology, cardiology, pharmacology, endocrinology, cancer, medical technologies.

Scientific domains

The research scope of the unit is genetics, genomics and bioinformatics. The unit clusters researchers with bioinformatics skills and experimental biologists. To answer biological and health-related questions coming from experimental biologists, the bioinformaticians develop computational concepts and bioinformatic tools for genomic data analysis and their integration. This includes the characterization of regulatory elements in the context of genetic variants, and networks within and between omics data. The unit applies these approaches to a broad range of biological systems and pathologies (sepsis, malaria, cancer, cardiopathy, cardiac aging and development, T lymphocyte differentiation).

Unit workforce

Unit workforce	Number on 30/06/2016	Number on 01/01/2018
N1: Permanent professors and similar positions	7	7
N2: Permanent researchers from Institutions and similar positions	6	9
N3: Other permanent staff (technicians and administrative personnel)	10	8
N4: Other professors (Emeritus Professor, on-contract Professor, etc.)	3	
N5: Other researchers from Institutions (Emeritus Research Director, Postdoctoral students, visitors, etc.)	0	
N6: Other contractual staff (technicians and administrative personnel)	4	
N7: PhD students	17	
TOTAL N1 to N7	**47**	
Qualified research supervisors (HDR) or similar positions	10	

Unit record	From 01/01/2010 to 30/06/2016
PhD theses defended	22
Postdoctoral scientists having spent at least 12 months in the unit	8
Number of Research Supervisor Qualifications (HDR) obtained during the period	0

2 • Overall assessment of the unit

Global assessment of the unit

The overall objective of the TAGC unit as a whole is to better understand the cellular and molecular mechanisms involved in the functioning of both normal and pathological complex biological systems, drawing on methodologies from genetics, genomics, and computational science. During the 2012-2017 evaluation period, the research activities were organized along three main axes. The thematic axis 1 “Complex traits and multifactorial diseases” aimed at identifying the molecular bases underlying the occurrence of multifactorial diseases, including haematological cancers, malaria and sepsis, in humans and various models (from in vitro model systems to Drosophila and mouse). The thematic axis 2 “Developmental genes and networks” analyzed genes and gene regulatory networks involved in various developmental processes, such as cardiogenesis in the Drosophila embryo, T lymphocyte differentiation, and male germ cell development. Finally, the thematic axis 3 “Network bioinformatics” pursued the aim at deciphering genome organization and gene regulation on the sequence level as well as at investigating protein functioning from a network perspective.

The scientific activity of TAGC during the 2012-2017 period has been carried out along the lines of the 2012 contract and, in accordance with its objectives, the unit has been very successful in attracting a number of complementary skills in genetics, genomics and computational science. The evolution of the scientific activities of the unit has led to a redefinition of the axes for the 2018-2022 period, so as to maintain internal coherence and to avoid thematic dispersal. Two research thematic axes are proposed: “Bioinformatics and genomics of molecular networks” and “Genetics and genomics of multifactorial diseases”.

Understanding the contribution of genetic variants to complex disease phenotypes requires a systems biology approach based on the production and analysis of large-scale datasets and data integration through computational modelling. The strength of the TAGC unit is to bring together experts in bioinformatics and experts in cellular, molecular and developmental biology to address physiological and pathological questions. The computational research and developments performed in the TAGC unit are thus inspired, validated and improved by challenging biological problems related to human health. Although the strategy defined by the TAGC unit has already led to technical and conceptual improvements in bioinformatics and in genomics, the valorization of the results in terms of a better understanding of the molecular bases of the complex disease phenotypes studied in the laboratory is on-going.

The output produced by the TAGC unit and the academic reputation and appeal of the unit are excellent. The interaction with the social, economic and cultural environment is very good. The management of the unit, the facilities, and the overall social and scientific atmosphere are excellent. The committee of experts recommends that the risk of thematic dispersal be continually controlled by the unit director jointly with the strategic advisory council.