GDEC - Génétique, diversité et écophysiologie des céréales

Rapport Hcéres

To cite this version:

Rapport d'évaluation d'une entité de recherche. GDEC - Génétique, diversité et écophysiologie des céréales. 2011, Université Blaise Pascal - UBP, Institut national de la recherche agronomique - INRA. hceres-02035232

HAL Id: hceres-02035232

https://hal-hceres.archives-ouvertes.fr/hceres-02035232v1

Submitted on 20 Feb 2019

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

Section des Unités de recherche

AERES report on the research unit

Genetics, Diversity and Ecophysiology of Cereals

From the

University Blaise Pascal

INRA

February 2011

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From the

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Le Président de l'AERES

Didier Houssin

Section des unités
de recherche

Le Directeur

Pierre Glorieux

February 2011

Unit

Name of the unit: Genetics, Diversity and Ecophysiology of Cereals GDEC

Requested label: UMR_A INRA

N° in case of renewal: UMR 1095

Unit director: Mr Gilles CHARMET

Members of the expert committee

Committee chairman

Mr. Dominique DE VIENNE, Université Paris 11, Orsay, CSS INRA representative

Other committee members

Mr Patrick SCHWEIZER IPK Gatersleben, Germany

Mr Paul NICHOLSON, JIC Norwich, UK

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(The CNU member was not available)

Report

1 . Introduction

Date and conduct of the visit

The visit took place on February 22nd and 23rd, 2011. The first day was divided into three parts. First the global presentation of the Unit was made by Gilles CHARMET, the Unit's Director, who presented the results for the past four years, and by Catherine FEUILLET, Deputy Director, who presented the project for the coming five years. The platforms and facilities were described in this session. Note that C. FEUILLET substituted for the future Director, Thierry LANGIN, who was absent for health reasons. Secondly, the leaders of the future six groups of the Unit presented the results and projects for their respective research teams. Thirdly, there were informal discussions with permanent and non-permanent staff (Engineers & technicians, PhD students & post-docs, scientists & teacher-researchers), with the directors board and with the representatives of the two organizations supervising the UMR, INRA and University Blaise Pascal of Clermont Ferrand.

The second day the committee met in closed session to prepare the writing of the report.

The members of the UMR were very well prepared for the visit of the committee, and the quality of their presentations revealed the great care they took in the preparation of the unit's five-year project. Committee members would like to congratulate the entire laboratory staff for their hospitality and for the high quality of presentations and discussions.

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

UMR 1095 GDEC was set up in January 2000 under the name of the "Plant Breeding and Health Unit", resulting from the fusion of the associate laboratory "Organization and Variability of Plant Genomes" (OVGV) and of the INRA Plant Breeding Unit. It took its present name at the beginning of the current four-year contract, in January 1st 2008. The two organizations supervising the Unit GDEC are the University Clermont II Blaise Pascal (UBP) and INRA. The Unit depends on the INRA Clermont-Ferrand-Theix-Lyon Research Centre, and to three INRA Scientific Divisions: GAP, EA and SPE. It is located in two geographical sites: the INRA buildings are located in the Domaine de Crouël (Clermont-Ferrand) and host more than 90% of the staff in their 3080 m2, and the Campus des Cézeaux (Aubière) hosts the University staff in 365 m². The GDEC is part of the "Clermont-Université" Higher Education Cluster (PRES) and is a founder member of the "Céréales Vallée" Competitiveness Cluster.

The research projects of the GDEC focus on bread wheat, the third most widely produced cereal in the world. At the Unit top-level fundamental research is performed with the final goal to improve the quality and yield of wheat in a context of sustainable agriculture and climate change. A part of the team works on the structure, function and evolution of the genome of the hexaploid bread wheat, others work on the genetic, molecular and physiological mechanisms involved in the control of traits of agronomical importance such as yield and grain quality, and finally some projects aim at applying the results obtained for understanding the genetic and environmental bases of agronomic traits and for improving these traits in plant breeding. The complementarities and integration of the various types of scientific activities are fully relevant and result from extensive and in-depth discussions within the laboratory over the past months.

Management team

The board of directors consists of the Director, G. Charmet, and two Deputy Directors, C. Feuillet and S. Mouzeyar. C. Feuillet is in charge of the scientific policy while S. Mouzeyar is responsible for the relationship with the University. In 2010 T. Langin joined this board, and he was involved in the preparation of the Unit's project for 2012–2016. The Unit management is assisted by P. Tixier Leyre, an administrative assistant, and by B. Debote who leads the administration/finance team. Finally there are various collective structures to help the directorate to make the decisions: an Executive Council, a Unit Committee with elected people representing the different categories of staff within the Unit, and an annual General Assembly. In addition there are regular team meetings.

- Staff members

	In the report	In the project
N1 : Number of professors (see Form 2.1 of the unit's dossier)	5	5
N2 : Number of EPST, (Public scientific and technological institution) or EPIC, (Public industrial and commercial institution) researchers (see Form 2.3 of the unit's dossier)	11	11
N3 : Number of other professors and researchers (see Form 2.2 and 2.4 of the unit's dossier)	0	0
N4 : Number of engineers, technicians and tenured administrative staff members (see Form 2.5 of the unit's dossier)	82.73	82.73
N5 : Number of engineers, technicians and non-tenured administrative staff members (see Form 2.6 of the unit's dossier)	28.5	15.5
N6 : Number of doctoral students (see Form 2.7 of the unit's project dossier)	16	12
N7 : Number of persons accredited to supervise research and similar	14	14

2 . Assessment of the unit

- Overall opinion

The Unit has an outstanding scientific output and a tight integration in international networks on bread wheat genomics, genetics and breeding. It has gained worldwide leadership in structural genomics of wheat, and a high potential for molecular dissection and identification of genes of agronomic interest, such as genes governing nitrogen use efficiency, biotic and abiotic stress resistance, recombination frequency, etc.

- Strengths and opportunities

The Unit capitalizes in an optimal manner on the results and genetic material generated throughout previous decades. The Unit has been able to recruit in recent years distinguished scientists in the field of genomics, plant pathology and eco-physiology. It has demonstrated its ability to raise funds from diverse national and international contracts thanks to the focused efforts on wheat as a complex experimental system of utmost agronomic and economic importance.

The Unit has developed highly efficient infrastructures and platforms to exploit all their extended genetic resources that are also integrated in the International Treaty for Plant Genetic Resources for Food and Agriculture. The Unit (C. Feuillet) will lead the recently approved project BreedWheat (Investissements d'Avenir), which will contribute to maintaining the integrated nature of the Unit project for the next nine years. Another opportunity facilitated by this grant will be the development of international collaborations with the CGIAR research program on Wheat at CIMMYT and ICARDA. The new organization and management structure seems highly appropriate to support the Unit overall project for 2012-2016.

- Weaknesses and threats

There are few weaknesses and threats in this laboratory. However, the massive and still increasing use of informatics tools makes it necessary to recruit local additional human resources in informatics and bioinformatics, because the URGI support cannot sufficiently respond to all the needs of the Unit.

Another problem is the lack of space. The Unit is expected to continue to grow, and at the present time the construction of new buildings is not an option for INRA. It is crucial for the development of the lab that this bottleneck will be solved. In addition, the dual location of the Unit at the Domaine de Crouël and the Campus des Cézeaux sites impedes the communication for some people. The increasing need for functional validation of genes will make it crucial that S2 facilities are made available.

- Recommendations for the unit director

The future director will have to continue the remarkable dynamics of the Unit, and pay attention to the need for a feeling of “ownership” among all the staff, to the communication strategy at all levels, including that within each team and platform. A challenge will be to maintain an appropriate balance and communication between the six teams in the new structure. We encourage the director to seek support from INRA and the University for hiring junior and senior scientists and teacher-researchers in the priority domains: genomic selection, plant physiology and plant-pathogen interactions. Bioinformatics and informatics are crucial needs for most of the projects, and all opportunities to reinforce the corresponding capacity of the unit must be explored.

- Production data

A1 : Number of *produisants* (professors and researchers whose names appear in a minimum number of “publications” over a 4-year period) as listed in N1 and N2 in the project column	16
A2 : Number of *produisants* among the other staff listed in N3, N4 and N5 in the project column	8
A3 : Proportion of *produisants* in the unit [A1/(N1+N2)]	16/16
A4 : Number of theses for accreditation (HDR) to supervise research defended	4
A5 : Number of PhD theses defended	9

3 . Specific comments on the research unit

Appreciation on the results

The Unit has an outstanding scientific productivity and output in high impact international journals, and is positioned as a worldwide leader in wheat genomics. There is a clear focus on wheat as a major crop, and an excellent representation and integration of the entire value chain, from basic science to applications in plant breeding for sustainable agriculture.

Compared to the previous periods, there has been a marked increase in the scientific output in appropriate and general journals. Over the review period, there are 141 publications in peer reviewed international journals, 86 % of them involving external collaborators (36% from foreign countries). The mean impact factor is very high (IF=6). All scientists (24) are publishing. There are 24 books or book chapters, 93 invited talks in international conferences, 2 patents and 10 plant varieties, 14 PhD and 4 HDR defended. The Unit organized two international meetings, the ITMI and Gluten workshop.

The Unit has engaged numerous national and international longstanding private and public partnerships (37). In wheat genomics, the Unit leads international partnerships for developing the wheat genome-sequencing program.

Appreciation on the impact, the attractiveness of the research unit and of the quality of its links with international, national and local partners

There were 93 invitations in international conferences. For her remarkable scientific results, one member of the research unit has received the Foulon Price of the French Academy of Agriculture and the Trophée des Femmes en Or.

The Unit has welcomed 16 foreign visiting scientists (36 months), 8 postdocs including 2 from abroad, and 14 PhD students. There is a possible limitation due to lack of space (lab and accommodation). The attractiveness of the Unit for French as well as foreign students should be improved by the planned review of the content of the current Master's Program "Biology and the Environment" with respect to the integration of genomic and genetic science at the Unit and by emphasizing more on career aspects e.g. by better integrating private partners from Céréales Vallée.

The Unit has proved outstanding ability to raise funds. About 90% of the resources come from external contracts (37) from ANR and international leading projects. The Unit just won a nine-year substantial funding from the "Investissementsd'Avenir" (Breedwheat) from the French Ministry of Research and Higher Education. The budget of the Unit roughly doubled in the past 4 years.

The Unit has collaborations with about 20 countries, not only in Europe, but also in the USA, Asia and Australia. The Unit has been a partner in three European projects (2 FP6, 1 FP7), one of them as coordinator, has obtained 15 ANR contracts (4 as coordinators), and obtained funds from FUI, FSOV and CPER. Thus it is extremely well integrated in both the local and international networks of wheat genomics, genetics and breeding.

Over the reviewed period, the Unit won 6 contracts with the private local or national sector, receives funds from CPER and has collaborations in the context of the Competitiveness Cluster "CéréalesVallée". The Unit has produced 2 patents and 10 plant varieties over the period.

- Appreciation on the strategy, management and life of the research unit

The organizational structure in place over the past four-year contract proved to be very efficient, and the management was extensively modified. Various committees were created to improve the communication within the Unit (see § 1a). In addition there is a quite active scientific life, with the “GDEC Thursdays”, the Journal Club and the seminars of the University. As an additional measure to further increase the feeling of “ownership” among scientific staff we encourage to open up the nomination of speakers and organization of “GDEC Thursdays” also for post-docs and PhD students. However the increasing use of English in the Unit represents a challenge. The scientists should continue to make sure that all the categories of personnel share the objectives and the results obtained, and should be careful to prevent the possible opening of a culture gap between the people using particular sophisticated new technologies and the other parts of the Unit. In this connection, the publication of the monthly Gazette of the Unit is encouraged, also for communication of science news and developments at GDEC in French using non-scientific language. It is also important to implement a homogeneous and clear policy of authorship and acknowledgements of the technical staff in research articles across GDEC teams and platforms.

Discussions took one year to define the new organization chart of the Unit comprising 6 teams, and thus were done in an extensive and very careful way. However, the new organization was finally not approved by the general assembly of the unit but only by the Unit Committee.

The initiatives mentioned above for the scientific life of the Unit are relevant. In addition, the Executive council of the Unit, which includes team and platform leaders, meets monthly to discuss the important strategic decisions.

Fourteen researchers teach in the University Blaise Pascal of Clermont Ferrand, three of them in other Universities, for a total of 156 hours (from 4 to 28 hours per person) in Licence and Master. The Unit would like to contribute to the creation of a Plant Science Master with emphasis on genetics and molecular genetics and genomics.

- Appreciation on the project

The long-term scientific project is ambitious and highly relevant both for the increased knowledge background of the structure, function and evolution of the wheat genome and for plant breeding for a sustainable, low input agriculture. The synergy between the teams is evident from the integrated structure of the overall project.

25 % of the running costs of the contracts are shared between the teams. All teams obtained public and private contracts (see above), with a high rate of success.

The major part of the Unit’s research is highly original and cutting edge, and is exploiting in an optimal manner the resources and knowledge developed in previous projects.

4 . Appreciation team by team and/or project by project

- Team E1: Structure, Function and Evolution of the Wheat genomes

  Team leader: Ms. Catherine FEUILLET

- Staff members

	In the report	In the project
N1: Number of researchers with teaching duties (Form 2.1 of the application file)		
N2: Number of full time researchers from research organizations (Form 2.3 of the application file)	3	3
N3: Number of other researchers including postdoctoral fellows (Form 2.2 and 2.4 of the application file)		
N4: Number of engineers, technicians and administrative staff with a tenured position (Form 2.5 of the application file)	10 (including 2 IR)	8 (including 2IR)
N5: Number of engineers, technicians and administrative staff without a tenured position (Form 2.6 of the application file)	12 (including 5 postdoc)	9 (including 3 postdoc)
N6: Number of Ph.D. students (Form 2.7 of the application file)	4	3
N7: Number of staff members with a HDR or a similar grade	3	3

*past: Team E1 part of the Area 1 research team which split into E1 and E2

- Appreciation on the results

The team has conducted research of outstanding quality and high impact in the last 4 years and took the world leadership in bread wheat genomics. The team is also coordinating or co-chairing national (BreedWheat),European (TriticaeGenome) and International wheat genome initiatives (ITMI and IWGSC). Breakthroughs of the last 4 years included the construction of a physical map of flow cytometry-sorted chromosome 3B, its partial sequencing (the on going full sequencing represents 3 rice genome equivalents), the analysis of its structure and organisation, and 3B-located gene expression surveyed on Nimblegene arrays. Distribution of recombination crossovers was also monitored over Chr 3B using high density markers unravelling relative importance of the position along the chromosome and of sequence homology for CO formation. Besides Chr 3B-targeted research the development of large series of markers (ISBP and COS combined with SNPs) will allow high density coverage of the 21 wheat chromosomes.

Also the reconstruction of the cereal ancestral genome structure has permitted the proposing of a novel evolutionary scenario of the monocotyledonous genomes and beyond of plant genomes, building on the famous crop circle scheme established by Gale, Moore and Devos in the 90s on the basis of RFLP markers. The scenario shows that from the proposed cereal protogenome with n=5 and 9138 protogenes has been prone to whole and segmental genome duplications followed by chromosome fusions and local rearrangements explaining the current structure of the cereal genomes. These events have also been followed with respect to neo/sub functionalization of cereal genes that may explain adaptation being reflected by possible para/orthologous position of meta QTLs, as exemplified in rice and wheat (see below). The leader of these activities will start up a new team (E2) to carry on this outstanding and innovative research, which has also largely contributed to the leadership of GDEC in the wheat research community.

Positional cloning approaches have been undertaken at several loci including that for crossability with rye (Skr locus) taking advantage of ortho-meta QTLs and collaborating closely with scientists of E2, E3 and E4 teams.

The recruitment of young scientists, and subsequently that of young talented scientists and engineers has clearly boosted the team towards the world wheat genomics leadership. This has been enabled by the strong INRA GAP support and a clear focus of GDEC on wheat. The major results mentioned above have been obtained thanks to the experience and accumulated knowledge in wheat genetics and genetic resources of GDEC and an efficient in-house genotyping facility.

This outstanding research has led to high quality publications of scientists of team E1 with an average impact factor of 6.22. The 5 scientists and 3 engineers staff of the E1 team have published 50 peer-reviewed papers and 6 book chapters over the last 4 years, a large part of which as leaders (first and/or last author). All these activities have been published in excellent journals (Science, TIPS, Plant Cell, PNAS…) and some of them are now considered as reference publications. Also the remarkable number of invitations to congresses clearly demonstrates the leading role of scientists of the E1 team.

The Genome team has established a large array of national, European and international collaborations and has been the driving force of numerous regional, national ANR, European FP6 and FP7 consortia as well as international consortia, often as coordinators. Beyond excellent research results, the charismatic personality and the high networking ability of the team leader have been instrumental in this leadership.

- Appreciation on the impact, the attractiveness of the team and of the quality of its links with international, national and local partners

The staff of E1 is regularly invited in international conferences dealing with wheat genomics, bioinformatics and cereal genome evolution. Communication has not been limited to scientific journals and conferences, as shown by the record of the intense dialogue with the society (numerous interviews, press releases, press articles) and obtained awards.

Due to its leadership, the attractiveness of the team in wheat genomic research is evident, with 15 master students, 6 PhD, 8 post docs (two of the latter having been recruited as permanent staff) over the last 4 years. Also the team has hosted 16 visiting scientists over the last 4 years. This clearly demonstrates that the GDEC unit is a focal point for wheat genomics research. It would be a pity if this attractiveness for high-profile scientists becomes compromised by the limited availability of office and laboratory space in the future.

The E1 team has been very successful in raising funds from regional, national and European origins with a high frequency of grants approved, notably 2 ANR white, 2 ANR Genomics, 2 FP6/FP7 projects and 7 other national/regional contracts. Contracts also include 5 grants from INRA calls for proposals (AIP). Currently the E1 team coordinates 5 projects and participate in 3 others. Very recently, the federative project BreedWheat that team E1 coordinates, has been granted by the Ministry of research in the frame of “Investissements d’avenir”, called “Biotechnology and Bioresources”, thus providing long term funding for developing activities notably tightly linked with national seed industry. Probably more important is the fact that this project will provide additional federative cement between all the teams of GDEC. The team is also strongly involved in the competitiveness cluster “CéréalesVallées”, since one researchers of GDEC C. is member of the scientific board.

The E1 team has largely contributed to GDEC being now a main actor in major international networks on wheat structural and functional genomics and it coordinates most of them (ITMI, IWGSC, ETGI). It will likely also be a major component of the wheat CGIAR research program (CRP) on wheat. The high scientific profile and charismatic personality of the E1 team leader have been instrumental in the launching of the highly coordinated wheat genome sequencing program on a chromosome-by-chromosome basis.

GDEC is based in CérealesVallées competitiveness cluster and located in a very active seed industry region. Relationships with the socio-economic environment (Biogemma, Limagrain) are therefore very important. A recent project DIGITAL has been developed and fully financed by new private partners (RAGT, ARVALIS, KWS, Bioplante and Syngenta) demonstrating the finalized outcome of E1 team research.

Appreciation on the strategy, management and life of the team

The team organization and management appear excellent. Despite a high international activity of the team leader, the communication policy and dialogue within the team has not been neglected. It is important to maintain such informal and informative dialogue among all the team members including technicians.

The Area 1 team of the previous 4-year contract has allowed the emergence of a young scientist project on the highly innovative and challenging theme of cereal genome structure evolution (see E2 project). This E2 team through an ANR young scientist project has gained his independence and will be starting up the E2 team within the next 5-year contract of the GDEC unit.

Due to the breakthroughs in wheat- and cereal genomics, the team has been invited for presentations in genetics, genomics, evolution and bioinformatics in Universities (36 hours for team E1). The attractiveness resulting from previous GDEC area 1 activities will likely lead UBP Clermont-Ferrand to organize a more visible pole in plant science including GDEC, PIAF and GReD and to renew its offer of a Master's qualification with a stronger component in plant genomics and physiology. The creation of an international Master with European vocation would be appropriate: This would enhance the flow of PhD students from UBP into GDEC (Currently, only 4 PhD over 15 in the unit come from UBP).

Appreciation on the project

Pursuing most of the activities of the previous 2008-2011 contract, the project for the next 4 years is subdivided in 6 subprojects aiming at (i) physically mapping and sequencing of wheat chromosomes 3B and 1BL, (ii) carrying the structural and functional analysis of the gene space in chr 3B, (iii) conducting comparative and evolutionary analyses of Chr3B and 1BL, (iv) developing of HTP molecular markers for breeding, (v) characterizing the recombination gradient and underlying factors along chromosomes, and (vi) determining the molecular bases and diversity of the crossability (Skr) trait. As the team is dynamic, experienced and attractive, benefits from highly efficient platforms and resources, and has demonstrated its ability to raise funds with a clear long term funding ahead, there is no doubt that it has the capability to accomplish the workplan and go beyond.

Given the know-how of team E1 in attracting institutional, regional, national and international funding there is no specific concern to be mentioned here. The government loan funds (BREEDWHEAT) will support on a long term basis (9 years) team E1 activities. However, the team should not neglect continuing its participation in new international consortia in the frame of FP8 and CGIAR.

All the above-listed 6 projects are cutting edge in the field of wheat genetics and genomics and have the premise of new breakthroughs with both fundamental and applied significance.

Conclusion

Summary

The E1 team has clearly taken world leadership in the field of wheat genomics in a 4-year time span with an efficiency rarely being mirrored elsewhere in plant science. Focusing GDEC activities on wheat, the support from INRA (recruitments, facilities, supporting actions (AIP)), a high profile of the scientists of the team, excellent support infrastructures (platforms) and a well organized and managed unit providing the team with a productive environment have been instrumental for its success. The project of team E1 is straightforward with well planned activities, clear leadership and strong links with other GDEC teams, well embedded in international initiatives and has the premise of new breakthroughs.

Strengths and opportunities

Focusing efforts on wheat genomics through the recruitment of high-profile scientists and building on excellent knowledge, resources and infrastructures of GDEC were excellent decisions. Clear leadership, high visibility and attractiveness, ability to raise funds (e.g. stable funding provided by BreedWheat), involvement in international initiatives, and well focused and high quality cutting edge research are the strengths of the team.

Weaknesses and threats

The major threat might be to successfully maintain a good balance between the leading of cutting edge science and the time- and effort- consuming activities of coordination of worldwide initiatives. Notably, while the team leader has demonstrated her ability to coordinate many initiatives in parallel, maintaining such a high level of coordination until high quality sequence for all 21 wheat chromosomes is obtained, might be an exhausting effort. It is important also to keep a good contact and dialogue within the team and with the other GDEC teams, which so far have been very efficient and productive. For these reasons the committee recommends that the team leader who will take on the role of deputy director of the Unit (the director is not an INRA staff and has only a recent experience in wheat and the Unit), be supported in her daily activities by a deputy team leader. This could be achieved by upgrading a team member as co-leader of the group. An additional recruitment into the team in order to take over some of the activities of the upgraded co-leader should also be considered.

Recommendations

The committee has been impressed by the outstanding quality of the achievements and projects of team E1 and is confident that the team will maintain a world leadership in the coming 4 years. It recommends that INRA and UBP continue and even strengthen their supportive effort, notably in providing facilities to the team to host foreign visitors. It appears to the committee that more responsibilities might be delegated to a team member, for instance in upgrading a team member as co-leader of the group to manage most of the daily business of the team.

- Team E2. Plants Paleogenomics for Traits Improvements
  Team leader : Mr. Jérôme SALSE
- Staff members

	Past	Future
N1: Number of researchers with teaching duties (Form 2.1 of the application file)	0	0
N2: Number of full time researchers from research organizations (Form 2.3 of the application file)	1	1
N3: Number of other researchers including postdoctoral fellows (Form 2.2 and 2.4 of the application file)	0	0
N4: Number of engineers, technicians and administrative staff with a tenured position (Form 2.5 of the application file)	1	2
N5: Number of engineers, technicians and administrative staff without a tenured position (Form 2.6 of the application file)	9	3
N6: Number of Ph.D. students (Form 2.7 of the application file)	1	2
N7: Number of staff members with a HDR or a similar grade	1	1

- Appreciation on the results

This young team emerged during the last four years from the “genome team” (see team E1). The originality and main strength of its research work is to link basic research on paleogenomics and genome evolution with more applied research on genes potentially involved in agronomic traits. On both aspects, the quality of the research performed is outstanding. Within a few years, the team has achieved an international leading position in plant paleogenomics. In the last four years this team has obtained important results, including:

A major contribution to the description of the global patterns and events involved in the evolution of the structure of plant genomes, by reconstructing ancestral chromosomes and establishing the chronology of major genomic events (whole genome duplications, chromosome fusion and fission). This will constitute a reference scenario for numerous basic and applied works.

- The proposition of a new mechanism of chromosome evolution based on the nested chromosome fusion.
- The characterization and the quantification of the divergence in expression of duplicated genes
- The involvement in large scale genomic projects (Brachypodium and Cacao genomes, wheat 3B chromosome) and the production of genomic resources (markers)
- The development of bioinformatics tools (e.g. orthology detection)
- The progress in identification and characterization of genes of agronomic interest

The emergence of this team from the “Genome” team during the last four years was thus highly justified.

The publication output of the team is very high, both in number and quality: 22 publications for one permanent scientist, including 15 as leading author, mostly in high-ranking journals (including 1 Nature, 1 Science, and 1 PNAS; mean IF > 9). The different results were presented in numerous international conferences. One PhD thesis has been defended and two are underway.

This team is involved in numerous and complementary partnerships with biological specialists of different plant species and bioinformaticians/theoreticians at different levels: locally within the unit, nationally and internationally. Principal national and international collaborations led to several articles, revealing continuity in partnerships.

Appreciation on the impact, the attractiveness of the team and of the quality of its links with international, national and local partners

The PI of the team, has a good international visibility and he is highly recognized in the field of plant genomics, and more specifically in paleogenomics. During the four last years, he was invited to 13 international conferences, which denotes the strong impact of his original work on the plant genetics and genomics community. His results on paleogenomics also have a impact on the media beyond the academic area.

Despite the small size and recent inception of the team, it appears to be very attractive and it welcomes numerous students (19) including three PhD (two are underway), and a post-doc will be recruited soon.

So far, the PI of the team has successfully raised funds both as a leader (6 grants) and as a collaborator (4 grants). This has helped the successful emergence of the team.

The work and the tools developed by this team appear pivotal within the unit. The work of this team is naturally tightly linked to the research done in team E1; the tools and knowledge developed will probably be very useful for cloning genes of agronomic interest (teams E3 and E5), and the markers developed in the team are used by team E6 for characterizing genetic resources and in selection programs. However, it remains to be seen to what extent important agronomic traits in different crops are controlled by orthologous genes of conserved function and to what extent the recently discovered high percentage of non-syntenic genes e.g. in bread wheat might be even more important.

The team has also developed important national and international networks around the plant paleogenomic research area, including international partners specialising in the genomics of other model plants (barley, Brachypodium, etc.). It is also involved in whole genome sequencing international consortium (Brachypodium, cocoa).

Results obtained by the team, in collaboration with team E3, led to one European patent registered in 2010. This clearly demonstrates the success of the integrative research strategy stretching from basic genomic research to applied aspects.

Appreciation on the strategy, management and life of the team

This small young team is organized around one PI and two permanent technicians. Non-permanent researchers and technicians are regularly hired through grant funding. This organization has proved to be very dynamic and efficient in the past and should continue in the future.

The creation of the team through an “ANR jeune chercheur” funding allowed to reinforce and to make emerging the cutting edge projects developed by the team.

The PI of the team is involved in some teaching in Clermont-Ferrand and in other French universities and “grandes écoles”, which should contribute to the attractiveness of the team and of the Unit for potential PhD students and others.

Appreciation on the project

The proposed project is very innovative and ambitious. It maintains direct continuity with previous works but also proposes new and original developments. It is well structured in three main tasks, from more basic to more applied. The whole project is built on evolutionary perspective to understand what evolutionary events have shaped plant genome structure and function (expression), and how it may help understanding the genesis of traits of agronomic interest. It will capitalize on the methodological tools, the genomic resources, and the strong networks developed in the past four years. The dynamism and the structure of the team with one scientist, a few permanent technical staff, and several students, have proved to be very efficient and will contribute to the feasibility and the success of the project.

Most of the project, especially tasks 1 and 2, is original and cutting edge.

- Conclusion

  - Summary

The team E2 is a young and very dynamic team that leads projects with strong integration from basic research on plant genome evolution to more applied one on the characterization of genes of agronomic interest. It obtained outstanding results and acquired an international leading position in plant paleogenomics. Based on the knowledge, tools, and resources previously developed, it proposed an ambitious, original, and well-structured project, with the all the resources and skills to manage it successfully.

  - Strengths and opportunities

The strengths of this team are its potential to carry on high level and original research, integrating very basic research with more applied aspects and to have acquired international leadership in plant paleogenomics. The methodological tools, the genomic resources and the fruitful national and international networks already developed are strong opportunities for the success and the development of this team.

  - Weaknesses and threats

There is no actual weakness because the team is very attractive and should continue to get funding and to attract students and post-docs.

  - Recommendations

The committee simply recommends continuing such a high quality research and working efficiently with other teams of the Unit, and maintaining the fruitful national and international partnerships already developed.

- Team E3. Yield adaptation of wheat to abiotic stresses

  Team leader: Mr. J. LE GOUIS

- Staff members

	Past	Future
N1: Number of researchers with teaching duties (Form 2.1 of the application file)	3	3
N2: Number of full time researchers from research organizations (Form 2.3 of the application file)	2	2
N3: Number of other researchers including postdoctoral fellows (Form 2.2 and 2.4 of the application file)	0	0
N4: Number of engineers, technicians and administrative staff with a tenured position (Form 2.5 of the application file)	7.1 (including 1 IR)	7.1 (including 1 IR)
N5: Number of engineers, technicians and administrative staff without a tenured position (Form 2.6 of the application file)	2	2
N6: Number of Ph.D. students (Form 2.7 of the application file)	5	4
N7: Number of staff members with a HDR or a similar grade	3	3

Area 2 split in 3 teams (E3, E4 and E5)

- Appreciation on the results

The E2 team stems from area 2 of the previous GDEC structure. Area 2 has been subject to extensive reorganization in the past 4 years with the end of the maize and sunflower programs in Clermont Ferrand in 2007 resulting in a profound change in the staff, through retirement, departure and recruitments, as well as integration of a group focusing on cereal diseases led by T. Langin in 2010, which will build on the existing plant pathology platform (formerly focusing on sunflower diseases). Significantly, UBP professors have had to shift their research focus from sunflower diseases to wheat grain development and recruit new assistant professors. INRA scientists from area 2 also belong to different INRA divisions (genetics (GAP) and agronomy and environment (EA)); this is of great benefit since it allows integration of genetic, modelling and ecophysiological approaches.

During the past 4 years, the research has focused on two major themes aiming at deciphering the genetic and ecophysiological determinants of i: grain size and composition and ii: nitrogen use efficiency combined with the inverse relationship between yield and grain protein content (so called Grain Protein Deviation or GPD).

Theme 1 comprised grain growth and grain composition axes: For Grain growth a descriptive proteomic approach and a molecular/transcriptomic approach have been used to survey grain formation/analyse peripheral layers at more mature stages and decipher the mechanisms governing wheat grain development, respectively. This has focused on E3 ligase enzymes involved in ubiquitination of regulatory proteins (transcription factors, cyclins, etc.). A first group of team E3 was the one conducting these latter activities while the former activities will continue in team E4. For grain composition, activities have focused on transcription factors (PBF, GAMYB, SPA) interacting with storage protein (Gliadins, glutenins) synthesis gene regulatory sequences, with association and functional validations on the way. A genetic approach including a metaQTLanalysis, has also been conducted for various grain traits (hardness, protein content, fibre content).

Theme 2 involved a modelling of GxE interactions for yield protein content and rate of development with the setting up of the Sirius quality1 model and the analysis of the genetic determinants of the GPD through QTL and innovative ortho meta QTL approaches (yielding a patent on a GoGAT gene). Here again theme 2 activities will split into team E4 (modelling approach) and team E3 (genetic and physiological approach grain protein content and influence of abiotic stresses)

Most of the activities of team E3 were launched 4 years ago in the aftermath of thematic shifts and extensive reorganization and embedding. E3 scientific research has yielded high quality results. The full potential will be realised shortly with 4 on going PhD theses (Publications submitted notably for the grain development part).

The E3 team emerging from Area2 has published 38 papers for 3 teachers-researchers and 3 researchers (4.5 ETP research) and 1 engineer. The average impact factor is good (3.4) and has tended to increase over time (notably through recent very good papers in J Exp Bot). The E3 team has developed one variety and filed two patents. A large number of publications involve collaboration with other French groups but the level of publication with international groups appears limited. The numbers of invited communications in congress proceedings have also recently increased.

The E3 team has had a strong partnership with England (U. Nottingham) and Australia (CSIRO) on the theme of water and nutrient use efficiency. A developing partnership is that with CIMMYT and ICARDA in the frame of the CGIAR research programmes (CRP). The team has embarked in two European consortium proposals in 2011 (Flowering time and cross talk between biotic and biotic stress) indicating a good networking and an internationally recognized expertise. Of particular note is the fact that the team has an excellent national networking with INRA research stations, technical institutes, and private seed industry.

- Appreciation on the impact, the attractiveness of the team and of the quality of its links with international, national and local partners

Due to its well-focused research and very good understanding in the area of nitrogen use and grain protein deviation, the reputation of the recently established team has been increasing. Invitations in symposia have consequently increased in the last few years.

Facilitated by the presence of teachers, the team currently hosts 4 PhD students which is a satisfactory number. On the other hand scientists of team E3 have apparently supervised a low number of masters or post docs. The attractiveness of this team as potential hosts for scientists and students appears to have been less than that for other, longer established GDEC teams.

The area 2 team has raised funds from ANR Génoplante and ANR Genomics (3 grants) and from competitiveness clusters and the private sector (5 grants). The team has been active in institutional calls for proposals notably in obtaining funding within a joint BBSRC (U. Nottingham) and INRA initiative. Therefore, the team has demonstrated its ability to raise funds often in partnership with industry and technical institutes, with a well focused and high impact research aiming at application in the field.

The team is very well integrated in national scientific networks but the level of international collaboration has been rather limited. Again, this may be explained by its relatively recent establishment and reflects the time required to develop international relationships.

Nitrogen use efficiency and grain protein content are both very important traits and the understanding of their genetic, physiological and cell and molecular bases is much needed to produce low input, high milling quality bread wheat. Therefore the topic is focused in an area of particular interest for end users and has received support from the seed and flour industry, technical institutes and the competitiveness cluster CéréalesVallée.

- Appreciation on the strategy, management and life of the team

Management and scientific animation of area 2 was clearly more challenging than for area1 due to its multidisciplinary components, diverse research aims, and its significant restructuring and need to efficiently integrate newcomers. In addition, some scientists had activities in both areas 1 and 2 which was good for interactions but may present difficulties from a management point of view. Following intense discussions, the decision was taken to split area 2 into three teams (E3, E4 and E5) each with a better delimited research focus. This was certainly a good thing.

It is difficult to appreciate this point but the successful emergence of 3 teams each with a well defined research focus and functioning at the forefront of their areas of expertise might be considered as a success in this area.

The team comprises 3 teachers from UBP who are heavily involved in university teaching. In addition, the INRA scientists have participated in the teaching of physiology, genetics, plant breeding and bioinformatics in several universities.

Appreciation on the project

The E3 team will focus its activities on two themes: the cell and molecular biology of grain development and the genetics and ecophysiological determinism of post flowering nitrogen absorption. 3 research projects will continue beyond 2011 but grants submitted to the government loan funds would provide running costs and infrastructures to secure the critical mass required for the team project. The scientific strategy is very well set and the project is feasible given the positive dynamics of the team.

While the activities on grain development are rather generic in their approaches, the GPD and abiotic stress activities have clearly a comparative advantage over competitors with a very good definition of scientific targets and the anticipated use of cutting edge phenotyping platforms.

Conclusion

Summary

In the last 4 year contract, scientists of team E3 have clearly built a well defined, high quality area of expertise ranging from the molecular and cellular aspects of grain development using “omics” approaches to the genetic and physiological bases of nitrogen use and grain protein content. This has allowed the team E3 to prepare a very clear strategic workplan with well defined scientific questions and targets for the new contract. The levels of publication, communication and international collaboration have been steadily increasing, while the team has become established. The team has a very good national and industrial networking portfolio and a very dynamic policy of fund raising in national, European and international initiatives.

Strengths and opportunities

Team E3 gathers complementary expertise in cell and molecular biology, and genetics and ecophysiology which will help in tackling major issues of the impact of climate change on grain filling and quality. The challenge is to integrate these approaches and, as a result, also make the association between INRA and UBP scientists a success. Excellent levels of foreseen funding (notably ANR, BreedWheat national program, EU FP7 and CRP), recognized expertise and know how and cutting edge infrastructure (Phénome national program) are certainly the main strengths of the team making a high probability of success. The strengths of the team are clearly its very good leadership, very well phrased research questions and high quality tools and strategy. The investissementsd’avenirBreedwheat project and the CGIAR research program are clearly outstanding opportunities to consolidate integration in the national community and strengthen international collaborations.

Weaknesses and threats

There is no specific concern at the scientific level since research is well focused and straightforward.Nevertheless, team E3 has a strong responsibility in maintaining and strengthening the successful association with the University UBP. The presence of the UBP group and the INRA group on two different sites though not very far from each other may lead to isolation. The risk of this might be enhanced by the fact that the two thematic foci, though converging on the grain, can be conducted in a largely independent manner: The BreedWheat project and other projects associating the two groups of team E3 and other GDEC teams will be instrumental for making this association a success.

Another important point which has been a weakness in the last 4 year contract is the rather low number of international collaborations contrasting with the excellent level of national and industrial collaborations. This can be explained by the fact that the team was still becoming established. During the presentations, the team has shown its willingness to develop collaborations with international centres and European research centres through FP7 consortia. This will be made easy by the now well established expertise of the team.

Recommendations

Another recommendation concerns the respective foci of teams E3 and E4. As these two teams stem from the same area 2 group, it is important that the domains of research are clearly defined and not overlapping but are complementary and developed to maximize interactions and collaborations. This is not an easy challenge. In that aim E3 should focus on stressful situations and absorption of nitrogen under abiotic stresses while E4 should focus on quality aspects of proteins and share materials

It might also be a recommendation to initiate studies by focusing on a particular type of abiotic stress: drought, thermal stress and elevated CO2 might be too wide and too diverse an array of stresses to investigate in parallel from the outset.

- Team E4. Integrative Biology of Grain Composition (BIG)

  Team leader: Mr. Pierre MARTRE

- Staff members

	Past	Future
N1: Number of researchers with teaching duties (Form 2.1 of the application file)	1	1
N2: Number of full time researchers from research organizations (Form 2.3 of the application file)	2	2
N3: Number of other researchers including postdoctoral fellows (Form 2.2 and 2.4 of the application file)	0	0
N4: Number of engineers, technicians and administrative staff with a tenured position (Form 2.5 of the application file)	7.5 (including 1 IR)	8.5 (including 1 IR)
N5: Number of engineers, technicians and administrative staff without a tenured position (Form 2.6 of the application file)	3	4 (including 1 Post-Doc)
N6: Number of Ph.D. students (Form 2.7 of the application file)	6	3
N7: Number of staff members with a HDR or a similar grade	1	1

*Figures from former Area 2 which split into 3 teams (E3, E4 and E5) in the next 4 year contract

- Appreciation on the results

The research provides a balance of complementary approaches to understand the mechanisms and genetics underlying grain development, and composition and the impact of environment on these. The integration of proteomic and targeted transcriptome (E3 ligases, transcription factors) analyses, with QTL analysis and modelling (SiriusQuality1) provides a powerful and original approach to understanding these processes. Furthermore, the integration of research into an environmental context (G x E interactions) ensures that the research addresses problems of immediate and future concern for the production of high quality wheat. Some notable highlights (not exhaustive) are:

The identification of the five main profiles and four developmental phases of protein expression during development of the peripheral layers of grain.

The identification of an E3 ligase (orthologous to rice GW2) as a potential candidate involved in determining grain size.

The cloning of five wheat orthologous of the ten recognised transcription factors of barley controlling grain reserve protein synthesis. Particularly as this includes sequencing of their promoter regions to identify cis-motifs.

The identification of the optimal leaf area index for maximal efficiency of nitrogen storage.

The identification of the link between post flowering absorption of nitrogen and ‘grain protein deviation’.

Identification of putative genes underlying NUE involved in nitrogen metabolism.

The number of publications is commensurate with that of other GDEC teams. The team has published 73 peer reviewed papers with about half as leading author, and with a substantial number involving national or international collaboration. This is very high for only 3.5 FTP researchers. The average IF of 3.48 is high for the discipline. The team has contributed to 9 book chapters, 5 as leading contributor indicating that they have a recognized expertise in the field. One special issue on modelling quality traits of the Eur J Agronomy was edited by the future team 4 leader. In addition, team E4 has also created transcription factor and expression databases. Some notable publications marking significant advances were produced, among these being A2.48, A2.51 and A2.58.

The evidence from the publications and research activities indicates a high quality and stability of partnerships within the team. Collaborations span from regional, e.g. CNRS-UBP LIMOS unit in modelling and seed industry to European (FP6 project HEALTHGRAIN) and involvement in international networks notably in seed protein nomenclature. The team has organized an international gluten workshop with 150 participants from 30 countries in Clermont Ferrand demonstrating its international profile and contacts.

- Appreciation on the impact, the attractiveness of the team and of the quality of its links with international, national and local partners

All thirteen 'invited speaker' presentations were as leading author and some of these were at prestigious international meetings.

A large number of doctoral candidates have worked within the team, including students jointly supervised from North Africa. The team composition combined with the high level of output indicates that it is successful in recruiting high level candidates for posts, including those from abroad.

The team has a very good record of obtaining research contracts. They have an impressive record of working successfully with industrial partners, particularly Biogemma. A large proportion of the funding involves close collaboration within industrial and scientific clusters. Some particularly large grants include QualitNblé and "NutriPAN".

The team enjoys a significant number of national and international collaborations as evidenced by the high proportion of peer review publications produced in collaboration with other French (35) or international (19) partners. For example the novel work on isohomoeoallelic lines involving collaboration and work on starch composition with colleagues from China and Japan

Research on the role of wheat-based products in human ailments provides evidence of a focus on identifying and ameliorating potentially negative effects on particular individuals. The underlying theme of enhancing nitrogen use efficiency and grain composition in low input agriculture further demonstrates engagement with socio-economic concerns.

- Appreciation on the strategy, management and life of the team

The team has structured its research program to exploit the skills within it. This demonstrates good team organisation through being aware of its strengths, which it will utilise, while not attempting to overstretch itself.

The initiatives present a good balance of cutting-edge projects combined and integrated with those employing robust well-tried technologies and approaches.

Evidence for a modest contribution to teaching is presented within the paperwork.

- Appreciation on the project

A clearly described and well integrated scientific research project is presented. The proposed approaches appear entirely appropriate with the resources available and the scientific questions being addressed. Main axes are 1: the environmental and genetic variability of wheat nutritional density and 2: the environmental, genetic and molecular bases of the nutritional regulation of grain protein composition. Strong interactions with team E3 which deals with interactions between environmental factors on grain development and protein content are foreseen. Axis 2 involves a holistic approach of physiology, omics, interactions (protein:protein and DNA:protein), network modelling and allelic diversity which is ambitious and challenging but the team has comparative advantages to enable it to reach the objectives.

The schematic presentation of the integrated approach makes clear that the scientific resources (high calibre researchers, teacher-researchers and engineers) have been appropriately allocated to the diverse components of the overall project.

The high level of integration between the groups working on transcriptomics and proteomics with modellers is cutting edge. Similarly, the analysis of the interaction between the transcription factors involved in transcriptional regulation of storage proteins is also original.

Conclusion

Summary

Overall, the evidence presented demonstrates that this team is working in an integrated manner and utilising cutting edge approaches to understand and ultimately manipulate grain composition.

Strengths and opportunities

The overall aims of the project are excellent and align very well with INRA strategy. The aims of the project are entirely appropriate, making maximum use of the skills of the team members and the resources available to them.

The modelling work has the potential to inform on potential candidates for detailed scrutiny within the project outlined by the BIG team and those of other GDEC partners.

Every effort should be made to continue and enhance the integration of project 4 with others, in particular project 3. This includes the genomics platforms and the wheat germplasm collection. This should provide significant synergy among the projects and enhance the overall programme of the Unit.

Participation in EU applications such as GRAINFILL strengthens the international status of the group and provides an opportunity to expand the global reputation of the unit.

The ABBAH and BREEDWHEAT projects will open new and exciting opportunities to extend the range of their work and their influence through collaboration with partners both within the Unit and elsewhere in Europe.

Weaknesses and threats

Axis 1 of the team project group is well defined, building on strong expertise, but it should remain vigilant that it does not become isolated from the rest of the team.

While the hypothesis presented is that scaling laws are emerging properties of regulatory networks it is unclear how the programme might be modified if this hypothesis were to prove incorrect.

Some aspects of this Project have clear relevance to those of Project 3. The present description does not, perhaps, emphasise how close collaboration with the project of team E3 would benefit both parties.

The combination of association genetics and synteny to be employed in plan 3.3 may be optimistic. While synteny between cereal species exists there is no guarantee that genes in other species that are syntenous in regions underlying PQTL are those responsible for the observed QTL. A clear back-up strategy is required for such situations.

The number of PhD students is low. The team should take advantage of the presence of a teacher researcher of UBP to attract students and propose topics on the areas of research covered. The range of cutting edge tools and techniques mastered in the team should be attractive.

Recommendations

The project currently consists of a diverse set of objectives, some of which are highly ambitious, for example the functional characterisation of candidate transcription factors for the regulation of grain storage proteins. Care should be taken within the overall project to ensure that outputs from each of the components feeds optimally into others, both within this project and others within the Unit. Continued scrutiny of progress will be required to ensure that the overall balance of the project is maintained throughout the forthcoming period.

- Team E5.: Cereal Diseases

  Team leader: Mr. Thierry LANGIN

- Staff members

	Past	Future
N1: Number of researchers with teaching duties (Form 2.1 of the application file)		1
N2: Number of full time researchers from research organizations (Form 2.3 of the application file)		1
N3: Number of other researchers including postdoctoral fellows (Form 2.2 and 2.4 of the application file)		
N4: Number of engineers, technicians and administrative staff with a tenured position (Form 2.5 of the application file)		6 (including 1 IR)
N5: Number of engineers, technicians and administrative staff without a tenured position (Form 2.6 of the application file)		1 Post - Doc
N6: Number of Ph.D. students (Form 2.7 of the application file)		1
N7: Number of staff members with a HDR or a similar grade		3

- Appreciation on the results

Team E5 was set up at the end of 2009, and results are still preliminary and have not been published yet. Therefore, no appreciation of results is currently possible.

- Appreciation on the project

The prime aim of the team is to work with reducing disease levels and mycotoxin production by Fusarium fungi. These fungal pathogens are important not only for their potential in causing severe yield losses but also because infection leads to the accumulation of toxic metabolites in the infected tissue which includes grain consumed by man and livestock. This area is very relevant for meeting the INRA goal of sustainability, namely low input agriculture and will consider the effects of abiotic stress on pathogen interactions. Not only is infection encouraged by stress but is more prevalent in low tillage systems. However, the relevance of studying this disease is apparent worldwide: this is a highly competitive area and it is therefore imperative that this team sets clear goals which reflect and exploit the strengths of this Unit and do not try to compete with research groups which are well established and ahead. The current project ideas do not do this adequately though they reflect considerable knowledge and thought.

It is intended to provide an extra position of a scientist in 2012 to support this area. Also, INRA will be moving wheat-disease projects from Rennes to CF, which may create an opportunity to reach sufficient impact in this field, provided the core funding can be substantiated by external funding? The latter is absolutely necessary given the size of the team at present and given the imminent retirement of the university (UBP) partner. The fact that the team leader has been appointed as the new Unit director and that this area is not well established here will put some strain on lifting this area to the level of other programmes in the Unit.

This team has a high level of experience in a number of plant-pathogen interactions. The established “local” part of the team has previously worked on sunflower: they bring considerable technical expertise and profound knowledge of a difficult plant-pathogen interaction to, for them, a new system. The experiments made so far have focussed on establishing that their biological material behaves as has been seen elsewhere, a necessary introductory move but has not contributed to cutting edge scientific progress. The new team leader, who joined recently (2009) from a leader position at another Unit – has in the past worked on Fusarium, but mostly on the pathogen side and not so much on plant genetics. The projects presented at present are promising but not cutting edge, and others are doing similar things. Thus Jim Anderson at USDA has a contig 3BS QTL from the Chinese variety Sumai 3, which is apparently being transformed into “standard material”: very clear goal and materials. Other experts including H. Buerstmayr at BOKU/IFA Tulln, A. Mesterhazy from CRI Szeged, T. Miedaner from Hohenheim Univ., or D. Somers from AAFC Winnipeg have been working with FHB resistance QTL’s localized on chromosomes 3BS, 5AS etc. in many projects. Thus almost 20 resistance meta-QTL for FHB have been identified, and several of those are already used in backcrossing programmes (as summarized by Löffler et al. 2009, Mol. Breeding).

Other approaches taken, e.g., using Tri5-GFP fusions are also used elsewhere, e.g. at Rothamsted Research institute.

Conclusion

Summary

This team has the potential to exploit the expertise and materials available at the Unit, but needs to plan carefully to prioritise the ideas to achieve this.

Strengths and opportunities

Aims are excellent and there is much potential for developing relevant leading research programmes in the INRA context and internationally.

There are clear opportunities for exploiting the genome project resources in this environment. In particular this programme should be developed to exploit the materials developed by other pillars at the Unit. This includes both the genomics platforms and the wheat (core) collection.

There are good team members who have a lot of relevant knowledge and technologies who are moving into wheat from a background in sunflower diseases and from other INRA units.

There is a good network of INRA field stations and Units, and other institutes, working with other model systems.

Participation in EU applications gives an opportunity to provide resources to others and reap the benefits for the unit.

Weaknesses and threats

This is a small and newly established team with other important functions as the team leader will also be a new director for the Unit will not be able to place all his efforts into establishing this new area here, which would be necessary to be able to establish the cereal disease programme at the same level as the other programmes. We have the impression that the teamleader has been focussing more on general unit management in recent years rather than being actively involved in research. Although the emphasis will be on the FHB complex, perhaps too many diseases (FHB, Septoria, Rust) are planned to be studied for the resources available, there is a clear need to prioritise, perhaps by “delegating” diseases to collaborators and not try to cover everything. Furthermore, the approaches suggested do not build enough on the strengths at this Unit. The role of the Unit as an internationally leading centre for wheat genetics and genomics gives an unique opportunity to support efforts in resistance breeding for many diseases on a national and international level and this unique platform should be exploited ruthlessly. We do not think that studying the fungal side of the FHB interaction will leverage the synergistic potential of the Unit in an optimal manner.

It is possible that ultimately transgenic approaches will prove to be the only way for defeating this disease complex. However, we consider that the idea of using glycosylation in transgenics to detoxify mycotoxins is risky. Is this relevant? What is the risk that glycosylated forms of the mycotoxins can be metabolised in mammals to the active mycotoxins? Furthermore, no mycotoxin has proven to be an essential pathogenicity factor for any Fusarium species and the published evidence suggests that the toxins are produced always during fungal development in the plant. Furthermore, the disease is caused by a range of different species producing a plethora of different known mycotoxins and other metabolites. A successful transgenic approach must therefore focus on preventing initial infection.

The proteomic and transcriptomic approaches taken do not have clear goals and in essence copy work done in the strong groups at USDA, Austria and elsewhere. In our experience, proteomic and transcriptomic analyses of cereals during Fusarium infection primarily demonstrates tissue destruction rather than identifying targets conferring resistance.

- Recommendations

Allocation of resources to this team is essential otherwise it cannot survive scientifically and pull its weight in developing the Unit.

Given that the planned effort will be on Fusarium, there is a need to develop a clear prioritisation of their resources especially to exploit the strengths of this Unit by using the genetic and genomic resources at this Unit i.e. the core collection and the genetically anchored physical maps for individual chromosomes that harbour FHB resistance QTL. Exploitation of the existing known QTLs should be considered in collaboration with others, with the final aim of map-based cloning of the underlying genes. Moreover, the upcoming sequence of the 3B chromosome will offer even better opportunities to clone genes responsible for resistance QTLs. In this respect it might be wise to carefully re-consider joining efforts for the cloning of the major Sumai3-derived QTL on this chromosome.

Most research results internationally suggest that mycotoxin accumulation is very closely linked to fungal development in the infected cereal tissue. The best strategy for achieving low levels of mycotoxin contamination would therefore be to develop plants which do not become infected rather than trying to remove the numerous metabolites produced by different species of Fusarium that can infect wheat in the field. The most effective strategy for achieving this in the short term would be to look for sources of resistance in gene bank material under local conditions, including the known – and perhaps new QTL's which could be identified in the French material.

Nevertheless, transgenic strategies may ultimately prove to be necessary and a real success story leading to the prevention of poisoning the French (and other European) public with insidious toxins in the baguette may well help to turn the tide of popular negative attitude to the technology in France and elsewhere.

There is a clear need to ensure that activities at Rennes are integrated in the Cereal Disease programme here. This will need efficient flow of information and joint planning of lab (GDEC) and field (Rennes) research and could be achieved by scheduling regular visits by senior scientists from GDEC to Rennes (and vice versa). Otherwise we see a risk that results and conclusions from field trials in Rennes as a breeding facility might become somewhat uncoupled from the research activities of the Cereal Disease team.

The committee recommends the re-naming of the team into "Resistance of wheat to biotic stresses" in order to more clearly emphasize on the output value of this team in the context of the unit.

- Team E6. Genetic diversity and selection

  Team leader: Mr. Gilles CHARMET
- Staff members

	Past	Future
N1: Number of researchers with teaching duties (Form 2.1 of the application file)		
N2: Number of full time researchers from research organizations (Form 2.3 of the application file)	1	1
N3: Number of other researchers including postdoctoral fellows (Form 2.2 and 2.4 of the application file)		
N4: Number of engineers, technicians and administrative staff with a tenured position (Form 2.5 of the application file)	19,3 (including 2.8 IR)	16,3 (including 2.8 IR)
N5: Number of engineers, technicians and administrative staff without a tenured position (Form 2.6 of the application file)	3 (including 1 Post-Doc)	2 (including 1 Post-Doc)
N6: Number of Ph.D. students (Form 2.7 of the application file)		
N7: Number of staff members with a HDR or a similar grade	2	2

- Appreciation on the results

The research objective of this team is the phenotypic and molecular characterization and the analysis of wheat genetic resources in preparation for exploiting them in breeding programs. This team is well integrated in the general scheme of the unit as it has efficiently exploited tools and knowledge generated by other teams in an applied perspective. They defined clear objectives on using genetic resources to increase the breadth of the genetic basis for breeding and on the development of high quality, low input, and hardy wheat varieties. These objectives are well justified in the context of reinforcing sustainable agriculture and because they are not (or weakly) taken into account by private breeding companies. Over the four past years, they developed useful tools (e.g. characterization of genetic diversity on new traits, development of new selection criteria) and material (e.g. pre-breeding genetic material, new varieties).

Given that the objectives of this team are partly orientated to direct breeding applications and not only to academic knowledge production, the publication level is good, with 43 publications in well-targeted journals, including 19 as a leading authors.

Partnerships are strongly developed inside the Unit as this team takes advantage of genomic tools and resources developed by the teams involved in more basic research. For instance, most publications are co-authored with other members of the Unit. National partnerships are also well developed, especially with other INRA research groups and with private partners (GIE). In the last year, the team has also reinforced and increased international partnerships, especially with genetic resource institutes.

- Appreciation on the impact, the attractiveness of the team and of the quality of its links with international, national and local partners

The members of the team are internationally recognized in the field of plant genetic resources and were invited to five international conferences.

During the last year the team recruited three foreign post-docs and numerous students (16).

The team has a very good record of attracting funding. So far, the projects have been very well funded through numerous national and European grants, including private funding, 10 as a coordinator, and nine as a collaborator.

National networks with other INRA groups and private collaborators are well developed (see above). In the past year, they strengthened their international partnerships, especially in relation to genetic resource conservation and breeder networks.

Valuable genetic material has been created in the pre-breeding program and 10 varieties (7 wheat, 3 triticale) have been registered, especially three interesting prototype “high quality hardy” varieties to respond to sustainable agriculture objectives. The team also increased the distribution of seeds from the genetic resources collection, which promotes the use of genetic resources. Take-up of the resources was particularly high among private breeding companies demonstrating the socio-economic benefit of the work of this team.

- Appreciation on the strategy, management and life of the team

This team includes people and research projects from former area 1 and area 3. This new organization is logical and has been well articulated into two main parts from characterization of genetic resources to their uses in breeding programs. Thanks to this new organization, team 6 has a clearly defined role and position within the Unit project.

This point is difficult to evaluate specifically with respect to team 6 and we must refer to the general evaluation of the Unit.

Some members of the team are locally involved in teaching (22H) in license and master programs.

- Appreciation on the project

The project is well structured and clearly integrates its activities with those of other teams within the Unit, for example through exploitation of the tools and resources developed by other teams. The proposed project provides logical continuity with past work (e.g. linkage disequilibrium analyses, pre-breeding program) but it also proposes the ambitious objective of developing genomic selection in wheat. The hiring of a CR scientist (due this year) will be important to strongly support this part of the project and will further increase the strong links with the other teams, especially E1, to push the project forward along the envisaged value chain.

The objective of developing high quality, low input varieties for sustainable agriculture is innovative and the aim of introducing genomic selection into the wheat breeding program undoubtedly provides a significant cutting-edge component to the project.

- Conclusion

  - Summary

This team develops research and programs with direct applied objectives to produce low input hardy wheat for sustainable agriculture. It is well integrated into the whole Unit organization and develops strong links with other teams. Based on the important genetic resources that the team manages (wheat collection) and its past experience, the team proposes a well structured and ambitious research program that should have concrete impact in the challenging context of developing sustainable alternative agricultural practices.

  - Strengths and opportunities

One of the main strengths of the team is the management and use of the national wheat (and other Triticeae) collection. These genetic resources have already been well exploited and will be a key to carrying through the objectives of this team and of the whole Unit. Another strength is the strong reciprocal interactions with the other teams within the Unit.

  - Weaknesses and threats

The association mapping and genomic selection parts of the project are challenging. The strategy of collaboration with national and international teams more involved in theoretical developments is clearly appropriate, but the team should pay attention to also maintain its local strong population-genetic skills, especially because methodological developments are foreseen.

  - Recommendations

Given the quality of the project, the committee simply recommends carrying it through and to maintain and reinforce the fruitful collaborative works within the Unit. The team will also have to ensure good collaborations on the emerging genomic selection program and to be well positioned at the interface of theoretical development and breeding applications.

Intitulé UR / équipe	**C1**	**C2**	**C3**	**C4**	**Note globale UR**
Génétique, Diversité et Ecophysiologie des Céréales (GDEC)	**A+**	**A+**	**A+**	**A**	**A+**
Description, gestion et valorisation de la diversité génétique	A+	A	non notée	A+	A+
Structure, fonction et évolution des génomes de blé	A+	A+	non notée	A+	A+
Maladies des céréales	non notée	non notée	non notée	B	non notée
Rendement et adaptation du blé aux contraintes abiotiques	A	A	non notée	A+	A
Biologie intégrative de la composition du grain	A+	A	non notée	A	A
Paléogénomique des plantes pour l'amélioration variétale	A+	A+	non notée	A+	A+

C1 Qualité scientifique et production

C2 Rayonnement et attractivité, intégration dans l'environnement

C3 Gouvernance et vie du laboratoire

C4 Stratégie et projet scientifique

Statistiques de notes globales par domaines scientifiques
(État au 06/05/2011)

Sciences du Vivant et Environnement

Note globale	SVE1_LS1_LS2	SVE1_LS3	SVE1_LS4	SVE1_LS5	SVE1_LS6	SVE1_LS7	SVE2 _LS3 *	SVE2_LS8 *	SVE2_LS9 *	Total
A+	7	3	1	4	7	6		2		30
A	27	1	13	20	21	26	2	12	23	145
B	6	1	6	2	8	23	3	3	6	58
C	1					4				5
Non noté	1									1
Total	**42**	**5**	**20**	**26**	**36**	**59**	**5**	**17**	**29**	**239**
A+	16,7%	60,0%	5,0%	15,4%	19,4%	10,2%		11,8%		12,6%
A	64,3%	20,0%	65,0%	76,9%	58,3%	44,1%	40,0%	70,6%	79,3%	60,7%
B	14,3%	20,0%	30,0%	7,7%	22,2%	39,0%	60,0%	17,6%	20,7%	24,3%
C	2,4%					6,8%				2,1%
Non noté	2,4%									0,4%
Total	100,0%	100,0%	100,0%	100,0%	100,0%	100,0%	100,0%	100,0%	100,0%	100,0%

*** les résultats SVE2 ne sont pas définitifs au 06/05/2011.**

Intitulés des domaines scientifiques

Sciences du Vivant et Environnement

- **SVE1 Biologie, santé**
  - **SVE1_LS1 Biologie moléculaire, Biologie structurale, Biochimie**
  - **SVE1_LS2 Génétique, Génomique, Bioinformatique, Biologie des systèmes**
  - **SVE1_LS3 Biologie cellulaire, Biologie du développement animal**
  - **SVE1_LS4 Physiologie, Physiopathologie, Endocrinologie**
  - **SVE1_LS5 Neurosciences**
  - **SVE1_LS6 Immunologie, Infectiologie**
  - **SVE1_LS7 Recherche clinique, Santé publique**
- **SVE2 Ecologie, environnement**
  - **SVE2_LS8 Evolution, Ecologie, Biologie de l'environnement**
  - **SVE2_LS9 Sciences et technologies du vivant, Biotechnologie**
  - **SVE2_LS3 Biologie cellulaire, Biologie du développement végétal**

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N/Ref : 15-2011

Monsieur le Directeur,

Nous nous associons aux remerciements émis par la direction du laboratoire " ***Genetics, Diversity and Ecophysiology of Cereals***" (GDEC: UMR INRA_A 1095) aux membres du comité d'évaluation pour la qualité de leur travail. Vous trouverez ci-jointe la réponse de l'équipe de direction du laboratoire.

Nous partageons l'avis extrêmement positif du comité qui identifie l'unité comme leader mondial dans le domaine de la génétique du blé.

Le soutien conjugué de l'université et de l'INRA doit se concrétiser dès 2012 par la création d'une chaire mixte (UBP-INRA). Les tutelles travaillent également avec un de leurs partenaires industriels (Limagrain) pour la création d'une chaire industrielle sur le dispositif offert par l'ANR.

L'excellente dynamique scientifique du laboratoire, son implication et sa reconnaissance internationales se sont récemment concrétisées par l'obtention dans le cadre des investissements d'avenir d'un projet Biotechnologies - Bioressources intitulé « BREADWHEAT », financé pendant 9 ans.

Nous vous prions d'agréer, Monsieur le Directeur, l'expression de nos salutations distinguées.

Clermont-Ferrand, le 14 avril 2011

La Présidente,

Nadine LAVIGNOTTE.

REPUBLIQUE FRANCAISE
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE
CENTRE DE CLERMONT FERRAND - THEIX - LYON

Clermont-Ferrand
April 13, 2011

Comments from UMR 1095 on the AERES report.

All the members of the UMR 1095 GDEC would like to thank the AERES committee for the fair and in depth assessment of our research unit and their helpful remarks and suggestions. We are especially pleased to observe that the committee found our scientific project coherent, of high scientific quality, competitive at the international level and judged our scientific production of excellent quality. We do share the views of the committee concerning our need of strengthening local human resources in bioinformatics and informatics and the lack of place that can limit our future developments. We will take the suggestions into account while continuing to work towards comforting our strengths and increasing our efficiency. We also acknowledge that the committee validates our current and future management structures. Since this report is going to be published on the AERES website, we feel it necessary to correct some errors in particular in the tables that summarize the staff members and do not correspond to the latest version that was sent last month in response to the AERES request. An updated version of the tables for the unit and teams staff is provided in a second file.

Below are **specific responses to point 4: "specific appreciation team by team and/or project by project"**

Team 1: no particular comment

Team 2: no particular comment

Team 3 and Team 4: a few references to the work accomplished by the two groups have been cited wrongly in one or the other groups. This is due to the fact that the structure has evolved from one axis embedding these groups and that it was likely difficult for the committee to trace back the origin of the work in some cases. This is not a problem and does not need to be addressed specifically at that stage.

Team 4: There are 2 comments that are based on erroneous assumptions and maybe related to a lack of clarity in the original document:

p19: "Evidence for a modest contribution to teaching is presented within the paperwork": This is surprising since the E4 team has made a major contribution in teaching with about 300h of teaching just for the INRA members of the team in the past 4 years (not taking into account the MCF and professors at UBP)
p. 20: "The number of PhD students is low"
This remark probably stems from the fact that our report was not clear enough, if we refer to the exact numbers of 6 PhD during the period for 1 HDR.

Team 5:
Even though the report has rightly pointed out some of the strengths and weaknesses of this team, there are several points we think unveil some aspects that escaped the attention of the committee. The absence of the team leader due to exceptional circumstances (for health reasons) did not allow him to answer questions and have a real discussion with the members of the committee in order to precise some aspects of the scientific project. We feel that this point needs to be mentioned at the beginning of the written report for the E5 team as this has had strong consequences on the final evaluation. Thus, this response is the only opportunity to address a number of comments and statements made by the committee:

"Although the emphasis will be on the FHB complex, perhaps too many diseases (FHB, Septoria, Rust) are planned to be studied for the resources available, there is a clear need to prioritize, perhaps by "delegating" diseases to collaborators and not try to cover everything. "
We don't understand this comment. All the current project of Team 5 is focused on FHB and there was for example no mention of plan to perform research on rust in the written or oral presentations. Project on septoria will be performed in the first place in collaboration with BIOGER and will only be developed further at GDEC after new scientists have been hired.

"We do not think that studying the fungal side of the FHB interaction will leverage the synergistic potential of the Unit in an optimal manner".
We do not share this point of view. We think that a better understanding of the biology of *Fusarium* can help us to define new and original strategies to limit durably the infection and the contamination. Nevertheless, our direct work on *F. graminearum* is

limited to a contribution to the analysis of population structures in order to define an optimal inoculum.

"The proteomic and transcriptomic approaches taken do not have clear goals"
There is a limited understanding of the molecular mechanisms involved in plant resistance against FHB. So, this part of our project aims to identify genes and function involved in wheat resistance to FHB. As mentioned in our project, the objective is to compare and identify differentially expressed genes or proteins in FHB-susceptible and -resistant wheat lines under infection and uninfected conditions. This part of the work is plane in BREEDWHEAT in collaboration with the MH Lebrun's team (BIOGER-INRA Versailles)

"In essence copy work done in the strong groups at USDA, Austria and elsewhere. In our experience, proteomic and transcriptomic analyses of cereals during Fusarium infection primarily demonstrates tissue destruction rather than identifying targets conferring resistance. "
These two comments appear to be a little bit contradictory?! On one side, this strategy is an uninformative approach, on the other side, it is developed in many competitive research groups?!

"However, we consider that the idea of using glycosylation in transgenics to detoxify mycotoxins is risky. Is this relevant? What is the risk that glycosylated forms of the mycotoxins can be metabolized in mammals to the active mycotoxins?"

Some authors describe correlations between toxin resistance and field FHB resistance. For example, trichothecenes could suppress the expression of plant defense proteins induced after host infection. Therefore, we propose that molecular mechanisms conferring trichothecene resistance might be important components of the polygenic FHB resistance trait. Biochemical mechanisms of resistance to DON, such as catabolism and conjugation of DON, have been previously reported. So, glucosyl transferases appear to be good candidates to be involved in these processes of detoxification.

"Furthermore, no mycotoxin has proven to be an essential pathogenicity factor for any Fusarium species and the published evidence suggests that the toxins are produced always during fungal development in the plant."
Yet, we do not agree with this comment. Recent studies on mutants exhibiting a disrupted trichodiene synthase (*tri5* gene) show a dramatically reduced virulence on wheat and an incapacity to colonize the floret: tox- strains can still colonize the first inoculated

spikelet but the mutant is not able to protube into the rachis. Its growth is confined to the point of inoculation. So, a better understanding of the physiological relevance of mycotoxins is required to develop resistant crops or specific inhibitors to decrease mycotoxin wheat contamination. Therefore, most of the evidence supports the hypothesis that mycotoxins act as a virulence factor.

"Exploitation of the existing of known QTLs should be considered in collaboration with others, with the final aim of cloning of the underlying genes – The most effective strategy for achieving this in the short term would be to look for sources of resistance in gene bank material under local conditions, including…"

The review committee suggests focusing the projects of team 5 on the genetic and molecular characterization of FHB resistance QTL. The paradox that this comment creates is interesting. Almost all the projects of the team 5 aim to develop tools to identify new sources of FHB resistance (using the GDEC genetic resources collection) and at term to develop map-based cloning strategies to clone the most interesting QTLs in collaboration with other teams of the unit. Therefore, we agree with the committee that these projects should be pursued in priority during the next years.

"Allocation of resources to this team is essential otherwise it cannot survive scientifically …"

We would like to remind that this team has been created only recently and its size should increase in the future. For example, the team is in the process of recruiting a post-doctoral fellow, and the recruitment of a researcher and a researcher with teaching activities (*Maître de conférence*) is planned for next year. This should ensure sufficient manpower to carry out the team's projects.

"There is a clear need to ensure that activities at Rennes are integrated in the Cereal Disease programme here. This will need efficient flow of information and joint planning of lab (GDEC) and field (Rennes) research and could be achieved by scheduling regular visits by senior scientists from GDEC to Rennes (and vice versa). Otherwise we see a risk that results and conclusions from field trials in Rennes as a breeding facility might become somewhat uncoupled from the research activities of the Cereal Disease team."

The Small Grain Cereal group of the GAP division, led by GDEC scientists (C Feuillet and G Charmet), is aware that research programmes on wheat resistance to major diseases must be continued after INRA's decision to close them in Rennes. Scientists of GDEC and BIOGER are discussing since one year to develop a new project that will integrate the former results and material from Rennes. In this project, Rennes will remain as the major location for disease evaluation for the INRA breeding programmes, and surely for new research programmes too. The transfer of genetic material created in Rennes is already organized and will be achieved in May. For what concerns the possibility of pyramidizing QTL for FHB and septoria, this task can be accomplished by the E6 team using markers developed in Rennes and in the new project of team E5.

Team 6: no particular comment

Gilles CHARMET Director of UMR 1095	Thierry LANGIN & Catherine FEUILLET Future Director & Deputy-Director