Institut de génomique - génoscope

Rapport Hcéres

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

Section des Unités de recherche

AERES report on the research unit

GENOSCOPE

From the

CEA

May 2010

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

Section des Unités de recherche

AERES report on the research unit

GENOSCOPE

From the

CEA

Le Président
de l'AERES

Jean-François Dhainaut

Section des unités
de recherche

Le Directeur

Pierre Glorieux

May 2010

Research Unit

Name of the research unit : Institut de Génomique Genoscope - Centre National de Séquençage

Requested label

N° in the case of renewal

Name of the director : Mr. Jean WEISSENBACH

Members of the review committee

Chairperson :

Mr. Philippe GLASER, Institut Pasteur, Paris

Other committee members

Mr. Pascal BARBRY, Université de Nice- Sophia Antipolis

Mr. Emmanuel BARILLOT, Institut Curie, Paris

Mr. Catherine FEUILLET, Université Clermont-Ferrand 2

Mr. Frank Oliver GLÖCKNER, Jacobs University, Bremen, Allemagne

Mr. Julian PARKHILL, Wellcome Trust Sanger Institute, Cambridge

Mr. Jean-Louis REYMOND, Université de Berne, Suisse

Committee members nomminated by staff evaluation committees (CNU, CoNRS, INSERM and INRA CSS....)

Observers

AERES scientific advisor

Ms. Michelle DEBATISSE

Research Organization representatives

M Gilles BLOCH

Ms Anne FLÜRY-HERARD

Report

1 • Introduction

- Date and execution of the visit :

The visit took place on March 25 and 26, 2010. The Genoscope Director made a general presentation of the Genomic center, starting with its history and describing its initial missions and their evolution. The sequencing activity (data production, finishing and major projects), the bioinformatics and the applications (high throughput cloning and biocatalytic activities screening, and metabolism engineering) were presented and discussed in three separate sessions. The committee had a quick tour of the center and heard separately the scientists and engineers, the technical staff, the group leaders and the Director. It met also the Director of the CEA SDV department.

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

The Genoscope was created as a GIP (groupement d'interêt public) in 1997 as a national sequencing center combining sequence production with sequence analysis and annotation. In 2000, a research Unit CNRS/Genoscope/Evry University (UMR8030) was created within the Genoscope . The UMR has already been evaluated in 2008. Genoscope was included in the CNRG in 2002 and finally integrated in the DSV of the CEA in 2007 leading to a modification of the status of the employees.

The 5000 m2 laboratory is located in the Genopole campus at Evry. The lab space is perfectly well adapted for the different activities conducted by the Genoscope, which are high throughput sequencing and bioinformatics for both services and internal projects and two connected fields: high throughput cloning and biocatalytic activities screening and metabolism engineering (synthetic biology). The focus of this expertise concerns the service to the community, the sequence production and technological developments, the sequence annotation and the research activity of the two small research groups that are not part of the UMR 8030.

- Management team

The management team is constituted by the director of the Genoscope together with the six team leaders (Sequence production, finishing, mutation analysis, Bioinformatics, Application (synthetic biology), and biocatalytic activities screening) with a strong interaction with the UMR team leaders. There is no formal management organization with for example a management board. The Director together with the team leaders meet once a month, but in fine the Director takes the decisions. The different categories of personal are satisfied by this management organization.

Historically a Genoscope scientific committee was in charge of the selection of sequencing projects submitted by the community but also to evaluate the in house project and the strategy. This committee was replaced in 2008 by an IBISA scientific committee only in charge of the selection of community sequencing projects performed on the Genoscope budget.

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

	Past	Future
N1: Number of researchers with teaching duties (Form 2.1 of the application file)	0	0
N2: Number of full time researchers and engineers from research organizations (Form 2.3 of the application file)	40	40
N3: Number of other researchers including postdoctoral fellows (Form 2.2 and 2.4 of the application file)	1	1
N4: Number of technicians and administrative staff with a tenured position (Form 2.5 of the application file)	56 (54 ETP)	56 (54 ETP)
N5: Number of other engineers, technicians and administrative staff (Form 2.6 of the application file)	1	1
N6: Number of Ph.D. students (Form 2.7 of the application file)	0	0
N7: Number of staff members with a HDR or a similar grade	3	3

2 • Overall appreciation on the research unit

- Overall opinion

The Genoscope combines service to the community for small to large sequencing projects with its own genome projects. It has elaborated an efficient pipeline of sequence production from cloning to genome annotation for both microbial and large eucaryotic genomes. The Genoscope has recently diversified its activities and is developing two new research areas: (1) the functional annotation of genes through screening for biocatalytic activities after gene cloning and protein production and (2) metabolic engineering, for which promising preliminary results have been shown.

The Genoscope is recognized internationally for its contribution and leadership in major sequencing projects starting with the human chromosome 14 and reflected by publications in top-level journals. At an international level it is considered as a medium size genome center. But in fact its number of deep sequencers (6) positions Genoscope as a rather small size genome center. The service to the community is largely recognized by the French community and has contributed to the development of Genomics in France. However, due to budget limitations and to the difficult task of providing services to the community with a broad range of diverse projects, Genoscope sequencing throughput and its competitiveness and visibility has decreased during the last years. For this reason, the Genoscope does not have any more its own projects.

The Genoscope has decided to focus its activity on plant and environmental (in particular marine protists) genomics. Few genome centers are dedicated to these two fields. The solid infrastucture of the Genoscope, the expertise and knowledge of its staff and the acquisition of new generation sequencers by local IBISA platform to perform small and medium size projetcs, should allow the Genoscope to gain again its position at the international level (provided that Genoscope is given a significant increase of its budget).

- Strengths and opportunities

The Genoscope has a long lasting expertise in Genomics to combine different technologies on diverse systems: microbes, metagenomes and Eucaryotes.

The combination of research and platform activities, in particular through the association with the UMR, ensures state of the art methods in the field of sequencing and bio-analyses.

The Genoscope is well prepared to face an increase of its sequencing capacity given its solid information technology (IT) infrastructure supported by an efficient team and a granted access to super computer facilities (Genci).

Its stable teams in terms of technicians, engineers and group leaders with strong interactions are highly motivated.

The emergence of new sequencing technologies provides opportunities for new projects and motivates the teams. The decision to acquire a 3rd generation long read sequencer is promising, especially for environmental sequencing projects.

The two major projects considered for the future: plant genomics and protists genomics were considered as the right niche to become again a significant Genomic center at the international level.

The development of new research topics connected to genomics, in particular the characterization of new catalytic functions, will contribute to improve protein function annotation.

- Weaknesses and threats

The lag in terms of acquiring and using new equipment at a high level compared to other genomic centers has contributed to reduce the capacity of the Genoscope to perform really large genomic projects.

The duty to perform a large number of diverse small projects as a service to the community is extremely costly in terms of resources and limits the possibility of future development of the Genoscope.

Projects are managed centrally by the production or finishing teams according to the type of project. An identified informatician is in charge of data control and flow between production and collaborators. However, the management system appears poorly adapted to the large number of ongoing projects, which leads to rather weak user interactions.

The communication with collaborators, which quite often lack expertise in Genomics and bioinformatics, remains an issue. The external collaborators need to be informed regularly on the status of the project , what has been done, what they have to do.) There is no formal user committee. This project management system may contribute to get a feed back on the collaboration and to improve the whole process.

There is no clear evaluation processes of the cost of operations since two years, which hinders the possibility to evaluate the cost / benefit for each project. In particular to evaluate the cost of finishing.

- Recommendations to the head of the research unit

It is recommended:

-to reduce the number of collaborative projects by focusing on large scale projects and on fewer types of projects (e. g. genomic projects). Small projects should be oriented to IBISA genomic platforms. This must be discussed with the IBISA sequencing scientific committee,

-to set up a management system that will enable regular and semi-automatic communication with the collaborators on the status of their project,

-to reevaluate the status of long lasting projects, or projects that did not start after a certain period, e.g. 1 year,

-to improve the estimate of cost / benefit of each project, and to evaluate carefully if finishing of genomes is worthwhile since a large number of unfinished (draft) genomes can be done for the same price. This needs to be carefully discussed with the users.

-to improve the procedure to implement new methods and take more risk in implementing them,

-to extend the role of the IBISA scientific committee to evaluate internal sequencing projects and the Genoscope strategy.

- Data on the work produced :

(cf. http://www.aeres-evaluation.fr/IMG/pdf/Criteres_Identification_Ensgts-Chercheurs.pdf)

A1: Number of permanent researchers with or without teaching duties (recorded in N1 and N2) who are active in research	
A2: Number of other researchers (recorded in N3, N4 and N5) who are active in research	
A3: Ratio of members who are active in research among permanent researchers [(A1)/(N1 + N2)]	
A4: Number of HDR granted during the past 4 years	
A5: Number of PhD granted during the past 4 years A6: Any other relevant item in the field	1

These numbers are not significant given the missions of the Genoscope.

3 • Specific comments on the research unit

- Appreciation on the results :
  - Relevance and originality of the research, quality and impact of the results

In the context of a genome center, results are the production of sequences, their annotation and analyses. The platform had a major contribution in the development of genomics at the national level by performing both small and large-scale projects. Many collaborators lacking expertise in genomics and bioinformatics, the involvement of the Genoscope teams in data analysis and interpretation was often more important than initially foreseen. The large number of small size projects, although greatly acknowledged by the community, led to an increased cost per base and reduced the capacity to perform large projects with international visibility.

The major genome projects published these last years by the Genoscope are the protist *Paramecium tetraurelia*, the black truffle and the grape vine. It has also been a pioneer in environmental metagenome projects by the analysis of the microbiota from a wastewater plant from Evry and it contributed to the recently published extensive genomic investigation of the gut microbiome. However, for this last project Genoscope was unable to compete with the sequencing capacity of the BGI-Shenzhen.

Sequence production: The Genoscope has progressively incorporated new technologies in its different sequencing pipelines (Roche-454 and more recently Illumina) in an efficient but somehow also cautious manner. The rather conservative way of implementing new technologies is partly due to the commitment of Genoscope to fulfill projects previously accepted by the Scientific Committee as a service to the community. These commitments explain why Genoscope is for instance still using more intensively capillary sequencing than most genome centers. The focus on *de novo* sequencing with the goal to produce high quality finished genomes corresponds to a demand from the community. However the benefit of dealing with draft genome sequences of multiples samples need to be further explored. A more extensive use of short reads and multiplexing would allow the Genoscope to improve the ratio between cost and benefit for many projects. For the future, in view of the expected reduction in finishing, the mission of the Finishing group will have to be reevaluated.

Bioinformatics: the scientific information technology (IT) lab shows strong skill in terms of data management, storage, heavy computation and provides efficient support both to the sequencing and bioinformatics teams. The technological solution is well adapted and they use state of the art methodologies for developments of software tools. Peak needs for computation are outsourced to large computing national centers. The strong interaction between the IT lab and the other groups both in terms of equipment and software is extremely beneficial. The interaction of the Genoscope with the Bioinformatics groups from the UMR provides the tools and the strategy for genome sequencing and genome annotation.

Screening for biocatalytic activities: this small team has implemented an efficient strategy for high throughput cloning and expression of proteins predicted by genome annotation. It has focused on few protein families (*i. e.* thiamine pyrophospahe-dependent enzymes or nitrilase) and has expressed almost all proteins from *Acinetobacter bayli* ADP1, a bacteria selected as a model organism by the Genoscope. They have also set up a procedure for the identification of catalytic activities by combining different methods and using state of the art technologies including mass spectrometry. This group interacts strongly with different teams from the UMR in particular in bioinformatics and organic chemistry.

Metabolic engeeniring: this team has initiated several innovative projects in the field of synthetic biology including the engineering of *E. coli* strains able to fix CO2 by a non-canonical pathway or with a simplified metabolism devoid of reactions requiring thiamine pyrophosphate and the implementation of a new pathway for the biosynthesis of deoxyribose. It combines the expression of new activities in *Escherichia coli* with directed evolution and chemistry. For the purpose of directed evolution, it has set up an automatic device allowing long lasting bacterial continuous culturation that has proven to be extremely efficient. Significant achievements were shown for the different projects. However, most if not all these projects result of collaborations with a single industrial partner and it has been difficult to define the exact contribution of the CEA team in terms of innovation.

- Number and quality of the publications, scientific communications, thesis and other outputs

The number and the quality of the collaborative projects led to co-authorships in a significant number of publications, including 20 as major authors and in high-ranking journals, such as Nature, Nature Biotechnology Genome Research. The new topics (metabolism engineering and biocatalytic activities screening) did not yet lead to any publication, however there is a great potential for original results there. The Director of the Genoscope and one of the team leaders are regularly invited at national and international conferences. As a technological infrastructure, no PhD thesis were expected, however, the Genoscope may contribute more to training by hosting students at the level of Master-Pro, engineer school or License for example as "apprenti".

Quality and stability of partnerships *(optional)*

- Appreciation on the impact, the attractiveness of the research unit and of the quality of its links with international, national and local partners :
  - Number and reputation of the prizes and distinctions awarded to the unit members, including invitations to international conferences and symposia

The reputation of the Director is a key element in the international recognition of the Genoscope. The Genoscope is recognized for the quality of its achievements and their impact. However, the relative decrease in sequence production compared to that of some other sequencing centers, if not corrected, may impact on the future reputation of the center.

- Ability to recruit top-level scientists, post-docs and students, and more particularly from abroad

As a platform, the Genoscope is not expected to recruit top-level scientist, but projects. There are few genomic centers dealing with non-human or non-disease related genomics. The Genoscope is therefore an attractive center for international projects focusing on plant genomics and environmental genomics, and metagenomics.

- Ability to raise funds, to successfully apply for competitive funding, and to participate to scientific and industrial clusters

The Genoscope has been and remains an important partner in numerous national and international sequencing projects funded both by the national research agency (ANR) and by the EU. This funding represents a substantial part of the budget of the Genoscope. The genomic part of the Tara Ocean project is only funded on a pilot level (ANR grant) so far but Genoscope aims at developing a larger project as a follow up. Although a person was recruited with a

part-time activity dedicated to the specific task of fund raising, the possibility to raise adequate funding for this ambitious project remains hypothetical. For the catalytic activities screening group, the Genoscope is partner in one ANR project (coordinated by a group from the UMR) and this group is expected to raise additional funds both from public sources and industrial partners in the near future.

- Participation to international or national scientific networks, existence of stable collaborations with foreign partners

Since its creation, the Genoscope has been a partner in numerous international genome projects. For the future, the Genoscope is expected to become the leading genomic partner of the Tara Ocean project. It will be responsible for the choice of the best strategy to gain maximum information from the samples (sequencing of reference strains from cultured protists, single cell sequencing of unculturable protist, and sequencing of metagenomes). It should take a leading role for the sequencing per se and for the first levels of sequence analysis.

- Concrete results of the research activity and socio-economic partnerships

The diversification of the Genoscope in the screening of enzymatic activity and metabolic engeenering is associated with strong interaction with a company and they are seeking for further industrial collaborations. The person with a part-time activity dedicated to the specific task of fund raising is also in charge of the development of additional industrial partnerships. This will help Genoscope to fulfill one of its original missions.

- Appreciation on the strategy, governance and life of the research unit:

  - Relevance of the unit's organization, quality of the governance and internal and external communication

The Genoscope is organized in six teams, each headed by a team leader. This organization allows it to fulfill efficiently its mission. There is a very good internal communication between these groups and with the research groups of the UMR in particular with the two groups involved in microbial and eukaryote genome annotation. Regular meetings are organized for the different teams and for projects. Engineers and scientists are fully satisfied with the internal communication. The technicians stated that they miss global view on the different projects. This could be achieved in the frame of general assemblies.

Conversely, the external communication deserves to be improved. As previously stated, regular information on the status of the projects should be sent to the external partners and a mechanism that enables regular feedback from the partners of a project could be put in place. The Genoscope may also contribute more significantly to the promotion of genomics for example by organizing (or co-organizing) courses and meetings. The Genoscope website is set up to provide extensive and didactic information on the ongoing and performed projects and their status. Unfortunately, this web site has not been updated since two years. This needs to be rapidly changed as it also participates to the international visibility of the center.

- Relevance of initiatives aimed at scientific coordination, emergence of cutting edge projects and taking of risks

As a technological platform, the Genoscope is in most cases identified as a partner in large consortia. However, the emergence of new sequencing technologies provides opportunities to coordinate ambitious and cutting edge projects in the study of plant evolution and of marine protist as examplified by the Tara Ocean project. To achieve this, a strong involvement of the research teams of the UMR is necessary.

There is no coordination of the activity of the Genoscope with that of the CNG (Centre National de Génotypage). The specificity of these structures relies on their thematics, the CNG being in charge of human genetics and genomics, and the Genoscope of the rest. However, it would be more efficient and costless to better coordinate the activity of both Institutes, in particular with respect to bioinformatics and technology development.

- Involvment of the unit's members in teaching activities and in organizing research at the local level

Not relevant

- Appreciation on the project:
  - Existence, relevance and feasability of a medium- or long-term scientific project

In the recent years, due in part to budget limitation, the Genoscope had to reduce the number of in house projects. With the raise of new high throughput technologies, the Genoscope aims to gain leadership in two different areas: plant and protist genomics. In addition, the Genoscope will continue to be in charge of large genomics projects submitted by the national community, in some cases within international consortia.

Plant comparative genomics: Genoscope has published outstanding results on genome duplications that occurred during the evolution of mono and dicotyledonous plants. Thus far, the strategy has been to perform the analysis of plant genome duplications through projects proposed by partners in the French community (*e. g.* grape, banana). This approach, however, may become limited as the genomes chosen by the community may not be the most adapted for analyzing the history and mechanisms of genome duplication. Given the sequencing capacities at Genoscope and the availability of other plant genome sequences in the databases, the evaluation panel suggests for the Genoscope to develop its own strategy alongside these collaborations and select plant genomes to be sequenced and re-sequenced in view of answering their evolutionary questions.

The Tara Oceans project and protist genomics: The Tara Ocean project is a three year global expedition to explore the photic zone of the worlds ocean's. Similar to the well known Venter global ocean sampling cruises, Tara Ocean also makes use of the advances in high-throughput sequencing technologies. In contrast to the Venter cruises which have a clear focus on prokaryotic biodiversity of surface waters, Tara Oceans will analyze the biodiversity of protists, zooplankton, prokaryotes and viruses and heavily link this information with images and environmental parameters of the different sampling sites. Global questions like: Who is out there? What are they doing? and How does the environmental select? will be addressed in times of global changes. It is expected that the project will provide significant new insight especially in the biodiversity and distribution of the eukaryotic plankton. The Genoscope has started to take a leading role in protist sequencing. The sequencing efforts are split into the sequencing of around 50 reference protist genomes from culture collections, single-cell genomics to address the uncultivated fraction and finally metagenomes and metatranscriptomes of the sampling sites. In the ongoing pilot phase all steps and standards will be developed for sampling, DNA/RNA extraction, sequencing and bioinformatics. In terms of standardized submission of sequences and contextual data from genomes and metagenomes, the Genoscope should get in contact with Genomic Standards Consortium and implement the emerging Minimum Information About a (Meta)Genome Sequence (MIGS/MIMS) standards to facilitate data exchange.

The committee strongly supports the engagement of the Genoscope in this internationally visible project and further steps should be taken to extend the leading role of the Genoscope. The scale and topic of the project fits nicely to the mission of the Genoscope and it is expected that it will guide technological advancements on the sequencing and bioinformatic platform. The strong involvement of the Genoscope on currently emerging long reads sequencing technologies, especially for the metagenomes and metatranscriptomes, was appreciated. This must be accompanied by significant investments in the sequencing platform, including consumables.

Screening of bio-catalytic activities: the group leader has shown a clear strategy to develop this new activity through national collaborations, and an ANR project has been submitted with an external unit in organic chemistry. The team has developed a solid infrastructure and the interaction with the Genoscope teams together with the access to a rich collection of genomic and metagenomic DNAs, put it as an attractive partner for ambitious projects in the biocatalyst field. The team leader is aware that a critical aspect will be the choice of the enzymatic families that will be selected for screening.

  - Existence and relevance of a ressource allocation policy

Genomics is costly and even if the Genoscope has been successful to raise funds from the ANR and EU, money has been limiting for the development of the Genoscope. Given the choice made to address questions unrelated to human health, raising money is a difficult issue. Several alternatives to the classical funding on project were

considered, like to apply to the National Loan or to obtain the status of TGIR (très grand instrument de recherche). As already mentioned, a person has been recruited for this purpose and for development of industrial partnerships but funding presently remains an important issue.

Originality and risk-taking

As a platform to take risk is probably not a necessity, and one would expect more that the community submits risky and original projects. This was the case in several instances, for example in the choice of the sequenced organisms. However, it is important that Genoscope is prepared to take such projects forward and tests some risky strategies. The bio-catalytic screening group is also expected to screen more original but also more difficult families of enzymes.

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

Réponse du Génoscope au rapport Aeres

Nous nous réjouissons que le comité ait apprécié la qualité de l'informatique et de la bioinformatique, notre motivation, nos intentions sur les équipements de séquençage de troisième génération, nos projets futurs dans le domaine de la biodiversité notamment des protistes et nos nouvelles orientations dans des aspects plus fonctionnels de la génomique. Le comité souligne que ces aspects sont peu considérés dans les autres centres de génomiques.

Comme nous, le comité déplore que Genoscope ait perdu une grande partie de sa visibilité en raison de son sous-équipement notable qui a pris le pas ces dernières années, du fait des limitations budgétaires.

Un certain nombre de critiques ont aussi été émises auxquelles nous souhaitons apporter une vue plus nuancée ainsi que quelques explications.

- La mise en place des nouvelles technologies serait lente. Ceci est vrai quand on compare notre situation à celle des grands centres. A l'inverse de ceux-ci, Genoscope n'est plus un centre assez important pour bénéficier de programmes d'accès "en primeur" (souvent avec un an d'avance) réservés aux grands centres. Nous avons aussi tenté de comparer les différents instruments avec une équipe de développement restreinte, sans doute au détriment de la rapidité de déploiement d'une technologie donnée dont le choix aurait pu intervenir plus tôt. Du fait du service à la communauté nous sommes tenu d'offrir une large palette de techniques et donc d'instruments associés. En outre, le déploiement rapide de nouvelles procédures n’est pas compatible avec un centre travaillant à grande échelle en intégrant des procédures d'assurance qualité. La montée en puissance des techniques nouvelles nécessite une mise en place progressive.

- le Centre est occupé à trop de petits projets et trop de finition. Il est indéniable que ces activités très exigeantes en personnels (souvent hautement spécialisés) sont très onéreuses pour Genoscope. Les petits projets ont souvent été initiés en réponse à des sollicitations des équipes externes (projets financés par l'ANR) ou de l'appel à projets IBiSA à des périodes où des solutions alternatives existaient peu. La nécessité de finition est un débat ancien, dans lequel nous sommes très souvent placés devant une forte pression des équipes demandeuses. Nous sommes en plein accord avec le comité qui recommande de réduire finition et petits projets. C'est la mise en œuvre de ce type de recommandation qui s'avère délicate.

- Les équipes seraient insuffisamment informées sur le déroulement de leur projet. Nous sommes étonnés de cette critique qui peut bien sûr concerner certains projets, mais qui à notre sens ne résulte pas d'une consultation générale des nombreux collaborateurs qui ont fait appel au Genoscope durant la décennie écoulée. Il nous semble que seule une enquête de satisfaction aurait permis de trancher cette question et d'avoir un retour utile pour les orientations futures des activités de service. Nous réfléchissons à la réalisation d'une telle enquête.

- La gestion des projets extérieurs serait défaillante. Nous nous étonnons aussi de cette constatation. Plusieurs formules de gestion des projets extérieurs ont été expérimentées par le Genoscope. Au terme de ces expérimentations, portant sur plusieurs centaines e projets, il apparaît que la plus efficace est celle qui assure le plus court chemin entre l'utilisateur et le laboratoire de séquençage du Genoscope. Nous nous sommes longuement expliqué, notamment dans la discussion entre le comité et les responsables de laboratoire. Ces éclaircissements n'ont manifestement pas retenu l'attention du comité. Ce dernier au contraire a formulé des propositions qui nous apparaissent purement théoriques, essentiellement adaptée aux petites plateformes.

- la mise en place d'un système d'information utilisateurs semi-automatique a été recommandée. L'information semi-automatique aboutit très souvent à susciter plus de questions qu'il n'apporte de réponses.

- L'absence d'un comité d'utilisateurs a aussi été soulignée.
La grande majorité des utilisateurs avec qui nous avons développé des projets, reconnaît le sérieux et le professionnalisme de ses interlocuteurs du Genoscope. Nul doute qu'une enquête de satisfaction sera nécessaire pour étayer ces affirmations. Mais, parmi nos convictions, nous estimons être à l'écoute des utilisateurs. Et même si les projets peuvent être regroupés par objectifs généraux, chacun est un cas particulier, surtout dans ses tenants et aboutissants, son stade de départ et son but final. Ce ne sont pas les recommandations d'un comité d'utilisateurs qui vont faire progresser la situation du "sur mesure" que nous nous sommes toujours efforcé de prendre en compte pour amener les données dans leur meilleur état. Les desiderata réitérés des utilisateurs nous sont à l'inverse bien connus et visent surtout à recommander (1) la finition des projets de séquençage portant sur des génomes entiers, voire sur des collections de cDNA et (2) la prise en charge de plus de petits projets. Le principal effet d'un comité d'utilisateurs représentatifs serait donc d'augmenter la fraction de finition et de petits projets et donc d'aller à l'opposé des recommandations de ce comité d'évaluation.

- L'absence d'évaluation des coûts qui empêcherait d'estimer un rapport coût/bénéfice pour les projets. Nous avons effectivement nous-mêmes mentionné que nous ne pouvions contrôler certains éléments de coûts et que le caractère volatile des protocoles ne permet de remplir cette tâche de façon rigoureuse. Mais ceci ne nous jamais empêché de procéder à des approximations assez précises pour éclairer des choix sur les approches expérimentales. Et c'est dans ces termes que les choix sont expliqués et discutés avec les utilisateurs.

- Il y aurait depuis quelques temps une diminution de la production de résultats de premier plan sous-entendant un certain déclin. Nous constatons que la dernière publication dans Nature parue au moment de l'évaluation (génome de la truffe) n'a pas été prise en considération dans le rapport du comité. Est-ce délibéré pour étayer la démonstration ? Une autre publication (génome d'Ectocarpus) dans Nature est actuellement sous presse

- Il est indiqué que le site web n'a pas été mis à jours depuis deux ans. Ceci est vrai pour quelques aspects sur les projets extérieurs que nous avions indiqués au comité. Mais cette généralisation à l'ensemble du site web est une contre-vérité.

- Il est indiqué que le directeur, consulte ses proches collaborateurs (chefs de laboratoires), mais qu'il décide seul. Le directeur du Genoscope est seul responsable devant ses tutelles (passées et présentes). Aussi évite-t-il de mettre en oeuvre des propositions collégiales de personnes non mandatées qu'il désapprouverait.

- Il est recommandé d'étendre le rôle du comité "séquençage" du GIS IBiSA à l'évaluation des projets propres et de la stratégie du Genoscope. Cette fonction se situerait clairement en dehors du rôle attribué à ce comité dans la convention constitutive du GIS IBiSA. Mentionnons aussi que les projets propres actuels font tous l'objet de financements extérieurs, principalement par le canal de l'ANR, et sont donc évalués à ce titre.

Dr Jean Weissenbach
Directeur du Génoscope