LMGM - Laboratoire de microbiologie et génétique moléculaire

Rapport Hcéres

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

Section des unités de recherche

AERES report on the research unit:

Laboratoire de Microbiologie et Génétique Moléculaires-UMR 5100

From the

Université Toulouse 3 Paul Sabatier

CNRS

Mai 2010

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

Section des Unités de recherche

AERES report on the research unit

Laboratoire de Microbiologie et Génétique Moléculaires-UMR 5100

From the

Université Toulouse 3 Paul Sabatier

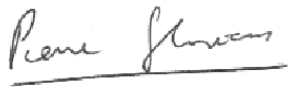
CNRS

Le Président
de l'AERES

Jean-François Dhainaut

Section des unités
de recherche

Le Directeur



Pierre Glorieux

Mai 2010

Unit

Name of the unit: Laboratoire de Microbiologie et Génétique Moléculaires

Requested label: UMR - CNRS / Université Paul Sabatier toulouse 3

No. in case of renewal: UMR 5100

Unit director: Mr Agamemnon J. CARPOUSIS (former director:Mr Claude GUTIERREZ)

Members of the expert committee

Chairperson:

Mr Ivan MATIC, University of Paris 5

Reviewers:

Mr Philippe BOULOC, University of Paris 12

Mr Martin BUCK, Imperial College London, United Kingdom

Mr Fernando DE LA CRUZ, University of Cantabria, Spain

Ms Hilde DE REUSE, Pasteur Institute, Paris

Mr David LEACH, University of Edinburgh, United Kingdom

Mr Gianni POZZI, University of Siena, Italy

Reviewer(s) nominated by the staff evaluation committees (CNU, CoNRS, CSS INSERM ...):

Ms Bénédicte MICHEL (CoNRS representative)

Representatives present during the visit

Scientific delegate representing AERES:

Ms Claire POYART

University representative :

Mr Guillaume BECARD

Research organisation representative :

Mr Bertrand DAIGNAN-FORNIER (CNRS representative)

Report

1 • Introduction

- Date and conduct of the visit:

The expert committee visited the Laboratory on November 26 and 27, 2009. The meeting started with a presentation by the current head of the laboratory. Subsequently, each team presented the past activity and the projects. Experts also met, in separate committees, the representatives of: researchers with permanent position, PhD students, postdoctoral fellows, engineers, technicians and administrative assistants. The representatives of the University and the CNRS were also met. Final meetings were held separately with the outgoing and then the new director. The site visit ended with the closed-door meeting of the committee. The visit was executed smoothly and without any problems.

- History and geographical location of the unit and brief description of its field of study and activities:

The laboratory, which is located in the CNRS building on the University Paul Sabatier Toulouse III campus, was created in 1992. The members of this laboratory study the organization, plasticity, evolution and expression of the genomes of bacteria and bacteriophages. Their research ranges from the study of single molecules via particular systems of interacting regulatory components (most often protein- nucleic acid, but several protein-protein systems) to living bacterial cells and their interaction with the environment. This research is based on approaches that include molecular genetics, biochemistry, genomics and bioinformatics. The studied bacteria and bacteriophages are often model organisms of major interest for fundamental research through offering paradigms, as well as for applications in biotechnology, the food industry and the medical sciences.

- Management Team:

The current direction (C. GUTIERREZ, director, and O. FAYET, assistant director) will be replaced by a new team (Mr A. CARPOUSIS, director, and Mr P. POLARD, assistant director) in the future unit.

- Staff: (according to the dossier submitted to AERES):

	In the report	In the project
N1: Number of professors (see Form 2.1 of the unit's dossier)	13	12
N2: Number of EPST, (Public scientific and technological institution) or EPIC, (Public industrial and commercial institution) researchers (see Form 2.3 of the unit's dossier)	16	15
N3: Number of other professors and researchers (see Form 2.2 and 2.4 of the unit's dossier)	14 post-doc	0 post-doc
N4: Number of engineers, technicians and tenured administrative staff members (see Form 2.5 of the unit's dossier)	21,25	22,25
N5: Number of engineers, technicians and non-tenured administrative staff members (see Form 2.6 of the unit's dossier)	1 IR, 1 IE, 2 AI	1 AI
N6: Number of doctoral students (see Form 2.8 of the unit's report dossier and 2.7 of the unit's project dossier)	16	9
N7: Number of persons accredited to supervise research and similar	21	19

2 • Assessment of the unit

- Overall opinion:

Globally, the research carried out at the Unit can be qualified as good to very good. The Unit is clearly visible in the French and international research landscape. However, the committee noticed heterogeneity in the performances of the various groups. While the quality and originality of the research of some groups is clearly at the highest international standard, some are below this level. This is also evident when one considers the level of funding that the various groups can attract into the Unit. The committee members consider that the Unit is now at an important point of transition because several major group leaders will soon retire, already present young groups have yet to prove that they can have qualitatively and quantitatively important scientific productivity, and new high caliber group(s) will and need to be recruited. The challenge for new director will be to take advantage of this fluid situation to impose a new momentum.

- Strengths and opportunities:

-This Unit provides a prime example of the value of an association CNRS & University by providing excellence in teaching, research and the training of PhD students.

-Several of the research teams are world-leaders in their specialties with excellent publication record.

-Collaboration between some groups based on shared complementary conceptual and/or methodological approaches results in strong synergy.

-Staff of this Unit, belonging to all professional categories, maintain pleasant professional and human interactions.

- Weaknesses and threats:

-Several major group leaders will retire in near future.

-Some teams, in spite of their small size, seem to carry a number of unrelated or poorly related research projects.

-Some groups in the unit are considering testing whether the systems that they have successfully characterized in one bacterial species are also present in other bacteria. This should be avoided as much as possible. The rationale for such a move must include the expectation of major new discoveries, rather than demonstrating commonality of molecular mechanisms with only a modest divergence of functionality.

-Some teams are not attracting external funding, nor post-docs or PhD students.

-The difficulties of some teams result from the heavy teaching load of their members.

- Recommendations for the unit director:

The committee strongly urges the director to instigate a transparent and collective decision-making process to help assure high quality long-term scientific performances of the unit. Formation of a horizon-scanning group might be useful. The new director is now facing three important challenges / difficulties that must be faced rapidly. First problem is existence of the very small teams of which some work on a large spectrum of unrelated projects and that have weak scientific productivity. A continuous support to these groups as such is unlikely to be the best solution for the science, and in term of institutional politics may lead to long-term problems. The committee recommends that these groups concentrate on a main themes in order to avoid dispersion, and /or that the members of these groups join, and thereby reinforce the other teams of the Unit in order to better align and improve their scientific productivity. This is particularly important for the university staff that has very heavy teaching loads. Second problem is retirement of the several world-leaders in their specialties. This serious problem must be tackled with extreme care. The proposed transition concerning leadership of the “Pneumococcal transformation” group is exemplar. On the other hand, the retirement of some leaders will be accompanied by the disappearance of their group. This provides two opportunities. (i) The members of these groups could join with and reinforce other groups. (ii) The liberated space could be used for the internal emergence and / or recruitment of the new groups. The recruitment of the new groups is the third challenge for the new director. Careful attention should be paid to new scientific recruitments. The director should discriminate between two categories of recruitments: those that will strengthen existing research projects by providing new inputs and skills and those that might be founders of new research projects. The latter are most critical to evolving the Unit into a form able to remain competitive and be positioned to take advantage of new developments (technical and as sub disciplines) in molecular microbiology and molecular genetics. Whatever the choice, the new recruits must be given adequate support to ensure rapid success and future developments.

- Data on work produced:

A1: Number of *produisants* (professors and researchers whose names appear in a minimum number of "publications" over a 4-year period) listed in N1 and N2 in the project column	28
A2: Number of *produisants* among the other staff listed in N3, N4 and N5 in the project column	31,20
A3: Proportion of *produisants* in the unit [A1/(N1+N2)]	28/29
Number of theses for accreditation to supervise research defended	2
Number of theses defended	12
Any other data relevant for the field (please specify)	

3 • Detailed assessments:

Overall, scientific productivity as measured by quantity and quality is good. In the period of evaluation, the Unit produced 120 scientific publications. Some of research papers were published in high impact generalist journals: 1 Science, 2 Cell, 4 Mol Cell, 5 PNAS, 3 EMBO J, 1 EMBO Rep., 4 J Mol Biol, which attests quality and originality of the research conducted. The impact and international visibility of the scientific results produced is also attested to by the invitation of the members of the Unit to speak at international meetings, to participate in the evaluations and to publish review articles in: Ann Rev Microbiol; Curr Opin Microbiol; Methods Enzymol; Microbiol Mol Biol Rev; Mol Microbiol; Nature Rev Microbiol; Trends Genet; Trends Microbiol. Most groups have important collaborations with French and foreign laboratories. It must be also noted that members of this Unit have participated in the organization of international scientific meetings, and that several researchers are members of editorial boards of scientific journals. Therefore, it can be concluded that the quality, originality of the research and international visibility of some groups is clearly at the highest international standard. However, several groups are below this level.

Most of the recurrent funding comes from the CNRS Life Sciences Department. Since 2005, this funding is stably around 183 k€/year. The financial support from the University is negligible. Financing coming from external sources is good, i.e., at average about 466 k€ / year. Hence, in the period of evaluation, the unit obtained two European and a dozen of French national contracts (principally ANR BLANC). Once again, some groups have a proven record in attracting funding at the highest level, while others do not.

The Unit showed that it is attractive for top-level researchers. In the period of evaluation two new group leaders joined the Unit, significantly reinforcing existing research projects by providing new inputs and skills and initiating new research projects. During this period, Unit attracted 14 post-docs, 12 PhD students obtained their grade, and 14 PhD students are now present in the Unit.

Many of the members of this Unit are heavily involved in teaching activities, which is important for the attractivity of the Unit to the students. However, such important time investment is affecting scientific productivity of most professors and assistant professors. This problem is not unique for this unit and could be resolved by careful reassessment of research priorities in order to avoid dispersion, as well as by restructuring groups in order to provide critical mass of staff required for successful research.

The Unit is very well integrated in its local environment. Besides excellent relationship with the University, it is also member of the alliance, l'IFR109 "Institut d'Exploration Fonctionnelle des Génomes" between several research units in which it plays a prominent role. This alliance promotes scientific interactions and provides technical platforms, which allows setting up projects that would have been beyond Unit's technical means.

All important decisions concerning governance and choice of strategy are made collectively by the heads of groups and the director. Staff belonging to all professional categories expressed positive opinion about professional and human interactions in the laboratory. Internal communication between the heads of groups, the director and the rest of the staff, should constantly be maintained. The laboratory council should hold three annual meetings as required by CNRS.

The committee members believe that the proposed project could maintain the reputation of the Unit. The human resources are there to make this possible. Recent recruitments of group leaders have reinforced the scientific excellence of the Unit. Projected recruitment(s) have the full support of the committee. However, some modifications of proposed project are necessary. In particular, adjustment of the adequacy between human resources and projects of the small groups is important. In addition, while it is not a real problem on a medium term, the retirements of the major group leaders will have a critical impact in the long-term. However, this is also an opportunity for the new management to reinforce the research quality and promote the implementation of novel research avenues.

4°•°Team-by-team and/or project-by-project analysis

Name of the team: RNA Metabolism in Prokaryotes

Name of the team leader: MR A.J CARPOUSIS

- Team staff or staff allocated to the project (according to the dossier submitted to AERES):

	In the report	In the project
N1: Number of professors (see Form 2.1 of the unit's dossier)		
N2: Number of EPST, *Établissement public à caractère scientifique et technologique* (Public scientific and technological institution) or EPIC, *Établissement public à caractère industriel et commercial* (Public industrial and commercial institution) researchers (see Form 2.3 of the unit's dossier)	2	2
N3: Number of other professors and researchers (see Form 2.2 and 2.4 of the unit's dossier)		
N4: Number of engineers, technicians and tenured administrative staff members (see Form 2.5 of the unit's dossier)	1	1.6
N5: Number of engineers, technicians and non-tenured administrative staff members (see Form 2.6 of the unit's dossier)	0	1
N6: Number of doctoral students (see Form 2.8 of the report unit's dossier and 2.7 of the project unit's dossier)	2	
N7: Number of persons accredited to supervise research and similar	2	2

This group has established a steady set of published outputs over the assessment period. These have clearly highlighted novel and in some cases founding observations made by the group. List of publications includes primary articles in both generalist (PNAS, NAR, Methods Enzymol, J Biol Mol, Trends Biochem Sci) and specialized microbiology journals (J Bacteriol, Mol Micro), as well as reviews (Ann Rev Microbiol, Prog Mol Biol Transl Sci) that are well cited.

The group is the leader in the field of the study of the RNA degradosome of *E. coli* for which novel properties are continued to be found.

One project deals with the structure/function relation and localization of RNaseE and of the RNA degradosome. This project has demonstrated the need to integrate molecular cell biology, imaging and structural biochemistry and genetics methods to full establish the functioning of this important member of the cells machinery for managing RNA metabolism. Prior work and proposed work in this area is to a very high standard, and the group has had the expected presence at national and international meetings.

For the future, the group is appropriately focused on the need to relate functionalities to localizations. The group should be encouraged to formalize joint efforts in the structural biology area, and to take up alternate complementary approaches (e.g. use of NMR for domain structures where these are sufficiently small), as well as

looking at RNase E homologues from other organisms for tractable materials for structure determination where possible. The group should benefit well from the recruitment of a cell imaging expert in the Unit.

A second project deals with the study of the non-coding RNAs in a hyperthermophilic archaea and the mRNA degrading enzymes in the archaea. The group needs to be mindful of (i) the impact deep sequencing may make on their future plans and the need to establish appropriate collaborations to start such a project, (ii) the need to have access to genetic methods as well as biochemical approaches in their organism of choice, and (iii) perhaps the need to focus on fully evaluating the substrate specificities of the RNase J they are currently studying. To make an impact, the relatively new RNase J project will need to produce robust new findings.

Finally, the collaboration with the group of Vilnius (Lithuania) for the sequence-specific labeling of RNA using the properties of the C/D guide RNPs previously established in this group has some biotechnological value, and may in itself provide important new resources with which to probe specificities of interactions and the nature of interaction interfaces in RNA-RNA and RNA-protein complexes.

Name of the team: Mobile genetic elements

name of the team leader: Mr M. CHANDLER

- Team staff or staff allocated to the project (according to the dossier submitted to AERES):

	In the report	In the project
N1: Number of professors (see Form 2.1 of the unit's dossier)		
N2: Number of EPST, *Établissement public à caractère scientifique et technologique* (Public scientific and technological institution) or EPIC, *Établissement public à caractère industriel et commercial* (Public industrial and commercial institution) researchers (see Form 2.3 of the unit's dossier)	3	3
N3: Number of other professors and researchers (see Form 2.2 and 2.4 of the unit's dossier)	2	1
N4: Number of engineers, technicians and tenured administrative staff members (see Form 2.5 of the unit's dossier)	2.5	2.5
N5: Number of engineers, technicians and non-tenured administrative staff members (see Form 2.6 of the unit's dossier)	2	
N6: Number of doctoral students (see Form 2.8 of the report unit's dossier and 2.7 of the project unit's dossier)	1	1
N7: Number of persons accredited to supervise research and similar	2	2

This is a very strong group as judged by the number of publications of high impact factor. The team is in its prime. Group leader has succeeded in harnessing all the energy that he and his group put in the analysis of mobile genetic elements. The list of publications of the group is impressive, probably in the top 10% for a French standard (more than 29 publications since 2005 both in high IF journals (Cell, Nature, EMBO J, Mol Cell, NAR) and in specialized journals (Mol Micro, J. Bacteriol, Trends Gent, PloS Genet, Trends Microbiol, Plasmid). They also published several review articles (MMBR, Res Microbiol, Microbe). Now they are extremely powerful in their ability to deal with

advanced scientific questions. They are supported also by an extended network of collaborators and scientific colleagues that help them in attacking any possible subject with a massive amount of high tech tools.

The group works on an extremely well set-up system that analyzes bacterial insertion sequences (3 main specific projects). It has been running and remained extremely productive for many years. Their work on the IS200/IS608 family of IS elements is a paradigm in the molecular attack of a problem of this type.

It should be stressed that research on mobile genetic elements (the bacterial mobilome) is not just another classic topic of molecular microbiology, but one of the most interesting subject of investigation in the genomic era, essential to understand the evolution of bacterial genomes, and also contributing to practical aspects such as genome annotation. In fact, automatic annotation of genomes is impaired by lack of knowledge of the mobilome, typically generating incorrect annotations each time mobile genetic elements, or parts thereof, are involved.

The IS finder database, developed by this team, deserves to be funded and kept within the LMGM. Closing this team will cause a significant decrease in LMGM productivity.

There are no real weaknesses in this group in the purely scientific aspects of the work. Nevertheless, the leader of the group is approaching the age of retirement. The group should work to find a substitute if they want to continue this line of research. It is not clear if the group already has a substitute. Nothing in the presentation suggested that they have.

Name of the team: Bacterial transformation & genetic plasticity

Name of the team leader: Mr. J.P. CLAVERYS

- Team staff or staff allocated to the project (according to the dossier submitted to AERES):

	In the report	In the project
N1: Number of professors (see Form 2.1 of the unit's dossier)	2	3
N2: Number of EPST, *Établissement public à caractère scientifique et technologique* (Public scientific and technological institution) or EPIC, *Établissement public à caractère industriel et commercial* (Public industrial and commercial institution) researchers (see Form 2.3 of the unit's dossier)	2	3
N3: Number of other professors and researchers (see Form 2.2 and 2.4 of the unit's dossier)	2	
N4: Number of engineers, technicians and tenured administrative staff members (see Form 2.5 of the unit's dossier)	1.8	2.8
N5: Number of engineers, technicians and non-tenured administrative staff members (see Form 2.6 of the unit's dossier)		
N6: Number of doctoral students (see Form 2.8 of the report unit's dossier and 2.7 of the project unit's dossier)	2.5	2
N7: Number of persons accredited to supervise research and similar	4	5

This evaluation is based on the achievements of the "Bacterial transformation & genetic plasticity" group and on the project of the merged groups "Bacterial transformation & genetic plasticity group" and "Molecular assemblages and genome dynamics in bacteria". For the report on the former group see further down.

The "Bacterial transformation & genetic plasticity" group leads world research in the field of natural genetic transformation. Their work is of the highest standard of scientific rigor and originality. In the period of evaluation they have published ten research papers (*PNAS*, *Science*, *Cell*, Mol Micro, J. Bacteriol, Microbiology). In addition they have published nine review articles or other contributions in FEMS Microbiol Rev, Nature Rev Microbiol, Ann Rev Microbiol, Trends Microbiol, Mol Microbiol. The group has important and stable national and international collaborations with top research laboratories. The members of the group provide approximately eight contributions to international meetings per year and the group leader is invited to give several lectures at international meetings per year. The group leader organizes approximately one international meeting per year. This level of international engagement is a testament to the group's high international scientific profile. The group has been very successful in rising funding from several EU, Swiss and French sources that have enabled scientists to join the group from the UK, Switzerland, Norway, China and France. The group has also benefited from the dual support to the unit, from the University (two positions) and the CNRS (four positions). The group has a consistent track record of combining risk taking with safe projects. This has resulted in both an innovative and consistent record of achievement. The group provides leadership in good research practice for the unit and high quality teaching through the staff associated with the University. This is a prime example of the value of a mixed CNRS/University group providing excellence in teaching, research and the training of PhD students.

The research project proposed is highly original and inventive. It combines the strengths of two internationally competitive research groups, "Bacterial transformation & genetic plasticity" and "Molecular assemblages and genome dynamics in bacteria", to address fundamental questions of scientific interest in the area of natural genetic transformation. The fusion of the two groups will provide significant critical mass in this area of excellence. The "Molecular assemblages and genome dynamics in bacteria" group brings top-level biochemistry and experience in the field of DNA replication that complement the strengths of the "Bacterial transformation & genetic plasticity" team. The joint team proposes to investigate the regulation of DNA uptake and processing; regulation of the X-state; the intersection of recombination and DNA replication following DNA uptake; and cell cycle and chromosomal events consequent on transformation. These are important questions of basic science that have implications for understanding the behavior of pathogenic organisms.

In summary, this is an excellent program that is well thought-out to combine appropriate risk-taking with safe science, in the hands of two world leaders of the fields of transformation and DNA replication. It is likely that opportunities will emerge to develop this research in new directions, which might include bacterial cell biology and bacterial pathogenicity. There are no significant weaknesses or threats to this group and we recommend that they carry out the program as proposed including the merging of the groups for the period of 2011-2014.

Name of the team: Genetic recombination and the cell cycle

Name of the team leader: Mr F. CORNET

- Team staff or staff allocated to the project (according to the dossier submitted to AERES):

	In the report	In the project
N1: Number of professors (see Form 2.1 of the unit's dossier)	1	1
N2: Number of EPST, *Établissement public à caractère scientifique et technologique* (Public scientific and technological institution) or EPIC, *Établissement public à caractère industriel et commercial* (Public industrial and commercial institution) researchers (see Form 2.3 of the unit's dossier)	1	1
N3: Number of other professors and researchers (see Form 2.2 and 2.4 of the unit's dossier)	1	
N4: Number of engineers, technicians and tenured administrative staff members (see Form 2.5 of the unit's dossier)	1	1
N5: Number of engineers, technicians and non-tenured administrative staff members (see Form 2.6 of the unit's dossier)		
N6: Number of doctoral students (see Form 2.8 of the report unit's dossier and 2.7 of the project unit's dossier)	0.5	2
N7: Number of persons accredited to supervise research and similar	2	2

This team studies the mechanisms by which chromosome segregation and dimer resolution are coupled, and the roles of the FtsK protein in the activation of XerCD and in chromosome segregation.

The team has co-discovered the existence of specific short sequences that are used by FtsK to segregate the chromosome in the correct orientation (KOPS). This has led to two publications in excellent journals and a review article. In parallel, the team has described the constraints on chromosome organization for XerCD/dif resolution and the physiological essential role of FtsK in chromosome segregation (definition of the FtsK domain of activity), which also led to two publications in excellent journals and one submitted. Finally, an additional publication reflects the participation of the team in an international collaboration. In conclusion, the scientific production of the team is very good qualitatively (EMBO reports, Mol Cel, EMBO J, PloS Genet, Nature Struct Mol Biol and quantitatively (7 articles since 2005).

In addition to its major activity in *Escherichia coli*, the team has collaborated, still on FtsK, XerCD and chromosome segregation, with the "Evolution of bacterial genome" team, with the aim of understanding which aspects of the Xer/FtsK interactions are general or specific to certain bacterial species.

The team is supported mainly by an ANR contract that will end in 2010, and will apply for a new one. The team has regularly attracted PhD students and has developed collaborations in several directions.

The projects are the weak point of the team since the way they are presented does not highlight their originality. In addition, the projects are quite dispersed and the most important questions that the team wishes to put

forward in the future are somehow unclear. Given the national and international competition in the field, more focus should be given to projects aiming at fundamental novelty. For example, it is unclear how studying bacterial species in the light of what is known in *E. coli* is expected to bring answers to fundamental questions; it is also unclear how the proposed new mutant and chimeric proteins will solve the remaining questions, knowing that the field in already rich of a lot of specific mutants and chimeric proteins.

In conclusion, the scientific production of the team is important qualitatively and quantitatively, and the team is well introduced in the field to which it has brought essential original contributions. The projects are less strong than the past realizations and the committee recommends that the team better defines its strength and originality and focuses more on fundamental questions. Finally, it is important that the team avoids a dispersion of its projects and remains leader in most of the collaborations in which it participates.

Name of the team: Biology of decoding and translational control

Name of the team leader: Mr O. FAYET

- Team staff or staff allocated to the project (according to the dossier submitted to AERES):

	In the report	In the project
N1: Number of professors (see Form 2.1 of the unit's dossier)	1	2
N2: Number of EPST, *Établissement public à caractère scientifique et technologique* (Public scientific and technological institution) or EPIC, *Établissement public à caractère industriel et commercial* (Public industrial and commercial institution) researchers (see Form 2.3 of the unit's dossier)	1	1
N3: Number of other professors and researchers (see Form 2.2 and 2.4 of the unit's dossier)	1	
N4: Number of engineers, technicians and tenured administrative staff members (see Form 2.5 of the unit's dossier)	1	1
N5: Number of engineers, technicians and non-tenured administrative staff members (see Form 2.6 of the unit's dossier)		
N6: Number of doctoral students (see Form 2.8 of the report unit's dossier and 2.7 of the project unit's dossier)	1	
N7: Number of persons accredited to supervise research and similar	2	3

This small team has been developing two projects over the assessment period.

The first project is devoted to the detailed study of the mechanisms of programmed -1 ribosomal frameshifting (PRF1) in bacterial transposable elements. This issue is well integrated in the overall topic of the CNRS unit. The results on these studies have generated a set of publications (3) in microbiological (J Bacteriol,)or biochemical journals (J Biol Chem) as well as a review and a book chapter.

The second project concerning the genetic exploration of bacterial virulence is very descriptive, the approaches used are not up to date and at the exception of collaborative works the results generated have been published in low impact journals.

In general, the productivity during the assessment period is modest.

The work on PRF1 testifies of a good specialized expertise, though is presently supported by one researcher and a technician.

The overall team is small with a restricted number of collaborations. There is presently no specific funding associated with the topics of this team. There is a general lack of coherence among the present research topics and among the proposed projects of this team. The project on antibacterial targets was difficult to judge given the lack of detail, especially important when intending to change research directions, and could be flawed unless the Unit conducts an internal project review and subsequently supports a more detailed and focused proposal.

We strongly recommend that the contribution of the members of this team should be redistributed within the CNRS unit. The work on PRF1 is appreciated and could benefit from integration in another team of the unit.

Name of the team: Genomics of integrated systems

Name of the team leader: Ms G. FICHANT

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

	In the report	In the project
N1: Number of professors (see Form 2.1 of the unit's dossier)	1	2
N2: Number of EPST, *Établissement public à caractère scientifique et technologique* (Public scientific and technological institution) or EPIC, *Établissement public à caractère industriel et commercial* (Public industrial and commercial institution) researchers (see Form 2.3 of the unit's dossier)	1	1
N3: Number of other professors and researchers (see Form 2.2 and 2.4 of the unit's dossier)	1	
N4: Number of engineers, technicians and tenured administrative staff members (see Form 2.5 of the unit's dossier)		1
N5: Number of engineers, technicians and non-tenured administrative staff members (see Form 2.6 of the unit's dossier)		
N6: Number of doctoral students (see Form 2.8 of the report unit's dossier and 2.7 of the project unit's dossier)		1
N7: Number of persons accredited to supervise research and similar	2	1

The team leader was recruited in 2004 as bio-informatics Professor at the University Paul Sabatier and to setup a research team at the LMGM. She succeeded in establishing i) a complete de novo teaching bio-informatics program at the University ii) and many productive collaborations within the LMGM by providing a bio-informatics analytical

support. Prior to 2004, the team developed a sophisticated database on ABC transporters; during these past years, it pursued its development by improving its interactivity. Based on their experiences, they developed methods for identification and reconstruction of complexes (e.g. competence cascades) and other bioinformatics tools such as PEGR to analyze recombination events between genomes.

Considering the small size of the team and the involvement of its researchers in heavy teaching duties, the scientific productivity is of good quality (11 publications in: Bioinformatics, J Bacteriol, Mol Microbiol, BMC Genomics, co-author of the Cell paper of Clavery's team). In the past 4 years, the laboratory has been directly involved in supervising seven master students, however, no PhD students were trained. This is explained by the absence of a bio-informatics program at the University, prior the recruitment of the team leader. This problem will be overcome by the recent integration of a PhD. student.

Team members actively participate in international meetings including one invitation of the team leader. In 2008, the team recruited an assistant professor. The team succeeded in rising funding, being PI or co-investigator on several national or international programs, most of them associated with collaborations.

The proposed project is a continuation of the past activity. The committee supports the maintenance of the collaborative activities within the LMGM as this association has been highly productive for all partners. It recommends the group to be vigilant concerning the biological relevance of the research performed and to ensure the development of tools that fulfil real needs of biologists. At the same time, it recommends the development of a specific team project that would provide identity and visibility, while keeping close contact with external bio-computing teams as already indicated in the project.

Name of the team: Structure and Function of Molecular Chaperons

Name of the team leader: Mr P. GENEVAUX

- Team staff or staff allocated to the project (according to the dossier submitted to AERES):

	In the report	In the project
N1: Number of professors (see Form 2.1 of the unit's dossier)	0	1
N2: Number of EPST, *Établissement public à caractère scientifique et technologique* (Public scientific and technological institution) or EPIC, *Établissement public à caractère industriel et commercial* (Public industrial and commercial institution) researchers (see Form 2.3 of the unit's dossier)	1	2
N3: Number of other professors and researchers (see Form 2.2 and 2.4 of the unit's dossier)	1	
N4: Number of engineers, technicians and tenured administrative staff members (see Form 2.5 of the unit's dossier)	2	1
N5: Number of engineers, technicians and non-tenured administrative staff members (see Form 2.6 of the unit's dossier)		
N6: Number of doctoral students (see Form 2.8 of the report unit's dossier and 2.7 of the project unit's dossier)	1	2
N7: Number of persons accredited to supervise research and similar	1	1

The team leader was previously appointed at the "Centre Médical Universitaire" in Geneva (Switzerland) where he mainly studied bacterial chaperons. In 2007, he joined the LMGM with the financial support of a "CNRS ATIPE". His recent work concerns i) molecular and genetic studies on DnaJ, ii) investigation of the role of chaperones in adaptation to cold, iii) studies on the trigger factor and SecB proteins. Studies are mainly on *Escherichia coli* but also on *Desulfitobacterium*. The team leader's scientific productivity is very good (9 publications: 7 original articles in Protein Sci, J Biol Chem, Infect Immun, PNAS, Mol Microbiol and 2 reviews), however due to his recent move, none of the actual publications originates for a work performed with Toulouse collaborators.

The PI participated in international meetings (one invitation) and has several international collaborations that led to publications and the arrival of two post-doctoral fellows with short term fellowships. The team succeeded in recruiting two PhD students and two researchers with tenure tracks. In addition to the "ATIPE", the team is financed by an "ATIPE Plus" and by an "ANR" grant (as a co-investigator). All of this put the team in excellent manpower and financial conditions.

The chaperone field is highly completive with numerous laboratories addressing the relation between structures and functions with highly sofisticated approaches. The proposed project relies mainly i) on classical genetic screens and ii) molecular biological studies. Despite the fact that these methods have successful in the past, they might currently have some limitations. Uninteresting candidates resulting from genetic selections could handicap the development of the proposed project. In addition to the experiments that the team intend to perform, we

recommended that the team considers alternative approaches to investigate the mechanistic understanding of chaperones.

Name of the team: Global regulation and stress resoponses in bactaria

Name of the team leader: Mr C. GUTIERREZ

- Team staff or staff allocated to the project (according to the dossier submitted to AERES):

	In the report	In the project
N1: Number of professors (see Form 2.1 of the unit's dossier)	3	
N2: Number of EPST, *Établissement public à caractère scientifique et technologique* (Public scientific and technological institution) or EPIC, *Établissement public à caractère industriel et commercial* (Public industrial and commercial institution) researchers (see Form 2.3 of the unit's dossier)	1	
N3: Number of other professors and researchers (see Form 2.2 and 2.4 of the unit's dossier)		
N4: Number of engineers, technicians and tenured administrative staff members (see Form 2.5 of the unit's dossier)	0.6	
N5: Number of engineers, technicians and non-tenured administrative staff members (see Form 2.6 of the unit's dossier)		
N6: Number of doctoral students (see Form 2.8 of the report unit's dossier and 2.7 of the project unit's dossier)	1	
N7: Number of persons accredited to supervise research and similar	1	

The group will now close, and members will be distributed to other groups. Comments on some of the issues associated with the moves are made in the overall Unit assessment. The Global regulation group was known for its solid expertise in bacterial gene regulation. As examples, the team was a reference for their studies on osmoregulation and on the role of transcriptional sigma factors. During these last four years, several projects were developed: i) the phosphorelay involved in the regulation of *Escherichia coli* capsule synthesis, ii) the osmoregulation in *Lactococcus lactis*, iii) biosynthesis of arginine in *Escherichia coli*, iv) the role a Spx regulator in the competent state of *Streptococcus pneumoniae* or vi) the role of sigmaE in *Xanthomonas campestris* stress response.

The group closes with a good number of publications in some of the best journals in the field (even though that lab members had heavy teaching or administrative duties), reflecting a clear set of useful outcomes for the majority of the projects (9 publications in J Bacteriol, Microbiology, Mol Microbiol, FEBS Lett). The initial problems tackled were very worthwhile, and the researchers have been successful in taking forward many of these projects at the level of genetic and some biochemistry and physiology.

However, the diversity of the research subjects affected the group external visibility with one direct consequence, the incapacity of the group to obtain external funding. A weakness that may have emerged if the group had continued was the depth with which each problem was being studied, and whether the problems would sustain sufficient long-term interest in the scientific community. To do so, commitments to either a more challenging single problem in stress regulation (e.g. the integration of stress responses) or an in-depth multidisciplinary approach to mechanistic studies would seem to be required.

Name of the team: Diversity, evolution, ecology and genome structure of the T4 Superfamily of bacteriophages

Name of the team leader: Mr H. KRISCH

- Team staff or staff allocated to the project (according to the dossier submitted to AERES):

	In the report	In the project
N1: Number of professors (see Form 2.1 of the unit's dossier)		
N2: Number of EPST, *Établissement public à caractère scientifique et technologique* (Public scientific and technological institution) or EPIC, *Établissement public à caractère industriel et commercial* (Public industrial and commercial institution) researchers (see Form 2.3 of the unit's dossier)	1	
N3: Number of other professors and researchers (see Form 2.2 and 2.4 of the unit's dossier)		
N4: Number of engineers, technicians and tenured administrative staff members (see Form 2.5 of the unit's dossier)	0.8	
N5: Number of engineers, technicians and non-tenured administrative staff members (see Form 2.6 of the unit's dossier)		
N6: Number of doctoral students (see Form 2.8 of the report unit's dossier and 2.7 of the project unit's dossier)		
N7: Number of persons accredited to supervise research and similar	1	

The team has produced important and original work through international collaborations with top groups. The diversity of T4 phage has been explored, and the outcomes in some cases published in the top journals for the field. The lab has clearly been instrumental in driving the international effort, and has sustained a high quality program throughout the period. The group should be commended on their abilities and original contributions to a field with emerging importance in gene flux in the environment, especially for photosynthetic activity in the oceans. The latter

is clearly an area many molecular based environmental studies should pay increased attention to, and one where the group can be viewed as setting the scene for the next generation of phage molecular biologists.

Given the special situation of this group, it was considered not relevant by the evaluation team to emphasize the possible weaknesses of the unit. There was certainly no intent, on the part of the PI during his presentation, to present a project for the future of the unit.

It is entirely reasonable to suggest the program would continue at its strong international quality level should the lab head not be retiring. But team leader himself recognized the team will close after his retirement. The team can be closed without trauma.

Name of the team: Dynamics of Bacterial Replicons

Name of the team leaders: Mr David LANE ; Mr Jean-Yves BOUET and Mr Franck PASTA

- Team staff or staff allocated to the project (according to the dossier submitted to AERES):

	In the report	In the project
N1: Number of professors (see Form 2.1 of the unit's dossier)	1	1
N2: Number of EPST, *Établissement public à caractère scientifique et technologique* (Public scientific and technological institution) or EPIC, *Établissement public à caractère industriel et commercial* (Public industrial and commercial institution) researchers (see Form 2.3 of the unit's dossier)	2	2
N3: Number of other professors and researchers (see Form 2.2 and 2.4 of the unit's dossier)	1	
N4: Number of engineers, technicians and tenured administrative staff members (see Form 2.5 of the unit's dossier)	1	1
N5: Number of engineers, technicians and non-tenured administrative staff members (see Form 2.6 of the unit's dossier)		
N6: Number of doctoral students (see Form 2.8 of the report unit's dossier and 2.7 of the project unit's dossier)	2	
N7: Number of persons accredited to supervise research and similar	2	2

The group works on a well set-up system (2 main specific projects as shown below), which are already running and are productive. They have characterized the molecular mechanism of action of the F plasmid partition system. This work has led to the understanding of the mode of action of ParA and ParB. It allowed the regular production of several publications (8 publications since 2005 in very good specialist journals: Mol Microbiol, J Bacteriol, J Biol Chem, Appl Environ Microbiol) . The second main topic is the characterization of the partition systems of the several chromosomes of *Burkholderia*. It was shown that the partition systems of these chromosomes function independently of each other, leading to one publication. The group also signed a paper in collaboration on the N15 partition system and a review in Mol Microbiol. The scientific questions they try to answer are meaningful and are well oriented. They

have started new technological approaches (e.g., microfluidics) to analyze their systems, which are promising and should be reinforced. Thus, they ensure the rejuvenation of the project.

The leadership has to be substituted. From the presentation, it seems that the members of the group have not coordinated the "transfer" very well. Probably they do not feel the urge to do it, since the present leader remains in place for a time. But this was a weakness of the presentation (the present leader talked almost exclusively about the past achievements, leaving little time for projects). A co-direction by two group members is proposed. This is another potential source of trouble. Considering the size of the team, a single leader should be chosen within the next two years. Another putative weakness is the multiplication of the projects. Although each of the individual proposals is quite sensible, altogether the sum of the proposed work may not be realistic for such a small team, even if a PhD student and/or a post-doctoral fellow would join the group.

Although both main topics should be maintained, a clear-cut project is required for each topic, and should be planned ahead of time. The structure of the group will have to be defined more precisely. A single leader has to be chosen. The project on the *E. coli* Par system seems more inspiring. If the group chooses to be led by the other senior researcher (working on *Burkholderia*) this decision has to be well motivated.

Name of the team: Molecular assemblages and genome dynamics in bacteria

Name of the team leader: Mr P. Polard

- Team staff or staff allocated to the project (according to the dossier submitted to AERES):

	In the report	In the project
N1: Number of professors (see Form 2.1 of the unit's dossier)		
N2: Number of EPST, *Établissement public à caractère scientifique et technologique* (Public scientific and technological institution) or EPIC, *Établissement public à caractère industriel et commercial* (Public industrial and commercial institution) researchers (see Form 2.3 of the unit's dossier)	1	
N3: Number of other professors and researchers (see Form 2.2 and 2.4 of the unit's dossier)	1	
N4: Number of engineers, technicians and tenured administrative staff members (see Form 2.5 of the unit's dossier)		
N5: Number of engineers, technicians and non-tenured administrative staff members (see Form 2.6 of the unit's dossier)	1	
N6: Number of doctoral students (see Form 2.8 of the report unit's dossier and 2.7 of the project unit's dossier)	1.5	
N7: Number of persons accredited to supervise research and similar	1	

This team studies (i) how the proteins required for replication restart are maintained in the proximity of replication forks by interaction with SSB in *B. subtilis* and (ii) what happens to transforming DNA in *Streptococcus pneumococus*.

This team has an excellent scientific productivity (9 publications in: Mol Microbiol, J Bacteriol, Virology, EMBO J, Cell, J Mol Biol; and one review in FEMS Microbiol Rev.). In *B. subtilis*, the team has defined the molecular mode of action of the helicase loading machine and has shown that SSB acts as the physical support of proteins needed in case of replication arrest. This work has led to two publications in excellent journals, a publication in collaboration, and a meeting review. In *S. pneumococcus*, the team has participated in the definition of the new role of a protein as a recombination mediator during natural DNA transformation. The team is co-author in a publication in the prestigiousjournal Cell and in a review article. In addition, the team had collaborated at INRA with different laboratories on several topics to share its expertise of the Tap Tag technique, which has led to four publications in collaboration.

The team has moved from Jouy en Josas (Unit Génétique Microbienne, INRA) to the LMGM in 2007. This move has proven to be a great success for two reasons. First the team leader has been able to maintain a productive collaboration with the previous co-workers at INRA on the *B. subtilis* part of the ongoing projects, and to move this topic to the LMGM successfully. Second, the team has strengthened the links with the "Bacterial transformation and genetic plasticity" team on *S. pneumoniae*.

The team has been successful in raising financial supports from Europe and from ANR and is applying to ANR for a very promising joint project on *S. pneumoniae* competence and transformation.

The projects have the particularity of involving the fusion of two teams, as "Bacterial transformation and genetic plasticity" will fuse with "Multiprotein assemblies and bacterial DNA dynamics". The *B. subtilis* replication restart project will be terminated within one or two years, with the identification of all SSB partners at replication forks and the characterization of the specificity of the SSB C-ter sequence that promotes these interactions. The fused teams will concentrate on *S. pneumoniae* transformation, which is an excellent choice. All types of questions concerning competence and DNA transformation will be addressed (see "Bacterial transformation and genetic plasticity" project). The expertise of the "Multiprotein assemblies and bacterial DNA dynamics" ex-team will allow it to focus on the characterisation of the role of PriA and of the two *S. pneumoniae* SSB proteins during DNA transformation, a question that is crucial to the understanding of the mechanism of genetic exchange that drives pathogenicity and antibiotic resistance in streptococci.

In conclusion, the excellence of the team is clear from its past productivity and future projects. The fusion of the two excellent teams is well prepared and very promising. The committee recommends that the proposed fusion and the accompanying projects are realized as planned.

Name of the team: Evolution of Bacterial Genomes

Name of the team leader: Mr P. RITZENTHALER

- Team staff or staff allocated to the project (according to the dossier submitted to AERES):

	In the report	In the project
N1: Number of professors (see Form 2.1 of the unit's dossier)	3	3
N2: Number of EPST, *Établissement public à caractère scientifique et technologique* (Public scientific and technological institution) or EPIC, *Établissement public à caractère industriel et commercial* (Public industrial and commercial institution) researchers (see Form 2.3 of the unit's dossier)		
N3: Number of other professors and researchers (see Form 2.2 and 2.4 of the unit's dossier)		
N4: Number of engineers, technicians and tenured administrative staff members (see Form 2.5 of the unit's dossier)	1	1.5
N5: Number of engineers, technicians and non-tenured administrative staff members (see Form 2.6 of the unit's dossier)		
N6: Number of doctoral students (see Form 2.8 of the report unit's dossier and 2.7 of the project unit's dossier)	3	1
N7: Number of persons accredited to supervise research and similar	1	1

All scientists that are permanent members of this group are heavily involved with teaching duties at the University Paul Sabatier. This fact is appreciated and taken into consideration in the drawing this evaluation report.

In the period 2006-2009 this group has been carrying on its specific research work on recombination in lactic acid bacteria, with special attention to bacteriophages, a field in which group leader is internationally recognized. This work on the directionality control in phage mv4 site-specific recombination, and on the characterization of the atypical Xer recombination system in *Lactococcus*, yielded publications in good journals such as PLoS Genetics, Virology, and J Bacteriol. However it should be noted that, during the assessment period, the overall productivity in terms of scientific publications was considered low (only 3 articles, one recently accepted in J Bacteriol, not in the report). During this period, a new project on the genome diversity of the *L. lactis* species was supported (from 2006 to 2008) by an ANR grant for a program associated to human nutrition research. This descriptive work, which started with a PFGE typing of several different isolates and the development of a novel Multilocus Sequence Typing (MLST) scheme, demonstrated that diary strains are phylogenetically separated from the environmental strains.

The planned future research activities of the group are on genome plasticity and evolution of the genome of *Lactococcus lactis*, and include essentially two different projects: (i) the study on the Xer recombination machinery, which has unraveled novel characteristics that distinguishes the *Lactococci* from the other firmicutes and has been well published, and (ii) a project on the pan genome and the core transcriptome of *L. lactis.*

The group benefits of recognition in the field of the *Lactococci*. The project on the atypical Xer recombination system is well integrated in the general topic of the CNRS unit. It has generated important results and is planned to be

developed in close and synergistic collaboration with both the “Bacterial transformation & genetic plasticity” and the “Genetic recombination and the cell cycle” teams.

The weaknesses of this team are following:

The objective of the project on the genomics of *L. lactis* appear to extend beyond the general interests of the CNRS unit

The comparative approaches proposed to try to define a core-transcriptome for *L. lactis* should be considered unlikely to succeed.

Essential lack of coherence among the proposed projects

Limited international visibility of the research group

Limited scientific communication skills

Limited capability of attracting external funds

Limited capability of establishing international collaborations

We recommend that the members of this group (i) focus their research efforts on the project on site-specific recombination and (ii) expand their collaboration with other scientists at LMGM by joining other teams of the CNRS unit.

Note de l’unité	Qualité scientifique et production	Rayonnement et attractivité, intégration dans l’environnement	Stratégie, gouvernance et vie du laboratoire	Appréciation du projet
A	A	A	A	A

Nom de l'équipe : RNA METABOLISM IN PROCARYOTE

Note de l'équipe	Qualité scientifique et production	Rayonnement et attractivité, intégration dans l'environnement	Stratégie, gouvernance et vie du laboratoire	Appréciation du projet
A	A	A	A	A

Nom de l'équipe : ELÉMENTS GÉNÉTIQUES MOBILES

Note de l'équipe	Qualité scientifique et production	Rayonnement et attractivité, intégration dans l'environnement	Stratégie, gouvernance et vie du laboratoire	Appréciation du projet
A+	A+	A+	A	A+

Nom de l'équipe : TRANSFORMATION BACTÉRIENNE ET PLASTICITÉ GÉNÉTIQUE

Note de l'équipe	Qualité scientifique et production	Rayonnement et attractivité, intégration dans l'environnement	Stratégie, gouvernance et vie du laboratoire	Appréciation du projet
A+	A+	A+	A	A+

Nom de l'équipe : RECOMBINAISON GÉNÉTIQUE ET CYCLE CELLULAIRE

Note de l'équipe	Qualité scientifique et production	Rayonnement et attractivité, intégration dans l'environnement	Stratégie, gouvernance et vie du laboratoire	Appréciation du projet
A	A	A	A	A

Nom de l'équipe : BIOLOGY OF DECODING AND TRANSLATIONAL CONTROL

Note de l'équipe	Qualité scientifique et production	Rayonnement et attractivité, intégration dans l'environnement	Stratégie, gouvernance et vie du laboratoire	Appréciation du projet
C	B	C	B	C

Nom de l'équipe : GENOMICS OF INTEGRATED SYSTEMS

Note de l'équipe	Qualité scientifique et production	Rayonnement et attractivité, intégration dans l'environnement	Stratégie, gouvernance et vie du laboratoire	Appréciation du projet
A	A	A	A	A

Nom de l'équipe : STRUCTURE AND FUNCTION OF MOLECULAR CHAPERONS

Note de l'équipe	Qualité scientifique et production	Rayonnement et attractivité, intégration dans l'environnement	Stratégie, gouvernance et vie du laboratoire	Appréciation du projet
A	Non noté	A	A	A

Nom de l'équipe : GLOBAL REGULATION AND STRESS RESPONSES IN BACTERIA

Note de l'équipe	Qualité scientifique et production	Rayonnement et attractivité, intégration dans l'environnement	Stratégie, gouvernance et vie du laboratoire	Appréciation du projet
Non noté	A	B	A	Non noté

Nom de l'équipe : DYNAMICS OF BACTERIAL REPLICONS

Note de l'équipe	Qualité scientifique et production	Rayonnement et attractivité, intégration dans l'environnement	Stratégie, gouvernance et vie du laboratoire	Appréciation du projet
A	A	B	B	A

Nom de l'équipe : MOLECULAR ASSEMBLAGES AND GENOME DYNAMICS IN BACTERIA

Note de l'équipe	Qualité scientifique et production	Rayonnement et attractivité, intégration dans l'environnement	Stratégie, gouvernance et vie du laboratoire	Appréciation du projet
A+	A+	A	A	A+

Nom de l'équipe : EVOLUTION OF BACTERIAL GENOMES

Note de l'équipe	Qualité scientifique et production	Rayonnement et attractivité, intégration dans l'environnement	Stratégie, gouvernance et vie du laboratoire	Appréciation du projet
B	A	B	A	C

Université Paul Sabatier
TOULOUSE III

Direction de la Recherche

Toulouse, le 22 mars 2010

Affaire suivie par
Ghislaine MACONE-FOURIO
téléphone
05 61 55 66 05
télécopie
05 61 55 69 53
courriel
seccs@adm.ups-tlse.fr
GF/GMF/FW

Le Président

au

Président du comité d'experts de l'AERES

Monsieur le Président,

Je vous remercie pour l'évaluation du Laboratoire de Microbiologie et Génétique Moléculaires (LMGM, UMR CNRS/UPS 5100) dirigé par Claude Gutierrez, dont le porteur de projet est Agamemnon Carpousis.

Je me réjouis que le Comité d'Experts de l'AERES ait reconnu la grande qualité des recherches menées au LMGM et le rôle-clé que joue ce laboratoire au sein de l'Université. Les points à améliorer seront discutés avec le porteur de projet dans un esprit constructif pour l'avenir de la recherche à l'Université.

Vous trouverez ci-dessous un message du porteur de projet apportant quelques observations sur le Rapport d'Evaluation de l'AERES.

Je vous prie de croire, Monsieur le Président, à l'expression de ma meilleure considération.

UNIVERSITE PAUL SABATIER

Gilles FOURTANIER

Response to the preliminary report of the AERES on the project to renew the LMGM

The leader of the project, Agamemnon Carpousis, prepared this response to the preliminary version of the report by the AERES after a meeting (March 11, 2010) in which all the current group leaders and the new group leaders in the project participated. The meeting and the resulting response reflects the transparent and collective decision-making process that the leadership of the unit has practiced in the past and that we intend to continue in the future.

This response is divided into two sections, the first part responding to the overall assessment of the research unit and the second part responding to the team-by-team assessments.

We would first like to thank all of the members of the committee for a frank, succinct and complete report that we believe will aid the LMGM particularly with respect to the task of building new teams when four of the current group leaders retire at the end of the next mandate.

I. Overall assessment

We note a number of very positive comments in the overall assessment of the unit including:

- Several of the research teams are world-leaders in their specialties with excellent publication records.
- The unit has shown that it is attractive for top-level researchers.
- Collaboration between some of the groups is based on shared complementary conceptual and/or methodological approaches resulting in strong synergy.
- The unit is well integrated into its local environment.
- The unit provides a prime example of the value of an association of the CNRS and the University by providing excellence in teaching, research and the training of Ph.D. students.
- Staff of this unit, belonging to all professional categories, maintains pleasant professional and human interactions.

In light of the number of groups that had favorable comments in the team-by-team assessments, we were surprised to read that the scientific productivity of the research unit as measured by quantity and quality was only 'good' (p. 6, Detailed assessments). Since a considerable proportion of our research funding comes from a block grant to the laboratory from the CNRS, we would like to make the following observations about the global scientific production of the research unit. For the period covered by the report, the permanent scientific staff comprised 16 members of the CNRS and 13 members of the University. 28 of the 29 of the members of the scientific staff were considered 'productive' by the criteria of the AERES. Based on a finalized list of publications that was sent to the AERES (January 2010), the research unit produced 140 publications of which 100 are research articles and the remaining 40 are reviews, perspectives, commentaries or book chapters. Of the 140 publications, 100 can be considered 'primary' scientific production of the research unit since the corresponding author and/or the lead author of these articles are members of the research unit. Twenty-eight of the publications were in journals or reviews with an impact factor greater than 8 including *Cell* (2), *Science* (1), *Annu Rev Microbiol* (2), *Mol Cell* (4), *TIGs* (2), *PNAS* (4), *PloS Genet* (4) and *EMBO J* (3). In addition, we published 18 articles in *Molecular Microbiology*, which is arguably the best specialized journal covering the research area of the unit, and 14 articles in the *Journal of Bacteriology*, which we consider to be the journal of reference for research in bacteriology. Considering the relatively modest size of the research unit, we believe that the overall scientific productivity is 'very good' if not 'excellent'.

We believe that the laboratory can be considered to be amongst the most visible in France engaged in fundamental research in molecular microbiology. We would like to point out that the specificity and originality of the LMGM is its thematic coherence, in which the teams share a common interest in fundamental research on model prokaryotic organisms. This is an important part of the attractiveness of the research unit and maintaining this specificity is essential for maintaining the reputation of the unit.

We are happy to note that the committee emphasized the importance of the staff scientists of the University in teaching, and in the training of Masters and Ph.D. students. We will maintain these activities, which contribute to the attractiveness of the research unit and its integration into the University. In spite of the heavy teaching load, the University staff, as underlined in the positive evaluation of most of the teams, has maintained a productive research activity. During the discussion of the AERES evaluation amongst the group leaders, it was suggested that the University staff needs the opportunity to develop their own research projects to maintain morale within the unit. There is nothing that precludes this possibility although it is evident that heavy teaching and administrative duties within the University make it difficult to assume the responsibility of leading a group. It is also obvious that a team wholly composed of University scientific staff is at a disadvantage. These sensitive issues result in part from well-known endemic deficiencies in the organization of the French University system, which lacks well-defined mechanisms for balancing teaching and administrative loads with the level of research activity of the members of the University staff. The leadership of the LMGM will be attentive in seeking opportunities to participate in discussions with the University aimed at helping to reduce teaching and administrative loads of the University staff.

The committee noted heterogeneity amongst the teams in the research unit in terms of their size, scientific production, and capacity to attract funding, students and postdocs. This is admittedly the case. We would like, however, to make a few brief comments. Four of the teams in the current research unit are recent additions to the laboratory. Two of the teams were created in the previous mandate of the laboratory and two in the current mandate. The creation of these teams is the result of an effort to renew the research unit that began in the previous mandate. These teams have managed to attract funding, students and/or postdocs, and their creation can be viewed as proof of the capacity of the LMGM to attract top-notch researchers and to build new teams. Although the new teams are not as large or as productive as some of the established teams in the research unit, the new teams can be considered to be correctly installed in the laboratory and they have access to resources that should permit them to contribute qualitatively and quantitatively important scientific production over the next four-year period. The committee paid particular attention to two small teams in the research unit. We will comment on these teams in the second part of the response dealing with the team-by-team assessments.

The committee has emphasized that we face a major challenge involving the creation of several new research teams with the retirement of four group leaders at the end of the next mandate. We agree with the committee that this situation should be viewed as an opportunity to build new groups that will maintain the reputation of the research unit. We have already dealt in part with this situation. The committee has given very strong support for the transition concerning the leadership of the 'Pneumococcal transformation' team and it supports the continuation of the 'Dynamics of bacterial replicons' team. As already detailed in the written project and in discussions with the committee, meeting the challenge of building new groups will be a major preoccupation of the leadership of the laboratory during the next mandate. We plan to recruit at least one new group leader from outside the research unit. Our objective will be to build dynamic teams that develop ambitious new projects.

Although we understand the rationale, we regret the detached style that the AERES has imposed on the evaluation process. In the life of the laboratory, the evaluation was traditionally the moment when the committee acknowledged the investment of time and effort of the leadership in managing the laboratory, and they also commented on other aspects of the life of the laboratory. We would therefore like to use this response to thank the current direction of the unit for all their efforts in the day-to-day administration of the unit. Much of this work is invisible to the rest of the unit and we need to be reminded from time to time of the sacrifice that the leadership makes in contributing to the collective good of the laboratory. We would also like to thank the leader of the Bacteriophage T4 group, which will close with the retirement of the group leader, for his internationally recognized contributions to the field of bacteriophage diversity. Over the past two decades, this group has been instrumental in work that has revitalized interest in bacteriophage. With the explosion of genomic and metagenomic research, bacteriophages are now known to be important vectors in the flux of genes in the environment. It is unfortunate that with the closure of this group, the major laboratories training the next generation of bacteriophage molecular biologists will be located almost exclusively in North America.

II. Team-by-team analysis

In this section, we will only comment on the evaluation of teams where the committee detected a potential weakness.

Name of the team: Biology of decoding and translational control.

This small team is currently composed of a CNRS staff scientist, a University and Hospital staff scientist, and a CNRS technician. During the period covered by the report, the team had ANR funding and a postdoc. The team produced 3 publications on translational control and 12 publications on bacterial virulence. The leader of the team is the current assistant director of the research unit. The appreciation of the committee of the work on decoding and translation control was positive, but they found the work on bacterial virulence 'very descriptive'.

We regret that we did not explain better the structure of this group in the written and oral presentations. The University and Hospital staff scientist (MCUPH) divides her time between a clinical microbiology laboratory in a teaching hospital and the LMGM. The publications on bacterial virulence originate from work in the clinical laboratory. The MCU contributes on a daily basis to the principal research of the LMGM team as evidenced by her authorship on papers on decoding and translational control. Over the years, the MCU has provided the LMGM with a variety of clinically important strains and she has had important interactions with other groups as evidenced by recent work with the Bacteriophage T4 team, which resulted in two publications and a patent. In addition, the MCU is an expert on the growth of non-standard bacterial strains, an expertise that has contributed significantly to work in other teams (for example, work with the Mobile Genetic Elements team on growing non-standard bacteria to isolate transposons). Taking all of these factors into consideration, we believe that the bacterial virulence work should not be viewed as a dispersion of the scientific research of the team. The MCUPH has no choice but to continue the bacterial virulence work as part of her duties in the hospital.

Another potential weakness detected by the committee was with the project, in which the current head of the research unit plans to join the team to develop a new line of research. We regret that the committee viewed this as a dispersion of the research interests of the team. The attachment of this University staff scientist to the Decoding and Translation Control team should be viewed as an administrative decision giving him some 'breathing room' to develop a new project on the identification of new targets for antibacterial compounds. We agree that a detailed and focused project needs to be developed, and that this proposal will require an internal review before allocation of resources to this project is decided.

We strongly support the continuation of the Decoding and Translational Control team until the staff scientists retire at the end of the next quadrennial.

Name of the team: Dynamics of bacterial replicons.

We are happy that the committee supports our decision to continue this group under new leadership, which is necessary due to the retirement of the current leader. It is unfortunate that insufficient time was allotted in the oral presentation to enable the new leadership to present the research project adequately, but this seems to have been a relatively minor glitch since the project was detailed in the written report. The committee detected a potential weakness due to the proposed co-direction of the future team. The co-direction emerged during our discussions of how to renew the group. The co-leaders head two related and complementary research projects within the group, and the committee supported the continuation of both lines of research. The research unit has managed the co-direction of a restructured group under similar circumstances in the past. The leadership of the unit recognizes the need for a single leader when the team is re-evaluated in four years. One further point is that the current group leader, who has been continuously active at the bench throughout his career, will remain in the team for two years in the next quadrennial. His role and responsibility have been defined by consensus with the new leadership, and his presence should be viewed as a valuable aid in helping the team to advance their projects.

Name of the team: Evolution of bacterial genomes

This small team is currently composed of three University staff scientists, a CNRS technician and two Ph.D. students. The Ph.D. students are co-directed, one with another team in the LMGM and the other with a team in another laboratory on the University campus. During the period covered by the report, the team had ANR funding, trained two Ph.D. students who graduated in 2006, and produced three publications in good journals including an article in PloS Genetics. The leader of the team is recognized internationally for his work with lactic acid bacteria and their phage. The committee, however, noted deficiencies in the research project and stated that some of the planned work extended beyond the general interests of the LMGM.

As described in the written project, this team will close with the retirement of the group leader in 2013. We support the continuation of this team until 2013 to permit them to finish ongoing work, in particular a Ph.D. project that will continue through 2012 if the student obtains a fourth year of support. This time scale will permit the members of this team to investigate other lines of research in other teams. With the retirement of the group leader, the other members of the group will have the opportunity to participate in efforts to build new teams in the period 2012-2015.