IPS2 - Institut des Sciences des Plantes de Paris Saclay

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 unit:

The Institute of Plant Sciences Paris-Saclay

IPS2

Under the supervision of
the following institutions
and research bodies:

Université Paris Sud

Université D'Evry - Val d'Essonne - UEVE

Université Paris Diderot

Centre National de la Recherche Scientifique - CNRS

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[1]*,*

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

On behalf of the expert committee,

- Mr Pere PUIGDOMENECH ROSELL, chair of the committee

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[1] 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 assessment contained herein are the expression of independent and collegial deliberation of the committee.

Unit name:	Institute of Plant Sciences Paris-Saclay
Unit acronym:	IPS2
Label requested:	UMR
Present no.:	
Name of Director (2013-2014):	N/A
Name of Project Leader (2015-2019):	Mr Martin CRESPI

Expert committee members

Chair:	Mr Pere PUIGDOMENECH ROSELL, Centre for Research in Agricultural Genomics, Spain
Experts:	Mr François BRIAT, INRA Mr Josep CASACUBERTA, Centre for Research in Agricultural Genomics, Spain Mr Mark COCK, CNRS Mr Pascal GAMAS, CNRS Mr Jean-Pierre JACQUOT, Université de Lorraine (representative of CNU) Ms Cathie MARTIN, John Innes Center, United Kingdom Mr Olivier PANAUD, Université de Perpignan Via Domitia Ms Susana RIVAS, CNRS (representative of CoNRS) Mr Dominique ROLIN, Université de Bordeaux (representative of CSS INRA) Mr Andreas WEBER, University of Duesseldorf, Germany Mr Cyril ZIPFEL, The Sainsbury Laboratory, United Kingdom

Scientific delegate representing the AERES:

Mr Steven BALL

Representative(s) of the unit's supervising institutions and bodies:

Mr Jean-Michel CAMADRO, Université Paris-Diderot

Mr Patrick CURMI, Université Evry Val d'Essonne

Mr Thierry GAUDE, CNRS, INSB

Mr Frédéric GAYMARD, INRA, Département BAP

Ms Sylvie RETAILLEAU, Université Paris-Sud

Ms Jacqui SHYKOFF, Doctoral School n° 145

1 • Introduction

History and geographical location of the unit

The IPS2 emerges from an important restructuration and consolidation of 3 of the 4 Plant Biology institutes involved in the Cluster of Excellence or LabEx SPS "Saclay Plant Sciences". The selection of SPS by an international committee and funding by the ANR emphasize the academic quality and potential for innovation of this cluster. The reorganization of IPS2 will involve the institute of Plant Biology (IBP, Orsay), the Research Unit of Plant Genomics (URGV, Evry) and part of the institute of Plant Sciences (ISV, Gif). The longstanding collaborations and coordination with the fourth institute "Jean-Pierre Bourgin" (IJPB, Versailles) is being reinforced through Labex activities. **The creation of IPS2 is a unique opportunity to ensure the quality and sustainability of the research and teaching activities in Plant Sciences on the Paris-Saclay campus.** The IPS2 will bring together most of the research in **Plant Biology from the Paris-Saclay Campus** with the aim to strengthen its existing potential, by improving the synergies and by creating a higher visibility of Plant Sciences at the national and international levels. It is perfectly in tune with the activities and objectives of the SPS Labex that is supported by 5 institutions; the universities of Paris Sud and Evry, the CNRS, the INRA and the FCS that coordinates the Excellence Initiative of Paris-Saclay. The creation of the IPS2 will integrate around half of SPS members at a single Unit instead of the actual geographical dispersion between three distant locations. The creation of IPS2 is the fruit of important discussions taking into account the future University of Paris-Saclay and the visibility of Plant Sciences in this area. **A variety of indicators of the Idex project shows that Plant Sciences is a major force of the Paris-Saclay Campus** in terms of scientific impact and quality, as well as University teaching at Master and Doctoral levels.

During the discussions that led to this proposal, several options were studied including the possibility that the institute could be located initially at several sites. A large consensus emerged among the project and group leaders and three of the four Institutions (CNRS, INRA and PSud) that gathering the different teams at a single site would be a significant advantage for the visibility, the efficiency, the economy and the development of the project. These Institutions cannot afford the costs of staying at different sites on the long term. Among the different possibilities analysed, the renovation of the "Batiment 630" at the "Saclay Plateau" appeared to be the best solution since it can host all of the potential research groups/platforms (with 5500 m^2 dedicated to research space) and can profit from 2500 m^2 dedicated to training and teaching surfaces. Nevertheless, the building requires important renovation and additional facilities to grow plants (growth chambers, greenhouse space) and to carry out cell biology experiments (confocal, DMI and epifluorescence microscopes). Meetings with permanent staff from the 3 plant units involved (IBP, ISV and URGV) and the creation of several working groups have been carried out to prepare the creation of IPS2 and to identify the renovation and equipment required before the start in 2015. The following working groups have been formed: **"Plant Culture and greenhouses"; "Administration", "Support Functions", "Computing", "Imaging", "GMOs, Radioactivity, hygiene and security"** and **"« omics » platforms"**. These discussions notably established priorities for the building renovation, identified absolute needs not currently available at the Bat. 630, and established priority equipment that must be available and functional before the anticipated start of the IPS2 unit in 2015. This equipment is mainly linked to plant growth facilities (greenhouse space, growth chambers) and cell biology (microscopy). An inquiry for the actual demands (in laboratory and office space, growth surfaces and computing) of all future groups has been requested and will be analysed before the end of the year to establish the best distribution of space for laboratories, platforms (with a capacity to host external users) and teaching facilities.

Management team

The **management of IPS2** will be assured by a "direction committee" composed of a director Mr Martin CRESPI, three vice directors (dealing with infrastructure, human resources and translational biology) and the IPS2 manager or "administrator".

AERES nomenclature

SVE2_LS3 Biologie cellulaire et biologie du développement végétal

Unit workforce

Unit workforce	**Number as at 30/06/2013**	**Number as at 01/01/2015**
N1: Permanent professors and similar positions	25	25
N2: Permanent researchers from Institutions and similar positions	20	20
N3: Other permanent staff (without research duties)	60	60
N4: Other professors (Emeritus Professor, on-contract Professor, etc.)		
N5: Other researchers from Institutions (Emeritus Research Director, Postdoctoral students, visitors, etc.)	19	19
N6: Other contractual staff (without research duties)	18	18
TOTAL N1 to N6	**142**	**142**

Unit workforce	**Number as at 30/06/2013**	**Number as at 01/01/2015**
Doctoral students	26	19
Theses defended	31	
Postdoctoral students having spent at least 12 months in the unit	17	
Number of Research Supervisor Qualifications (HDR) taken	20	
Qualified research supervisors (with an HDR) or similar positions	20	20

2 • Assessment of the unit

The Evaluation committee had the opportunity to hear about the work that the different groups are doing and to discuss with them their current and future research plans. The institutions and the staff, technicians, students and scientists, as well as the Director expressed their views and the committee discussed with them and had some documents that were provided. The analysis of the individual groups is presented later in following sections of the AERES report.

In general terms the committee unanimously agreed that the project to integrate Plant Biology research groups from CNRS, INRA and universities in the same institute in Saclay is an excellent idea that will consolidate this important field in an institute with an international visibility. As the institutions confirmed their commitment with the project, the committee recommends that actions are taken as soon as possible to start the adaptation of the building to its new functions.

Strengths and opportunities related to the context

The IPS2 presents the opportunity to integrate groups working in the study of plant growth and development in relation to both biotic and abiotic environment, and, therefore, has a strong potential to become an important institute for Plant Science at the European and international level.

In the IPS2, groups working in basic science and in translational research will coexist. It is therefore an original initiative to explore applications of the results produced by basic research and to generate new ideas taking into account the needs of farmers and breeders.

The institute will integrate scientists working full-time in research and professors from three different universities in the Paris area. This fact will create a unique opportunity to become a major pole of attraction for higher education in Plant Sciences.

Presently two well equiped platforms exist devoted to functional genomics and metabolomics.The new institute will offer the opportunity to further develop these technological platforms in efficient services to scientists inside and outside the institute and will enable optimising infrastructures in a field that is quickly adopting new methodological approaches.

The institute has already a large, strong and dynamic community of technicians, engineers, students, researchers and professors with a competent and highly motivated proposed director. They have the elements necessary to develop their scientific program at the international level.

Weaknesses and threats related to the context

The project displays at this point logistic and financial questions requiring clarification notably with respect to funding. It is still not clear for instance in what conditions at the different levels of staff (for example technicians) will work in the new institute.

The infrastructures of the new institute are presently not adequate, starting with the building that needs renovation and facilities including growth chambers and greenhouses. If the institute wishes to attract top class scientists, these aspects should be solved as fast as possible.

Recommendations

For the project to start with a sufficient level of credibility, the renovation of the building must start as soon as possible. The project has to be clear to everyone. It should include sufficient space for laboratories and offices and some common space dedicated to interaction of IPS2 members, especially students and postdocs. A budget for equipment is also necessary, mainly for growth chambers and greenhouses, as well as image acquisition and analysis (confocal microscopy).

Both Institutions and the proposed Director should inform continuously the IPS2 members of the state of advancement of the project, in order to maintain their motivation for the new project they are involved in.

The new institute should ask their Funding Institutions and (or) agencies to appoint an external Scientific Advisory Board that will be consulted for the essential scientific decisions taken. It could meet every year and should start as soon as possible.

The transcriptomic and metabolomic platforms should be restructured in order to offer full service to the whole community. They need clear rules for access and management and must meet IBiSA platform recommendations. The same principle can be applied in the case of the newly proposed “Translational Department” and “Axe Biological Networks”. The existence of groups working in these directions and collaborating with groups of the institute will be enough to influence the work of all of them in these two important directions, without creating any new structure.

The informatics and bioinformatics infrastructure should be reconsidered from scratch. The need for storing data and for informatic treatment of genomic, transcriptomic and metabolomic data and from image analysis will most probably require an increasing access to computing facilities and specific sotfware.

The new institute must have the best possible relations with neighboring centers such as IJPB in Versailles, using the framework of the SPS program but also with Plant Biology groups at the I2BC, Le Moulon Centre where groups are working in plant breeding and with INRIA in informatics. Sharing plant growth facilities, instruments for genome and image analysis and bioinformatics will be necessary in the coming years.

The recruitment of new groups formed around young scientists of international quality working in novel approaches of Plant Science should be actively explored. Building an attractive scientific, teaching and technological environment is an essential requirement for the success of such actions.

3 • Detailed assessments

Assessment of scientific quality and outputs

The scientific production of the different groups is excellent and the evaluation of the individual projects is presented later. The evaluation of the work done by different groups ranks from excellent to outstanding. The outputs are not only publications in high ranked international journals but also materials and tools (databases or patents for instance) that are or could be of interest for industry. Several of the teams are recognized international leaders in their fields.

Assessment of the unit's academic reputation and appeal

The new institute belongs to the only Doctoral School specifically devoted to Plant Sciences in France (Doctoral School n° 145). It has the potential of becoming one of the major poles of research in Plant Biology in France and the major one, together with IJPB in the Paris area, especially if it efficiently cooperates with the surrounding universities and research Centres.

Many of the members of the new Centre have already an international recognition and there is an excellent opportunity to place IPS2 as an attractive place at the international level for training in Plant Sciences. Importantly, the Doctoral School has already set up strong connections with some of the best European Doctoral Schools in Plant Sciences, which is an excellent initiative and a clear asset for the future.

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

The Units that constitute the new institute have an excellent reputation for their facilities and scientific standards and some of the groups already have a strong interaction with industry. This may be used as an entry point to strengthen the interaction with society in general. Moreover, some IPS2 members have been very active in public debates, notably regarding GMOs.

Assessment of the unit's organisation and life

The institute will have around 110-120 permanent personnel (around 50 researchers from universities, INRA and CNRS) of which 2/3 will be in the 12 research groups and 1/3 will be in support functions.

The **management of IPS2** will be assured by a "direction committee" composed of a Director, three Vice Directors (dealing with infrastructure, human resources and translational biology) and the IPS2 Manager or "Administrator". This group will reach decisions based on discussions and proposals of different committees: "Conseil de Laboratoire" and "Conseil Scientifique". The "Conseil de Laboratoire" is the place to debate and propose solutions for all aspects of the institute's life (career evolution, technical choices, information exchanges between the personnel, day-to-day functioning of the Unit). It is composed of elected and nominated members representing the entire personnel of the Unit according to French legislation. The "Conseil Scientifique" will play a major role in debating the scientific perspectives of the Unit (evolution of research teams, incorporation of new teams, scientific activities and meetings, technical demands) and will be formed by all group leaders, the direction committee and it will also include 2-4 members elected by the personnel that are interested to contribute to the scientific life of IPS2. The organization of the work within the teams will be carried out by the group leaders, having a key role in the management of the laboratory and, through the participation in Department Meetings and the "Conseil Scientifique", they will highlight issues related to research programs. All group leaders will interact directly with any member of the direction committee to address any matters dealing with administration or infrastructure to be discussed in the monthly meetings of the "Comité de direction". The Department Directors will have mainly a scientific role by organizing periodic meetings of the department where PhD students and other non-permanent personnel will present and discuss their work. They will also name a representative of the Department for the "Comité technique" to indicate functioning or other problems linked to the research demands of the different groups. Finally, Department directors will be in charge of discussing PhD projects and ANR projects with the "Comité de direction". The "Comité technique" will address the maintenance and functioning of the building and the interaction with the teams and will include personnel from the support staff dedicated to infrastructures, the Administrator, a Vice director, and one representative per Department. These committees will interact with the direction committee to propose priorities based on their different areas of competence and thus help in the final decisions to be made for the Unit.

The definition of an organisation of the new institute is not finished. It has nevertheless already some elements of its structure established with three Departments that have been formed on a voluntary basis. Many details will need to be worked out but a strong leadership exists at the institute’s future Management, and it needs to be supported by the Institutions (CNRS, INRA and universities) to perform its mission at best.

Assessment of the unit's involvement in training through research

The groups have a number of students at the postgraduate level. The students are part of two Doctoral Schools (Ecole doctorale n°423 des Génomes Aux Organismes (GAO) and Doctoral School n° 145 Sciences du Végétal (SdV)) . This is the only institute in the Paris area teaching Plant Biology. Supervisors are recommended to take care of the publication record of their students, a factor that may have important consequences for their future.

Assessment of the strategy and the five-year plan

The organizational project of the institute is not yet finished, but it is on the good track and will become an outstanding research Centre in the future. The direction, in conjunction with scientists, staff and Institutions should continue working on the basis of the present structure with eventually the assistance of an external Scientific Advisory Board.

4 • Team-by-team analysis

Team 1 :	Signalling pathways controlling legume root system development
Name of team leader:	Mr Florian FRUGIER

Workforce

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

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

• Detailed assessments

Assessment of scientific quality and outputs

The group "Signalling pathways controlling legume root system development" is using *Medicago truncatula (Mt)* as a model to decipher genes and signalling pathways involved in root and nodule development under normal and salt stress conditions. Forward and reverse genetics, as well as bioinformatic and transcriptomic tools are used for this purpose and the resulting output can be considered excellent.

Original data reported by the group concern the role played by the cytokinins (CK) in these pathways. In particular, a CRE1 CK receptor, a RR *cis*-element and two transcription factors, one of them being post transcriptionally regulated by a miRNA, were characterized. Transcriptomic analysis of meristems from *Mt* reference, *cre1*, and salt tolerant genotypes, coupled with reverse genetics analysis of candidate genes were performed. It enabled to characterize two transcription factors involved in the regulation of root architecture in response to salt stress, and to nodule senescence responses.

Over the period 2008-2012, the group has published 2 book chapters and 21 papers in peer review international journals, including 3 Plant Cell, 3 Plant J, 1 Mol Plant, 1 New Phytol, 1 Plant Physiol, 1 J Exp Bot, 1 Trends Plant Sci.

Assessment of the team's academic reputation and appeal

This research group achieved an excellent level of recognition in its field. It gives ten invited lectures to meetings (2 national and 8 international). It has an important local (with at least 3 other groups of IPS2), national (Dijon, Montpellier, Toulouse) and international (Germany, Belgium, Italy, UK, Spain, Hungary, China, Australia, USA, South Korea) network of collaborations. Some of these collaborations are funded by international programs (ANR KBBE, EC FP7) or bilateral exchanges (Italy, China). The group was also successful to obtain competitive grants both at the national (ANR) and EC levels.

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

Team members are conducting basic research, and are not mentioning any interactions with the economic or social environment. Joining the IPS2 project which aims at facilitating translational research should make the team more open to initiate project(s) on legume crops.

Assessment of the team's organisation and life

This research group started to exist 5 years ago and its organisation and management by the PI have proven to be efficient, as attested by its ability to raise funds, to develop national and international networks, to train graduate students and to publish results in the highest ranking Plant Science journals.

Assessment of the team's involvement in training through research

Two post-doc, 1 ATER, 5 PhD students and 10 "Master" level students were trained during the last period. Furthermore, three members of this research group belong to the University, and therefore the group as a whole has a strong commitment in teaching (800 hours / year, essentially at University of Paris 7 in Licence and Master levels). In addition to teaching *per se*, members of the group are involved in the management of a teaching department, and in the teaching and funding committees of a doctoral school (ED 145). The group is therefore very active in training and teaching activities.

Assessment of the strategy and the five-year plan

The research project of the group will follow up on previous research lines with the main objective of integrating the regulatory cross-talks which contribute to adapt *Mt* root architecture to environmental constraints.

An in depth analysis of the CK pathway and of the CK / flavonoid cross-talk which potentially affect auxin transport will be performed. The impact of various biotic and abiotic (including N starvation) stresses on the pathways regulating the root system development will also be scrutinized.

The project is sound. However, although collaborations are well identified the number of stress conditions that will be considered is too high and these aspects of the project would deserve to be more prioritized. Also, concerning the signalling role of flavonoids, it should be considered that a paper (Li et al, 2010, Plant Cell, 22:1620-1632) ruled out this possibility. Consequently this part of the project needs to be reconsidered.

Conclusion

The overall quality of this “young” group ranks from very good to excellent with an outstanding involvement in teaching / training activities. It has proven by the past to be attractive and able to raise funds for producing first rank papers in the field of Plant Sciences.

- **Strengths and opportunities:**

The group has in hand tools to study cross talks of pathways involved in stress responses and root system architecture. It has therefore the opportunity to be involved in a hot topic at the international level, and consequently to participate in front science programs.

- **Weaknesses and threats:**

Many stress conditions are considered in the project. Although some of these stresses will be studied in collaborations, the group should be careful to not spread their efforts thin in too many directions. It is even more critical due to the fact that (i) a strong percentage of permanent scientists are University teachers with time consuming teaching duties, and (ii) the international competition in this field of research is high.

- **Recommendations:**

We would recommend for the next contract (i) to be careful to rank the various programs according to research priorities, in particular concerning the high number of stresses considered (ii) to reinforce the group by attracting full time researcher(s) (iii) to try to publish part of the work in top “multidisciplinary or more general biology” journals, outside from the strict “Plant science” field, in order to extend the visibility of the group, and (iv) to consider to initiate project(s) on legume crops.

Team 2 : Regulatory non-coding RNAs in root plasticity

Name of team leader: Mr Martin CRESPI

Workforce

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

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

• Detailed assessments

Assessment of scientific quality and outputs

The group “Regulatory RNAs in root developmental plasticity” investigates the regulatory mechanisms involved in root architecture using a combination of cell biology, genetic, genomic and molecular approaches.

During the last few years, the group has identified several regulators of root development in *Medicago truncatula*, including the salt-induced receptor-like kinase MtSRLK1, the RNA-binding protein MtRBP2, and bHLH, NAC and MtRR1transcription factors. In addition, the mechanism of action of long and small non-coding RNA riboregulators in *Arabidopsis thaliana* and *Medicago truncatula* root growth and development, as well as in response to biotic and abiotic environmental cues has also been investigated. The group has uncovered a variety of non-coding RNAs that, through the interaction with RNA-binding proteins, modulate the expression of various regulatory genes, encoding transcription factors and DNA methylases, involved in the developmental adaptation of the root system to the environment.

Over the period 2008-2012, the group has published 35 papers in peer-reviewed international journals, including 4 Plant Cell, 1 Genome Res, 4 Plant J, 1 New Phytol, 1 Plant Physiol, 1 EMBO J, 1 Trends Plant Sci, 1 Sci Signal,...

Based on these facts, the quality of the scientific production and approaches is excellent.

Assessment of the team's academic reputation and appeal

The attractiveness of this group is excellent. The group (mainly the group leader) has been frequently invited as speaker in scientific conferences (10 national and 25 international) and has also participated to the organization of 4 international workshops. The group leader has established successful local (Versailles, Evry, Gif sur Yvette, Orsay), national (Dijon, Cadarache, Toulouse) and international (Argentina, Germany, Belgium, Spain, Brazil, Portugal) collaborations. The group has obtained competitive grants [local (Labex SPS), national (ANR) and international (KBBE, FP7-EEC)] that, in some cases, fund these collaborative projects.

The group leader is “Chargé de Mission” for the CNRS (Integrative Plant Biology Section; assistant to the INSB Deputy Director in charge of this section), representative of EPSO, member of evaluation committees of (national and international) research institutes, peer reviewer for scientific journals and (national and international) research agencies. In addition, he is co-responsible (together with the SPS Director) for the IPS2 project (coordination of different tasks and funding applications) and applies to become IPS2 director.

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

Social/economic integration of the group is rather weak (for instance, one lecture by one team member at the University Paris VII) and it should be improved in the future by the development of translational research and diffusion of acquired knowledge into the general public.

Assessment of the team's organisation and life

The composition of the team has greatly changed in 2010 with one permanent staff member (CR1 CNRS) joining the University of Heidelberg to start his own group and a second permanent staff member (DR2 CNRS) quitting the team to start his own group and being joined by 3 additional permanent staff members (PR2 Paris VII, MdC Paris VII and AI CNRS).

Assessment of the team's involvement in training through research

Over the period 2008-2012, 6 post-doc, 3 ATER, 6 PhD (ED 145), 13 Master students and 10 foreign visiting workers were trained.

One group member is a Professor and two members are Lecturers at the Univ. Paris VII, and therefore strongly involved in teaching-related activities (192 hours per year each). In addition, they are responsible for 2 Master programs (Univ. Paris 7 and Paris 11) and a Licence course (Univ. Paris Diderot). Finally, one of them is member of the Labex SPS Training committee.

In summary, the implication of the group in teaching and training activities is outstanding.

Assessment of the strategy and the five-year plan

The proposed project builds on previous research with the major goal of understanding the role of ncRNAs in determining root plasticity in *A. thaliana* and *M. truncatula*. Two major research questions will be addressed. First, the natural diversity of ncRNAs will be analysed (genome-wide ncRNAs evolution and polymorphism) and correlated with phenotypic diversity in response to low phosphate (*A. thaliana*) and low nitrate/rhizobial symbiosis (*M. truncatula*). Second, the group will investigate regulatory mechanisms of root organogenesis involving ncRNAs [(i).24 ntsiRNAs during epigenetic regulation of symbiotic nodule formation, and (ii) lincRNAs that control *Arabidopsis* lateral root formation by modulating the pattern of alternative splicing].

The group leader is an expert in the field and the project is based on previous work which led to solid results, high ranking publications and the establishment of important collaborations both nationally and internationally. The quality of the proposed research project is therefore excellent.

Conclusion

The group has solid expertise in the study of developmental mechanisms involving ncRNAs and the proposed research project is sound.

- **Strengths and opportunities:**

The group has developed a significant number of experimental tools and established key national and international collaborations that should contribute to the success of the proposed research programme. The team has also been successful in raising funds to support ongoing research.

- **Weaknesses and threats:**

The group has lost a significant number of permanent staff members in 2010 (1 DR2 CNRS, 1 PR2 Paris7, 1 MC Paris7, 1 AI CNRS, 1 CR1 CNRS). Moreover, the only full-time researcher is the group leader, who is actively involved in a variety of tasks related to research management and administration and, importantly, has also applied to become IPS2 director. The remaining three permanent staff members are actively involved in teaching. All this may have a negative impact on the scientific production in the coming years, especially considering that the research topic is highly competitive at the international level.

- **Recommendations:**

Considering the weaknesses indicated above, strategies should be implemented that would enable the team to hire one or more permanent scientists. In addition, identifying crucial topics to focus on and setting priorities with respect to research activities is also recommended.

Team 3 : Cell Cycle Chromatin and Development

Name of team leader: Ms Cécile RAYNAUD/Mr Moussa BENHAMED

Workforce

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

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

• Detailed assessments

Assessment of scientific quality and outputs

The group has been working on the analysis of the factors that control the transition between cell proliferation and differentiation, under normal or stress conditions. Their model system is *Arabidopsis thaliana* (although they also used *Physcomitrella patens* for specific purposes) and they combined genetic approaches with cytology and flow cytometry, as well as transcriptomic analyses. The group worked on various subjects with connexion to the central objective of the team. These included the analysis of the regulation of S-phase onset, of the factors governing transition from cell proliferation to differentiation, as well as studies on the control of programmed cell death by the myo-inositol pathway. In spite of the diversity of subjects studied, and the dispersion of efforts this implies, the team managed to obtain interesting data and publish the results obtained. Of particular relevance are the results showing the implication of CDT1 proteins in genome integrity and the role of KRP5 in controlling chromatin structure. These recent results are the basis of the recent focus of the team on the control of cell cycle and associated chromatin remodelling, which has already produced interesting results and high quality publications.

The present members of the team have published several book chapters and 15 articles in the 2008-2013 period, including 2 Plant Cell, 1 New Phytologist, 1 Mol Plant, 1 Plant Physiology, 1 NAR, as well as others published by present members of the team in their former laboratories.

Assessment of the team's academic reputation and appeal

The group is well recognized in its field and has collaborations both with French research groups and some of the leading international teams in the field. They have participated in a number of international meetings and have been invited to give lectures in French and foreign laboratories. The team members act as reviewers for a number of high quality scientific journals and have participated in a high number of PhD and HDR jurys as well as national and international research project calls.

The group has been successful in getting local (IFR) and National (ANR blanc, ANR Jeunes Chercheurs) grants and ressources.

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

Members of the team have given many conferences on social issues related to plant sciences, such as GMOs, for example at Sciences Po (Paris), and participation in TV shows and public debates. Members of the lab also participated in the " Fête de la science" and "plant fascination day" regularly. One group member has also a contract with a private company, "Arvalis".

Assessment of the team's organisation and life

Although there is no specific information on this point in the dossier, the comparison of the past and proposed teams shows that it has been heavily remodelled in the last few years. These changes include a change in the leadership that is now shared by two scientists with complementary expertise. The focus of the team project has also been modified to include a new interest in chromatin.

Assessment of the team's involvement in training through research

The members of the team are strongly involved in teaching activities. Half of the team scientists have a Faculty positions. In addition to their teaching activities, scientists of the team coordinate PhD (Plant Sciences 145) and MSs (Plant sciences) programs. They also coordinate a network project for Plant Sciences teaching in the Paris area and they are leading an effort to extend this initiative to several EU universities.

The group includes at present three PhD students and two Postdocs, and has trained 3 PhD students, 3 M2 students, 1 L3-M1 student and 3 BTS student during the 2008-2013 period.

Assessment of the strategy and the five-year plan

The team has been heavily remodelled in the recent past, with an important fraction of the team leaving and several scientists joining the team. These changes have been accompanied with a reorientation of the scientific project of the team. The objectives of the team continue to be centered on the analysis of the control of cell cycle, but with two major projects and a particular interest in the interaction between cell cycle control and chromatin modifications. More specifically they propose to study the function of the interaction of CDT1 with Pol έ, and second, to explore the function of BAF60 and SWI/SNF proteins in the control of cell cycle progression. This important change in the composition and strategy of the group can be seen as a risk in a highly competitive field. However, the group has already published a number of articles in high quality journals in the last two years that seem to validate the strategy; it has defined an original niche which perfectly fits the expertises of the team member, and importantly it benefits from collaboration with some of the best international teams in the field. This group will also benefit from the IPS2 environnment, with collaborations with several teams.

Conclusion

- **Strengths and opportunities:**

The team has been substantially remodelled and has incorporated two new young scientists. The team is very dynamic, has complementary skills and expertises, as well as excellent collaborations. Its competence on chromatin structure analysis will be particularly valuable to continue or develop collaborations with other IPS2 teams.

- **Weaknesses and threats:**

The project proposed requires developing first a delicate technique to get access to specific cell types (Task 1). This could be considered as a threat, but the team has a backup plan with another technique that is already mastered by the group.

Team 4 : Translational Research Group

Name of team leader: Mr Abdelhafid BENDAHMANE

Workforce

Team workforce	Number as at 30/06/2013	Number as at 01/01/2015
N1: Permanent professors and similar positions	1	1
N2: Permanent EPST or EPIC researchers and similar positions	3	3
N3: Other permanent staff (without research duties)	3	3
N4: Other professors (PREM, ECC, etc.)		
N5: Other EPST or EPIC researchers (DREM, Postdoctoral students, visitors, etc.)	3	3
N6: Other contractual staff (without research duties)	5	5
TOTAL N1 to N6	15	15

Team workforce	Number as at 30/06/2013	Number as at 01/01/2015
Doctoral students	3	
Theses defended	4	
Postdoctoral students having spent at least 12 months in the unit	8	
Number of Research Supervisor Qualifications (HDR) taken	2	
Qualified research supervisors (with an HDR) or similar positions	2	2

• Detailed assessments

Assessment of scientific quality and outputs

The translational research team leaded is well known at both national and international levels in the field of plant genetics. The major discovery of the team was the cloning and characterization of sex determinism genes in melon. The 2 papers published in Nature (2009) and Science (2008) by the team (full leadership -first and last author) speak by themselves, regarding the very high academic level of this past achievement. The team authored or co-authored a total of 37 articles in the last 5 years, which is another strong indicator of scientific excellence.

The team is also known for the development of TILLING platforms, which have fueled many fruitful collaborations, as shown by the many high profile papers where members are co-authors.

Assessment of the team's academic reputation and appeal

The team is one of the most dynamic in the field in France. The number of collaborations at both national and international levels is a good indicator of its reputation and appeal. So is the co-authorship of the team leader of an article in Annual Review of plant biology (not many french researchers have co-authored publications in this journal).

The total of external funding received by the team in the 5 years period is ~7000 k€.... (37 projects in total). In addition, the PI of the group received a senior ERC grant of 2500 k€ for the period 2014-2019.

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

The group has achieved an outstanding level of interaction with the private sector. Among the 37 projects mentioned above, 13 involved a partnership with private seed companies (more than 10).

Assessment of the team's involvement in training through research

The team has been involved in doctoral (7 PhDs) and post-doctoral (8 post-docs) training. The PhD students are directly involved in the high profile publications of the team (2 are first authors of the Nature and Science papers). As a team, the involvement in teaching is not very high, although there is a full professor from UEVE strongly committed in both teaching and research.

Assessment of the strategy and the five-year plan

The strategy proposed for the 5 years period is to develop both basic and applied aspects of the study of sex determinism in Plants. From a fundamental point of view, the team endeavours deciphering the genetic, cellular and physiological networks that lead to the development of male and female flowers (in cucurbits, solanaceae and Arabidopsis). From an applied point of view, the objective is to engineer new parthenocarpic crops. The team also proposes to create a translational research platform with the objective of creating new "ideal plant prototypes" which will provide an added value to IPS2.

Conclusion

- **Strengths and opportunities:**

Probably one of the best teams in France when scientific production, attractiveness and interactions with both public and private sectors are considered.

- **Weaknesses and threats:**

Project potentially too ambitious, in particular if team members are asked to devote significant part of their time to the horizontal activities of the translational research department.

Team 5 : Genetic Control of the symbiosis

Name of team leader: Mr Pascal RATET

Workforce

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

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

• Detailed assessments

Assessment of scientific quality and outputs

This group's work focuses on plant-Rhizobium interactions, in particular the establishment of the identity of root nodules and the mechanisms that prevent the plant from mounting an immune response in the presence of the bacterium. The group has made a significant investment in the establishment of a retro-transposon-based insertion mutagenesis collection. Analysis of mutants derived from this collection has allowed the identification of genes involved in symbiotic immunity and nodule identity. A PhosphoInositol-PhosphoLipase C-XD-containing protein and a cysteine-rich receptor kinase have been implicated in two independent pathways involved in suppressing the immune response. The analysis of NOOT loci suggests that aerial developmental genes may have been recruited to suppress root identity in the nodule. The group has also been involved, through collaborations, in the analysis of developmental mutants and in a study aimed at understanding how plant root exudates affect root-associated microbial communities.

During the period 2008-2012, the group produced 12 primary publications, including five reviews and book chapters, plus 30 additional secondary publications (secondary authorship) in collaboration with other groups. The primary publications include 1 Plant Cell, 1 New Phytologist, 1 Plant Physiology and 1 PLoS One.

Assessment of the team's academic reputation and appeal

Investment in the transposon insertion mutant collection has allowed multiple international collaborations to be established and has been an important factor in enhancing the international visibility and attractiveness of the group. During the period 2008-2012, the group leader gave six invited talks at meetings, five of which were international including two International meetings on Legume Genetics and Genomics. The group has hosted three visiting scientists (from New Zealand, Russia, Egypt - each for two months) and one UNESCO-L'Oréal postdoctoral fellow (2 years). The group was involved in the organisation of four conferences and workshops at the national level. The group coordinates a Franco-Russian PICS project and an international ANR project (Legumics) and is involved in two additional, national ANR projects. No information was provided regarding work for journals.

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

The group is conducting basic academic type research with little translational activities.

Assessment of the team's organisation and life

The group consisted of one scientist, one technician, one postdoc and two PhD students at the beginning of the previous contract, and currently consists of two scientists, one technician, one contract technician and two Masters students. During the contract, the group therefore gained one scientist and lost one technician and the contracts of three PhD students, two postdocs, three visiting scientists, two contract technicians and three master students were completed. Although relatively small, the size of this group has remained stable over time. No information was provided concerning the management of the group.

Assessment of the team's involvement in training through research

The group trained four PhD students and three Masters students during the previous contract and currently has two second-year Masters students. In addition, the two full-time researchers regularly do several hours of teaching at Masters level (15h in total, 2008-2012).

Assessment of the strategy and the five-year plan

The proposed project will be a continuation of the current work on symbiotic immunity and nodule identity. For the symbiotic immunity aspect, the group proposes to investigate "nodule immune status (NIS)" by comparing nodules with roots and looking at the effects of the symbiotic bacteria and nitrogen fixation. The effects of a complex rhizospere will also be taken into account. This approach will use both existing and newly identified mutants. The concept of nodule immune status needs to be more rigorously defined but this is expected to emerge from the studies carried out within the project.

The nodule identity part of the project will concentrate on understanding the functions of the two NOOT genes identified by the group and will involve multiple approaches including the use of mutant plants, double NOOT mutants, reporter constructs and transcriptomics and the identification of NOOT protein interactors. The aim is to characterise signalling pathways and identify downstream targets of these genes (including studying candidates such as TGA transcription factors and NPR1-like proteins).

Overall, the project builds on interesting mutants identified by the group during the previous contract and has the advantage of being focused but the project lacks ambition for a five-year project and no timeline is provided for the planned work.

Current collaborations, including work on-site with three groups at Gif-sur–Yvette and Orsay and with other French groups, will be maintained. A new collaboration will be established with the ”Stress signalling” group (Team 11) to work on MAPKs and CDPKs. The group will reduce the number of collaborative projects outside the scope of their proposed project, compared to the last research contract.

Conclusion

This group has carried out excellent quality research on its own research topics and has used the development of an insertion mutagenesis resource to very effectively establish additional collaborative projects.

- **Strengths and opportunities:**

The group has an excellent publication record and the project builds on solid, mutant-based approaches developed during the previous contract.

- **Weaknesses and threats:**

A large proportion of the papers published by the group correspond to collaborative projects led by other groups. Whilst this activity has been important in terms of generating publications, given the small size of the group, care should be taken that this activity does not negatively affect work on the group's own research topics. The project is feasible on the whole but lacks clear, long-term planning and could be more ambitious.

- **Recommendations:**

The group should carry out an in-depth reflection about the long-term objectives, within a five-year perspective. A clear strategy is also needed to reinforce the group, particularly in terms of PhD students and post-docs. It may also be beneficial to develop collaborations at the international level directly related to the group's research project.

Team 6 :

Genome Dynamics and Pathogen Resistance

Name of team leader:

Ms Valérie Geffroy

Workforce

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

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

• Detailed assessments

Assessment of scientific quality and outputs

This group is interested in the evolution of NBS-LRR genes that constitute the major class of resistance (*R*) genes, and uses mostly the legume crop *Phaseolus vulgaris* (common bean) for their research. They have studied several NBS-LRR loci (namely *Co-x*, *Co-2* and *B4*) that are associated with resistance of the common bean to the fungal pathogen *Colletotrichum lindemuthianum*. The *Co-2* and *B4* loci contain large clusters of NBS-LRR genes. Notably, phylogenetic analysis between the two loci revealed that many of these NBS-LRR genes are related, suggesting that they evolved through ectopic recombination. Indeed, sequence comparison identified a subtelomeric satellite repeat, named *Khipu*, that is interspersed between NBS-LRR sequences. This repeat is specific to the *Phaseolus* genus and is present in most *Phaseolus* subtelomeric regions. An additional centromeric repeat, *Nazca*, has also been identified.

Despite the small size of the group and the non-model crop studied (common bean), the group has been very productive over the period 2008-2013. It produced a total of 20 publications, including 9 primary publications. The primary publications have been published in New Phytologist, Plant Physiology, Theoretical and Applied Genetics, Molecular Genetics and Genomics, Frontiers in Plant Science, Functional Plant Biology, Genetics and PLoS One. Given the 'non-model' status of common bean, the publication of some of these studies in generalist journals or top plant-specific journals clearly reflects the excellent nature of the research performed by this group. Notably, the group has recruited 2 MCFs who have a good publication track-record and who have expertise very well-aligned with the objectives of the group for the proposed projects in the next cycle.

Assessment of the team's academic reputation and appeal

The group attracted funding from diverse sources generally as coordinator (INRA, IFR86, ANR (as participant), Genoscope and IDEEV) during the period 2008-2013, but the total amount (134,000 euros) could be seen as rather low. The group is well-connected internationally and directly participates in current efforts in legume genomics. This is directly reflected by past and future joint-publications with different laboratories abroad. The visibility of the team leader is reflected by invitations to give lectures at major international conferences, such as the International Meeting on Legume Genetics and Genomics (2010, 2012), and to present a Plenary Lecture at the forthcoming International Congress on Molecular Plant-Microbe Interactions (2014), which is the most important conference in the field of plant-microbe interactions.

In addition, the team leader is a member of the Editoral Board for the journal Frontiers in Plant Genetics and Genomics, frequently reviews manuscripts for international journals (including New Phytologist, Theoretical and Applied Genetics, and BMC Genomics), as well as national (e.g. INRA) and international (e.g. BARD) research proposals. She is also involved both nationally and internationally in the organisation of conferences (Vth Internation Congress on Legume Genetics and Genomics; 8ème Colloque de la Societe Francaise de Phytopathologie).

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

The group has apparently some contacts with the industry (Clause and Vilmorin), but no specifics are given in the report. The team leader is a member of the scientific committees of IBP and IDEEV. One IE is responsible of equipment at IBP.

Assessment of the team's organisation and life

The group consists currently of one full-time researcher (with a HDR), two researcher-teachers (MCFs) (NB: one is currently preparing the HDR), two research assistants, and one PhD student who will finish his PhD in 2014. While it is mentioned that the group hosted four Master students, it is not possible to judge from the information provided if any of these students is still present. During the period 2008-2013, two PhD students defended successfully (in 2010 and 2011, respectively).

The group never had any post-doctoral scientists. This is an issue to address.

No specific information is provided on how the group is organised, but it is likely that the HDR currently prepared by one MCF may enable the group to host more students.

Assessment of the team's involvement in training through research

The group trained two PhD students and four Masters students during the period 2008-2013, and currently has one PhD student. The group has two researcher-teachers (MCFs) teaching at the University Paris-Sud, and the team leader is teaching ~10h/year at the Master level at the universities of Paris Sud, Paris 6 and Paris 7. One MCF is involved in continous training programmes for the UMR 8618 and for the doctoral school ED145.

Assessment of the strategy and the five-year plan

Based on their previous work on NBS-LRR evolution and repetive sequences, the group proposes in a first objective to study in more details the role of repetitive genetic elements, chromosomal organisation and epigenetic-based regulations on *R* gene varability and expression. This will first involve some 'upstream' work required to gather more genomic, genetic and cytogenetic data on NBS-LRR genes in *Phaseolus* and more specifically on *Khipu* repetitive sequences, as well as on the *B4* and *Co-2* loci. This will be complemented by studying the evolution of the repetive sequences *Nazca* on a short-time scale. In a major second objective, the group proposes to study how pathogen infection affects meiotic recombination and small RNAs. The work on somatic recombination will be performed in both *Phaseolus* and *Arabidopsis* making use of previously published materials available through a collaboration with the group in Versailles (IJPB) working on meiotic recombination.

A third objective is focused on developing virus-induced gene silencing (NB: *Phaseolus* is recalcitrant to plant transformation) to identify the responsible gene(s) present in the *Co-x* locus underlying resistance to C. *lindemuthianum*. The succesful development of this technique will have obvious significant impact on the public and private legume community beyond the specific interests of this group and beyond the field of plant-microbe interactions.

The group is already involved in national and international successful collaborations, and has identified novel collaborations that could direcly benefit the proposed projects. It is not yet clear why the collaboration with the Plateform PAPPSO at INRA Le Moulon on phosphoproteomics is proposed. Regarding the proposed work on the impact of pathogen infection on small RNAs, collaborations with local groups (at ENS Paris) working on similar questions in model plants could also be beneficial. Similarly, the proposed work on NBS-LRR evolution, small RNAs and the *Co-x* locus should be accompanied by 'effectoromics' and comparative genomics between different C. *lindemuthianum* strains to identify the actual effectors secreted by C. *lindemuthianum* and that affect the processes studied.

Conclusion

This group has carried out excellent research in the period 2008-2013 despite its small size and the challenging nature of the crop model studied.

- **Strengths and opportunities:**

The proposed projects for the future cycle clearly capitalises on the strengths and expertise of the researchers in this group.

The group is well-postioned to make major discoveries on NBS-LRR evolution and to identify R genes *against C. lindemuthianum* in *Phaseolus*.

- **Weaknesses and threats:**

The questions addressed are major questions in biology (which is good), but this also means that many other groups may address these questions as well (and maybe more efficiently) in Arabidopsis or in other legumes that are better models (e.g. *Medicago*). It is clear that the group has a competitive advantage as they identified *Phaseolus*-specific repetitive sequences, but they should be aware of these potential issues and think carefully about which plant species is best to address which specific scientific question.

- **Recommendations:**

Possible recommendations could include:

1) develop additional collaborations related to small RNAs and potential effectors of *C. lindemuthianum* ;

2) recruit addtional full-time scientists; optimally this should include PhD students and post-doctoral scientists (no real need to have more permanent scientists). The latter could be achieved by making efforts to attract more long-term funding in order to tackle succesfully the many interesting questions addressed ;

3) develop links with industry.

Team 7 : Functional genomics of secondary metabolism in monocots-microbes interactions

Name of team leader: Ms Marie DUFRESNE

Workforce

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

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 unit		
Number of Research Supervisor Qualifications (HDR) taken	2	
Qualified research supervisors (with an HDR) or similar positions	2	2

• Detailed assessments

Assessment of scientific quality and outputs

The output of the team over the review period has been very good. The focus up until now has been on studying the roles of plant glycosyl transferases in pathogenesis, of crop and model plants. The team has published a significant number of papers on the relationship between secondary metabolism and plant pathogenesis, in both models and crops. These publications have been in medium impact journals. The director of the team is due to retire within the forseeable future. To mitigate against this, and to ensure the continued productivity of the research, a new team leader has been appointed who joined the institute in 2010, meaning that this new team has been classified as emerging, and will be re-evaluated in 2017. There has been rather few publications from the new group leader on plant pathogenesis, with respect to mycotoxins and their detoxification by plants. Rather, the focus of the majority of her publications has been on fungal biology/genetics and tools for investigating fungi. Nevertheless, the focus of the team in the new institute will be on detoxification of mycotoxins, firstly in Brachypodium (a model for cereals) with later translation to important cereal crops.

Assessment of the team’s academic reputation and appeal

The academic reputation and attractiveness of this team is excellent, particularly given the expertise in fungal genetics of the newly elected team leader, which offers the possibility of novel insights into the interactions between the metabolism of fungus and plant host in pathogenic relationships of agronomic importance. However, with the pending retirement of the present group leader, there was a concern that expertise in plants and, in particular, plant secondary metabolism will be somewhat more restricted in the future, and this will impact negatively on the scientific profile of the team. The newly appointed group leader has enthusiastically embraced the possibilities of plant biology, but it is a lot to master in a short time, and some of the future objectives of the team seem a little naive. While there has been great benefits of uniting expertise on fungal molecular biology and expertise on plant pathology, and likely considerable added value from this interdisciplinary association in the future, it will be very important for the group to maintain a strong reputation in plant pathology in the long term, either by encouraging further collaborations with teams outside IPS2, or through recruitment of a pathologist to the team, particularly one with expertise in cereal crop diseases caused by fungal pathogens. This would enable the team to move beyond their quite limited current objectives to address the broad importance of fungal toxins in cereal crops, and to develop methods for reducing the levels of such toxins in grain, which would have large economic benefits for Europe and be of considerable translational significance.

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

The team was assessed as very good in their interactions with their social, economic and cultural environments. The team has the potential to improve their social impact significantly by moving from work focussed on a model (Brachypodium) to work on crops of agronomical importance. While it might take a little longer to generate the initial data in crops, the impact of studies of direct relevance to agricultural problems will be much greater and the team will discover that there is considerably enhanced commercial interest in their work.

Assessment of the team’s involvement in training through research

The team was assessed as excellent in their contribution to teaching and training, because of the teaching commitments of two of the permanent team members the traininng and supervision of 3 PhD students within the reporting period, with an additional student still to complete their thesis, and training of 3 M2 and 3 M1 students. In addition, one of the team members has joined overall responsibility for the Masters course ‘Science du végetal’ for the University of Paris Sud.

Assessment of the strategy and the five-year plan

The strategic plan for the team was assessed as very good. Two exciting results were outlined in the written report, one suggesting that increasing the activity of a specific glucosyl transferase that glycosylates and so detoxifies DON (deoxynivalenol), could improve resistance of *Brachypodium* to *Fusarium graminearum*. Metabolically, this is quite surprising. Unfortunately these data were not expanded upon in the presentation and so it was not clear, whether this would become a core strategy for cereal crop improvement by the team in the future.

The second fascinating observation was the suggestion, in the written report, that *F. graminearum* induces metabolism of the plant, particularly the mevalonate pathway and that this induction of metabolism might fuel the synthesis of mycotoxins such as DON. If this were the case then this would be a very unique observation that should be prioritised in future research. It would also be a perfect project for IPS2 because of the expertise in metabolic flux analysis and the technology platform focussing on fluxomics would provide unique facilities for understanding the importance and mechanisms of these effects. Nothing was described on this objective in the presentation, suggesting that this preliminary, exciting observation, may not yet be ready for further research. Since this constituted one of the three tasks outlined as priorities for the team in the new institute, there were some concerns about the formulation of priority research objectives by the team.

More work is probably necessary for developing a robust strategy for how the outputs of the team will be translated into agronomic improvements. Are the genes involved in detoxifying the DON mycotoxins suitable for developing resistance in cereal crops by TILLING? If wheat is the primary target for improvement which TILLING populations are available? There are publically available wheat TILLING populations being developed for screening by sequence comparison. These would seem to be ideal materials for developing translational opportunities for this research.

Conclusion

- **Strengths and opportunities:**

Combination of expertise in fungal molecular biology/genetics with expertise in plant secondary metabolism and pathology. The possibilities for innovative discoveries from this interdisciplinary team are obvious.

Attractive and dynamic team leader, with enthusiasm to expand the research profile of the team.

- **Weaknesses and threats:**

Potential loss of expertise in plant pathology/secondary metabolism may limit the team in its ambition. Some naivety about identification and functional characterisation of enzymes of plant secondary metabolism.

- **Recommendations:**

There are real possibilities to build on the interdisciplinarity of this team and to address major questions of considerable agronomic importance. Prioritisation of toxins to work on, based on their agronomic significance would be a good idea. In addition movement to working directly on crops rather than using Brachypodium as a model would improve the attractiveness of the team and the impact of their research.

Team 8 : Organellar gene expression- & transcriptomic platform

Name of team leader: Ms Claire Lurin

Workforce

Team workforce	Number as at 30/06/2013	Number as at 01/01/2015
N1: Permanent professors and similar positions		
N2: Permanent EPST or EPIC researchers and similar positions	2	2
N3: Other permanent staff (without research duties)	7	7
N4: Other professors (PREM, ECC, etc.)		
N5: Other EPST or EPIC researchers (DREM, Postdoctoral students, visitors, etc.)	1	1
N6: Other contractual staff (without research duties)	1	1
TOTAL N1 to N6	11	11

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

• Detailed assessments

Assessment of scientific quality and outputs

The research of the team is concerned with the regulation of organellar gene expression, with specific emphasis on plastidial gene expression. This work is important because, to a large degree, the abundance of plastidial-encoded proteins is controlled at the post-transcriptional level and many fundamental aspects of this are not yet understood. Specifically, RNA-editing and splicing as well as translational regulation are involved in determining the amount of plastid-encoded proteins. In this context penta-tricopetide-repeat-proteins (PPRs) are playing an important role in RNA-editing and splicing, but also in other processes, such as the control of translation and the assembly of multiprotein complexes. PPRs are encoded by the nuclear genome and through this provide a means for nuclear control over organellar gene expression. The Arabidopsis genome encodes close to 500 PPRs and a large share of these specifically binds to a particular sequence motif on RNA. The team has contributed to the discovery of PPRs in plants more than 10 years ago and during the past 5 years analysed the specific functions of a few gene family members in much detail. In cooperation with international partners, the group contributed to several large-scale projects. Including one aiming at identifying the protein-protein interaction networks in Arabidopsis, the results of which were recently published in Science. In another large-scale effort, 166 PPRs were fused to the reporter GFP and the sub-cellular localization of the tagged proteins was examined by epifluorescense microscopy. This work confirmed that the majority of PPRs are organelle-targeted, many being dual-targeted to plastids and mitochondria. One particular notable result was recently published in the Plant Cell, showing that two interacting proteins are required for the editing of the NdhD-1 site in Arabidopsis chloroplasts. This publication was the most prominent among the publications on which the group played a leading role.

Overall, the group has successfully managed to combine large-scale with gene-by-gene functional approaches and through this has contributed to the mechanistic understanding of the role of PPRs in plants. It has to be noticed, though, that this topic was initially pioneered in Evry by a PI who has left several years ago. Consequently, one of the major discoveries in the field, the decoding of a PPR sequence-specificity code, was achieved in the former PI's group in Perth. As demonstrated by joint publications, the team interacts with other leading groups in this field, indicating its international visibility and competitiveness. It has to be mentioned, though, that scientific output was relatively low over the past five years (9 papers listed in NCBI between 2008 and 2013) and the group leader is senior author on only 4 manuscripts during this time. On the positive side, most manuscripts have been published in the top-rated journal in the field (Plant J, Plant Cell, Mol Plant) and also in general-interest journals (Science). In summary the quality of the published work is very high, the quantity shows substantial room for improvement in the coming years.

When reflecting on the scientific impact and productivity, it is important to consider that this group consists of two pillars – the organellar gene expression team and the transcriptomics platform. The latter provides transcriptomic analyses as a service for a large number of other national and international laboratories. This is documented by co-authorships of platform scientists on a very substantial number of papers. Clearly, the platform part of the team is very strong and will also be an asset to IPS2, although it will have to be re-structured upon integration into IPS2 and it is important that this restructuration takes into account the very rapid evolution that the transcriptomics field is undergoing at the present time.

Assessment of the team's academic reputation and appeal

Group members have been invited to give presentations at several (mostly) national and (some) international meetings. Invitations to present at major international conferences are not apparent from the materials provided in the proposal. According to the proposal text, group members do not serve on the editorial boards of scientific journals. A very positive aspect is the organization of the URGC-Genopole transcriptomic days in 2012 that attracted approx. 100 attendants. The success of this meeting prompted a follow-up meeting in 2013. Through several ANR projects and one FP 6 European project the group interacts with a substantial number of other groups, frequently through integration of the transcriptomics platform in these joint activities.

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

There was no mention of such activities in the proposal text.

Assessment of the team's involvement in training through research

The group trained five graduate and 4 master students during the past 5 years. One postdoctoral researcher has been trained during this time. Contribution to teaching at the undergraduate level was low.

Assessment of the strategy and the five-year plan

The research team has realigned its research strategy to integrate its future research with the proposed research plan of IPS2. Some of the previous work on the role of PPR proteins in regulating organellar gene expression will be continued to finish up currently running projects. On the basis of protein-protein interaction studies and TAP-tagging approaches binding partners of RNA-binding proteins have been identified and these clomplexes will be analysed in detail. However, it is envisaged that the group will move away from gene-by-gene analyses of PPR proteins in the context of regulation of organellar gene expression. In the process of integrating with IPS2, the program will be extended to include the organellar gene expression response to biotic and abiotic challenges, with particular emphasis on pathogen attack/defense. The latter is based on the exciting finding that two different bacterial plant pathogens encode in their genomes PPRs, which might have the functions of secreted pathogen effectors that are injected into to plant cells upon infection, targeted to chloroplasts and involved in de-regulating plastidial gene expression. This excellent project is innovative and original and integrates the group well into the biotic interaction department. Jointly with the "Genomic network" group (Team 9) transcriptomic responses to abiotic and biotic challenge will be studied usingnovel bioinformatic and biostastistical analyses of large transcriptomic datasets that have been obtained with the CATMA platform at Evry. The advantage of this dataset is the consitency with which it has been obtained, which might enable discoveries that have not been possible by analysis of other large-scale datasets.

The team leader will also be responsible for the transcriptomics platform. In the future, the transcriptomic platform will need to be integrated with other 'omics-level platforms of IPS2, such as the metabolomic and fluxomic platforms. Potential for exciting new discoveries can only be leveraged by coordinate experimental design and data analysis across various 'omics domains.

Conclusion

This group is one of few at the international level that study the role of nuclear-encoded RNA-binding proteins in organellar gene expression. Overall, the contributions to the field are frequently in supporting roles and in future a clear and recognizable profile within the field should be developed. The proposed work on organellar gene expression regulation in response to biotic and abiotic factors is an exciting new step in this direction. The transcriptomics platform is an asset to IPS2 and to the larger scientific community. It will have to be made sure, though, that this platform will be integrated with efforts of the other IPS2 laboratories.

- **Strengths and opportunities:**

The group through its platform activities is very well connected with other labs and it is on the way of developing a clear scientific profile in RNA-protein interactions and their role in governing organellar gene expression.The new project on secreted pathogen effectors with PPR activity opens new avenues for research and integration with research of those groups interested in the response to biotic challenges.

- **Weaknesses and threats:**

The publication record of the organellar gene expression group is not as strong as it could be. Frequently, the group members act as one of several co-authors, but not as the lead or senior authors. This is clearly acceptable for the platform activities of the group, but not with respect to its core scientific profile. Relatively few postdocs have been recruited on extramural funds and contributions to graduate and undergraduate training are moderate.

- **Recommendations:**

Increase publication output as lead or senior authors. Do not underestimate the importance of hypothesis-driven research – the unbiased 'omics approaches are certainly important and worthwhile doing; nevertheless it will be crucial for high-impact publications to put more focus on functional analyses that reveal novel concepts and mechanisms in plant biology. Leverage the potential of IPS2 by thinking beyond the borders of the previous unit and develop a clear concept for interacting with the other groups

Platform analysis Transcriptomics Platform

Name of plateform leader: Ms Sandrine BALZERGUE

The Evry transcriptomics platform over the past five years has contributed to a large number of studies in France, Europe, and at the international level, which is documented by > 70 papers that list platform staff as co-authors. Originally most of the work was predominantly done using the CATMA Arabidopsis microarray, in addition to custom arrays and Affymetrix and other manufactured chips. Recently the platform has adopted next-generation sequencing systems for RNA-seq approaches and corresponding bioinformatics and biostatistics pipelines to analyze such data have been established. Mostly based on Illumina sequencing technology, all recent RNA-Seq protocols are now offered and the platform has recently been extended by including IonTorrent sequencing technology. While sequencing is also offered at competitive rates commercially, the platform distinguishes itself by offering a comprehensive package that ranges from experimental planning through data analysis and thus makes NGS experiments easily accessible to non-experts. Hence in general the platform over the past years has done an outstanding job with providing the community with transcriptomics services. Upon moving to and integrating the platform with the new IPS2, it will be important to reconsider the platform concept and allocation of resources to platform staff and instrumentation. Given that sequencing is now available on the market at relatively low cost, it might be advisable to direct less of the resources to running and maintaining sequencing hardware and to focus more on the pre- and after-sequencing aspects. Also, application of NGS in mapping of mutations, re-sequencing, and ChIP-Seq should be included.

Team 9 : Genomic Networks (Gnet)

Name of team leader: Ms Marie-Laure MARTIN MAGNIETTE

Workforce

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

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 unit	1	
Number of Research Supervisor Qualifications (HDR) taken	1	
Qualified research supervisors (with an HDR) or similar positions	1	1

• Detailed assessments

Assessment of scientific quality and outputs

Over the period 2008-2012, the group has developed original statistical methods to classify genes according to their expression profiles as well as methods for omics data analyses. It has developed and released four databases (CATdb, FLGdb++, ATOMEdb, UTILLdb) as well as several R packages dedicated to omics projects, in connection with URGV platforms. It has been involved in gene annotation and analysis, with software development for the prediction of regulatory motifs in promoters. Finally, it has collaborated with the URGV transcriptomics platform to carry out statistical analyses for a variety of studies.

The group has published 43 papers, including 37 in journals referenced in the Web of Knowledge. Those included six papers dedicated to developments in biostatistics, in journals with very good (Bioinformatics, BMC Bioinformatics) to average impact factor (Computational Statistics and Data Analysis; Journal of Multivariate Analysis; Biometrics; ESAIM-Probability and Statistics), seven very good papers related to gene annotation (Plant Physiol., J. Mol. Evol, BMC EvolBiol, Genome, BMC Genomics, BMC Plant Biol., Plos One) and three describing the databases developed by the team in connection with URGV platforms (two in excellent journals : Genome Biology, Nucl Acids Res, the third in Plant Methods). The contribution of the group to other papers was mostly related to statistical analyses of gene expression (published in excellent to good journals : Plant Cell, EMBO J., Plant Physiology, 2 Plant J., Plos One, BMC Genomics, BMC Plant Biol.).

The team production including database production and publications was therefore overall excellent for the past five years.

Assessment of the team's academic reputation and appeal

The group leader is associate editor of BMC Genomics since 2009 and has been reviewer for statistics for Plant Cell for four years. She is well recognized in France since she has been co-animator of the methodological network NETBIO since 2011 (about 80 researchers in statistics, computer science, bioinformatics and biology; network funded by the INRA department "Mathématiques et Informatique Appliquées"). She also has collaborations with excellent French teams in statistics (INRIA; MIA INRA…). The former group leader was member of the bioinformatics board of INRA, of MASC (multinational Arabidopsis steering committee) and member of the scientific program board of the annual meeting JOBIM, but he has now left the team. The team was recently (dec 2011) joined by a talented young lecturer.

The very good reputation and appeal of the group could be improved by a wider international recognition, as suggested by the low number of invitations to international meetings and international collaborations.

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

All members of the team take part in annual Fêtes de la science events and participate in presentation in schools of various professions at INRA.

Assessment of the team's organisation and life

The team is facing an important change with the replacement of the group leader. The group keeps however five experienced people with permanent positions, including three engineers with skills in bioinformatics and statistics and two researchers in statistics. Moreover, the new group leader is well recognised in the national community of researchers in biostatistics and bioinformatics and has a long-standing experience of fruitful collaboration with the URGV/IPS2 transcriptomics platform.

Assessment of the team's involvement in training through research

Over the period 2008-2012, the team has supervised or co-supervised five PhD students, as well as one post-doc. One group member is an associate Professor (Univ.d'Evry-Val d'Essonne). The members of the group are involved in teaching computer sciences, bioinformatics, statistics and genomics in six Master 2 of Univ Paris 7, Univ. Evry, Univ. Paris 11, Univ. Rouen, as well as in Pasteur institute, ENS and AgroParisTech.The team activity is therefore very good.

Assessment of the strategy and the five-year plan

The team plans to focus its activity on functional annotation of *A. thaliana* genes involved in stress responses, by meta-analysis of transcriptome data already available in CATdb or to be produced by the IPS2 transcriptomics platform. The goal is to characterize in particular numerous orphan genes that encode unknown proteins, as well as non-protein coding genes, including small RNA genes.

The principle will be to identify clusters of co-regulated genes (Task 1), using original (model-based) clustering methods developed by the group, interesting notably because the quality of clusters is assessed with a probabilistic score. Importantly, methods will be developed to analyze high through put sequencing/RNA-seq data in addition to microarray data. The co-expression clusters will then be analyzed from a biological point of view, to validate and annotate the clusters directly or indirectly involved in general or specific stress responses (Task 2). Various information and analyses will be integrated (GO classification, promoter sequence analyses, interactomes, possibly proteomes and metabolomes…) in close interaction with plant pathologists from and outside IPS2. These results will be made accessible *via* a database currently developed by the team. Finally, regulatory networks,i.e. sets of direct interactions between genes, will be inferred (Task 3). Methods will be developed, based on Gaussian graphical models, which raise some methodological problems when applied to transcriptomics data. Close collaborations with biologists and researchers in statistics are planned or have already started (with MIA INRA researchers, and University Evry researchers, from the Statistic & Genome team).

The goals and the strategy are therefore clearly defined for the coming years, thereby leading to an overall very good research plan. Important biological and methodological questions will be addressed, supported by a wealth of existing data and the team expertise, as well as a network of solid collaborations, within and outside IPS2.

Conclusion

The project proposed is very interesting and timely in view of the current challenges in plant genomics.

- **Strengths and opportunities:**

The team has a sufficient size and all required skills, supported by an excellent network of collaborators, to envisage an ambitious project; it has access to high quality data and the IPS2 context appears excellent to foster collaborations with biologists.

- **Weaknesses and threats:**

The team visibility may not be good enough at the international level.

- **Recommendations:**

Gene network analysis is a very dynamic field both in plant and animal/human biology, and it is important to be known and in close contact with the main groups worldwide. The team should try to increase its international visibility (by increasing its participation in international congresses, and concentrating on peer-reviewed papers in international journals) and develop some international collaborations.

Team 10 : Oxidative stress redox signalling and chromatin

Name of team leader: Mr Graham NOCTOR

Workforce

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

Team workforce	Number as at 30/06/2013	Number as at 01/01/2015
Doctoral students	3	
Theses defended	6	
Postdoctoral students having spent at least 12 months in the unit	2	
Number of Research Supervisor Qualifications (HDR) taken	3	
Qualified research supervisors (with an HDR) or similar positions	3	3

• Detailed assessments

Assessment of scientific quality and outputs

Oxidative stress group (OSG) contributions

At the beginning of the contract the group featured two permanent staff members, several PhD's and one post doc. At the end the contract the MdC has left, but an IE has arrived stabilizing the number of permanent members at two. Given the small size of the group, the scientific output is remarkable with 35 papers published in international journals. Of these 14 are review papers and 21 research articles. The PI of the group is either first or lead author of Ca 20 of the papers. The international recognition of the group leader is high. He has coordinated two ANR contracts co-edited special issues of journals, made invited conferences in many countries including China and Poland. He is an EBM of several journals and his advice is sought concerning scientific evaluation in several countries. He has participated in many international meetings. The major findings made by this group concern the use of a cad2 mutant deregulated for H_2O_2 production. The subsequent generation of *cad1 cad3* and multiple Arabidopsis mutants is recognized internationally and these mutants have been used by other groups. The scientific quality of this group is clearly very high with an obvious international status and recognition. One concern is the small size of the group and the lack of local aggregation on this theme in the last contract. The project together with the redox and signalling group developed for the next contract aims at correcting this flaw.

In terms of training through research, the OSG group has delivered 5 PhDs in the last contract. Social economic and cultural interactions are quite shallow due to the small size of the group as indicated in the document.

Redox signalling group (RSG) contributions

At the beginning of the contract, the group consisted of two CNRS researchers and one "maître de conférence (MC). The departure of one CNRS researcher to IBPC and the arrival of one IE have left the group stable in terms of permanent members (including a CNRS *Emeritus* volunteer collaborator during the whole period). The production of the group has been of high quality during the last contract with 25 articles in peer-reviewed journals. They have contributed mostly to the clarification of the thioredoxin chloroplastic network with interesting papers concerning G6PDH regulation, SEX4, ADPGPP and MsR. The contributions of this group has helped clarify the functions of plastidial Trxs x, y and z. The RSG group has also enjoyed an international recognition for a long time. Nevertheless, the departure of one of the CNRS researcher is a severe blow to this group and it is clearly desirable to associate it with the OSG group in the project. The RSG group has trained 4 PhD students in the last contract. The team is an active member of two GDR structures. The PI of the RSG group has given several conferences nationally and internationally (including one in Germany where she has a contract in Bavaria). The PI has reviewed several contracts and articles internationally. The group has been involved in ANR Genoplante till 2008. This group is also involved regularly in the promotion of science *via* la Fête de la Science.

Assessment of the team's academic reputation and appeal

The PIs of the three groups joining forces in the present project have had many international invitations to present their data in meetings. They have participated/ coordinated a large number of contracts including ANRs and EC contracts for a total of ca 900 k€. They are active members of the EB of several high reputation plant journals. Also they have been able to attract at least three post docs in the last contract.

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

This point is not very detailed in the document. The research performed is very basic-science oriented and there are few connections with industry. Nevertheless the study of redox systems is an opportunity to create new stress resistant cultivars and this could lead to industrial contacts and should be developed if possible. There are efforts to reach out to the general public and explain this research *via* participation to the Fête des la Science. A single paper resulted from a collaboration with Bayer.

Assessment of the team's organisation and life

Not relevant for team analysis, but this point may become sticky in the next contract. The three teams joining in the new project will have to "learn" to work together in the new project and particular attention should be given to polish the organization of the new team.

Assessment of the team's involvement in training through research

Three out of the four permanent staff members of the group have teaching duties. The group is heavily involved in teaching with ca 700 hours teaching yearly and this is a very big load. Also they have trained a large number of doctoral students in the last contract and their output on this item is excellent.

Assessment of the strategy and the five-year plan

The proposed project has merits and flaws. The principal merit is to join forces by combining the expertise of the oxidative and metabolic signalling and redox signalling groups. Clearly the themes of these two groups are very close and they even have published together in the past and participated to ANR Genoplante together. It has already been pointed out earlier that these two groups have shrunk too much to remain competitive on the international scene in the long run. Combining them now is clearly necessary. What is less clear is the input of the Chromatin and plant development group to the project. The theme of this group seems to be remote from the core of this project. Clearly the "Chromatin"group has had an excellent scientific output in the last contract although it is not always clear if the contributions were made in Orsay or Wuhan. The tasks of objective 1 are well delineated and integrated, but objective 2 is more heterogeneous, it remains to be seen how well the histone acetylation /methylation story will blend with redox aspects central to the first theme. Still the overall size of the projected research group is quite reasonable provided a true scientific graft between the partners can be reached.

Conclusion

The partners of the new group have had an excellent scientific activity in the last contract with more than 60 articles in peer reviewed international journals of high quality. Their international recognition and attractiveness are very high and they had the capacity to attract grants. Interactions with the social and private sectors could be improved but efforts have been made to explain the research done *via* mechanisms such as Fête de la Science or La main à la pâte. The project is of interest, the connections between the redox and oxidative signalling groups is natural, it is more difficult to predict if those with the chromatin group will be truly successful especially as the head of the group is spending also part of his time in his lab. in China. Nevertheless, scientifically such connections between the two areas exist, they will need to be exploited in the next contract.

Team 11 : Stress signalling

Name of team leader: Mr Heribert HIRT / Mr Jean COLCOMBET

Workforce

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

Team workforce	Number as at 30/06/2013	Number as at 01/01/2015
Doctoral students	2	▨
Theses defended	7	▨
Postdoctoral students having spent at least 12 months in the unit	3	▨
Number of Research Supervisor Qualifications (HDR) taken	1	▨
Qualified research supervisors (with an HDR) or similar positions	1	1

• Detailed assessments

Assessment of scientific quality and outputs

In the last contract the group based at URGV in Evry comprised up to two CNRS researchers, one INRA researcher, three technical assistants, 4 post docs and 3 PhD students. In the last contract, the group Signalling and Proteomics has worked in the area of Stress signal transduction in plants. They have especially characterized signalling cascades based on mitogen activated protein kinases (MAP kinases). This includes MAP4Ks, MAP3Ks, MAP2Ks and MAPKs. Physical interactions between these kinases are important as well as their phosphorylation status. Serines, threonines and tyrosines are phosphorylation targets depending on the kinase considered. These cascades are involved in stress signalling following cold treatment and pathogen attacks. Mutants have been isolated,in particular forMKK2, and via transcriptomics analyses more than 150 targets of this kinasewere identified. Conversely, MKK2 overexpressors exhibit increased freezing tolerance. A bioinformatics analysis made in this group has revealed 10 to 80 genes for the various categories of MAP kinases. Manipulating the level of these MAP kinases seems to be promising for improving stress resistance of plants. MAP kinases can phosphorylate transcription factors, but gene expression is also affected by chromatin modifying enzymes as histone deacetylases, methylases or acetylases. A large scale phosphoproteomics technology was developed at Evry and also Tap-tag technology to identify and purify protein complexes involved in transcription regulation.

The group has generated 37 publications in peer-reviewed journals including papers in leading journals as EMBO J, PNAS, Plant Physiol, Proteomics and Plant Cell. In most of these contributions they are either lead authors or first authors. Of these, *ca* 30 articles are research papers and 5 review articles. A few papers concern projects unrelated to this central theme (essentially on the *Salmonella typhimurium* system). A few book articles have been produced and a book edited by the PI. Incidentally, the PI has retained a lab. in Vienna (Austria) for some time, and some of these publications seem to be more closely linked to this affiliation (nearly half of the papers of the list are credited to the Vienna lab.). Nevertheless, given the relatively small size of the Evry's group, this is clearly an outstanding scientific output.

Assessment of the team's academic reputation and appeal

The international recognition of the PI is outstanding (elected EMBO member, highly cited ISI, selected as one of the 1000 most important French scientists, president of EPSO, etc…). It is also an associate editor of many plant journals and he performs an important editorial work. The work carried out in Evry has led to the creation of a technological platform for the isolation and analysis of protein complexes. Six international congresses in the last contract were organized or co-organized.

In the last contract, the team Signalling and Proteomics has been able to secure 4 ANR grants (1 coordinator) and two EU grants (not indicated if they are participant or leaders).

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

The research performed is rather basic science oriented in nature and few contacts have been established with industry although their work should open the possibility to create stress resistant crops. While translational research is not present, the PI of the group has reached out to the social groups to explain the nature of modern agriculture giving a large number of conferences to very diverse audiences.

Assessment of the team's involvement in training through research

This is the weakest point of this group comprising exclusively INRA and CNRS researchers. Little effort has been made to integrate teaching programs either at Evry or at other sites. They should participate a little more in this area. Nevertheless, the group has trained 7 PhD in the last contract, indicating a good participation in this domain.

Assessment of the strategy and the five-year plan

In the next contract, the composition of the group will be essentially identical with three permanent researchers and three technical assistants plus students and post docs (a number of those ie 7, listed in the project document have already left). The project of the group is a direct evolution of the former project. It will deal with the isolation and functional characterization of protein kinases and substrates, genetic screens for isolating key stress regulatory components, MAPK gene expression and epigenetic heritability and modeling of signalling cascades. Given the achievements of the group in the last contract, they should be able to deliver in the next contract, especially since there seems that no technological breakthrough will be needed. Still the situation of the group leader is not completely clear. He has apparently quit the direction of the Vienna lab but seems now to be heading for Saudi Arabia where he has been nominated as a distinguished fellow in 2010. This opens a number of questions on how will he splits his research time between Saudi Arabia and France, and how much of his time will he be able to dedicate to the IPS2 group? In any case, it will now be the task of another younger INRA researcher to lead the group effectively, on a day-to-day basis. The departure of the actual PI, even if it is only partial, also depletes the group of one of its members, reducing it to two permanent researchers and this is a concern.

Conclusion

This research group has had an outstanding scientific output in the domain of MAPK signalling in the last contract. The international recognition of the work achieved by the groupis enormous. On the other hand, there is little translational effort and this could be improved. Also the formal teaching is absent in this group, which has nevertheless trained several PhD students. The project is the direct continuation of their present activity and thus offers few risks. However, the departure of the actual PI, even if only partial, raises concerns about the functional aspects of this group, but at least a successor is clearly identified. The new direction of IPS2 should pay attention that this group maintains its outstanding standards in the new situation.

Team 12 :

Signalling regulation and metabolic interactions

Name of team leader:

Mr Michael HODGES

Workforce

Team workforce	Number as at 30/06/2013	Number as at 01/01/2015
N1: Permanent professors and similar positions	6	6
N2: Permanent EPST or EPIC researchers and similar positions	2	2
N3: Other permanent staff (without research duties)	7	7
N4: Other professors (PREM, ECC, etc.)		
N5: Other EPST or EPIC researchers (DREM, Postdoctoral students, visitors, etc.)	2	2
N6: Other contractual staff (without research duties)		
TOTAL N1 to N6	17	17

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 unit	3	
Number of Research Supervisor Qualifications (HDR) taken	3	
Qualified research supervisors (with an HDR) or similar positions	3	3

• Detailed assessments

Assessment of scientific quality and outputs

The team investigates interactions between primary metabolic pathways (photosynthesis, respiration, photorespiration, and N assimilation), to highlight limiting and new regulatory steps allowing plant metabolism adjustments to fluctuating environmental conditions. They developed two main approaches. The first one is devoted to study the role of protein kinases (*PII* and *SnRK1)* in signalling cascades involved in plant metabolic regulation. The second approach is to get a dynamic and realistic point of view of metabolic interactions and bypasses between C and N metabolism including NADH synthesis and photorespiration.

The results on the PII protein highlight a new role in regulating lipid metabolism through acetyl-CoA-carboxylase interactions. While the work on SNRK1 suggests that the SnRK1 (a energy sensor inhibited by AMP and DP) might play a significant role in the control of cell proliferation in *A. thaliana* through inhibition of KRP6 (a negative regulator of cell division). By using a combination of stable isotope labelling experiments with gas exchanges, measurements and NMR, MS analyses, the team has pointed out the critical role of NAD in C/N interactions and gave a set of explanations to understand the key regulatory mechanisms to coordinated plant metabolism interactions.

The scientific production, quantitatively and qualitatively is excellent. The team has published 44 research papers published in high profile peer reviewed journals + 20 paper with the metabolome platform. Among them, the committee underlines 12 Plant Cell Environ, 7 Plant Physiol, 7 New Phytol, 5 Plant J, 3 PNAS, 2 PLoS One, 2 FEBS Letter, 1 Trends Plant Science, 1 Curr Opin Plant Biol, 1 JBC, etc.

Assessment of the team's academic reputation and appeal

The team has an excellent reputation in the field of plant physiology and metabolism, and has active collaborations within and outside France. A long list of participation at national and international conferences is mentioned, as well as invitations as contributing and keynote speakers. Team members have built a strong lab network at local plant institutes (mainly the IJPB INRA Versailles), national (Nantes, Grenoble, Nice) and international institutes and universities (Germany, Portugal, Spain, Belgium, UK, Italy and Australia).

The team has been successful to get public funds from ANR (Jeunes chercheurs, Genoplante) and local infrastructure (IFR 87).

One team member has been awarded the CNRS "Bronze medal" and also benefits from a Young Professor IUF position. The excellence and attractiveness of the research carried out in the team was recognized by the SPS labeX, this research activity has become one of the four SPS Flagship projects.

Team members are largely involved in expertise as reviewers and committee members (<100 international scientific journals, 18 international research projects, recruitment committees). The team leader contributes to the collective management of the IBP as Deputy Director.

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

Team members are conducting mainly basic science-oriented research. Their implication in social and cultural interactions are limited to animation of the "Fête de la Science" each year and interactions with high school classes. For economic aspects, the team develops interactions with private companies in the context of the Metabolome Platform. But the overall actions are limited.

Assessment of the team's organisation and life

The group leader has been able to bring together many competences in order build a strong team devoted to metabolism studies. The integration is in good adequation within the institute (good interactions with others teams through the platform activities, contribution of scientists to collective tasks). The team is in charge to run the Metabolomics facility, which is central for many research projects in the institute.

Assessment of the team's involvement in training through research

Overall, the team has high international visibility and an excellent capacity to attract post-docs (3) and PhD students (6) linked to the high success in competitive funding. Taking in account the teaching/scientist ratio, the contribution of the team to teaching is outstanding. Members of the team have numerous responsibilities in teaching units from Licence, Master to PhD grade. One member of the team has published a book on "isotopie en biologie" that can be used by scientist as well as student.

Assessment of the strategy and the five-year plan

For the coming years, the team proposes to pursue its successful work on various aspects 1) Interactions between metabolisms (including Photosynthesis, photorespiration, N assimilation, NAD synthesis, C1 metabolism and Amino acids metabolism), 2) flux-patterns associated with day and night metabolism, 3) intrinsic regulatory mechanisms (phosphorylation cascades, redox regulation of enzyme activities) and 4) effect of environmental cues on metabolic interactions, fluxes and regulations. The final aim in terms of translational research is to allow to predict how to increase plant yield while reducing inputs.The main risk taken by the team is linked to the fact that most of the proposed research directions are not related to real agronomic traits that can be transferred to agriculture. The risk exists that, while the research excellence will be maintained during the next period, it might be difficult to establish direct links with respect to agricultural challenges. The second risk is linked to the fact that one of the scientific leaders will leave the unit on January 2015 for Australia. He will leave a void in the stable isotope labelling approach to study metabolism and plant physiology. Clearly, the urgent strategic need exists to find a young scientist that can provide the required leadership in the field of metabolism and metabolomics.

On the top of these research directions, the team will continue to take in charge any developments (protocols, new equipment) to anticipate user needs relevant from IPS2 teams. The objective is to be a major player in the phenotyping pipeline of IPS2 projects.

Conclusion

This team is a very productive group with dynamic members, an excellent publication record in major journals and has had success in securing national funds, and good collaborations. In summary, the necessary technical tools and permanent personnel are in place and the project can be expected to generate interesting and internationally visible results over the next four years.

- **Strengths and opportunities:**

The team established a panoply of techniques for metabolite profiling and flux analysis that is more or less unique at the national level, and also competitive at the international level.

- **Weaknesses and threats:**

With the departure of the young and successful professor to Australia, the team will have to manage the transition and overcome this drawback through strategic recruitment of a replacement.

- **Recommendations:**

The team needs to find an excellent scientist in metabolism and metabolomics in order to keep on track the research team, the external funding and the platform activities. The manager will have to take in consideration the translational direction taken by the unit and has to propose a project which includes both integrative biology and translational aims.

Platform analysis : Metabolism-Metabolome Platform

Name of plateform leader: Mr Guilllaume TCHERKEZ

The platform is dedicated to the qualitative and quantitative analysis of metabolites in plant matrices with metabolomics approaches, natural abundance enrichment measurements of stable isotopes (mainly C and N) and measurement of metabolic fluxes. The facility is well equipped with GC-MS, LC-MS, IR-MS and recently a 400 MHz NMR spectrometer with a cryoprobe. The group's mission is to serve the teams of the institute and beyond. A team of 5 engineers and technicians have the main competences needed to run the facility. So far, the available analysis offer as a service primary metabolites analysis by GC-MS, elemental analysis, the measure ^{13}C and ^{15}N enrichment and determination of nucletotides and cofactors, and amino acids by HPLC. In the near future, they should evolve towards lipidomics, quantification of phytohormones, use of NMR 1D and 2D to do classical metabolomics, coupling LC-IRMS, etc.

- **Strengths and opportunities:**

In the national and international context, the platform appears as the platform that has developed forefront skills in the analysis of the isotopic enrichment in natural abundance. The platform has established a panoply of techniques for metabolite profiling and flux analysis that is more or less unique at the national level, and also competitive at the international level. The platform will be able to combine this expertise with classical metabolomics. The platform should become a reference tool for the IPS2 project.

- **Weaknesses and threats:**

The first weakness concerns the management of the PF. No information is given to explain how projects are selected which will perhaps be a problem with the number of teams that increases in the IPS2 project. In view of the rise of the PF in terms of equipment, it is important to have an analytical management so as to identify the costs (consumables, maintenance, repair, replacement of equipment, extended warranties, nitrogen and helium liquid NMR, etc.) and find appropriate resources to maintain the activity. Different business models exist to maintain a PF, but a vision of the costs and resources is essential for sustainability of the PF.

The question for the future is how to develop the activity of the PF. The platform plans to develop a set of new competences (lipidomics, *in vivo* NMR, LC-IRMS coupling, phytohormone quantification, etc). Considering the size of the team and the fact that the platform team leader is leaving, the risk for the PF could come from a too large dispersion in terms of number of technological developments to implement and ensure service delivery in adequation with the available personnel.

The departure of the young and successful professor to Australia requires to manage the transition to overcome this drawback.

- **Recommendations:**

It is strategically important for the platform and for the IPS2 project to keep an efficient metabolomic platform. For this, an excellent scientific leader in metabolism and metabolomics is needed in order to keep on track the technological development on the platform and the strong link to the research team. Without leader, the platform will not survive in the national and international context of research. The choice of the platform leader who has the state of art competence in metabolism is a strategically urgent need.

5 • Conduct of the visit

Visit dates:

Start: 1st December 2013, at 20.30

End: 3rd December 2013, at 16.30

Visit site: Institut de Biologie des Plantes

Institution: CNRS, INRA, University Paris Sud, Paris 7, Evry

Address: Institut de Biologie des Plantes, Batiment 630. Université de Paris Sud, Gif-sur-Ivette

Specific premises visited

The visit included only presentations and discussions with members of the institutes that will form the Institute of Plant Sciences Paris-Saclay and the institutions.

Conduct or programme of visit

The programe included:

December 1st. Dinner of members of the committee

December 2nd: Presentations of the Director of the institute and of the different Departments

Discussion of the Evaluation committee.

December 3rd: Meeting with Representatives of the Institutions, with technicians and engineers, with students and postdocs, with researchers and team leaders and with the proposed Director. Presentations of Platforms.

Discussion of the Evaluation committee.

The detailed agenda was as follows:

December 2:

8:30	Welcome of Evaluation committee (EC) members and AERES scientific delegate
8:30-8:45	Presentation of evaluation procedures and of members of the EC by the scientific delegate of AERES
8:45-9:45	Presentation of the IPS2 Project by the unit's director (discussion together with IBP and URGV Directors)
9:45-10:15	Group "Signalling pathways controlling legume root system development"
10:15-10:45	Group "Regulatory non-coding RNAs in root plasticity"
10:45-11:00	*Coffee break*
11:00-11:30	Group "Cell Cycle, Chromatin and Development"
11:30-12:00	Group "Translational research Group"

12:00-12:15	Platform TILLING and positional cloning
12:15-13:15	Evaluation committee meeting *Review board*
13:15-14:00	*Lunch*
14:00-14:30	Group “Oxidative stress, redox signalling and chromatin”
14:30-15:00	Group “Stress signalling”
15:00-15:30	Group “Signalling, regulation and metabolic interactions”
15:30-15:45	Platform Metabolome
15:45-16:30	Evaluation committee meeting *Review board*
16:30-16:45	*Coffee break*
16:45-17:15	Group “Genetic control of the symbiosis “
17:15-17:45	Group “Genome Dynamics and Pathogen resistance”
17:45-18:15	Group “Functional genomics of secondary metabolism in Monocots-microbes interactions”
18:15-18:45	Group “Organellar gene expression”
18:45-19:00	Platform Transcriptome
19:00-19:30	Group “Genomic networks (Gnet)”
19:30-20:30	Evaluation committee meeting *Review board*
20:30	*Dinner* Evaluation committee *members Review Board*

December 3

8:15-8:30	*Welcome of* Evaluation committee *members and scientific delegate*
8:30-8:45	Translational Department
8:45-9:00	Axe Biological Networks
9:00-9:15	Meeting with Doctoral School representatives
9:15-9:45	Meeting with University and Organisms representatives: CNRS, INRA, PSud, UEvry, Paris-Diderot
9:45-10:00	*Coffee break*
10:00-10:30	Meeting with technicians and engineers
10:30-11:00	Meeting with PhD students and post-docs
11:00-11:30	Meeting with researchers, professors and lecturers
11:30-12:00	Meeting with team leaders
12:00-12:30	Discussion with Proposed Director IPS2
12:30-14:00	*Lunch Review Board*
14:00-16:30	Evaluation committee members meeting *Review Board*
16:30	*Departure*

Specific points to be mentioned

The Evaluation committee was presented with written and oral information about the project of the new institute and the groups that will integrate it. The committee had time to discuss with scientists and with other members of the new institute as well as with representatives of the Institutions. It was also time for internal discussions.

The committee had the very useful collaboration of the staff of the new institute, and in particular of its new Director, Dr. Martin CRESPI, as well as the representative of AERES, Mr Steven BALL.

The only point that members of the committee indicated was the low level of heating in the Auditorium of the institute.

6 • Supervising bodies' general comments

UNIVERSITÉ
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Le Président de l'Université Paris-Sud

à

Monsieur Pierre GLAUDES
Directeur de la section des unités de recherche
AERES
20, rue Vivienne
75002 Paris

Orsay, le 24 mars 2014

N/Réf. : 68/14/JB/LM/AL

Objet : Rapport d'évaluation d'unité de recherche
N° S2PUR150007659

Monsieur le Directeur,

Vous m'avez transmis le 3 mars dernier, le rapport d'évaluation de l'unité de recherche Institut des Sciences des Plantes de Paris Saclay - IPS2 - n° S2PUR150007659 et je vous en remercie.

L'université se réjouit de l'appréciation portée par le Comité sur cette nouvelle unité et prend bonne note de ses suggestions. Elle sera en particulier attentive à la restructuration de la plateforme Métabolome, et discutera avec le directeur de l'unité de la mise en place d'un comité scientifique externe.

Vous trouverez en annexe les éléments de réponse de Monsieur Martin CRESPI, directeur de l'unité de recherche.

Je vous prie d'agréer, Monsieur le Directeur, l'expression de ma sincère considération.

Jacques BITTOUN
Président

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CENTRE NATIONAL
DE LA RECHERCHE
SCIENTIFIQUE

Gif-sur-Yvette, le 25/03/2014

Institut des Sciences Végétales

OBJET : Réponse au rapport d'évaluation AERES du projet IPS2

Les équipes constituantes du projet Institut des Sciences de Plantes de Paris-Saclay, IPS2, ont pris connaissance du rapport d'évaluation AERES et remercient le comité pour le travail d'évaluation réalisé sur la construction du projet. Nous avons pris bonne note des points forts et des points faibles de la prochaine Unité soulignés par le comité et enregistré les recommandations qui feront l'objet de travaux approfondis au cours des prochains mois en préparation du démarrage de l'Unité en Janvier 2015. Après une appréciation de portée générale sur les recommandations du comité, certaines équipes et plateformes ont souhaité préciser certains points sur leurs activités passées ou futures.

Nous avons analysé les recommandations faites par le comité et partageons l'importance du financement du projet. Depuis la visite du Comité AERES (le 2-3 décembre), nous avons obtenu le projet 3P, for Plant Phenotyping Platform, qui nous permettra de disposer d'un budget (autour de 1.2 Meuros) cette année pour améliorer les moyens de culture de l'Unité ainsi que d'autres équipements de biologie cellulaire et translationnelle. En plus, une promesse ferme de soutien nous a été donnée par la Région Ile de France pour permettre la préparation du Bâtiment 630 à l'accueil de nouvelles équipes d'autres Unités. Cette somme sera aussi utilisée pour la préparation de la nouvelle infrastructure informatique nécessaire pour l'IPS2, qui aura une forte composante génomique. La nomination d'un « Scientific Advisory Board » sera aussi proposé afin d'être mieux accompagnés dans les futures décisions stratégiques de l'Unité et améliorer son attractivité nationale et internationale.

Groupes de Recherche

L'équipe « Genetic control of symbiosis » dirigée par P. Ratet, a pris note de la remarque sur l'évaluation de ses objectifs à long terme. Depuis plusieurs années, cette équipe a développé des outils génétiques chez *Medicago truncatula* qui ont été utilisés par une grande partie de la communauté scientifique pour l'identification de nombreux gènes de légumineuses. En conséquence, ils ont été associés à plusieurs publications relatives à ces identifications de gènes. Toutefois, comme indiqué dans le projet de recherche, l'équipe se concentrera sur deux projets innovants qui sont l'immunité nodule et l'identité de l'organe de nodule.

L'équipe « Genome dynamics and pathogen resistance » dirigée par V. Geffroy a pris note de la remarque sur le recrutement postdocs. En fait, cette équipe a recruté 1 postdoc universitaire (ATER) et a déjà mise en place une collaboration avec l'équipe de Blake Meyers (University of Delaware, USA) pour l'analyse des petits ARNs dans ses recherches futures.

L'équipe « Genomic Networks » dirigée par M-L. Martin-Magniette accepte la remarque du comité sur sa visibilité à l'international. Cette équipe a développé plusieurs collaborations à l'international sur les aspects méthodologiques (e.g. A. Raftery Univ of Washington on mixture models) et compte renforcer les interactions avec les biologistes et participer plus activement dans des Congrès internationaux.

La plateforme Transcriptome a anticipé la recommandation du comité et travaille sur son intégration à l'Observatoire du végétal à l'IJPB à de l'INRA-Versailles. Cette plateforme est déjà

Gif-sur-Yvette, le 25/03/2014

labellisée IBiSA et voudrait garder une certaine capacité de séquençage en plus de continuer à développer et valider des nouveaux protocoles d'analyse informatique et des services de construction de banques afin d'offrir un service le plus complet possible.

Dans le prochain plan quinquennal, l'IPS2 portera un projet original dans le continuum recherche fondamentale-enseignement supérieur-innovation en sciences végétales.

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