

Research evaluation

EVALUATION REPORT OF THE UNIT Génétique des génomes

UNDER THE SUPERVISION OF THE FOLLOWING ESTABLISHMENTS AND ORGANISMS: Institut Pasteur Paris, Centre national de la recherche scientifique, CNRS Inserm

EVALUATION CAMPAIGN 2023-2024 GROUP D

Rapport publié le 27/05/2024

High Council for evaluation of research and highter education



In the name of the expert committee¹ :

Tal Dagan, Chairwoman of the committee

For the Hcéres² :

Stéphane Le Bouler, acting president

Pursuant to Articles R. 114-15 and R. 114-10 of the French Research Code, evaluation reports drawn up by expert committees are signed by the chairmen of these committees and countersigned by the Chairman of Hcéres.



To make the document easier to read, the names used in this report to designate functions, professions or responsibilities (expert, researcher, teacher-researcher, professor, lecturer, engineer, technician, director, doctoral student, etc.) are used in a generic sense and have a neutral value.

This report is the result of the unit's evaluation by the expert committee, the composition of which is specified below. The appreciations it contains are the expression of the independent and collegial deliberation of this committee. The numbers in this report are the certified exact data extracted from the deposited files by the supervising body on behalf of the unit.

MEMBERS OF THE EXPERT COMMITTEE

Chairperson:	Ms Tal Dagan Kiel University Allemagne
Experts :	Ms Julie Chaumeil Inserm — Institut national de la santé et de la recherche médicale Ms Juliette Hamroune CNRS — Centre national de la recherche scientifique (supporting personnel) Mr Robert Lahue University of Galway Irlande Mr Pierre Mandin

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REPRESENTATIVES OF SUPERVISING INSTITUTIONS AND BODIES

Institut Pasteur Mr Patrick Trieu-Cuot
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- CNRS INSB Mr Christian Muchardt
- Délégation régionale CNRS Ile de France Mr Eric Migevant Meudon



CHARACTERISATION OF THE UNIT

- Name: Genetics of Genomes
- Acronym: GoG
- Label and number: CNRS UMR 3525
- Composition of the executive team: Unit direction: Eduardo Rocha

SCIENTIFIC PANELS OF THE UNIT

SVE Sciences du vivant et environnement SVE4 Immunité, infection et immunothérapie

THEMES OF THE UNIT

Research in the unit is centred around diverse aspects of genome biology, with a focus on the maintenance and evolution of genetic information. This includes genome organisation and replication, gene expression and the evolution of genes and genomes over time through the process of mutations, gene acquisition, DNA loss and genome rearrangements. The key biological models include enterobacteria, Vibrio, and yeast, with recent research directions and teams (Berthelot) further expand the model systems to include also humans and other mammals. The recruitment of the Bernheim team is expected to strengthen the interface between microbial and vertebrate genetics.

HISTORIC AND GEOGRAPHICAL LOCATION OF THE UNIT

The UMR3525 Genetics of Genomes (GoG) was established twelve years ago and is situated in the campus of Institut Pasteur in Paris where it is a large part of the Genomes and Genetics department (G&G). The unit was originally established in order to tackle the challenges of whole-genome sequencing, e.g. of model organisms such as *Saccharomyces cerevisiae* and *Bacillus subtilis*. Later developments of the unit led to the addition (and application) of additional OMICS technologies in order to study key processes in genome biology, such as the quality control of gene expression (team Jacquier), DNA mutagenesis, repair, and recombination (teams Mazel, Arcangioli, Richard), and molecular evolution (team Rocha). Additionally, the unit spurred the application of sequencing technologies to the analysis of chromosome structure and metagenomics (team Koszul). More recently, the study of evolutionary genomics using single-cell approaches in mammals was added to the unit portfolio (team Bethelot). Furthermore, the unit integrated team Bernheim whose work in comparative and functional genomics bridges both Bacteria and Eukaryotes. At the same time, teams having a focus on microbial pathogens that were initially included in the unit were regrouped into a different own unit on that topic. With the current team composition, the unit is focusing on fundamental aspects of genetics, genomics, and molecular evolution.

RESEARCH ENVIRONMENT OF THE UNIT

The unit is affiliated with the CNRS and the institut Pasteur. The teams correspond to a large part of the department of Genomes and Genetics (G&G) at the Institut Pasteur. There is thus a tight link between the direction of the department and that of the unit. The teams in the G&G department share activities such as seminars, PhD/postdoc presentations, PI meetings, and a bi-annual retreat – that practically also correspond to the unit's event.

The partnership established by institut Pasteur with universities in Paris enables the unit to benefit from university doctoral contracts from Université Paris Cité and from Sorbonne Université. The unit's scientists also have the possibility to teach in those universities.

The unit is well integrated in the institut Pasteur as well as the French research ecosystem. Members of the unit are part of several panels and committees at institut Pasteur and CNRS. The teams of the unit are integrated in diverse large collaborative or federative research projects.

The unit is also well integrated in the European research community via collaborative grant proposals (ITN, EraNET) and diverse scientific collaborations.

Thanks to several applications, teams in the unit are, furthermore, associated with a number of industrial partners.



UNIT WORKFORCE: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	0
Maîtres de conférences et assimilés	0
Directeurs de recherche et assimilés	9
Chargés de recherche et assimilés	11
Personnels d'appui à la recherche	19
Sous-total personnels permanents en activité	39
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	14
Doctorants	19
Sous-total personnels non permanents en activité	33
Total personnels	72

DISTRIBUTION OF THE UNIT'S PERMANENTS BY EMPLOYER: in physical persons at 31/12/2022. Non-tutorship employers are grouped under the heading 'autres'.

Nom de l'employeur	EC	С	PAR
INST PASTEUR PARIS	0	8	16
AUTRES	0	12	3
Total personnels	0	20	19

GLOBAL ASSESSMENT

The unit encompass complementary teams that perform innovative research on timely topics. Research fields covered by the unit range from bacterial genetics to genome stability and evolution. Major scientific achievements include novel mechanisms of phage-bacteria interactions, mechanisms of genome compartmentalisation, novel characteristics of mobile genetic elements and development of synthetic molecular units to combat antibiotic resistant pathogens (these are just several examples out of a long list). The unit goal to integrate diverse topics in bacterial and eukaryotic genetics, genomics and evolution within the framework of human microbiome research supplies a promising research direction for the future. The researcher's ambition is met by a highly supportive research environment. The teams in the unit lead an innovative line of research that is characterised with an outstanding productivity and success rate in attracting third-party funding and excellent recruits. These achievements are accompanied by specific distinguished prizes. Research in the unit is conducted with the highest standards of ethics, data guality, and data sharing principle. The unit also contributes to important development of methodologies, databases and computational tools. The unit contributes to the training of PhD students and post-docs and has a long-lasting impact on the scientific community thanks to the success of its alumni (in France and beyond). The unit is led and managed very effectively and has a structured vision of further developments in the fields of synthetic biology and metagenomics. Societal activities in the unit include multiple activities aimed to reach out to a diverse audience. While there are no obvious weaknesses to report, it seems that the coordination between the hosting institution and CNRS could be improved. The global assessment of the unit is excellent to outstanding.



DETAILED EVALUATION OF THE UNIT

A-CONSIDERATION OF THE RECOMMENDATIONS IN THE PREVIOUS REPORT

The previous evaluation concluded that the unit has excellent achievements and listed several aspects where the unit could further improve (note that the evaluation was done for the entire G&G department, not only the UMR). The following six aspects were commented:

- 1. The scientific output and quality was deemed excellent. A recommendation to invest more efforts in science outreach led to the development of science communication activities.
- 2. The internationalisation and collaborations were deemed excellent. A main comment was the very skewed gender balance. Consequently, the unit made efforts to integrate more female scientists and currently three out of eight teams are led by female Pls.
- 3. The unit was encouraged to consider their societal and economic impact. For the economic outputthe focus in Pasteur is mainly on basic science rather than applied research. Nonetheless, the report includes diverse examples for knowledge transfer. Similarly, the unit made an effort to establish and develop public outreach activities.
- 4. Comments on centralised facilities led to the development of bioinformatics services that are specific to the groups, while software maintenance is done centrally.
- 5. A strong emphasis was put on the unit involvement in training through research, which constitutes a significant portion of the unit's activities. The assessment of the unit performance was excellent, and the unit was motivated to further invest in bioinformatics training and transferable skills for PhD students. Both of these topics were tackled via the supplement of additional courses and mentorship for PhD students.
- 6. Comments on the strategy and future plans led to the recruitment of two teams with a focus on evolutionary biology and genetics (Berthelot, Bernheim). There was no change in the spatial organisation of the groups in separate building (which is likely impossible to change).

B-EVALUATION AREAS

Considering the references defined in the unit's evaluation guidelines, the committee ensures that a distinction is made on the outstanding elements for strengths or weaknesses. Each point is documented by observable facts including the elements from the portfolio. The committee assesses if the unit's results are consistent with its activity profile.

EVALUATION AREA 1: PROFILE, RESOURCES AND ORGANISATION OF THE UNIT

Assessment on the scientific objectives of the unit

A key goal is the integration of bacterial and eukaryotic genomics, e.g. in the context of the human microbiome, which is seen as a promising research direction for the future.

The integration of novel interdisciplinary approaches is driven by large scale sequencing (HiC and single cell) and comparative genomics. The research approaches are interdisciplinary. The unit also contributes to the development of research software and resources.

Assessment: excellent to outstanding

Assessment on the unit's resources

The space resources remain limited. The annual budget exists yet the net worth has decreased over the years. The unit sees its personnel as the most important resource. Budget for specific projects and PhD/postdoc personnel was increased very successfully via third-party funding. Access to various central platforms (including research facilities and resources) is secured via the Pasteur institute.

Assessment: excellent to outstanding



Assessment on the functioning of the unit

The teams in the unit lead an innovative line of research that is characterised by high productivity and success rate in attracting third-party funding and excellent recruitment. The unit comprises teams with compatible research interests and is its research objectives offer new routes for synergistic interactions. With the exception of space, the unit has excellent resources (including its early career researchers) to

With the exception of space, the unit has excellent resources (including its early career researchers) to conduct research.

Research in the unit is conducted with the highest standards of ethics, data quality, and FAIR principles. Assessment: outstanding

1/ The unit has set itself relevant scientific objectives.

Strengths and possibilities linked to the context

The unit is located at the Institut Pasteur, which supplied an excellent research environment for the stated objectives. The aim to focus on human microbiome research is well founded on a strong track record of the unit on microbial genetics. The unit PIs have a high success rate in attracting third-party funding, also in highly competitive and prestigious funding instruments (e.g. ERC grants). The newly added groups in the unit (Berthelot, Bernheim) have a research agenda that is highly relevant for the stated objectives.

Weaknesses and risks linked to the context

There are no obvious weaknesses or risks.

2/ The unit has resources that are suited to its activity profile and research environment and mobilises them.

Strengths and possibilities linked to the context

The unit members have access to the excellent facilities and research platforms at the institut Pasteur. Multiple ERC grants supply additional funds for the respective groups. Close research interests supply possibilities for collaborative projects (as the track record also shows). Possibilities: the Pls could consider applying for collaborative grant proposals (e.g. ERC synergy grants).

Weaknesses and risks linked to the context

The working space remains limited. This is a recurrent issue that also makes it difficult to apply for additional funding. Administrative support of the CNRS scientists seems to have recently improved but according to the CNRS, personnel for such administrative position in the coming years cannot be fully guaranteed. Possible risk: the annual budget has not been modified for several years to face the increase in the costs of both personnel and consumables.

3/ The unit's practices comply with the rules and directives laid down by its supervisory bodies in terms of human resources management, safety, environment, ethical protocols and protection of data and scientific heritage.

Strengths and possibilities linked to the context

The unit is largely following directives put in place by the institut Pasteur. There are diverse mechanisms set in place to educate and motivate the personnel to follow the required regulations and also monitor diverse measures, e.g. of efficient and sustainable use of resources. All scientists are required to attend a one-day ethics education and are well aware of the contemporary directives in this topic.

The groups that conduct data-rich research are well up to date with data management plans as well as sharing scientific softwares.



Weaknesses and risks linked to the context

There are no obvious weaknesses or risks.

EVALUATION AREA 2: ATTRACTIVENESS

Assessment on the attractiveness of the unit

The unit has an excellent to outstanding reputation thanks to an excellent quality of the scientific production, good quality policy regarding support staff, outstanding success rate in calls for applications from third-party funding agencies and access to state-of-the-art technologies.

1/ The unit has an attractive scientific reputation and is part of the European research area.

2/ The unit is attractive because for the quality of its staff support policy.

3/ The unit is attractive through its success in competitive calls for projects.

4/ The unit is attractive for the quality of its major equipment and technical skills.

Strengths and possibilities linked to the context for the four references above

1. Scientific reputation

The unit organises internal scientific activities that are essential for the formation of new collaborations.

Scientists in the unit are well involved the respective national and international scientific communities thanks to their contribution to scientific conferences, editorial responsibilities, and scientific societies.

The unit organises several international conferences, helped by the pluridisciplinarity and the quality of the different teams. The unit's reputation is also reflected by the numerous prizes awarded to nine PIs and senior scientists. Commitment to the European research environment can be noted: many invitations to international conferences and more than 150 communications in congresses across France and Europe.

2. Staff support

The unit has set policies for staff integration and mentoring for early career scientists. The unit's attractiveness is firmly established as it welcomes over 30 PhD students and postdocs, representing almost half of the unit's workforce. Networking and access to training is visibly promoted, and supported for career advancement, even outside Institut Pasteur or the academic field, this is a part of the unit's policy.

3. Third party funding

The global amount of grants obtained in the evaluation period reaches more than 15M€, on national and European level. This clearly reflects the attractiveness of all teams. Two teams have obtained ERC grants in the past and there are currently three ongoing ERC grants in the unit.

4. Major equipment and technical skills.

The unit has access to infrastructure such as the Pasteur Institute's Department of Technology, which guarantees access to state-of-the-art technologies and machines.

Weaknesses and risks linked to the context for the four references above

1. Scientific reputation

No obvious weaknesses.

2. Staff support

Administrative support of CNRS and ERC grantees seems to be lacking.

The proportion of non-permanent staff in the different teams of the unit is rather large. This addresses the question of upkeeping technical skills throughout the years with the turnover of PhD students and postdocs, as well as the continuity of all research projects. This risk is aggravated by the limited number of research support personnel in the unit.

3. Third party funding

Only one team has received funding from regional and local call for projects (such as Idex or territorial collectivities).

4. Major equipment and technical skills.

No obvious weaknesses.



Assessment on the scientific production of the unit

The scientific production of the unit is outstanding.

- 1/ The scientific production of the unit meets quality criteria.
- 2/ The unit's scientific production is proportionate to its research potential and properly shared out between its personnel.
- 3/ The scientific production of the unit complies with the principles of research integrity, ethics and open science. It complies with the directives applicable in this field.

Strengths and possibilities linked to the context for the three references above

1. The scientific production of the unit meets quality criteria.

The scientific output of the unit includes the results of highly innovative research approaches and ample novel findings on diverse biological phenomena. Examples for novel findings by the unit members include the following (to name just a few):

The contribution of quiescence to the mutation spectrum in yeast (Team Arcangioli)

A dictionary of antiviral arsenal in prokaryotes (Team Bernheim)

Novel players in DNA repair pathways (Team Koszul)

Synthetic weapons against pathogenic bacteria (Team Mazel)

Additionally, the unit produces databases, tools and software that are all publicly available for the scientific community. These are often corresponding to highly cited publications (e.g. CRISPR annotations in bacterial genomes; Team Rocha)

2. Scientific production is proportionate to the research potential of the unit and shared out between its personnel.

All teams have a high scientific productivity.

3. The scientific production of the unit complies with the principles of research integrity, ethics and open science.

Scientists in the unit are instructed regularly about matters of research integrity and ethics.

Members of the unit are active in scientific societies, which includes publication in society journals and attendance in society meetings.

The large majority of publications by the unit is in open access journals. All data produced by the unit is shared with the public as part of scientific publications.

Weaknesses and risks linked to the context for the three references above

There are no obvious weaknesses or risks.



Assessment on the inclusion of the unit's research in society

The unit contributes to multiple activities of interactions within the scientific community, industrial partners and the society and this was assessed as excellent.

- 1/ The unit stands out for the quality and the amount of its interactions with the non-academic world.
- 2/ The unit develops products for the cultural, economic and social world.
- 3/ The unit shares its knowledge with the general public and takes part in debates in society.

Strengths and possibilities linked to the context for the three references above

1. The unit stands out by the quality of its non-academic interactions.

The unit members are highly active in the scientific community in their roles as editors in journals, reviewing of scientific publications, serving in diverse review panels and organising workshops or conferences.

2. The unit develops products for the socio-economic world.

Several of the unit team members have close ties with industrial or commercial partners and several members issued patents. Examples are: synthetic alternatives against antibiotic resistance (Team Mazel), development of antibodies for gene therapy (Team Richard) and novel anti-phage systems (Team Bernheim).

3. The unit shares its knowledge with the general public and takes part in debates in society.

The unit members initiate and take part in multiple science communication activities. About a third of the unit members regularly volunteer to take part in outreach activities. This includes actions in schools and for seniors, activity in social networks, generation of educational material such as books or booklets. Engagement in outreach was also done i the form of art exhibition.

Weaknesses and risks linked to the context for the three references above

There is no obvious weakness or risk.



ANALYSIS OF THE UNIT'S TRAJECTORY

The unit has a sound basis to keep the excellent scientific work and interactions with the society also in the future. The unit plans to add to their current portfolio expertise (i.e. teams) with foci on synthetic biology and metagenomics. These two fields are highly relevant for the unit's research objectives and will help the unit to further develop a strong profile in applied microbiology and biological data science.



RECOMMENDATIONS TO THE UNIT

Recommendations regarding the Evaluation Area 1: Profile, Resources and Organisation of the Unit

The unit may consider increasing its visibility within the unit members.

Recommendations regarding the Evaluation Area 2: Attractiveness

1. Scientific reputation

Keep the excellent work.

2. Staff support

Keep asking for more permanent positions for technicians and/or engineers that could help strengthen the unit's workforce and maintain technical expertise on a long-term perspective. This would also be beneficial for team leaders and senior scientists who could clear some time to supervise PhD students.

3. Third-party funding

As suggested above, consider applying to ERC synergy grants would help raise more money than applying individually. Teams are also encouraged to apply to regional and local call for projects to diversify the sources of funding, and maximise chances of receiving financial support.

4. Major equipment and technical skills None.

Recommendations regarding Evaluation Area 3: Scientific Production

Keep the excellent work.

Recommendations regarding Evaluation Area 4: Contribution of Research Activities to Society

Additional teams could be motivated to contribute to outreach activities.



TEAM-BY-TEAM OR THEME ASSESSMENT

Team 1:

Dynamics of Genomes

Name of the supervisor: Benoit Arcangioli

THEMES OF THE TEAM

The Dynamics of the genome team focuses on the study of DNA damage/repair and the consequences on genome integrity/instability in two important processes in the fission yeast *S. pombe*, the mating-type switching and quiescence. The latter is becoming the primary focus of the team.

CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

The previous report mainly recommended strengthening internals collaborations within the team, and to secure fundings. The team has reoriented its main focus towards the mechanisms of quiescence, and most of the permanent members will be involved in the three work packages. Although several grant applications have been submitted or obtained, substantial additional funding remains an issue.

WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	0
Maîtres de conférences et assimilés	0
Directeurs de recherche et assimilés	2
Chargés de recherche et assimilés	1
Personnels d'appui à la recherche	2
Sous-total personnels permanents en activité	5
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	0
Doctorants	1
Sous-total personnels non permanents en activité	1
Total personnels	6

EVALUATION

Overall assessment of the team

The scientific quality of the team is overall very good to excellent.

Strengths and possibilities linked to the context

The team is well known for its work on the mating-type switching type in S. pombe and is progressively moving towards the study of the genetics of quiescence. This represents a great opportunity as it strengthens some priority axes of the unit, the institut Pasteur and the CNRS section 21. Indeed, the team is fits into two out three of the major topics of the unit, 'organisation and maintenance of the genomes' with the study of DNA repair and replication, and 'Evolution' with the study of molecular evolution of the genome with the accumulation of mutations during quiescence. Moreover, this project fits into one of the three priority axes of the Institut Pasteur, neurodegenerative diseases, and has the potential to bring new insights on aging and associated pathologies



as well as on drug resistance. The work of the team is well aligned with the key topics of 'Stability of the genomes' and 'Evolution' of the CNRS Section 21.

The team can rely on its excellent experience in yeast genetics and epigenetics, DNA repair and replication, having obtained numerous mutants and mastered numerous techniques from molecular and chemical assays, microscopy, to high-throughput techniques with extensive bioinformatic analyses. The team can also rely on strong, long-lasting national and international collaborations. The team leader has long been involved in the participation and organisation of courses and conferences, at local (Institut Pasteur), national and European levels. Finally, the team leader shows a strong investment in PhD and staff mentoring and strong support for their future opportunities.

The publication record of the team is very strong considering its size, with five research articles as first and/or last authors in the period in high quality journals (in Nature communications, eLife, and microbial cell...), and five collaborative publications. The team managed to keep constant funding through two ANR and two FRM grants (total over 700k€).

Weaknesses and risks linked to the context

As mentioned by the team itself, the risks are mostly linked to the difficulties to secure funding. Another risk is linked to the retirement of the team leader and another permanent researcher at the end of the five years. The team is refocusing the primary Aim towards the genetics of quiescence, with three ambitious work packages. The risk is whether these WP could be achieved within the timeframe and with the taskforce available in the team.

Analysis of the team's trajectory

The team will mostly focus on the study of quiescence. Following two important publications in yeast (2017) and primates (2022), two Aims will work on the physiological, genetic and epigenetic mechanisms leading to DNA damage (WP1) and instability of the trinucleotides repeats (WP2) in quiescent cells. The third aim will follow up a publication in 2020 and analyse the initiation program of nuclear DNA degradation and its relationship with DNA replication (WP3). The team relies on its conceptual and technical skills to build this project and ask important fundamental questions about the process of senescence that can lead to new insights in degenerative diseases and aging.

RECOMMENDATIONS TO THE TEAM

Overall, the proposed project is very interesting. It will be important to secure funding and taskforce, and focus on key questions to be able to finalise publications before the retirement of the team leader.



Team 2:

Molecular Diversity of Microbes

Name of the supervisor: Aude Bernheim

THEMES OF THE TEAM

The Molecular Diversity of Microbes team takes a multidisciplinary approach to address three stated themes.

- 1) Understanding antiviral defence systems in bacteria;
- 2) Discovery of naturally occurring, antiviral molecules from bacteria;
- 3) and seeking novel antiviral genes in eukaryotes.

CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

Not applicable, as the team was recruited to the unit in the second half of 2023.

WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	0
Maîtres de conférences et assimilés	0
Directeurs de recherche et assimilés	0
Chargés de recherche et assimilés	0
Personnels d'appui à la recherche	0
Sous-total personnels permanents en activité	0
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	0
Doctorants	0
Sous-total personnels non permanents en activité	0
Total personnels	0

EVALUATION

Overall assessment of the team

The team is off to an outstanding start, with appropriate focus on important goals and multidisciplinary approaches to achieving them. The unit has appropriate plans to integrate the team and to synergise efforts towards highly significant outcomes.

Strengths and possibilities linked to the context

The team leader has an outstanding background, with ongoing momentum in terms of attracting an ERC Starter grant, assembling a research team of six, and beginning to publish as an independent group. There are more than ten publications since 2020, with at least four as first or last author. Journals include Nature, Nature Communications, and Nucleic Acids Research. In addition, the team leader indicated during her presentation that an additional three publications are under review, and that these same manuscripts are available on bioArchives. The multidisciplinary approach is cutting-edge and well suited to compete in a challenging field. The unit proposes highly suitable integration of the team and availing of complementary scientific strengths to maximise chances for success. The team leader is also to be commended for outreach efforts, such as YouTube videos that explain the work to a broad audience.



Weaknesses and risks linked to the context

The approach is broad, covering a diversity of organisms, and may pose risks in terms of working with collaborators with suitable expertise and keeping the project well organised. To date, the team leader has managed this risk well.

Like any new hire, the team leader may be faced with new or unfamiliar responsibilities such as administrative, training of personnel, or budgetary. Similarly, career development and strategic planning are sometimes fruitful areas for advising. In the interview, the team leader indicated she receives strong mentoring support within the unit.

Analysis of the team's trajectory

The project is ambitious, but the aims are well thought-through and the team leader has good control over the project. The team leader informed the panel that she recently received EMBO Young Investigator status, which allows access to EMBO facilities such as mass spec. Overall, the project is in a very strong position to continue its successes and to open new areas in the field of microbial immune systems.

RECOMMENDATIONS TO THE TEAM

The team is in great shape, with strong funding and a very fast start to publishing independently. The team leader and the unit will need to keep a careful track of how broad a diversity of organisms can be managed and how to organise the work. The unit leadership and the team leaders should continue advisory/mentorship to help assure optimal development of the PI, and their integration into the unit and best outcomes for the team.



Team 3:

Comparative Functional Genomics

Name of the supervisor: Camille Berthelot

THEMES OF THE TEAM

The newly incorporated team is currently working on deciphering the evolution of uterine traits in mammals and humans, relying on cutting-edge technologies such as single-nuclei sequencing and organoids models. The team relies on pluridisciplinarity, combining functional and evolutionary genomics and computational biology to study the functions, and their evolution, of the female reproductive tract.

CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

Not applicable, as the team has joined the unit only in 2021.

WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	0
Maîtres de conférences et assimilés	0
Directeurs de recherche et assimilés	0
Chargés de recherche et assimilés	1
Personnels d'appui à la recherche	2
Sous-total personnels permanents en activité	3
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	2
Doctorants	2
Sous-total personnels non permanents en activité	4
Total personnels	7

EVALUATION

Overall assessment of the team

The team has an excellent to outstanding start, and its arrival in 2021 presented the opportunity for the unit to broaden its research topics with the addition of mammal models and new technologies, such as single-cell genomics and organoids culture. The research topic is rather original, indeed very few teams work on the evolution of the uterine traits in mammals, giving the team the opportunity to advance in a mildly competitive environment.

Strengths and possibilities linked to the context

The team, recently added to the unit, brings an original research topic, along with expertise in single-cell technology. The research quality is very high, with three research articles in high-profile journals, including Science, Genome Research and Nature Ecology and Evolution, all published prior to joining the unit. Successful applications to European and national grants in the past few years show how good the team's work is perceived by competitive programs: 1.2 M€ from ERC EVOMENS, 20 k€ from EndoFrance, and 20 k€ from Fondation pour la Recherche sur l'endométriose, all obtained as PI or supervisor.

The different projects are supported by numerous collaborations with other Pasteur teams, and teams in France (Institut Cochin, Station de Primatologie Strasbourg, MNHN, APHP), Europe (DKFZ Heidelberg, BPRC Netherlands) and USA (Seattle), showing envy to move forward with the support of other scientists and to share knowledge with other teams.



Weaknesses and risks linked to the context

The team is currently relatively small, with only two permanent positions in the wetlab part. The work overload for the PI is a potential risk: having to supervise two postdocs and two PhD students, while managing the progress of the four work packages described, day-to-day activities and administrative charges.

Four work packages show much enthusiasm, but also carry a risk of dispersion, aggravated by the fact that four lab members are non-permanent. The work packages' sustainability regarding the turnover pace is a risk not to be underestimated.

Analysis of the team's trajectory

The team's objectives show a very strong will to explore all the possibilities offered by their original research topic. The aim to better characterise the uterus at the cell level is clearly innovative, and the search for evolutionary events of the uterine traits in mammals will most certainly help with a better understanding of the female reproductive system. The impact of the team's research on societal questions such as fertility or uterus diseases is worth noting.

RECOMMENDATIONS TO THE TEAM

Overall, continue the good and innovative work.

Keep on developing their collaboration with teams from the unit and from other research centres. We recommend that the team take some time to spread their quality work to society, by communicating with the general public.

Recruitment of a senior scientist, possibly with an HDR, would help the team to grow accordingly to their ambitious five-year plan.



Team 4:

Genetics of Molecular Interactions

Name of the supervisor: Alain Jaco

: Alain Jacquier/Micheline Fromont

THEMES OF THE TEAM

The Genetics and molecular interaction team is closing in the coming months, following the retirement of the two team leaders. The team focused on the dissection of:

- 1) the mechanisms of mRNA degradation and how they are coupled to translation,
- 2) and the nonsense-mediated mRNA decay and the NMD complexes required for this degradation pathway.

To achieve these goals, the team developed and used large-scale functional genomics screens.

CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

The previous report was overall very positive, including outstanding scientific quality, excellent academic reputation, very strong in technological developments, and no specific recommendation were provided on the strategy for the past five-year plan. The main recommendation was to interact more with the industry and the general public.

WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	0
Maîtres de conférences et assimilés	0
Directeurs de recherche et assimilés	3
Chargés de recherche et assimilés	1
Personnels d'appui à la recherche	3
Sous-total personnels permanents en activité	7
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	1
Doctorants	1
Sous-total personnels non permanents en activité	2
Total personnels	9

EVALUATION

Overall assessment of the team

The overall scientific quality of the team is excellent.

Strengths and possibilities linked to the context

The team worked on the regulation of RNAs, in particular the process of the Non-sense-mediated mRNA decay (NMD), how this mechanism is coupled to translation and how it modulates gene expression. The team was also deeply involved in the technical development of large-scale functional genomics screens.

During the past five years, the team published five articles on the mechanisms of regulation of mRNAs, the mRNA degradation pathway and its link with translation in high quality journals (including NAR, EMBO journal, NSMB, as well as two collaborative studies. They further recently published two studies on mechanisms of post-transcriptional regulation of gene expression in *S. cereviciae*: one on the eIF2A factor and its role on the regulation of protein expression related to the cell wall to provide protection against environmental stress (Meyer et al., PIOS One, 2023), and one on how the sequestration of the Xrn1 exonuclease in exosomes preserves mRNAs



from degradation during post-diauxic shift (Courtin et al., MicroPubl Biol, 2023). Financial support was excellent, with three ANR grants as PI and one as collaborator (total around 900k€). The team was also awarded with three distinctions, two for the two team leaders, and one for a researcher.

Weaknesses and risks linked to the context

Major weaknesses were practically non-existent. The main risk was not to finish the projects implemented before the team's closure, but the recent publication of the two studies in 2023 show the will to wrap up everything.

Analysis of the team's trajectory

Not applicable as the team is closing.

RECOMMENDATIONS TO THE TEAM

Not applicable as the team is closing.



Team 5:

Spatial Regulation of Genomes

Name of the supervisor: Romain Koszul

THEMES OF THE TEAM

The Spatial Regulation of Genomes team was created as a G5 junior team in 2011 and upgraded as a senior team in 2017. The general aim is the study of the functional 3D organisation of prokaryotic and eukaryotic genomes, with the functional links with DNA transcription, recombination and repair and the dissection of phage-host interactions in different environments. The team develops and uses a wide range of omics approaches with extensive bioinformatics analyses, genetics, and synthetic biology, mainly in bacteria and yeast.

CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

The main recommendations were followed with a balance between technology development and projects. Constant technological development is pursued in the chromosome conformation capture approaches with:

- 1) tailoring protocols and developing bioinformatics analyses and programs for evolution studies, genome assembly, and mapping phage-bacteria genome contacts in different ecosystems,
- 2) and developing other techniques, like synthetic chromosomal regions allowing functional studies for the relationship between genome conformation and DNA repair.

Important biological questions are addressed with the dissection of the functional relationships between genome conformation and nuclear processes (transcription, recombination, repair), as well as host-phage interactions in different ecosystems including the human gut microbiota. The team has also recruited a third permanent researcher which secures further the taskforce and the possibilities of training.

WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	0
Maîtres de conférences et assimilés	0
Directeurs de recherche et assimilés	1
Chargés de recherche et assimilés	2
Personnels d'appui à la recherche	2
Sous-total personnels permanents en activité	5
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	5
Doctorants	6
Sous-total personnels non permanents en activité	11
Total personnels	16

EVALUATION

Overall assessment of the team

The scientific quality of the team is overall outstanding.

Strengths and possibilities linked to the context

The first strength of the team is the leadership in the field of 3D genome conformation and technological developments of chromosome capture approaches and the following bioinformatics analyses and modelling. The team follows the 'organisation and maintenance of the genomes' and 'Gene expression' key domains of



the unit, with the study of the links between genome organisation and DNA transcription/recombination/repair, and is directly linked to the goal to integrate bacterial and eukaryotic genomics. Moreover, the projects fit into two of the three priority axes of the Institut Pasteur, 'Host-pathogen interactions', notably with its collaborative work on the SARS-CoV2, and 'Antibiotics resistance', with its work on mobile genetic elements. The work of the team strengthens the key topics of the CNRS section 21, from technology development for genomics and interdisciplinary projects, to the expression and stability of the genomes, mobile genetic elements and diversity of life.

Publication record is outstanding with more than twenty publications as first and/or last authors with many in high-profile journals (including Cell, Mol cell, NSMB, NCB, Science advances, Elife...). National and international collaborations are very strong, as shown by the number of publications as collaborative (7) and co-last authors. Financial support is also outstanding, including an ERC consolidator and an ANR grants as PI and four ANR and one ANRS as collaborators (over 2 million euros). The team leader is the director of the Department of Genomes and Genetics of the Institut Pasteur since 2023 and an EMBO member since 2022. The team is involved in the Pasteur course on genome analysis.

Weaknesses and risks linked to the context

The risks and weaknesses, if any, are limited. The diversification and ambition of the work packages raises the question of the number of trained/permanent staff needed to carry out the projects, despite the recruitment of an additional permanent researcher. The team has always kept an excellent level of funding, and this should remain a priority to manage the ambitious project.

Analysis of the team's trajectory

The team's trajectory is divided into three work packages. The first one investigates the functional organisation of the yeast genomes and the relationship with genome expression and recombination. The second one focuses on bacterial chromosome folding, its interplay with transcription and how phage infection can affect the chromosomal metabolism. The third one aims to characterise phage-host genome relationships and their dynamics in diverse environments.

This project is very ambitious and can bring important fundamental insights on genome organisation as well as translational findings related to health issues, including human gut microbiota and antimicrobial resistance. The aims are carefully, though, with dedicated collaborations and substantial funding already acquired.

RECOMMENDATIONS TO THE TEAM

Overall, the achievements and projects are extremely exciting, and the team should keep up the outstanding work, with the high level of funding. Outreach activities may be developed further.



Team 6:

Bacterial Genome Plasticity

Name of the supervisor: Didier Mazel

THEMES OF THE TEAM

The team, established in 1998 and elevated to a Pasteur Unit in 2004, concentrates on three primary research domains: horizontal gene transfer via integrons, antibiotic-induced stress responses, and the genome architecture of bacteria featuring multiple chromosomes. The team usually comprises 14–16 members, including four tenured researchers and one engineer. Their research primarily employs, but is not limited to, *Vibrio cholerae* as a model organism. Methodological approaches combine genetics, functional genomics, and biochemical techniques, complemented by cutting-edge post-genomic methodologies such as 3C and single-cell analysis.

CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

The previous assessment of this team deemed it as outstanding, with no specific recommendations other than to continue their exemplary work.

WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	0
Maîtres de conférences et assimilés	0
Directeurs de recherche et assimilés	1
Chargés de recherche et assimilés	3
Personnels d'appui à la recherche	4
Sous-total personnels permanents en activité	8
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	3
Doctorants	5
Sous-total personnels non permanents en activité	8
Total personnels	16

EVALUATION

Overall assessment of the team

The global scientific quality of this team remains outstanding as demonstrated by the production record, the number of collaborations and the successful acquisition of funding.

Strengths and possibilities linked to the context

The team's work has greatly advanced understanding of integrons, revealing their unique recombination processes and their role in antibiotic resistance. Recent research explored sub-MIC doses of antibiotic effects on bacterial stress. The team has also investigated genome maintenance in bacteria with multiple chromosomes, discovering a replication checkpoint in *Vibrio cholerae*. Finally, the team has developed a targeted antibiotic device activated in specific pathogens, offering an alternative to broad-spectrum antibiotics and limiting resistance evolution.

The publication record of the team is excellent to outstanding with more 24 research articles in the period, most of high quality (including publications in Nature Biotechnology, Nucleic Acids Research, eLife, and Science Advances, etc.).



This work benefits from the team strong collaborative network, both locally, nationally and internationally. Specific projects benefit from collaboration with industry partners like EVOTEC. The team's focus on mobile genetic elements and genome organisation is perfectly aligned to that of the unit, maximising the potential for intern collaborations.

Visibility and international recognition of the team is outstanding as is attested by election of D. Mazel to the European Academy of Microbiology in 2017 and Academia Europaea in 2021.

Finally, financial support of the team research over the period is remarkable, including five ANR grants (3 of which are directed by 3 different staff members) one JPI AMR grant, Labex, and FRM team funding, totalling over 1.5 million euros. The team is also associated with the institute for technological innovations in microbiology BIOASTER, developing its socio-economic interactions.

Weaknesses and risks linked to the context

There are no weaknesses within this team. As noted by the team itself, a point of vigilance is the future retirement of the team head within the next 7–8 years, considering that Pasteur teams close at the end of the head's mandate. However, as noted below, the future of the senior permanent staff of the team has been thoroughly discussed and is well planned, so that should pose no problem.

Analysis of the team's trajectory

The team's research trajectory is focused on four distinct objectives.

- 1) The team aims to delve deeper into integrons, with a specific focus on unravelling the structure of the attl integrase synaptic complex and probing the determinants of cassette functions.
- 2) The team will further characterise the effects of low doses of antibiotics, with the aim of discovering novel molecules to enhance the efficacy of aminoglycosides and understanding the impact of RNA modifications on resistance.
- 3) The team will continue its pioneering work on the maintenance of multipartite genomes in bacteria like Vibrio cholerae, with the goal of unveiling the mechanisms governing replication synchronisation.
- 4) The team will pursue the development of a live antibiotic device, CoKiPs, tailored to combat antibioticresistant pathogens such as K. pneumoniae, S. flexneri, and S. enterica.

These projects are strongly supported by the team's outstanding expertise and strong preliminary data, which provide a solid foundation for further exploration. The objectives are clearly defined, and the team benefits from robust collaborations at both the national and international levels. Financial support is excellent with multiple funding sources, including JPI AMR MobTargets, ANR ChromIntEvol, and Labex IBEID.

Finally, while the team should close in the next five to six years, the future of the permanent staff has been thoroughly thought, discussed and planned, reflecting a very positive and well-coordinated approach.

RECOMMENDATIONS TO THE TEAM

Maintain this outstanding trajectory as it will undoubtedly yield success and impact.



Team 7:

Eukaryotic Genome Instability

Name of the supervisor: Guy-Franck Richard

THEMES OF THE TEAM

The Eukaryotic Genome Instability (EGI) team states three primary objectives.

- 1. double-strand break repair of expanded microsatellites;
- 2. alternative DNA structures in vivo;
- 3. and genomics of large microsatellites in DM1 [myotonic dystrophy type 1] families.

The team uses model eukaryotes, human genetics, and sequencing/bioinformatics to advance these themes.

CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

The previous report was generally positive about the scientific direction, the team leader, and the proposed five-year plan. The major negative was the small group size (4), due largely to limited external funding, and how this factor impacted the team's outputs.

WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	0
Maîtres de conférences et assimilés	0
Directeurs de recherche et assimilés	1
Chargés de recherche et assimilés	0
Personnels d'appui à la recherche	2
Sous-total personnels permanents en activité	3
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	0
Doctorants	2
Sous-total personnels non permanents en activité	2
Total personnels	5

EVALUATION

Overall assessment of the team

The team appears to be in a similar situation as the last review. Its science and outputs are strong for a team of its size. The team leader is internationally recognised. The team has engaged well with industry. The five-year plan is logical, builds on the strengths of the team, and has novel aspects in human genetics. The major limitation is funding, which limits team size. The overall assessment is in the very good to excellent range and could improve with additional funding and laboratory space. There is a downside risk if personnel support from the unit were to be reduced.

Strengths and possibilities linked to the context

The EGI team is currently competitive in all three themes of its work. One valuable resource is a long-time collaboration with the Institut de Myologie for access to key reagents. The team has made substantial progress in developing the new aspects of its work in all three themes of its plan. The research notes the exciting prospect to incorporate PacBio sequencing as a novel way to explore key questions in the microsatellite field.



The team's publication record since 2018 is quite strong considering the group size, with six original publications (five as senior author) in Cell Rep, Genetics, Nuc Acids Res and PLoS Genet. In addition, there are four methods papers, three reviews, two book chapters and editorship of a methods book on trinucleotide repeats.

The team has also engaged with industry, including funding from industry sources and the successful issuance of three patents stemming from the work. The team goals include advancing therapeutic approaches to important biomedical problems and the team is successfully pursuing this key goal.

Weaknesses and risks linked to the context

Funding in the last couple of years is relatively modest (<€100 K/year) with awards from AFM-Telethon, ARC, and Groupama. Several more funding applications are pending from AFM-Telethon, FRM, Fondation Maladies rares, and AstraZeneca.

Team size continues to be the major issue, largely stemming from external funding. In the interview, the team leader indicated that laboratory space is a key limiting factor. These issues will impact how far the research aims can go. Current personnel are identified to address each aim, so progress is likely, but clearly more funding and more personnel would accelerate the work. While the team is in position to contribute to the field on all three themes, this is a competitive area and acquiring additional resources is highly desirable.

The team relies quite heavily on collaboration with the Bioinformatics hub, including 40%-time contribution by one of its specialists. Loss of this resource would seriously damage the team's future, so the unit is strongly encouraged to ensure continued collaboration of the Bioinformatics hub with the EGI project. The team leader also refers to a growing demand on his time for administrative matters, which need to be reduced to allow full attention to the science. Both these points should be looked at by the unit to identify mechanisms to alleviate the risks.

Analysis of the team's trajectory

The proposed research is on the ambitious side for a relatively small research group. The team leader is interested in pursuing all three aims and the group is contributing to these aspects of the field at a reasonable level. Maintaining adequate lab staffing, including bioinformatics personnel, is key to continued success of the research team.

RECOMMENDATIONS TO THE TEAM

There is enthusiasm for the team's accomplishments and for the proposed new work. The team leader needs to seek additional funding. The team leader indicated that four new funding proposals that are pending from charities and industry, so funding may increase soon. The unit should look at ways to best support the team as described above.



Team 8:

Microbial Evolutionary Genomics

Name of the supervisor: Eduardo Rocha

THEMES OF THE TEAM

The Microbial Evolutionary Genomics team was established in 2008 as a G5 group at Institut Pasteur and later upgraded to a full unit in 2012. The team focuses mainly on horizontal gene transfer through mobile genetic elements (MGEs) and bacterial evolution. To do so, this highly interdisciplinary team uses a combination of comparative genomics, experimental biology, and computational modelling.

CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

The previous report was generally very positive about this team, praising it for both its outstanding scientific qualities and its involvement in the community, notably through knowledge dissemination. Continuous support for this team was recommended, particularly for its experimental needs. This consideration has been followed with the maintenance of a strong experimental activity.

WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	0
Maîtres de conférences et assimilés	0
Directeurs de recherche et assimilés	1
Chargés de recherche et assimilés	3
Personnels d'appui à la recherche	4
Sous-total personnels permanents en activité	8
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	3
Doctorants	3
Sous-total personnels non permanents en activité	6
Total personnels	14

EVALUATION

Overall assessment of the team

The scientific quality of this team is simply outstanding as is exemplified by the production record, the prizes earned, its funding capacities and its visibility.

Strengths and possibilities linked to the context

This team has achieved an important pioneering work on various aspects of bacterial evolution through MGEs. The team quantified the decisive impact of horizontal gene transfer (HGT) on bacterial genome dynamic through mobile genetic elements. Their work unravelled the prevalence of non-conjugative plasmids and the ability of certain plasmids to hijack conjugative functions. Their exploration of bacteriophages uncovered the prevalence of phage satellites across bacteria. They also demonstrated that transferred genes tend to concentrate in chromosomal hotspots, facilitating complex ecological interactions without disrupting overall chromosome structure. Investigating determinants of gene flow in bacterial populations, they identified functional consequences such as the spread of virulence factors and antibiotic resistance genes.



During the period, the team achieved an outstanding level of publication with more than 50 articles, including contributions to top-quality journals such as BMC Biology, ISME Journal, Nature Communications, Nature Microbiology, PLOS Biology, etc.

Financial resources are also outstanding, sourced from various avenues including the conclusion of the ERC CoG for the team leader in 2017, eight ANR grants (including 2 with a team member as leader), an FRM team support and resources from a Labex program, totalling over 1.5 M€.

The team's recognition and visibility are remarkable, as evidenced from the team leader being elected a member of the Academy of Microbiology and delivering a keynote address at ECCB/ISBM 2021 with over 2000 participants. Additionally, one team member received the bronze medal from CNRS.

In addition to being the unit director, the team leader has been part of the CID 51 of the CoNRS, has very strong editorial activities (editor for MBE), and has organised two workshops on Recent Computational Advances in Metagenomics (RCAM) in 2017 and 2019 and is a founding member of the French Society for the Study of Bacteriophages.

The team's collaborative network is extensive and robust, spanning from local (within the unit and Institut Pasteur) to national and international levels.

The team has produced notable software tools including four directly developed tools: SatelliteFinder, eVIVALDI, IntegronFinder, and PANACOTA, along with three indirectly contributed tools: BIGSI, CRISPRCasFinder, and PPANGOLIN. Finally, the team has pursued its efforts to maintain experimental approaches and to develop its wet space, despite the very restrictive space constraints in the institute.

Weaknesses and risks linked to the context

This team displays no visible weakness. Risks have been very well self-assessed by the team and are very limited, especially given the formidable management capacities displayed by the team leader over the years.

Analysis of the team's trajectory

The team's trajectory is described by a research project focused on four main work packages (WPs). WP1 aims to identify and characterise novel MGEs and their transfer mechanisms to complete the MGEs repertoire. WP2 investigates interactions between MGEs and bacterial cells, including capsule heterogeneity and eukaryotic hosts' roles. WP3 examines interactions between different MGEs and how it affects gene transfer. Finally, WP4 explores the functional innovation spurred by HGT, focusing on the accommodation of novel functions in genomes brought by MGEs (such as antibiotic resistance) and the co-option of MGE-encoded functions by prophages.

The project is very interesting and remarkably thought. The aim to enhance the global understanding of bacterial evolution through HGT is an important topic in biology that is perfectly in line with the global objective of the unit and of the section 21 of the CNRS. The different tasks involve a dense collaborative network of very high quality both at the national and international level.

Funding resources are secured and preliminary data and contingency plans are well planned.

RECOMMENDATIONS TO THE TEAM

Keep on this trajectory to maintain this outstanding scientific quality and impact.



CONDUCT OF THE INTERVIEWS

Dates

Start: 19 mars 2024 à 9 h

End: 20 mars 2024 à 18 h 20

Interview conducted: on-site or online

INTERVIEW SCHEDULE

Interview day 1: Tuesday 19th of March 2024

9 a.m. – 9:30 a.m. HCÉRES committee meeting

Closed-door meeting

9:35 a.m. – 9:40 a.m. HCÉRES rules and procedures by J. Dutrieux

Public session (all unit members)

9:40 a.m. – 10:40 a.m. Administrative and scientific presentation of the unit's achievements and future by E. Rocha

40 min presentation,20 min discussionPublic session (all unit members)

10:40 a.m. – 11 a.m.Committee debriefing and coffee break

Closed-door meeting

Teams audition #1 Public session (15 min presentation + 15 min discussion)					
Time	Zoom link	Team Number	Presentation by		
11 a.m. –	Same as unit presentation	1	B. Arcangioli		
11:30 a.m.					
11:35 a.m. –	Same as unit presentation	2	A. Bernheim		
12:05 p.m.					

12:10 p.m. – 1:40 p.m. Lunch break and committee debriefing

Closed-door meeting

Teams audition #2 Public session (15 min presentation + 15 min discussion)						
Time	Zoom link	Team Number	Presentation by			
1:45 p.m. –	Same as unit presentation	5	R. Koszul			
2:15 p.m.						
2:20 p.m. –	Same as unit presentation	6	D. Mazel			
2:50 p.m.						

2:50 p.m. – 3:30 p.m. Committee debriefing and coffee break

Closed-door meeting

Teams audition #3					
Public session (15 min presentation + 15 min discussion)					
Time	Zoom link	Team Number	Presentation by		
3:30 p.m. – 4 p.m.	Same as unit presentation	7	G-F. Richard		
4:05 p.m. – 4:35 p.m.	Same as unit presentation	8	E. Rocha		



4:35 p.m. – 6 p.m. Committee debriefing

Closed-door meeting

6 p.m. End of day 1 Interview

Interview day 2: Wednesday 20th of March 2024

- 8:45 a.m. 9 a.m. HCÉRES committee meeting Closed-door meeting
- 9 a.m. 9:45 a.m. Meeting with ITAs (in French) In the absence of managing staff
- 9:50 a.m. 10:35 a.m. Meeting with researchers In the absence of managing staff
- **10:40 a.m. 11:15 a.m. Meeting with PhD students and Postdoctoral fellows** In the absence of managing staff
- 11:15 a.m. 12:55 p.m.
 Committee debriefing and lunch break

 Closed-door meeting
- **1 p.m. 1:40 p.m. Meeting with institutions representatives** *Closed-door meeting*
- 1:40 p.m. 2:30 p.m. Committee debriefing and coffee break *Closed-door meeting*
- **2:30 p.m. 3:10 p.m.** Meeting with the unit direction *Closed-door meeting*
- **3:10 p.m. 6:30 p.m.** Redaction of the final report *Closed-door meeting*
- 6:30 p.m. End of the interview

PARTICULAR POINT TO BE MENTIONED

The PIs of teams 3 (Camille Berthelot) and 4 (Alain Jacquier and Micheline Fromont) were not present during the interview of the unit.



GENERAL OBSERVATIONS OF THE SUPERVISORS

The institution responsible for submitting the application, which is also responsible for coordinating the response for all the research unit's supervisory authorities, has not submitted any general comments

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