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## DGIMI - Diversité, génomes et interactions micro-organismes insectes

Rapport Hcéres

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

Department for the evaluation of  
research units

AERES report on interdisciplinary unit:  
Diversité, Génomes & Interactions Microorganismes-  
Insectes

DGIMI

Under the supervision of the following  
institutions and research bodies:

Nouvelle Université de Montpellier

Institut National de la Recherche Agronomique - INRA

December 2013



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

Department for the evaluation of  
research units

*On behalf of AERES, pursuant to the Decree  
of 3 november 2006<sup>1</sup>,*

- Mr. Didier HOUSSIN, president
- Mr. Pierre GLAUDES, head of the  
evaluation of research units department

*On behalf of the expert committee,*

- Mr. Thierry HEULIN, chair of the  
committee

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<sup>1</sup> The AERES President "signs [...], the evaluation reports, [...] countersigned for each department by the director concerned" (Article 9, paragraph 3 of the Decree n° 2006-1334 of 3 November 2006, as amended).



## Evaluation report

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

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

Unit name:	Diversity, Genomes & Microorganisms-Insects Interactions
Unit acronym:	DGIMI
Label requested:	UMR
Present no.:	1333
Name of Director (2013-2014):	Mr Patrick TAILLEZ
Name of Project Leader (2015-2019):	Ms Anne-Nathalie VOLKOFF

## Expert committee members

Chair: Mr Thierry HEULIN, CNRS-CEA

Experts:

- Mr David CLARKE, University College Cork, Ireland
- Mr Abdelaziz HEDDI, Insa Lyon (representative of CSS INRA)
- Mr Salva HERRERO, University of Valencia, Spain
- Ms Marie-Claire LETT, Université de Strasbourg (representative of CNU)
- Mr Jean-Christophe SIMON, INRA Rennes

Scientific delegate representing the AERES:

Mr Gabriele SORCI

Representative of the unit's supervising institutions and bodies:

- Mr Bernard GODELLE, Université Montpellier 2
- Mr Philippe HINSINGER (representative of Doctoral School n° 477)
- Mr Christian LANNOU, INRA



## 1 • Introduction

### History and geographical location of the unit

The UMR DGIMI was created in January 2011 by merging two UMRs: “Microbial Ecology of Insects & Interactions Host-Pathogens” (EMIP) and “Integrative Biology & Virology of Insects” (BIVI). The UMR EMIP moved from Saint-Christol-les-Alès to the Université Montpellier 2 (UM2) Campus in 2001 and the UMR BIVI in 2005. As a consequence, the team “Proteomic study of the interaction Spodoptera-microorganisms” was merged with the team “Biological resources & genetic of bacteria and entomopathogenic nematodes” in 2011. In 2013, this new team was merged with the team “Functional genomics & virulence factors” to constitute the current team “Integrative biology of bacteria-insects-entomopathogenic nematodes interactions” (BIBINE).

All members of the UMR DGIMI are now located on the Triolet Campus of UM2 (3rd and 4th floor, building 24), in Montpellier. The insectarium is located within the same Campus (building 55, Center for animal facilities).

The UMR DGIMI belongs to the “Plant Health & Environment” (SPE) Department of Inra and the “Environment, Lifesciences, AgriFood, Planetology” (EVAP) Department of UM2 (Section “Integrative biology, Plants, Interactions”).

### Management team

The current direction: Mr Patrick TAILLIEZ (director) and Ms Anne-Nathalie VOLKOFF (deputy-director)

The project leaders/future direction: Ms Anne-Nathalie VOLKOFF (director) and Mr Alain GIVAUDAN (deputy-director).

### AERES nomenclature

Domaine disciplinaire principal: SVE1\_LS6 Immunologie, microbiologie, virologie, parasitologie

Domaine disciplinaire secondaire 1: SVE1\_LS2 Génétique, génomique, bioinformatique

Domaine disciplinaire secondaire 2: SVE\_LS9 Biotechnologies, sciences environnementales, biologie synthétique, agronomie

### Unit workforce

Unit workforce	Number as at 30/06/2013	Number as at 01/01/2015
<b>N1:</b> Permanent professors and similar positions	3,5	4,30
<b>N2:</b> Permanent researchers from Institutions and similar positions	9,6	8
<b>N3:</b> Other permanent staff (without research duties)	18,6	16,6
<b>N4:</b> Other professors (Emeritus Professor, on-contract Professor, etc.)		
<b>N5:</b> Other researchers from Institutions (Emeritus Research Director, Postdoctoral students, visitors, etc.)		2
<b>N6:</b> Other contractual staff (without research duties)	6	
<b>TOTAL N1 to N6</b>	<b>37,7</b>	<b>30,9</b>



Unit workforce	Number as at 30/06/2013	Number as at 01/01/2015
Doctoral students	5	
Theses defended	8	
Postdoctoral students having spent at least 12 months in the unit*	9	
Number of Research Supervisor Qualifications (HDR) taken	3	
Qualified research supervisors (with an HDR) or similar positions	9	7

## 2 • Overall assessment of the interdisciplinary unit

### Global assessment of the unit

The overall assessment of the unit is excellent. In the socio-economic context of insect pest control and the necessity to propose biological alternatives to chemical insecticides, the unit DGIMI develops an original integrative approach (from molecules to organisms) in order to study the molecular mechanisms of the interaction between plants, *Lepidoptera*, pathogens and parasites (densovirus, nematodes and nematode-associated bacteria, hymenoptera and hymenoptera-associated viruses). The scientific production between 2008 and 2013 involves 54 papers (ACL), most of them being published in high standard journals. One major deliverable of their research activity is the contribution to three databases:

- I) a comparative genomics database on *Lepidoptera* pests of crops and their parasitoids (LepidoDB);
- II) a database on *Spodoptera* EST;
- III) a database on genome analysis of *Photorhabdus* and *Xenorhabdus*.

The unit is well funded by regional and national programs (six ANR projects, two projects as coordinator), and has strong links with two private companies (this includes the presence of four people from one company hosted in the unit, and a phase 2 product with the second one). The unit members are involved in training at both the License and Master level. In particular, they coordinate one Master specialty. The number of PhD students (8 theses defended and 5 in progress) should be increased in the future. Based on the meeting with the members of the unit (researchers-lecturers, engineers, technicians, administratives and students), the general feeling on the unit life and the scientific activities is excellent.

### Strengths and opportunities related to the context

- they manage a complete range of pathogens and parasites associated with crop-infesting *Lepidoptera*;
- they share common tools and methods to study the various partners (e.g., genomics);
- they share live material resources such as the Insect rearing facility (Insectarium), the Platform for experiments on Quarantine Insects (PIQ), three collections (nematodes, bacteria, insect cell lines), and tools for functional genomics;
- they have a very good level of economic interactions especially with two private companies;
- they are heavily involved in microbiology and parasitology teaching and networking (co-creation of a “Interaction Microorganism-Host” (IMH) network with the LSTM unit);
- according to previous recommendations, they increased their collaboration with the CBGP unit allowing studies at the population level.



### Weaknesses and threats related to the context

- the number of PhD students in average is quite low and can be easily increased;
- the absence of EU funding during the last period;
- the age pyramid is not favorable and will require recruitment or attraction of young researchers/lecturers and technicians/engineers in the near future;
- the teams have to adjust their objectives to their size (in terms of number of permanent positions) and strengths. On the other hand, the size should be increased by hosting more PhD students.

### Recommendations

- the members of the unit are encouraged to continue their efforts in building infrastructure in research and education and microbiology/parasitology networks at the regional scale. The animation of the IMH network and the construction of a SFR dedicated to “Invertebrates/environment” are particularly encouraged;
- they have to increase their international recognition through the coordination of larger international projects (EU projects/H2020 on biocontrol), the participation to international conferences as invited speakers, and publication in more generalist journals with high impact factor;
- they have to set research priorities both at the team and unit level that are appropriate with the size, strengths and skills of the teams/unit;
- they are encouraged to make the unit more attractive for PhD students and diversifying the origin of the PhD grants (e.g., CIFRE);
- associate-professors are encouraged to defend their HDR whenever possible;
- the teams are encouraged to increase collaborations between them through common projects;
- they are encouraged to, at the very least, maintain the current level of interactions with private companies.



### 3 • Detailed assessments

#### Assessment of scientific quality and outputs

The overall scientific production of DGIMI members between 2008 and 2013 is excellent, with 54 papers (ACL) published, many of them in high impact journals. The mean number of citations per paper is 9. The journals in which they published their results includes 'generalist' journals (Science, PNAS, PLoS One) and 'specialized' journals (BMC Genomics, Gene, Int J Syst Evol Microbiol, Insect Biochem Mol Biol, J Insect Physiol, J Invert Pathol, Environ Microbiol, J Virol, Mol Immunol). The average number of papers per permanent researcher/lecturer and per year is 0.8. Several members of the unit are co-authors of five patents in total.

Taking into account the quality of the research and its international positioning, the level of publications, especially in term of targeted 'generalist' journals with a high impact factor, could be easily increased.

Among the major results with high impact the experts committee would like to highlight the following:

- the role of holocentrism on evolution rates in Lepidoptera (PNAS in 2010, cited 40 times) and the characterization of the holocentric structure (PLoS One in 2011). One important result is the evidence that holocentric chromosomes allow faster evolutionary rates compared to monocentric ones;
- baculoviruses were shown to derive from the integration of a nudivirus in the genome of a braconid ancestor (Science in 2009, cited 94 times). Within the *Hyposoter didymator* genome, regions specialized in the production of proteins associated with IVs particles were shown to be amplified during viral replication (PLoS Pathogens in 2010, cited 36 times);
- the characterization of regulatory networks controlling pathogenicity in *Xenorhabdus*, involving the examination of *fliZ* expression at the single cell level (PLoS Genetics in 2013);
- a major contribution to the understanding of densovirus infection and replication (three papers published in J Virol).

Another important deliverable of their research activity is their involvement in the elaboration of three databases hosting genomic resources:

- I) a database on comparative genomics dedicated to Lepidoptera pests of crops and their parasitoids (LepidoDB), in collaboration with the BIPAA platform in Rennes;
- II) a database of Spodoptera EST created in 2006;
- III) a database on genome analysis of *Photobacterium* and *Xenorhabdus* (PhotoScope & XenorhabduScope) in collaboration with the Genoscope (CEA, Evry) and the 'Xenorhabdus US Consortium'.

They collectively manage a collection of living entomopathogenic nematodes (about 210 strains), a collection of their symbiotic bacteria (about 440 strains), and a collection of densovirus.

#### Assessment of the unit's academic reputation and appeal

The overall assessment of the academic reputation and attractiveness of the unit is very good. Several members of the unit contributed to the leadership in Lepidoptera genomics through the coordination of the Spodoptera sequencing project and the ADALEP (Adaptation of Lepidoptera to biotic environment) network. They also participated to the Fall ArmyWorm International Public Consortium (FAW-IPC) for the annotation of *Spodoptera frugiperda* genome and the 'Bombyx Genome Consortium'. They are members of the 'International Consortium on *Xenorhabdus* Genomic'.

They participated to the organization of two national meetings (Immunolnv 2008 and Entomo 2012 in Montpellier) as members of the Scientific Council. Several members of the unit were invited to ten international meetings in total.

They coordinated two Franco-Libanese projects (CEDRE 2007-09, 2009-10) and a project with Brazil (CAPES-COFECUB, 2009-10). They have been involved in two projects funded by ANR (Agence Nationale de la Recherche) as coordinator (ANR Blc 'Holocentrism'/2007-11 and 'ADA-SPODO'/2012-15), and four as partner (ANR Blc



'GnpAnnot'/2007-11, ANR Blc 'Paratoxose'/2009-12, ANR Systerra 'Biocosmac'/2009-12, and ANR BioAdapt 'ABC-PaPoGen'/2012-16). Several others projects (7) were funded by national (Inra-SPE, Inra AIP-Bioresources, Genoscope) and regional (UM2) programs, as coordinators or partners.

Their attractiveness can be measured by five invitations of researchers/professors and the welcoming of nine post-docs students. One member of the unit received a 'young lecturer' IUF grant (Institut Universitaire de France).

### Assessment of the unit's interaction with the social, economic and cultural environment

The interaction with the economic environment is very good. They have a strong link with two private companies: four people from the 'In Vivo Bioresources' company (two engineers and two technicians) are hosted in the unit to carry out programs on biological control of crop pests in collaboration with the DIDI team. The collaboration between the BIBINE team and the Nosopharm company on new antibiotics resulted in patents with license and a phase 2 product.

### Assessment of the unit's organisation and life

The organization and the life of the unit was evaluated as excellent. The organization of the unit is now stabilized with four research teams (EHA 'Epigenetic, Holocentrism & Adaptation', BIBINE 'Integrative Biology of Interactions Bacteria-Insects-Entomopathogenic Nematodes', DIDI 'Dynamics of Interactions of Densovirus-Insects' and B2iHP 'Integrative Biology of Host-Parasitoid Interactions'). They share live material resources such as the Insect rearing facility (Insectarium), the Platform for experiments on Quarantine Insects (PIQ), three collections (nematodes, bacteria, insect cell lines), and tools for functional genomics.

The quality of the unit's organization and life relies on the collegiality of the decisions at the unit level including researchers/lecturers, engineers, technicians and support staff, the frequent and regular meetings involving all the members (permanent positions) of the unit, and the organization of regular scientific seminars.

The meetings between the experts committee and the different groups of the unit confirm the very positive general feeling of the experts committee on the unit's management and life.

Three levels of decision taking exist: the Scientific Advisory Board involves the unit's direction and team leaders (about six meetings per year); the Lab Council (life organization of the unit) involves all unit members (three-four meetings per year); working groups dealing with Insectarium, Platform of Insect Quarantine (PIQ), Health/Safety/Quality.

### Assessment of the unit's involvement in training through research

They have a very important contribution in education at the Master level, including the coordination of the Master specialities (Section BioPMBB 'Plant and Microbial Biology-Biotechnology-Bioprocess'/Speciality IMHE 'Interactions Microbes-Hosts and Environment', Section EcoBioDiv 'Ecology-Biodiversity'/Speciality IEGB 'Engineering in Ecology and Biodiversity Management' at UM2, and Section BSE 'Biology-Health-Ecology'/Speciality SSIB 'Signalisation-Integrated Systems in Biology' at EPHE).

Two members of the unit contribute to the life of their Doctoral School (ED n°477 SIBAGHE, 'Integrated Systems in Biology, Agronomy, Geosciences, Hydrosociences, Environment') through the coordination of the 'Microbiology/Parasitology' Section and the participation to PhD committees as ED SIBAGHE representatives. They published two educational books for students (License, Master).

The number of PhD students (8 theses defended, and 5 in progress) should be increased in the future. All the PhD students (even a few master students) are associated to publications, confirming the good quality of student guidance.

The discussion with the deputy-director of ED SIBAGHE confirmed the important involvement of lecturers and researchers in the ED SIBAGHE functioning, and the quality in training of students through research.



### Assessment of the strategy and the five-year plan

Their five-year plan is very ambitious with the following original questions:

- expected breakthrough on the evolutionary of Ichnovirus and mechanisms underlying the success of parasitoid wasps attacking Lepidoptera species of economic relevance;
- genome scale analysis on the major moth pest *S. frugiperda*;
- population genomics and epigenomics (*S. frugiperda*) to identify mechanism of adaptation to plants;
- single cell approach to understand bacterial (*Xenorhabdus*)-host interaction;
- expanding research topics to include evolutionary and ecological aspects of densovirus in order to develop new tools for pest control.

The assessment of the strategy and the project was evaluated as excellent because of the real possibility to increase the interactions between teams due to the very good integration of biological models and approaches. The feasibility of the five-year plan is reinforced by a more intense collaboration with population geneticists of CBGP (Centre de Biologie et de Gestion des Populations, Montpellier) allowing integrative studies from molecules to populations.

Future associations with geographically and scientifically closely related research units could be the result of joint projects and publications, facilitated by the existing IMH 'Microbial-Hosts Interaction' network and the SFR (Structure Fédérative de Recherche) network 'Invertebrates/Environment' in preparation.



## 4 • Team-by-team analysis

**Team 1:** Epigenetics, holocentrism and adaptation of the insect

Name of team leader: Ms Emmanuelle D'ALENÇON

### Workforce

Team workforce	Number as at 30/06/2013	Number as at 01/01/2015
<b>N1:</b> Permanent professors and similar positions	0,5	0,8
<b>N2:</b> Permanent EPST or EPIC researchers and similar positions	1,6	1
<b>N3:</b> Other permanent staff (without research duties)	2,2	1,9
<b>N4:</b> Other professors (PREM, ECC, etc.)		
<b>N5:</b> Other EPST or EPIC researchers (DREM, Postdoctoral students, visitors, etc.)		1
<b>N6:</b> Other contractual staff (without research duties)		
<b>TOTAL N1 to N6</b>	<b>4,3</b>	<b>4,7</b>

Team workforce	Number as at 30/06/2013	Number as at 01/01/2015
Doctoral students	2	
Theses defended		
Postdoctoral students having spent at least 12 months in the team	1	
Number of Research Supervisor Qualifications (HDR) taken	1	
Qualified research supervisors (with an HDR) or similar positions	1,6	1

## • Detailed assessments

### Assessment of scientific quality and outputs

The main theme of EHA team is to describe the holocentric structure of the genomes of lepidoptera and its implications for functional organization, regulation and evolution of the genome. These questions are addressed on the noctuid *Spodoptera frugiperda*, on which the team has accumulated genomic resources (EST, RNAseq, BAC libraries), including a full sequenced genome, through an international consortium.



A search of centromeric proteins pointed the absence of some of them in *S. frugiperda* and the importance of Transposable Elements (TE) in the evolution of histone-like gene. Search for epigenetic marks in 1 % of the *S. frugiperda* genome showed that heterochromatine is associated with gene-poor, repeat-rich regions. Transcriptomic analysis of developmental stages of *S. frugiperda* allowed identifying genes involved in moth development, some of which being validated with siRNA experiments. One important result of the team is an evidence that holocentric chromosomes allow faster evolutionary rates compared to monocentric ones. Finally, the team is developing a project to identify genomic regions involved in plant adaptation in *S. frugiperda* by comparing genomes of the corn and rice specialized strains.

It is not always clear to understand the influence of holocentrism on genome and epigenome regulation and evolution, in terms of expectations and hypothesis-testing experiments. Although holocentrism is a unifying link of the team, some important issues addressed by the team are not very well connected to this central question.

For a small team like EHA, the production is excellent, both quantitatively and qualitatively, and diversified. Five papers, among which one in PNAS, two patents, and the building of LepidoDB, a dedicated database for lepidoptera of economic importance and their parasitoids.

### Assessment of the team's academic reputation and appeal

The team is very active and recognized in the field of Lepidoptera genomics. This has led to gathering many genomic resources on *S. frugiperda* and to propose the complete genome sequencing of this noctuid through an international consortium and supports from INRA and Genoscope. This team benefits from internal expertise in bioinformatics (two IE) and from supports from INRA platforms (PF Bipaa in Rennes and URGI in Evry). The team has also coordinated two ANR projects, one running till 2015.

The team also coordinates the French network ADALEP, supported by INRA SPE, and organized last year an international workshop on Lepidoptera genomics and adaptation. It also participates actively to the Bombyx Genome consortium.

The team has recruited in september 2011 an associate professor who is granted by IUF (Institut Universitaire de France) till 2018.

The team publishes in good to excellent journals (e.g. PNAS). The production is excellent and could be improved both quantitatively and qualitatively to make visible the efforts put on the acquisition of genomic resources. The team may increase its scientific recognition through invited participations to national or international symposia. The team has a relatively low number of PhD students (2) and post-doctoral fellowships (1).

The team has fully responded to the request of the Inra SPE division to interact more with the CBGP on population ecology, evolution and genomics of Lepidoptera. The EHA is a partner of an ANR project coordinated by CBGP (Adaptome), is co-supervising two PhD theses with CBGP, and hosts one researcher from CBGP to increase the links between functional and population genomics.

### Assessment of the team's interaction with the social, economic and cultural environment

The team develops in collaboration with bioinformatic platforms dedicated databases to gather and publically access genomic resources of Lepidoptera (LepidoDB) and Spodoptera (SpodoBase).

The team has developed patents to silence Spodoptera genes through siRNA delivery. Private partnership is ongoing but it is unclear how it is formalized.

### Assessment of the team's involvement in training through research

The team has a rather low activity of training through research (two PhD theses in progress). There is no self-analysis of the team to explain how this could be improved. The fact that the EHA team includes an associated professor (recruited in 2011) should be considered as an opportunity to attract more students on EHA research topics.

### Assessment of the strategy and the five-year plan

The project of the EHA team for the next 5 years is on the continuation of what has been done so far. It is still based on holocentrism in Lepidoptera and how this peculiar chromosome structure affects genome organization, functioning and evolution. Two changes are highlighted:



I) address these issues at a whole genome scale, taking advantage of the full genome sequence of *S. frugiperda*;

II) reinforce population genomics and epigenomics to identify the mechanisms of plant adaptation in the noctuid, taking advantage of the sequencing of the rice strain and the collaboration set up with CBGP.

The team should make clearer priorities on their scientific orientations, in relation with the actual human strengths of the team (two permanent people left or will leave soon). Interactions with other teams of DGIMI, with CBGP and other INRA teams working on insect genomics should be intensified to enhance research dynamics and overcome critical size effects.

## Conclusion

### ▪ Strengths and opportunities:

The team has an excellent recognition in the field of Lepidoptera genomics, through consortium initiatives, coordination of a network, development of dedicated databases and recent collaboration with CBGP. The use and valorization of genomic data obtained in Spodoptera are opportunities to better define further orientations and increase team reputation through publications in high ranked journals.

### ▪ Weaknesses and threats:

The team must be reinforced. The scientific strategy of the team should be better defined by making priorities, identifying essential needs and exploring important partnerships. There is a possible threat that the team could not reach their 5 year plan objectives mentioned in the document, because of insufficient resources and brainstorming on team priorities sized on actual strength and expertise.

### ▪ Recommendations:

The team should continue to lead projects on *Lepidoptera* genomics but needs to make clearer priorities, based on promising scientific issues, strategic aspects, human resources and expertise in presence. The team should continue and even reinforce collaborations with CBGP and other teams working in insect genomics. The team should also have more internal links within the unit and attract more PhD students and post-docs.



**Team 2:** Integrative biology of interactions between bacteria, insects and entomopathogenic nematodes

Name of team leader: Mr Alain GIVAUDAN

### Workforce

Team workforce	Number as at 30/06/2013	Number as at 01/01/2015
<b>N1:</b> Permanent professors and similar positions	2	2
<b>N2:</b> Permanent EPST or EPIC researchers and similar positions	3,6	4
<b>N3:</b> Other permanent staff (without research duties)	5,8	5,8
<b>N4:</b> Other professors (PREM, ECC, etc.)		
<b>N5:</b> Other EPST or EPIC researchers (DREM, Postdoctoral students, visitors, etc.)		
<b>N6:</b> Other contractual staff (without research duties)	1	
<b>TOTAL N1 to N6</b>	<b>12,4</b>	<b>11,8</b>

Team workforce	Number as at 30/06/2013	Number as at 01/01/2015
Doctoral students	2	
Theses defended	4	
Postdoctoral students having spent at least 12 months in the team	1	
Number of Research Supervisor Qualifications (HDR) taken	2	
Qualified research supervisors (with an HDR) or similar positions	4	3

## • Detailed assessments

### Assessment of scientific quality and outputs

The BIBINE team has resulted from the merger of three teams (the first merger in 2011 and a subsequent merger in 2013) and the team now has 16 permanent members of staff (11 supported by Inra and 5 supported by the Université Montpellier 2). This team has an excellent research output with 38 papers and three patents since 2008. Many of the papers are in excellent journals with high impact factors (i.e. five papers in *PLoS One*, three papers in *Environmental Microbiology*, two papers in *BMC Genomics*, one paper each in *Molecular Microbiology*, *Infection and Immunity*, *Applied and Environmental Microbiology*, *CurrOpinMicrobiol*, *Genome* and *Journal of Bacteriology*, and most recently a paper in *PLoS Genetics*). This represents a consistently high output for a laboratory in the area of molecular microbiology. In particular the latest research (just published in *PLoS Genetics*), involving the examination



of *fliZ* expression at the single-cell level, is very exciting and offers this team an opportunity to become research-leaders in the area of population heterogeneity.

This team is internationally recognized as being leading experts in the field of *Photorhabdus* and *Xenorhabdus* research. They have led the field in their work on the genomics of these bacteria since the publication of the *Photorhabdus luminescens* TTO1 genome in 2003. Importantly their contribution to the MaGE genomic analysis platform has led to the development of an extremely important resource for the field. Moreover since 2008 the papers published by this team have accumulated a h-index of 8 (calculated from 33 papers that were identified using the three researchers of the team as search terms in Web of Science) and their papers have been cited 172 times, suggesting that their work is having a significant impact in their research area.

Three members of the team have been invited to participate in a number of national conferences and some international conferences.

Finally it was interesting to see the protocol to help in the identification of *Photorhabdus asymbiotica* infections in humans.

### Assessment of the team's academic reputation and appeal

This team has an excellent reputation amongst their peers for performing (and publishing) excellent research. The team has secured five grants since 2008 primarily from the INRA SPE department. As outlined in the report, they have also participated in a number of national and international projects/networks ranging from an international *Xenorhabdus* consortium and a local regional network called “Interactions Micro-organisms-Hosts” (IMH). Their level of participation has ranged from collaborator to organiser. The team has been very active in regional and national networks in particular.

Much of the international work of this team has been with the characterization of nematode-bacteria complexes that have been isolated from around the world. This obviously speaks highly of the reputation of the team as experts in this area. The team has also collaborated with international groups (particularly in the USA) for the sequencing of *Xenorhabdus* strains. The team has hosted several short-term visits by foreign researchers and one French post-doctoral fellow since 2008. The post-doc has since been recruited by the INRA and is based in Clermont-Ferrand. Members of the team have also acted as *ad hoc* reviewers for a number of leading international journals and important funding agencies.

### Assessment of the team's interaction with the social, economic and cultural environment

The team has partnered with a small start-up company (Nosopharm) since 2009 and this partnership has resulted in three patents in 2012-2013 and a publication in the *Journal of Antibiotics* in 2013. The patents are protecting specific bioactive molecules (potential novel antimicrobials) produced by the genus *Xenorhabdus*. There has been much interest, particularly over the last few years, in *Xenorhabdus* and *Photorhabdus* as sources for novel antimicrobials and this team is well-placed to take advantage of this interest with their extensive strain collection (> 400 isolates) of *Xenorhabdus* and *Photorhabdus*. One of these compounds, NOSO-95, has been shown to be a first-in-class antibacterial molecule active against a number of antibiotic-resistant Gram negative bacteria and this compound is being developed by Nosopharm. The link-up between this team and Nosopharm does appear to be working well with both partners contributing to the interaction (i.e., BIBINE team brings bacterial strains and microbiology skills, Nosopharm brings path to market). Moreover Nosopharm and its academic partners have been successful in leveraging money from the French government for the development of NOSO-95, highlighting the potential for this partnership. Several press releases have also been linked to this partnership and there has been widespread on-line advertisement.

### Assessment of the team's involvement in training through research

Members of the team have been involved in the supervision of five PhD students that have graduated since 2008. Currently the team is supervising two PhD students. They have supervised nine Masters students (Master 1 and 2). Therefore this team has made a significant contribution to training through research in this unit.

Staff members are also involved in the running of post-graduate Masters programs and members of the team were critically involved in the development of new Masters course in “Integrative Parasitology”.



## Assessment of the strategy and the five-year plan

The BIBINE team is proposing to develop their work on the analysis of single-cell gene expression in bacterial populations. They appear to be well-placed to do this (with an excellent recent publication in PLoS Genetics) and this is going to be a very exciting new field of research in bacteriology. This work will be used to develop a better understanding of the roles of phenotypically distinct sub-populations of *Xenorhabdus* during the tripartite interaction. In addition the team proposes to study the nematode microbiome to determine the effect of other bacteria on the nematode-*Xenorhabdus* interaction. This is in line with an increased interest in studying how entomopathogenic nematodes and their symbiotic bacteria compete with the normal microbiota of their hosts.

## Conclusion

### ▪ Strengths and opportunities:

The team is composed of excellent researchers with a lot of experience in molecular microbiology. This experience will ensure rapid progress towards the objectives of the proposed project. The team is also well placed because of its access to the PIQ platform and its existing collaborations with other teams in the unit. These collaborations must also be seen as an opportunity and efforts to develop these links should be encouraged. Finally, the existing collaboration with Nosopharm is very exciting. In this collaboration the team has provided Nosopharm with access to their extensive *Xenorhabdus* strain collection. This collaboration must also be used as an opportunity to leverage more funding for the team from sources such as the EU.

### ▪ Weaknesses and threats:

The team is currently quite big and dynamic but it is imperative that new, young researchers are attracted to join it to ensure continuity. Moreover, the range of current funding sources are very limited and the team is encouraged to increase the diversity of funding sources to prevent any sudden changes in available funding.

### ▪ Recommendations:

The team is encouraged to exploit opportunities within Horizon 2020, including Marie-Curie fellowships, ERC fellowships (particularly early-stage and/or consolidator fellowships). The team have access to a number of resources that should attract potential EU-based collaborators (i.e. PIQ platform, strain collection). This would strengthen the funding base and also increase the profile of the team across Europe. The team is also encouraged to participate in more international conferences. This will increase their visibility and awareness of the exciting resources that they can access.



**Team 3:** Dynamics of densovirus-insect interactions

Name of team leader: Ms Mylène OGLIASTRO

Workforce

Team workforce	Number as at 30/06/2013	Number as at 01/01/2015
<b>N1:</b> Permanent professors and similar positions	1	1,5
<b>N2:</b> Permanent EPST or EPIC researchers and similar positions	1	1
<b>N3:</b> Other permanent staff (without research duties)	2,4	1,7
<b>N4:</b> Other professors (PREM, ECC, etc.)		
<b>N5:</b> Other EPST or EPIC researchers (DREM, Postdoctoral students, visitors, etc.)		
<b>N6:</b> Other contractual staff (without research duties)	5	
<b>TOTAL N1 to N6</b>	<b>9,4</b>	<b>4,2</b>

Team workforce	Number as at 30/06/2013	Number as at 01/01/2015
Doctoral students	1	
Theses defended	3	
Postdoctoral students having spent at least 12 months in the team	3	
Number of Research Supervisor Qualifications (HDR) taken	1	
Qualified research supervisors (with an HDR) or similar positions	2	2

- Detailed assessments

Assessment of scientific quality and outputs

During the last years, this team has made a major contribution to the understanding of the biology of densoviruses, using *Junonia coenia* densovirus (JcDENV) as a model. In that sense, the team has specially contributed to the understanding of the molecular mechanisms involved in the viral entrance, replication and systemic spread in the host. The excellent quality of such research is reflected by the publication records. Different aspects of JcDENV pathology and specificity have been published in top journals in the area of virology (*J. Virol* and *Virology*).

The team has also focused, more recently, on the study of densovirus evolution and ecology. Nevertheless, the team has made certain contributions that could have a major impact on that topic in the near future. Among such contribution, it is remarkable the discovery of changes in host behavior after viral infection and the development of methodologies for the finding of novel densoviruses in the field infecting new species of agronomical importance.



Such results are not published yet, although, according to the report, several manuscripts covering such aspects are in preparation.

### Assessment of the team's academic reputation and appeal

The team reputation is reflected in its interaction with other research groups (Mr Morena CASARTELLI, University of Milan, Italy; Mr Yi Li, Wuhan University, China; Ms Keiko KADONO-OKUDA, NIAS Tsukuba, Japan) working on related topics. Moreover, their studies have been published in top virology journals.

Recent and future studies on understanding densovirus evolution and ecology have increased their interdisciplinary from a conceptual as well as methodological point of view. It has been mainly realized by the establishment of national collaborations and consortiums (BGPI, Montpellier; INRA Bordeaux; INRA Avignon). It is expected that such collaborations will increase group reputation at the same time that will promote international visibility.

### Assessment of the team's interaction with the social, economic and cultural environment

Research conducted by the team has allowed the transfer of knowledge to a company for the development of novel agents for pest control. This gives an added value to the research with a possible substantial contribution to the economic developed of the region/country in the context of the “knowledge economy”.

Additional collaborations on the development of densoviruses as a delivery vector, although still very premature, could also contribute in a long term to the economy of the region.

### Assessment of the team's involvement in training through research

According to current and future plans, the team is broadening its research topic to evolutionary and ecological aspects of densoviruses, creating a more multidisciplinary environment. Such type of environment is especially attractive for national and international students and researchers, and has a major impact of the training capacity of the group.

### Assessment of the strategy and the five-year plan

Future plans are mainly focused on completing or getting more information on molecular and cellular aspects of the pathological process of densovirus infection as well as getting more information on ecological aspects. This should contribute to a better understanding of the pathological process occurring in the field and subsequently to the development of effective agents of pest control.

Having good connections with companies on the field, it would be interesting to focus on more applied aspects of densoviruses. For instance, very few aspects of the densovirus interactions with other biological control agents (parasitoids, predators and microbial control) being already in use for pest control are considered in the future plans. Knowing practical aspects of the interaction would strongly contribute to the development, alone or in combination, of densovirus as a biological control agent.

### Conclusion

#### ▪ Strengths and opportunities:

Densoviruses are restricted to arthropods and as a final outcome produce the death of the host, making them very attractive as biological control agents. The knowledge generated by the group on the viral pathology and ecology will be essential to allow a proper use of these virus insuring a safe transfer from the bench to the field.

#### ▪ Weaknesses and threats:

According to previous comments, research should not only focus on the development of basic knowledge but should also take the advantage of the collaboration with companies to focus on more applied issues.

They should increase international cooperation and funding, especially through the use of EU-instruments.



- **Recommendations:**

Recommendations are related to the above mentioned weaknesses. The team should give more value to the applied research and that could be mediated through the cooperation projects involving companies working on pest control and using, if possible, EU instruments.



**Team 4:** Integrative Biology of Host-Parasitoid Interactions

Name of team leader: Ms Anne-Nathalie VOLKOFF

### Workforce

Team workforce	Number as at 30/06/2013	Number as at 01/01/2015
<b>N1:</b> Permanent professors and similar positions		
<b>N2:</b> Permanent EPST or EPIC researchers and similar positions	2,7	1,5
<b>N3:</b> Other permanent staff (without research duties)	2,5	2,5
<b>N4:</b> Other professors (PREM, ECC, etc.)		
<b>N5:</b> Other EPST or EPIC researchers (DREM, Postdoctoral students, visitors, etc.)		1
<b>N6:</b> Other contractual staff (without research duties)		
<b>TOTAL N1 to N6</b>	<b>5,2</b>	<b>5</b>

Team workforce	Number as at 30/06/2013	Number as at 01/01/2015
Doctoral students		
Theses defended	1	
Postdoctoral students having spent at least 12 months in the team	4	
Number of Research Supervisor Qualifications (HDR) taken		
Qualified research supervisors (with an HDR) or similar positions	2	1

- Detailed assessments

#### Assessment of scientific quality and outputs

The B2iHP team conducts its research on insect parasitoids and is interested on the molecular mechanisms between the endoparasitic wasps and their insect hosts. Basically, two main fields are investigated to learn more about the parasitism success, including the identification and molecular characterization of maternal virulence factors mainly on the ichneumonid *Hyposoter didymator*, and studying their evolutive origin through different groups of hymenopterans and in collaboration with CNRS national groups. Only few national and international teams are developing this research because of the difficulty to access these non-conventional systems. B2iHP team uses comparative and functional genomics approach to identify candidate genes and to study their function and their impact on the physiology of the lepidopteran hosts. When possible, this team has evolved emerging technologies and concepts, such as the use of sncRNA as possible regulatory elements, and has tackled original questions. The scientific production is excellent (12 papers including one *PloS Pathogens* and one *Science*), taking into account the model



difficulties and the number of people being involved. B2iHP has a solid national collaboration and reputation while it should strengthen international interactions.

### Assessment of the unit's academic reputation and appeal

The B2iHP team is very dynamic both at the national and the international levels, although it should pay more attention to increase its international influence. It has been involved in the organization of two national meetings (ImmunInv08, Entomo12) and is currently working on a REID (Réseau Ecologie des Interactions Durables) network workshop. B2iHP team has also been involved on three ANR projects as a partner, several Inra SPE projects led by the team researchers, and other projects supported by the national Genoscope and the Université Montpellier 2. The team leader has chaired one CAPES/COFECUB project. The team has hosted four post-doc students and supervised one PhD student. Scientific expertise was mainly devoted to review papers and to participate to PhD and HDR evaluation committees. The team leader is also involved in many local, INRA, and national tasks, including the scientific council of the SPE department and the steering committee of the structuring issue "Biological Control".

### Assessment of the team's interaction with the social, economic and cultural environment

The research questions investigated by the B2iHP are academic but target a social and economic issue that is the identification of new methods and potential bio-pesticides to control insects damaging crops. The final objective through the understanding of parasitism efficiency is to select parasitoid traits and strains having detrimental impacts on the lepidopteran pests that cause huge damage on crops. The team members have actively contributed to development of a database for *Spodoptera* and the team leader has contributed to the dissemination of knowledge for educational purposes. Science dissemination and vulgarization is also made through book chapter publication and meetings.

### Assessment of the team's involvement in training through research

The team has supervised four post-doctoral students and one PhD student. They also have welcomed a pre-doc student from Brazil. The team leader has participated to the organization of two national meetings, ImmunInv 2008 and Entomo2012 as the coordinator of the scientific committee.

### Assessment of the strategy and the five-year plan

The five-year project will be focused on *H. didymator* to deeply understand how HdIV encoded proteins impact the Lepidopteran physiology by characterizing host pathways related to immunity and metabolism and to identify elements interfering with these functions. Genes of interest will be further explored with functional studies and extended phenotypes will be checked and characterized. At the evolutionary point of view, the team has previously demonstrated that two viral acquisition events have occurred within the *Campopleginae*. They aim now to further characterize the evolutionary history of virus acquisition within the ichneumonid wasps and to decipher the molecular nature of virus particles within this insect subfamily. Ecologically, B2iHP team intends to uncover how genetic variability of the *H. didymator* virus is correlated with the level of virulence and to identify genes involved in the fitness/virulence traits. While this project is in continuity with the previous one, it will help exploring the genomic and the transcriptomic data accumulated during the previous contract both at the mechanistic and the ecological levels.

### Conclusion

#### ▪ Strengths and opportunities:

- high rank of academic publication including one PLoS Pathogens and one Science paper in collaboration with a team from the Université de Tours;
- good involvement on national congress organization;
- good implication in national thesis, HDR and hiring committees;
- highly dynamic in national collaborations through ANR projects, sequencing projects, INRA projects, national networks, and consortia;
- local responsibility on insect resources and platforms.



▪ ***Weaknesses and threats:***

- weak involvement on education through research (one PhD student only) and socio-cultural initiatives;
- the team leader has already been invited and has attended several international meetings but should improve international influence through collaborations, international congress attending and organization.

▪ **Recommendations:**

The team should focus research on a limited number of models, (ideally one as it is the case in the team project), which will help increasing the efficiency and deciphering the molecular mechanisms that drive parasite virulence:

- strengthening international visibility through the leadership of international projects;
- reinforcing education through research by supervising more PhD/master students, but also by organizing public meetings for science vulgarization;

Now with three researchers (although the team leader will be chairing the lab), the team should increase the amount of papers published in high rank reviews.



## 5 • Conduct of the visit

Visit date:

Start: Tuesday December 17<sup>th</sup> 2013, at 8:30 am

End: Tuesday December 17<sup>th</sup> 2013, at 8:30 pm

Visit site: Triolet Campus, Building 24

Institution: Université Montpellier 2

Address: 2, place Eugène Bataillon, 34095 Montpellier Cedex 5

Specific premises visited: Platform of insect quarantine (building 24)

Conduct or programme of visit:

From 8.45 to 12.15 pm presentation of the unit results (by the head of the UMR), followed by the presentation of results/project of the four teams (by team leaders) and finally presentation of the unit project (by the new head of the UMR).

From 1.30 to 2.00 pm visit of the quarantine insect platform.

From 2.00 to 5.00 pm meeting with the 'researchers, lecturers' group, the 'technicians, engineers, administratives' group, 'PhD students and post-docs' group, the representatives of INRA and UM2, the deputy-director of the ED 'SIBAGHE' and finally the UMR direction (current director, next director and deputy-director).

From 5.00 to 8.30 pm meeting of the experts committee, writing of the report.



## 6 • Supervising bodies' general comments

Le Président

Montpellier, le 28 avril 2014

M. Didier HOUSSIN  
Président de l'AERES

M. Pierre GLAUDES  
Directeur de la section des unités de  
recherche

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Affaire suivie par :  
Ingrid CHANEFO,  
Directrice de la Recherche et des  
Etudes Doctorales

**Objet** : Réponse de l'établissement support au rapport d'évaluation de l'unité DGIMI –  
UMR 1333

Réf. : rapport d'évaluation S2PUR150008444

Messieurs

Je tiens à remercier le comité de visite pour la qualité de son rapport d'évaluation concernant l'unité de recherche DGIMI -Diversité, Génomes & Interactions Microorganismes-Insectes (UMR 1333), dirigée par M. Patrick TAILLEZ.

J'ai bien noté les remarques formulées par le comité de visite et veillerai à leur prise en considération par la future direction de cette structure.

En tant que tutelle universitaire de cette unité de recherche, je ne formulerai aucune remarque supplémentaire

Je vous prie d'agréer, Messieurs, l'expression de mes salutations les plus respectueuses.

Le Président de l'Université Montpellier 2,



Michel ROBERT

Pièce(s) jointe(s) :

Relevé des erreurs factuelles à rectifier dans le texte du rapport  
Observations générales formulées par le directeur



Institut National de la Recherche Agronomique

**Diversité, génomes et interactions  
microorganismes – insectes**

**UMR INRA-UM2« DGIMI » 1333**

**Objet : Réponse au rapport préliminaire AERES de l'unité DGIMI**

Rapport S2PUR150008444 - DGIMI - DIVERSITÉ, GÉNOMES ET INTERACTIONS MICRO-ORGANISMES  
INSECTES - 0342321N

Montpellier, le 25 avril 2014

Madame, Monsieur,

Par ce courrier, je souhaite signaler que nous n'avons pas d'observations de portée générale sur le rapport préliminaire d'évaluation par l'AERES qui nous a été transmis.

Cordialement,

Anne-Nathalie VOLKOFF

DUA, UMR DGIMI

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cc. Mr Patrick Tailliez, DU DGIMI