agence d'évaluation de la recherche
et de l'enseignement supérieur

Section des Unités de recherche

AERES report on the research unit

TAGC, Technologies Avancées pour le Génome et la Clinique, UMR_S 928

TAGC, Technological Advances for Genomics and Clinics, UMR_S 928

From the

Université de la Méditerranée, Aix-Marseille 2

February 2011

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Le Président de l'AERES

Didier Houssin

Section des unités de recherche

Le Directeur

Pierre Glorieux

February 2011

Research Unit

Name of the research unit : TACG, Technologies Avancées pour le Génome et la Clinique

Requested label : UMR_S INSERM

N° in the case of renewal : UMR_S 928

Name of the director : Ms. Catherine NGUYEN

Members of the review committee

Committee chairman :

Ms. Mireille CLAUSTRES, Université Montpellier I

Other committee members

Ms. Jane-Lise SAMUEL, Inserm, Université Paris-Diderot

M. Michel GOOSSENS, Université Paris-Est-Créteil

M. Claude THERMES, CNRS, Gif sur Yvette

M. François KARCH, University of Geneva, Geneva, Switzerland

Observers

AERES scientific advisor :

M. Pierre LEGRAIN

University, School and Research Organization representatives

M. Pierre CHIAPPETTA, Université de la Méditerranée

Ms Chantal LASSERRE, Inserm

Report

1 • Introduction

- Date and execution of the visit

The site visit lasted for one full day on February 2nd, 2011. After a closed door meeting with AERES representative, the committee listened a general presentation of the unit by the Director (history, scientific strategy, human, technical and financial resources) in the presence of all members. TAGC is a "monoéquipe" organized along three main research Axes (1: Complex traits and multi-factorial diseases ; 2: Developmental genes and networks; 3: Network Bioinformatics), and most group leaders gave a formal presentation. In the afternoon, the committee had three parallel meetings with students/post-docs, ITA/technicians and Researchers. Poster sessions gave the committee a good overview of young scientists research projects. The committee then met with representatives of the Institutions (Inserm, University) before a final closed door meeting.

- History and geographical localization of the research unit, and brief presentation of its field and scientific activities

TAGC was established in 2002 in the Centre of Immunology of the Scientific Campus of Luminy (Marseille) as an ERIT-M (research unit of technological and methodological innovation) ; under management of the same Director, it evolved as a ERM206 Inserm group (2004-2007), then a joint Inserm-University unit UMR_S 928 (2008-2011). The configuration has considerably changed : from 15 people in 2006 to 42 people in June 2010, and the unit will be soon a 1797,5 m2 laboratory, as it benefits from an extension of surface of 450 m2.

During the past years, a specific competency in Functional Genomics and Bioinformatics has been developed, completing the scientific landscape of the Luminy campus. The challenge for 2012-2015 is to transform the laboratory as a unit of integrative and systems biology, with applications to pathologies. The objective is to integrate new skills, resources and teams into a common project focused on deciphering the molecular networks that influence complex phenotypes (cancer, malaria, sepsis) or development (cardiogenesis).

- Management team

The management team consists of a Director and an Assistant-Director, assisted by an administrative staff of 3 persons shared with other Inserm units located in the building. An Executive Board and a Council of Laboratory contribute to facilitate the inderdisciplinarity and complementarity between the various programs.

- Staff members (on the basis of the application file submitted to the AERES)

	Past	Future
N1: Number of researchers with teaching duties (Form 2.1 of the application file)	5	5
N2: Number of full time researchers from research organizations (Form 2.3 of the application file)	4	7
N3: Number of other researchers including postdoctoral fellows (Form 2.2 and 2.4 of the application file)	5	3
N4: Number of engineers, technicians and administrative staff with a tenured position (Form 2.5 of the application file)	6,4	9,4
N5: Number engineers, technicians and administrative staff without a tenured position (Form 2.6 of the application file)	3	1
N6: Number of Ph.D. students (Form 2.7 of the application file)	17	14
N7: Number of staff members with a HDR or a similar grade	8	8

2 • Overall appreciation on the research unit

- Summary

The Committee has been very impressed by the fact that this unit presents an authentic multidisciplinarity, bringing molecular biology and medical questions together with bioinformatics and mathematics. This gives the unit all the skills necessary for projects that include the identification of gene networks as well as the determination of their alterations in human pathologies. Major efforts have been made to organize multidisciplinarity among the various themes and to optimize the common infrastructure. The overall management, facilities, social and scientific athmosphere are excellent and this is largely due to the enthusiasm and charism of the current applicant Director.

- Strengths and opportunities

TAGC has been successfull in gathering with an exceptional coherence, a number of complementary skills in genetics, epigenetics, genomics, bioinformatics and high throughput technologies. This gives to the unit his exceptional research potential. This potential is reinforced by a very good scientific environment clearly acknowledged by all lab representatives met by the Committee. They have developed a good level of scientific animation, with regular external and internal seminars, and a large number of PhD students (16 at present) who all recognize TAGC as a very good place for training. Strong internal collaborations, in particular between “wet” biology and bioinformatics, well organized services offered by their very efficient IBiSA platform (covering all branches of "omics" including NGS) and strong community spirit, have contributed to make the unit more and more attractive during the recent years. The last group leader recruitment should be very beneficial to the unit. They have also established a solid network of local, national and international collaborations. The unit is extremely successful in attracting financial support from various sources. They applied their skills and resources to the study of diseases of great interest for Public Health, with very successful interfacing with the Hospital.

- Weaknesses and threats

It was generally felt that while producing very good science, TAGC still needs to increase its number of higher impact publications. This objective should be facilitated by the arrival of the new senior scientists. The development of several biological-based projects will require significant staff input. In this context, TAGC will have to face the departure of two senior biocomputing scientists (although they still continue to strongly collaborate with TAGC). In the past, the development of this unit has always been tightly controlled to avoid dispersion. Recently, this development has accelerated, leading to a possible risk of thematic dispersal ; it will thus be essential to maintain in the future the same tight control as in the past years. The written documents raised some questioning about a possible risk of dispersion but the presentation and the discussions demonstrated the unique research objective of the lab with a real coherence between the projects.

- Recommendations

TAGC evolved from a technology-based to a solid well-organized research unit, so that the Director has now to be watchful on the choice of the research projects. This may require further focusing to remain scientifically competitive. The Committee strongly supports the recruitment of a Professor of Bioinformatics.

- Production results

A1: Number of permanent researchers with teaching duties (recorded in N1) who are active in research	5
A2: Number of permanent researchers without teaching duties (recorded in N2) who are active in research	7
A3: Ratio of members who are active in research among staff members [(A1 + A2)/(N1 + N2)]	1
A4: Number of HDR granted during the past 4 years	2
A5: Number of PhD granted during the past 4 years	9

3 • Specific comments

- Appreciation on the results

  – Relevance and originality of the research, quality and impact of the result

Efforts to gather complementary and cohesive competencies have now allowed TAGC to present several ambitious projects, some of which are very innovative (e.g. the study of multifactorial diseases by analysis of network modularity). The objectives are obviously of primary biological and medical interest. The work of this team is recognized at national and international levels as evidenced by different collaborations in France and abroad, as well as by the quality and the number of publications.

- Quality/number of publications, scientific communications, thesis and other outputs

During the period between 2006 and 2010, the unit totalized 105 peer-reviewed publications (the vast majority of them with members of the unit as principal authors) for 9 full-time researchers and teachers-researchers, all "publishing scientists". The impact factor ranges from 0,696 (Adv Appl Math) to 10,4 (Blood), 12,24 (Mol Syst Biol) and 12,8 (Br Med J). Around 66% of the publications referenced by ISI have an IF situated in the upper quartile of the category. New young members have published or have been associated with high IF articles (Science, Nature). The unit records 55 other articles, 10 book chapters, and 2 directions of scientific books. It participated in the creation of databases and software (TBrowser, RToll4TB, SimCT, GINsim) that are widely used by the scientific community. TAGC members organized or co-organized 19 congresses or conference sessions. A total of 8 PhD theses supervised by unit members were defended during this period. All PhD students published in peer-reviewed journals (1 to 6 articles per student).

- The quality and the stability of partnerships

Interdisciplinarity is the corner stone of the TAGC unit, with strong local collaborations (mathematics institute, hospital,..).The IBiSA labellisation of the functional genomic platform, which became a complete service with high expertise for transcriptomic, high-throughput sequencing and biocomputing analyses, is an essential element of TAGC dynamism that further contributes to establish new scientific collaborations.

- Appreciation on the impact, the attractiveness of the research unit and of the quality of its links with international, national and local partners

TAGC members regularly communicated at congresses: 49 invited lectures in international conferences, regular invitations to seminars (around ten/year), and 136 oral communications or posters. The bioinformatics was recognized by two international awards. They also participate in numerous expertises including evaluation committees for University, EPST, ANR, AERES, or Foreign agencies.

The unit is very attractive, The next arrival of three new groups (genetics, interactome, hematological malignancies) will considerably strengthen and expand the previous scientific strategies. The researcher's staff grew from 4 to 9 (2 Professors, 2 CR1 CNRS).

TAGC members are very successful in grant applications, with about 80% of their budget resulting from contractual resources including ACI, MERNT, MAE, CanceroPole, Regional and General Councils, INCA, ARC, AFM, ANRs (Piribio; Syscom; Jeunes Chercheurs), EU (ERAnetSysBio/ModHeart; ERAnetpathogenomics), etc..).

Most contracts obtained by the unit involve national or international partnerships.

It is remarkable that TAGC has a very active policy of partnership development, at the regional (Structural Genomic Institute; Cancer Research Center; Developmental Biology Institute; Immunology Center; Mathematics Institute; Nanotechnologies Institute; local hospitals, etc...), national (over 30 laboratories collaborate with TAGC) and international levels (mainly focused on modular modelling and analysis of biological networks ; a good example is the next creation of an "European Associated laboratory" with the prestigious Gulbenkian Institute of Science in Portugal)

- Appreciation on the management and life of the research unit

The committee has noticed an excellent management with an excellent spirit within the unit ; the staff scientists, post-docs, students and ITA expressed a clear satisfaction. The Director organizes very regular meetings with members of the unit, and is unanimously recognized for her availability by all categories of personnels. The vitality of the IBiSA platform favored the success in recruitment and promotion of engineers (one IR Inserm 2010 in bioinformatics, one IR in CDD from the University, one IE CNRS 2010, and three promotions (two IR2->IR1 and one AI->IE).

The strong policy of recruitment of young scientists (Inserm CNRS, University) favours the emergence of new strategies, such as protein-protein interactions and application of biological networks to malaria and hematological malignancies. These projects are a perfect illustration of the exceptional level of interdisciplinarity reached by TAGC.

The teachers-researchers are largely involved in teaching and training in LMD programs; several members are heading Master programmes or modules and participate in various steering committees and in the council of the Doctoral School of Life Sciences and Health ; most TAGC members are strongly involved in teaching and training abroad (partnerships with 7 countries). The unit demonstrates a very active participation to the ED 062 Vie et Santé (Faculty of Sciences) and IFR137 (Institute of oncology and immunology).

The overall organization and the governance of this structure is flexible enough to permanently evolve and allow the integration of new complementary skills. The Committee is confident that merging approaches developed in the three axes should provide a breakthrough in the development of system biology approaches.

The Committee has been very impressed by the fact that all PhD students benefit from a double supervision: biologic and biocomputing; this is highly novative.

Research axis 1: Complex traits and multi-factorial diseases

- ### Appreciation on the scientific strategy and networks:

This team presents an original and innovative project of integrative biology focused onto the immune system and aiming at deciphering the molecular networks that influence complex phenotypes and/or cause multifactorial diseases of major interest in public health (host malaria resistance; sepsis in intensive care units and in neutropenic patients; hematological malignancies such as HIV-related lymphomas, chronic leukemia, polycythemia vera or Sezary lymphoma). The working hypothesis is that interaction networks should reveal links of different nature between genes and proteins. Highly connected gene and protein groups potentially corresponding to functional modules will be identified from different networks (genome, gene regulation, co-expression, protein-protein and phenotype networks). This should lead to the identification of new susceptibility genes, of altered processes involving these genes and of potential therapeutic targets. The biological questions are appropriately approached by large-scale experiments, leaning on the high-throughput genomic platform, and are strongly interconnected with the highly experienced biocomputing research team.

- ### Conclusion:

  - #### Summary:

Based on the scientific results obtained in the previous mandate, this team has considerably magnified studies involving immune system and hematological components, by using an approach that combines human and mouse studies. For example, to decipher mechanisms involved in the acute respiratory distress syndrome, they are developing an original mouse model in which each stage of the inflammation and infection processes can be controlled independently.

  - #### Strengths and opportunities:

The group has attracted brilliant researchers and Hospital-University Professors who bring complementary expertises (genetics, statistics, molecular/cellular biology, approaches to study interactomes) and take advantage of the permanent interactions between specialists of animal models and specialists of human diseases. The local (Luminy campus and neighbor hospitals), national and international collaborations are relevant and well established. Partnerships with several countries in Africa and Israel (malaria) seem very productive (several good publications).

  - #### Weaknesses and threats:

Different and/or common leaders presented several projects in this axis, each of them referring to several different disorders; this may generate weaknesses for some groups that seem limited in size.

– Recommendation:

The Committee encourages further recruitments of young experimentalist researchers, due to the number of biological projects included in axis 1. The Committee recommends that the unit be careful to a risk of dispersion due to a large number of projects.

Research axis 2: Developmental genes and networks

- Appreciation on the scientific strategy and networks:

For the last two decades, work on the genetic control of heart development in Drosophila had been pioneered in Luminy in the IBDM. The current applicant has gradually taken over the destiny of the laboratory since the retirement of the team's leader. This is a leading group in this subject and the fly heart development is a paradigm for specification of mesoderm derivatives. The Committee believes that the idea of changing environment within the Luminy campus is very timely (see also reasons below). By joining the TAGC lab they will benefit from the tools, methods and concepts; vice versa the data generated by the fly heart axis will pave the way of the axis 3. The previous strategy allows the group to raise significant funding (ANR, AFM) and to build scientific networks (ERASysBio) of quality (Modheart). In addition constructive exchanges and collaboration with closed team (cardiac development in mammals) or with complementary expertise (electrophysiology of cardiac cell) will allow reaching the objectives.

- Conclusion:

– Summary:

The molecular genetics of heart development and morphogenesis in flies is so well understood that the system is ideally ripe for global genomics approach as they are carried out in UMR 928. Given the conservation of genes and mechanisms involved through evolution, the integration of this project within UMR 928 was found to be highly relevant by the Committee.

– Strength and opportunities:

The ability of quickly generating conditional knock-out alleles of any gene in almost any tissue in Drosophila brings a strong calibrating and validating tool to the "bio-informaticians" of the platform. Purity and homogeneity of the samples analyzed is one of the most challenging issues for any global "omics" experiment. Once again, the amenability of flies for molecular genetics allows the generation of strains with cell type- or tissue-specific fluorescent markers suitable for cell sorting. The recent publication record of the group over the last 5 years with 2 "PLoS Genet", 1 "Current biology" and 1 "Current Opinion Genet Dev", further proves the competence of the two senior scientists and their fellows in the field of fly cardiac development, role of mechanostransduction and cation channels. In addition the youngest scientist who joined recently the group demonstrated his expertise in cytoskeleton and cardiac development through one paper in one of the highest ranked journals (Nature Cell Biology).

– Weaknesses and threats:

The proposed integration of a team successfully devoted to a unique theme (genetic control of the cardiac differentiation) and model (Drosophila) entirely unrelated to those developed so far at TAGC may change in the long term the configuration and goals of the unit. However, it may offer an opportunity to all groups to take advantage of complementary technical and functional competences.

– Recommendation:

The Committee strongly supports the adhesion of the fly heart group to UMR 928

Research axis 3: Networks Bioinformatics: from data analyses to predictive models -

- Appreciation on the scientific strategy and networks:

The bioinformatics research performed by TAGC has considerably evolved in the recent years and in particular since 2006 with the arrival of a group who initiated the evolution from activities mostly centered on transcriptomics to gene network studies. This evolution was further reinforced by the recruitment in 2009 of two seniors specialized in protein interaction networks. All the bioinformatics activities are at the center of the research projects of the unit, being positioned upstream and downstream of experiments. They include activities related to the project on cardiac development (ERASysBio, Modheart) that consists in building a system level view of cardiac differentiation (see also the upper paragraph). Another project following the same outline consists in understanding the mechanisms of reprogramming the B-cells into macrophages. Other activities are dedicated to protein function prediction via interaction network analyses: prediction of moonlighting proteins from protein-protein interaction networks (by developing graph partitioning algorithms and by mining semantic representation of protein function in diverse organisms) will be tested experimentally, possibly leading to discovery of important new functions in normal or pathological cells and in the study and prevention of drug side- effects. The group is also involved in the development of new methods to identify genetic deregulated networks associated with the multifactorial diseases studied in the axis 1 (cancer, malaria and sepsis). All these analyses require strong knowledge in handling high-throughput data with in-house original dedicated methods to decipher gene networks. They are sustained by numerous collaborations with experts in bioinformatics and mathematics. The publications are numerous and provide many valuable tools acknowledged by the community.

The unit has set up a functional genomics platform (IBiSA) dedicated to high throughput technologies. It is remarkable that the unit has succeeded to integrate this platform as an essential component of its research activities. The platform has been reinforced by recent recruitments for the deep sequencing activity, an IR in bioinformatics (2009) and an IR dedicated to sample preparation (2010). The possibilities afforded by this platform and in particular by the Agilent microarrays and the SOLID deep sequencing facilities, sustained by a strong bioinformatics team, will obviously be essential for the future of TAGC.

- Conclusion

  - Summary:

To develop its research activities in the field of gene networks in normal and pathological situations, TAGC has successfully modified and strengthened its bioinformatics team. Together with the IBiSA platform, this team appears as the backbone that supports the experimental and clinical studies of the unit.

  - Strengths and opportunities:

The bioinformatics projects of TAGC are ambitious, innovative, and are at the center of its research activity. The authentic multidisciplinarity of these projects constitute an exceptional opportunity to address important biological and clinical problems.

  - Weaknesses and threats:

Considering the recent departure of two seniors (one PU and one MCU) from the bioinformatics team, the recruitment of bioinformaticians will be essential to sustain this activity.

  - Recommendation:

The Committee strongly supports the recruitment of a PU bioinformatician. The presence of a foreign Professor (sabbatical) in the unit may be considered as an excellent opportunity for this recruitment.

Intitulé UR / équipe	C1	C2	C3	C4	Note globale
TAGC - TECHNOLOGIES AVANCÉES POUR LE GÉNOME ET LA CLINIQUE	A	A	A+	A+	A

C1 Qualité scientifique et production

C2 Rayonnement et attractivité, intégration dans l'environnement

C3 Gouvernance et vie du laboratoire

C4 Stratégie et projet scientifique

Statistiques de notes globales par domaines scientifiques

(État au 06/05/2011)

Sciences du Vivant et Environnement

Note globale	SVE1_LS1_LS2	SVE1_LS3	SVE1_LS4	SVE1_LS5	SVE1_LS6	SVE1_LS7	SVE2 _LS3 *	SVE2_LS8 *	SVE2_LS9 *	Total
A+	7	3	1	4	7	6		2		30
A	27	1	13	20	21	26	2	12	23	145
B	6	1	6	2	8	23	3	3	6	58
C	1					4				5
Non noté	1									1
Total	**42**	**5**	**20**	**26**	**36**	**59**	**5**	**17**	**29**	**239**
A+	16,7%	60,0%	5,0%	15,4%	19,4%	10,2%		11,8%		12,6%
A	64,3%	20,0%	65,0%	76,9%	58,3%	44,1%	40,0%	70,6%	79,3%	60,7%
B	14,3%	20,0%	30,0%	7,7%	22,2%	39,0%	60,0%	17,6%	20,7%	24,3%
C	2,4%					6,8%				2,1%
Non noté	2,4%									0,4%
Total	100,0%	100,0%	100,0%	100,0%	100,0%	100,0%	100,0%	100,0%	100,0%	100,0%

*** les résultats SVE2 ne sont pas définitifs au 06/05/2011.**

Intitulés des domaines scientifiques

Sciences du Vivant et Environnement

• SVE1 Biologie, santé
- **SVE1_LS1 Biologie moléculaire, Biologie structurale, Biochimie**
- **SVE1_LS2 Génétique, Génomique, Bioinformatique, Biologie des systèmes**
- **SVE1_LS3 Biologie cellulaire, Biologie du développement animal**
- **SVE1_LS4 Physiologie, Physiopathologie, Endocrinologie**
- **SVE1_LS5 Neurosciences**
- **SVE1_LS6 Immunologie, Infectiologie**
- **SVE1_LS7 Recherche clinique, Santé publique**

• SVE2 Ecologie, environnement
- **SVE2_LS8 Evolution, Ecologie, Biologie de l'environnement**
- **SVE2_LS9 Sciences et technologies du vivant, Biotechnologie**
- **SVE2_LS3 Biologie cellulaire, Biologie du développement végétal**

UNIVERSITÉ DE LA MÉDITERRANÉE
AIX-MARSEILLE II

Objet : Réponse au rapport d'évaluation - **S2UR120001634 - TAGC - Technologies Avancées pour le Génome et la Clinique - 0131843H** - de l'unité TAGC - Technologies Avancées pour le Génome et la Clinique

Observations d'Aix-Marseille Université

To increase the impact of future publications, and reinforce the limited size of some groups, several strategies are simultaneously developing:

(i) To decipher molecular networks that influence complex phenotypes and multifactorial diseases, the strategy is to look for both the common molecular networks and the specific ones. All the contributors think along the same lines, and the approaches are converging, and are integrating skills and knowledge from different fields (genomics, genetics, epigenetics, bioinformatics). The goals are (i) sharing our specific expertise in order to enhance the novelty of each project by involving researchers regarding to their skills, and (ii) publishing in high IF reviews. This is particularly true for the several complex diseases treated in the axis 1. This should lead to a better understanding of pathogenic mechanisms and to identify new targets for several diseases.

(ii) Nowadays, the laboratory has become more visible, and expects to attract young scientists (post-docs and future CR or MC) to reinforce ongoing projects. This is effective for bioinformatics with two candidates already well identified, one at the professor level (Jacques van Helden) and the second one at the CR level (Benoît Ballester). The laboratory needs young experimentalist researchers and reinforcement of the technical staff to support increasing demand in both axis 1 and 2. The Université de la Méditerranée will do everything in their power, in collaboration with Inserm, to provide technical human resources to support the laboratory activity.

(iii) In order to reinforce the epigenetic skills, particularly for the questions relative to the integrative biology focused onto the immune system, TAGC has engaged a reflection to attract a young brilliant researcher with a high score publication, and already deeply involved in our subject through strong long term collaboration with us.

Jardin du Pharo . 58 Boulevard Charles Livon . 13284 Marseille cedex 07 . France
Tél. : +33 (0)4 91 39 65 00 . Fax : +33 (0)4 91 31 31 36 . www.univmed.fr

(iv) Regarding the fly group, its integration is already well engaged since it leverages on well established collaboration with axis 3 and the IBISA plateform. Integrating the TAGC will in addition provides this group the opportunity to steer some projects developed in axis 2 towards clinical questions. The establishment of collaborations with clinicians is indeed a midterm prospective.

En accord avec les deux autres établissements d'Aix-Marseille

Le Président
de l'Université de la Méditerranée

Yvon BERLAND

Le Vice-président du Conseil Scientifique
de l'Université de la Méditerranée

Pierre CHIAPPETTA

UMR-S- 928
Technologie **A**vancée pour le **G**énome et la **C**linique
Inserm U938
Parc Scientifique et Technologique de Luminy
Case 928 ï 13288 - Marseille - cedex 9
France
Téléphone: (33) 04 91 82 87 02
Fax: (33) 04 91 82 87 01

Marseille, the 13th of March 2011

To the review committee,

Dear committee chairman and members

First of all, I would like to thank all the committee for the work of synthesis they have done following the evaluation of our document and visit on site. The present report is representative of our projects, skills and objectives.

Nevertheless, I would like to clarify some aspects concerning the strategies to resolve the weaknesses and threats.
To increase the impact of our future publications, and reinforce the limited size of some groups, we are simultaneously developing several strategies:
(i) To decipher molecular networks that influence complex phenotypes and multifactorial diseases, we will look for both the common molecular networks and the specific ones. All the contributors think along the same lines, and our approaches are converging, and are integrating skills and knowledge from different fields (genomics, genetics, epigenetics, bioinformatics). We aim at (i) sharing our specific expertise in order to enhance the novelty of each project by involving researchers regarding to their skills, and (ii) publishing in high IF reviews. This is particularly true for the several complex diseases treated in the axis 1. This should lead to a better understanding of pathogenic mechanisms and to identify new targets for several diseases.

(ii) Nowadays, the laboratory has become more visible, and we expect to attract young scientists (post-docs and future CR or MC) to reinforce our ongoing projects. This is effective for bioinformatics with two candidates already well identified, one at the professor level (Jacques van Helden) and the second one at the CR level (Benoît Ballester). We are aware that we need young experimentalist researchers and strong reinforcement of the technical staff to support increasing demand in both axis 1 and 2. We are currently discussing with several young experimentalist researchers who may apply for a permanent position in the near future. We are also asking for new technicians and/or new engineers to support our laboratory activity.

(iii) Attract young brilliant scientists already involved in fields developed at TAGC. In order to reinforce the epigenetic skills, particularly for the questions relative to the integrative biology focused onto the immune system, we engaged a reflection to attract a young brilliant researcher with a high score publication, and already deeply involved in our subject through strong long term collaboration with us. His recent positive feedback let us to think that he will probably join us soon.

(iv) Regarding the fly group, its integration is already well engaged since it leverages on well established collaboration with axis 3 and the IBISA plateform. Integrating the TAGC will in addition provides this group the opportunity to steer some projects developed in axis 2 towards clinical questions. The establishment of collaborations with clinicians is indeed a midterm prospective.

Dr. Catherine NGUYEN,
Directrice Inserm UMR_S_928

*Plateforme **TGML** Plateforme de **T**ransciptomique et de **G**enomique de **M**arseille **L**uminy*