

CONTRIBUTION OF GENOMICS TO AGROECOLOGY

Report on projects funded over the period 2005-2019
and new horizons for research

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covers topics transversal to the various calls for proposals funded by the ANR. This collection, which first came out in 2009, gives an overview of the research projects, innovations and technological advances ongoing in a specific field. Without presuming to be exhaustive its objective is to retrace the societal and future challenges identified by research communities working on a specific topic. The research projects funded by the ANR are presented here in a concise summary. Each journal is aimed at researchers, political decision-makers and also the general public.

This journal is the result of invaluable collaboration between scientists from the field of animal, microbial and plant genomics and agroecology.

We would like to extend our thanks to all contributors.

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Introduction

Since its creation in 2005, the ANR has funded projects in animal, plant and microbial genomics along with projects aiming to support the development of a more sustainable agriculture. These projects received funds as part of programmes created in tandem with the agency's supervisory bodies, national research bodies and experts in their specific field.

Based on the finding that each of these major research fields had been financed for programmes set up independently, in "silo", issue no. 12 of this journal aims to bring into focus genomics projects with the potential to contribute to research in agroecology. It also aims to put forward priority areas of research and to demonstrate any obstacles in agroecology which could benefit from the contribution of genomics.

On the basis of the work in genomics and agroecology funded by the ANR, the first part of this journal provides an analysis of funding of animal, plant and microbial genomics projects of potential interest to agroecology.

Based on the results obtained in these three areas, and on the objectives to be reached to develop a more sustainable agriculture, The second part of the journal looks at new lines of thinking in genomics applied to agroecology. It focuses on the academic groups working together and covers clearly identified scientific concerns, while outlining the objectives to be reached to develop a more sustainable agriculture.

Finally, 33 projects funded by the ANR, potentially applicable to agroecology are presented individually in the table at the end of the journal.

Enlisting all life sciences for the profound transformation of our agricultural and food systems: genomics has a major role to play

How to make our agricultural and food systems compatible under the environmental pressure to achieve carbon neutrality and to protect biodiversity? This question spans as much the international political agenda, the European Green Deal proposal which explicitly mentions these two objectives, as the research and innovation agenda.

This goal of profound transformation, if we take the Green Deal example, is necessary as much to protect our global environment, as to protect the resources base and therefore the viability of our agri-food sectors, essential to preparing the economy of the future on a European level.

Research and innovation are therefore involved in two ways. First of all, the research organisation, the framework for its priority concerns and its funding priorities, may very well help reinforce business models and sectors as they exist today. This could lead for example to an economy of scale logic and specialisation on some key productions. It is this logic that is behind the tendency of production regions to specialise, behind the simplification of landscapes and shortening of rotations, incompatible with ambitious environmental objectives, despite the individual efforts of farmers. Conversely, research carries the seeds of potential for reorientation of innovation towards other forms of farm management, and management of the agricultural ecosystem at landscape or territorial level, to meet all economic, social and environmental objectives. Such is the promise of an agroecological innovation path.

French research organisations such as INRA and IRSTEA (today merged within INRAE), or Cirad but also the French National Research Agency and other French research bodies, have borne this framework or this research priority to re-ecologise agronomic research, which is essential for explaining why the agroecological transition represents major stakes for innovation, and not a return to old practices. This message was carried to the FAO, and to the confines of a certain number of international research programming organisations, especially at the interface between climate change, biodiversity loss and food security.

The prospect of driving research and innovation by setting widely ambitious objectives is the very core of the European Green Deal and the “missions” proposed by Mariana Mazzucato as methods of managing the European research area, directed by a tangible problem in our societies, with ambitious and non-prescriptive objectives on the type of research to be implemented.

All life sciences research is therefore relevant and potentially usable to answer to the objective of transforming the agricultural and food sectors to meet the deadlines for global carbon neutrality and protection of biodiversity. This ANR journal is essential as it shows that genomics, in all its diversity, can play a part and must play a part in this scientific dynamic to answer all societal questions. One of the major challenges of the agroecological innovation pathway was to remove the research framework from the central focus in order to concentrate on a single object, plant or animal organism to increase its performances, to look at the interactions between organisms in an agricultural setting, and to devise agronomic innovation on the scale of the ecosystem. This refocusing is essential for putting ecology back in agronomy. This journal shows that the frontiers of knowledge and research in genomics are in no way restricted to the scale of the individual organism, and that there is immense potential for exploring the contribution of genomics to understanding how agricultural ecosystems function, and ultimately to their management for production purposes, with the threefold objective of economic, social and environmental performance.

This journal therefore carries a double message. Besides demonstrating that genomics has a major contribution to make to this innovation pathway, with projects to support it, it also points to some major areas of questioning which could guide such a research agenda. In that, it provides major input to discussions on the French, European and international research agenda, and across the entire spectrum of the various disciplines, at the service of the food system’s transformation towards sustainable development. It is also a significant contribution to political discussions on projects as bold as the European Green Deal, the public debate on which has not yet apprehended how far it is bringing European economic sectors and the underlying visions of innovation into question. This project will of course be very high-yielding in terms of knowledge, as the example of genomics for agroecology illustrates.

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PART 1.

REPORT ON ANIMAL, PLANT AND MICROBIAL GENOMICS PROJECTS OF POTENTIAL INTEREST FOR AGROECOLOGY

ANR funding distribution in animal, plant and microbial genomics from 2005 to 2019

Following on from Génoplante, a plant genomics programme created in 1999 and which brought together public research and private stakeholders in plant improvement, the ANR launched the programme "Génoplante 2010" (2005-2010) from 2005. The programme aimed to maintain competitiveness within French research by 2010 in the field of plant genomics, and in particular to acquire new knowledge on the diversity of genes of interest and their functional validation. Génoplante 2010 was a joint programme between the Génoplante 2010 GIS and the ANR. This programme encouraged research within a public-private partnership. At the same time, a similar programme was launched in animal genomics, called "Genanimal" (2007-2010) in partnership with the Agenae GIS, aiming to promote bovine and small ruminant, aquaculture species, and pig and hen genomics. In 2007, the "large scale microbial genomics" programme was opened to the study of pathogenic micro-organisms and the gut microbiota.

The programme "Emergence and Maturation of biotechnology projects with high potential for recovery" funded projects in five editions from 2005 to 2008. It involved academic teams on biotechnology projects with economic interest and an innovative approach for industrial application.

From 2010, the ANR continued funding a unique "animal, plant and microbial genomics" programme divided into three sub-areas. This programme closed a cycle mainly and almost exclusively aimed at the acquisition of genomic data and sequencing methods.

In 2012-2013, the genomics projects became eligible to be part of the "Bioadapt" programme, for the production of knowledge in genetics and biology. The projects aspired to understand the functional mechanisms of or to create operational responses to global changes on a scale ranging from the gene to the species.

At the same time, from 2005 to 2013, the ANR's bottom-up "blue sky" programme also funded plant and animal genomics projects as part of the "Genomics, genetics, bioinformatics and biology of systems (SVSE6)" committee.

Since 2014, as part of the ANR's work programme, the Generic Call for Proposals (AAPG) is open to genomics works within the framework of basic or targeted biology projects. This in order to promote the development of living organisms adapted to global changes and to the food challenges of the years to come, especially in the "Biology of animals, photosynthetic organisms and micro-organisms" theme.

Internationally, the ANR has funded French teams on a basic research European call for proposals on plant genomics, "ERA- CAPS - Europe-USA joint call to expand the European research area in molecular plant sciences". From 2005 to 2013, bilateral agreements with Germany and Taiwan especially, enabled the financing of genomics projects within the "blue sky" programme. Since 2014, the AAPG serves to financially support French research teams working within bilateral partnerships between France and Germany, Taiwan, Mexico, Austria or Luxembourg.

By funding around 1,300 projects for an amount of up to €519 M (sequencing included) on plant, animal or microbial genomics (excluding the human field), the ANR has helped to further knowledge in genomics, has promoted the emergence or the consolidation of public-private partnerships in animal and plant genomics and has brought together a community by organising thematic events.

Concerning these themes the ANR has in particular, enabled (i) the financing of large-scale projects, in particular, sequencing of the trout, grapevine, banana plant, alfalfa, oak and wheat chromosome 3B genome, (ii) acquisition of new data on the organisation and regulation of genomes and (iii) furthering of knowledge on the functional characteristics of genes on species of interest for Humans and on several model species.

Concerning agroecology, as already described in detail in the ANR journal no. 8 "Emergence of agroecology and future perspectives", a series of three theme-based programmes:

- ▶ "ADD - Agriculture and Sustainable Development" (2005-2006);
- ▶ "SYSTERRA - Ecosystems, territories, living resources and agricultures" (2008-2010);
- ▶ "AGROBIOSPHERE - Viability and adaptation of productive ecosystems, territories and resources facing global changes" (2011-2013);

led to the launch of eight calls for proposals and funding of 93 projects for an amount of €54 M. They also encouraged the creation of a French approach to agroecology, based on the coming together of biological, agronomic, ecological and social sciences. It provides a general framework, a vision of the future of agriculture, and a set of alternative methods to the production models that are predominant today.

Agroecology is not just an additional option to be characterised and labelled, but a movement for a transition towards new forms of agricultural activities, towards a new relationship with natural resources and land, with the living world, leading to new relations between farmers and the rest of society.

The ANR currently continues to encourage the development of scientific communities working in agroecology in the GCP area "Dynamics of socio-ecosystems and of their components with a view to their sustainable management".

Internationally, the ANR is making a strong case for agroecology whether as part of its participation in programming initiatives (JPI FACCE) or as part of the agriculture and food call for proposals (ICT-AGRI-FOOD, Arimnet 2, ERANET FACCE SURPLUS, Leapagri, Sumforest, ForestValue, Prima, SusCrop, Fosc) to name but a few.



Genomics projects of interest to agroecology funded by the ANR

The ANR journal no. 8, "Emergence of agroecology and future prospects", made an in-depth analysis of the ADD-SYSTERRA-AGROBIOSPHERE programmes and presented the 93 projects funded for the amount of €54 M in the "report" section. Here it is not a question of counterbalancing this analysis for the genomics projects, but of presenting the genomics projects, the concepts, methods and results of which may contribute to agroecology research.

On the basis of a corpus of around 1,200 projects related to plant, animal and microbial genomics, funded mainly in the calls for projects cited previously, a scientific committee comprising members of the ANR, members of scientific steering committees having followed the ANR's programming on the themes of "genomics" and "agroecology" and qualified researchers, compiled three lists of projects according to their potential interest for agroecology, based on their project title and abstract (see table):

- ▶ 37 highly promising projects;
- ▶ 43 promising projects;
- ▶ 49 potentially promising projects;
- ▶ A little over 1,000 projects considered to be unrelated to agroecology.

Out of the 37 "highly promising" projects, and after having consulted with their coordinators, 33 projects are summarised here. The sheets are presented according to the three themes of the workshops from the colloquium "**Contribution of genomics to agroecology**" which took place in Montpellier in March 2018: 8 for the theme "bioaggressors", 11 for the

theme "inter- and intra-specific diversity" and 14 for the theme "plant-micro-organism interactions".

These 33 projects (see Table 1) mainly derive from three calls for projects:

- ▶ the GCP, which clearly states the importance of working towards a more sustainable agriculture, including agroecology, since it was set up in 2014;
- ▶ Bioadapt, the major objectives of which were to develop biology and genetics projects for adaptation of living things to global changes, as much in terms of understanding mechanisms as in terms of solutions to implement;
- ▶ non-theme-based programmes (one third of projects selected, which were more so open to upstream projects, some of which have the potential to contribute or to support the development of operational systems, including in the fairly short-term (2010, 2011 and 2012 editions).

The fact that some projects funded in the programmes within which genomics was a central focus were not selected or narrowly missed selection (e.g. plant genomics programme), is probably related to the reality of genomics only being in the development phase in France in the years 2005-2010, and the fact that its methods, tools and resources remained to be defined. The research having used these results for application purposes were developed at a later date. As for the other ANR programmes in which genomics qualified, but for which plant and animal genomics was not the central focus of the call, either they did not give rise to projects in the field of agriculture, or the proposals for agriculture were not selected due to contention between themes and fields, such as human health for example.

Table 1. Genomics projects funded by the ANR and projects selected for the journal

CALL FOR PROPOSALS TITLE	EDITIONS	NO. OF PROJECTS FUNDED	NO. OF PROJECTS SELECTED FOR THIS JOURNAL ¹
AAPG	2014-2019	402	13
Bioadapt	2012-2013	38	9
Blue sky, young researcher, International white "genomics" and "ecology"	2005-2013	521	10
GénoPlante, animal, plant and microbial genomics	2005-2010	212	1
Emergence and maturation of biotechnology projects with a high potential for recovery	2005-2012	19	-
European programmes	2005-2019	95	-
Other programmes	2005-2019	66	-

¹ To illustrate the sessions from the colloquium "**Contribution of genomics to agroecology**" (Montpellier, March 2018), 13 projects out of the 37 considered to be the most promising for agroecology were selected by keeping a balance between the young researcher projects and the collaborative projects, and between advanced projects and recently selected projects.

1) MAIN RESEARCH AND HIGHER EDUCATION BODIES INVOLVED

From an organisation standpoint, the projects selected are mainly coordinated by INRAE (54%) (Fig. 1), followed by the CNRS and the universities, each contributing for around 20% to coordination of the projects selected.

In terms of distribution of partner teams, which make up consortia of 3.3 teams on average for coordination, Figure 2 shows that INRAE is primarily involved? with 50% of partner teams for these 33 projects, followed by the CNRS and the universities. Nine private companies are working on eight projects, with none of those companies coordinating them.

Figure 1. Distribution of coordinators of the 33 agroecology genomics projects per organisation

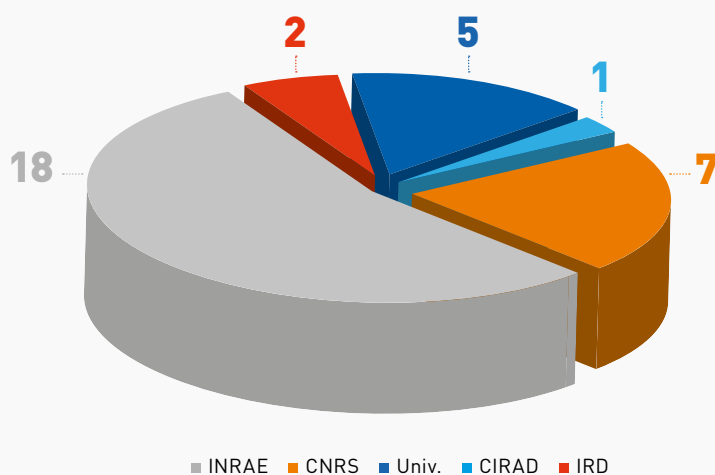
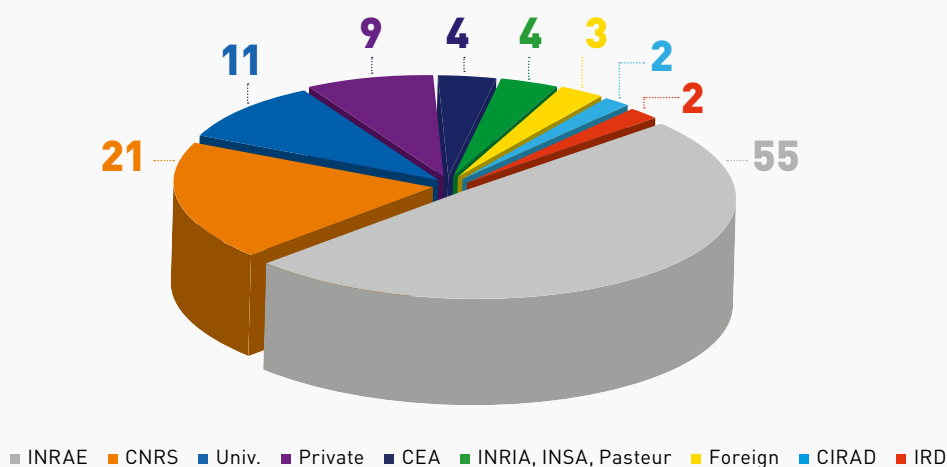


Figure 2. Distribution of partner teams of the 33 agroecology genomics projects per organisation



² The teams are shown to belong to their hosting supervisory bodies, where the research takes place. Researchers from other organisations not included in these data may also be part of the teams.

2) TEAM GEOGRAPHICAL DISTRIBUTION

The teams whose research covers agroecology are mainly located in the Paris region (15 in Paris and 9 in INRAE's centres in the Yvelines), followed by Toulouse and Montpellier showing equal distribution. French overseas territories only count one project located in French Guiana involving 6 partners in France and abroad (Fig. 3).

7 projects are coordinated in the region of Toulouse, in INRAE's centre in Castanet Tolosan in particular, on an equal footing with the Paris region (7 projects also coordinated), followed by Montpellier with 5 projects coordinated.

An additional analysis shows that the projects associate partners all over France and that for a given project, there are almost no partnerships among teams locally.

If we compare the distribution map of the 111 partners and coordinators of the projects presented in this journal (Fig. 3), to the geographical distribution of the 501 teams which proposed a project related to genomics in the "Animal, photosynthetic organism and micro-organism biology" of the 2019 GCP (Fig. 4). Team mobilisation for the 2019 GCP corresponds to effective representation of the scientific community conducting research in genomics in the broad sense of the term, in agriculture and livestock farming. On both figures we can see the same departments are highly represented, except for the departments in the PACA, Alsace and Western Brittany regions, where the projects funded were not or only partially selected for this journal.

Figure 3. Geographical distribution of the 111 teams participating in the 33 agroecology genomics projects

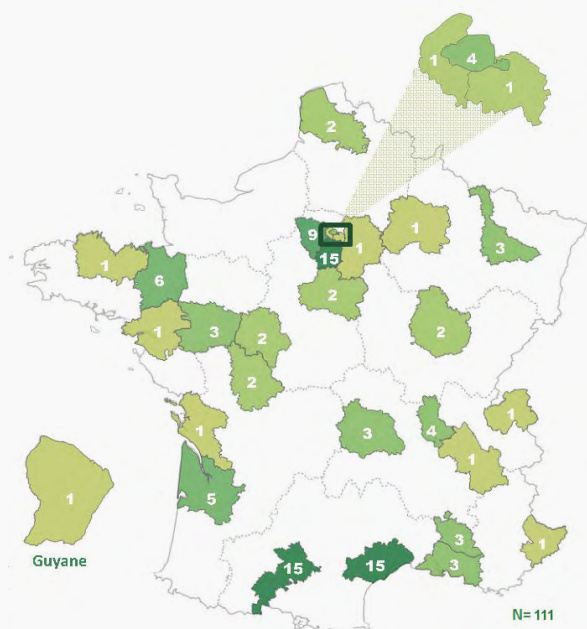
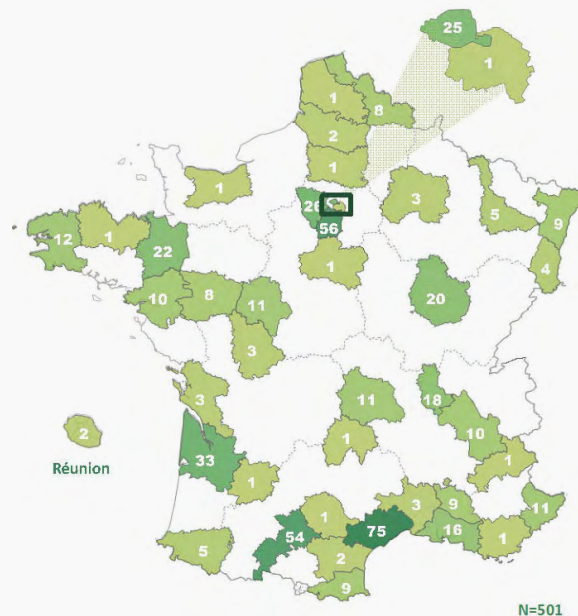


Figure 4. Geographical distribution of the 501 teams partnering the preproposals submitted to the ANR in 2019 in the area "Animal, photosynthetic organism and micro-organism biology"



3) PROJECTS BY DISCIPLINE

The projects selected mainly all focus on the field of plants (**Fig. 5**) looking at both plants and trees and their function (12), at nitrogen-fixing root symbioses (8), at fungi (3), at soil microbiota (2), at crop insect pests (2) or lastly at biocontrol for crop protection (2). Only 4 projects are related to livestock animals.

Figure 5. Number of projects according to the main fields

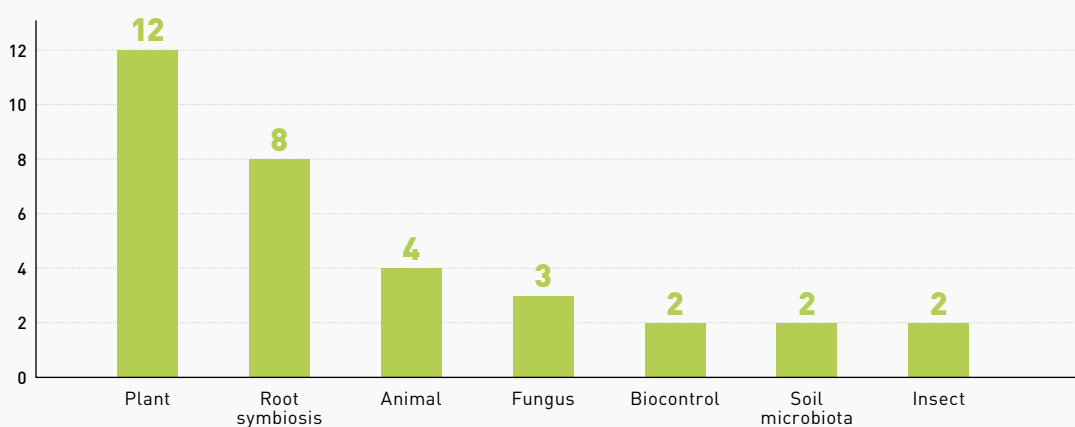


Figure 6 shows the team members per discipline (keywords for the team's research themes) leading the 33 projects presented.

Biological sciences teams are working on thirty-two projects. These teams herald from a wide range of backgrounds including biology, entomology, ethology, genetics, genomics and "omics" disciplines (metabolomics, proteomics, transcriptomics etc.), microbiology, physiology, phytopathology and virology.

Among them, sixteen projects are led exclusively by biological sciences teams and include seven Young Researchers projects (AATTOL, AeschyNod, DeCoD, INCITE, LCO-inNON-LEGUMES, POLLINET, SymbioMaize). By definition, these Young Researchers projects only involve one team and are selected mainly based on their innovative nature, with respect to the mainstream themes of their unit.

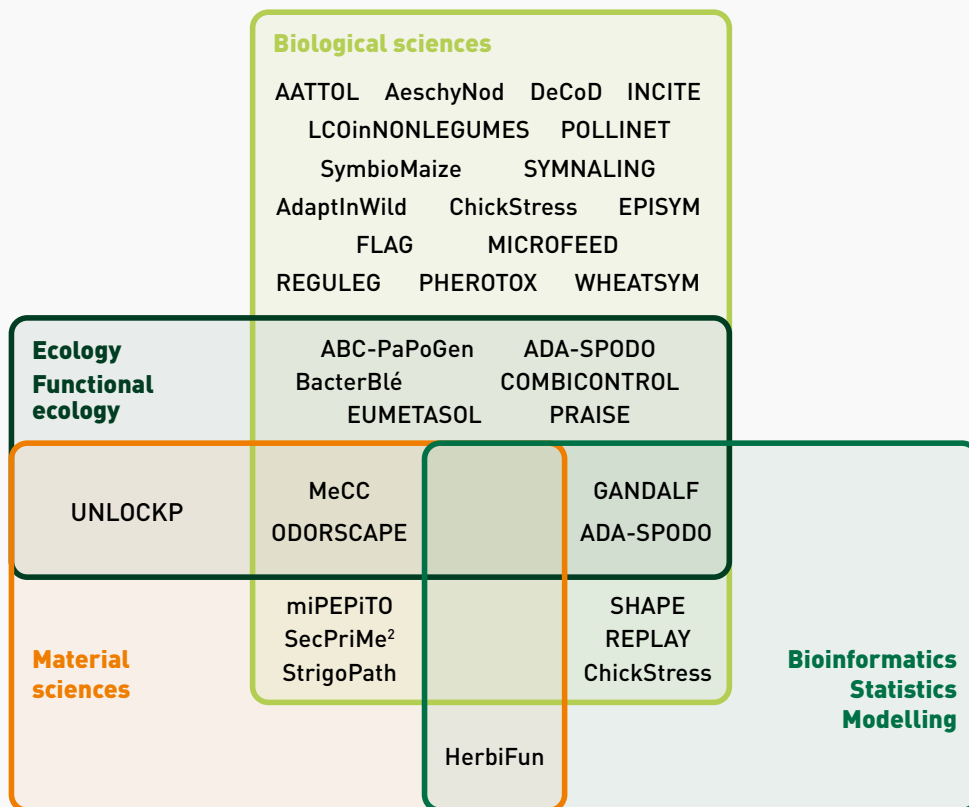
Sixteen other projects bring together teams from three other fields in addition to the biological sciences teams:

- ▶ Ecology teams (ecophysiology, functional ecology etc.) are involved in 10 projects;
- ▶ Material sciences teams (chemistry, analytical chemistry etc.) are involved in 6 projects;
- ▶ 6 projects have brought together bioinformatics, statistics and modelling teams.

Teams from three disciplines are involved in four projects: MeCC, ODORSCAPE, GANDALF, ADA-SPODO (**Fig. 6**).

The thirty-third project, HerbiFun, is led jointly by material sciences teams and mathematical sciences teams.

Figure 6. Distribution of projects according to the interdisciplinarity of the biological sciences, mathematical sciences, material sciences and environmental sciences partners



PART 2.

CONTRIBUTING TO MAJOR CHALLENGES IN AGROECOLOGY AND BEYOND: PRIORITY RESEARCH AREAS

Background and current context

Genomics was born at the end of the previous millennium thanks to the combined progress made in information technology and high-throughput automated analysis of biological samples. Its efficiency has only improved over the last 20 years (as seen in the spectacular progress in nucleic acid sequencing technologies). Genomics analyses and integrates biological information components derived from the various levels of organisation and functioning of an organism or from a community of organisms; (epi-)genome, transcriptome, proteome, fluxome, metabolome, ionome and phenome. Genomics is based on genetic code, an integrator universal language which builds bridges not only between disciplines, but also between the organisms studied.

The suffix shared by these various “omics” reflects a global analysis, derived from the holistic approach of the biome, as they aim to describe the structure, the functioning, and the regulation of the genome of all organisms found within an ecosystem, and to dissect the interactions between its components, and the roles played by the environment in the phenotypic expression of the various components. The challenge today is to integrate the responses of the organisms in the face of biotic and abiotic factors at the various levels of organisation and regulation. To do that, genomics relies both on the heterogeneous big data derived from multiple omics obtained at the different levels of organisation and on the data derived from temporal series, in order to correlate the said data. The objective is to optimise these interactions to promote the sustainability and the resilience of future agroecosystems.

It is widely accepted that agroecology comprises three inseparable dimensions: practice, politics and science. The latter notably refers to research aimed at protecting and recovering biodiversity and biological processes to cover both production requirements and all of the other ecosystem services provided by agroecosystems, by reducing the use of synthetic inputs. It therefore involves characterising, understanding and recovering functional biodiversity, among other things, to optimise biological regulations within agroecosystems, in order to improve the functionalities of these agroecosystems and devise practices for their long-term management. Like genomics, it involves observing, describing, and understanding, to then optimise complex and dynamic interactions and regulations between biological components found within a system, the agroecosystem in this case, and, as is most often the case, under the effect of human activities in a context of global change (climate change in particular). It thus involves understanding the effect of the genetic/specific structures of plant and animal material and the effect of crop growing and livestock farming practices on these functionalities, in order to design and develop economically-viable production methods, which protect those implementing them and which make a positive contribution to environmental concerns (soil functionality, nutrient cycles, preservation of biodiversity, attenuation of climate change and water quality etc.).

Agroecology, which involves furthering understanding of the interactions between the organisms found within crop and livestock farming systems which are subject to changes in their environment, may benefit from advances in the use of “omics” data through at least three approaches:

- 1) qualitative and quantitative description of the diversity of living communities in interaction within an agroecosystem, especially thanks to fast-growing metagenomics;

2) study at the various societal and temporal levels of interactions between the biological components within an agroecosystem. This represents one of the fields of integrative biology, molecular ecology or systems biology;

3) rapid and efficient transfer of results for a model or reference species, which has been extensively researched in genomics, to all related species for which the same functionalities are looked for. This is what is known as translational research.

The integration of these three approaches at different levels of organisation is of major importance to the understanding of friendly or hostile interactions which exist within an agroecosystem. It is necessary from now on to move towards a functional approach to (i) define how the dynamics of regulation networks is affected by the environment and how this environment affects the phenotype and the diversity of plants, animals and micro-organisms, and their interactions and (ii) put forward assumptions as to the functionality of a group or network of "omic" regulators among related species. This functional change in integrative biology and translational research can be used to develop predictive approaches as to the capacities of the various lines/races of the same species or different species to be used for the same functionalities.

Integration of "omics" data at the level of individuals representing a species and found within an agroecosystem, must also document a dynamic vision of biological systems, by taking several scales of organisation (from cells to the organ they are part of, or even the community in the case of microbes), time (long-term) and space (through to the landscape) into account.

The integration of "omics" data at the scale of a species or families of species can be used in the long-term to conduct predictive biology approaches, by modelling the impact of gene regulation and function on a phenotype of interest within a species based on "omics" knowledge acquired on the models (translational research).

This conceptual change in the integration of "omics" data must provide for a better understanding of the molecular and cellular mechanisms of the phenotypic response for the major characteristics entering into an agroecological design of agriculture and livestock farming (use of resources, immunity, tolerance to environmental stressors, optimisation of biological interactions etc.). It must lead to the discovery of predictive biomarkers (i.e. functional polymorphisms) for species grown and raised, their bioaggressors and synergistic organisms at the scale of genomes and the metagenome, or even up to the networks of interactions of these causal "omics" variations (interactome).

► Area 1:

Towards better multi scale integration of "omics" data for optimal use in agroecology

1) Optimising the analysis of big data for translational research into species cultivated/grown and at the service of predictive biology

The constant reduction in the cost of "omics" technologies (genomics, transcriptomics, proteomics, metabolomics, phenotypics etc.) today enables the production of large volumes of heterogeneous data at various levels of organisation of living things, bringing biology into the big data era. It is from now on crucial to develop tools and methods but also infrastructures (platforms) and to make them accessible to the scientific community as a whole.

The use of these new technologies for observing the functioning of living things will make it possible to reach a fine understanding of complex biological processes (determinisms of the development of or-

ganisms, diseases, adaptive mechanisms etc.), and ecological processes but also reactions to global changes (climate change especially). This requires redefining the processes and methods used to store, interpret, question and view these data, and especially provide for their successful integration.

The analysis of these big data is currently a bottleneck requiring the development of high-performance and reliable tools which are able to process heterogeneous data in terms of dimension (large number of variables measured), scale (hundreds of millions or even billions of data per experiment), resolution (able to include missing data), time (up to several weeks and months of analysis), heterogeneity (sequence, intensity, spectrum etc.), type (qualitative, quantitative etc.), and format (table, graphs, text etc.).

2) Integrating “omics” data for furthering understanding of the functioning of individuals in interaction in their agroecosystem

In the agricultural field where these “omics” data are increasingly produced, the technological challenges are major for identifying the combinations of “omics” variables explaining biological variability (especially phenotypes) observed at the various levels of organisation of living things (the cell, the tissue, the organ, the individual, the population, seed production area) making up an agroecosystem. It is now clear that it is only when knowledge of the functioning of an individual at its various levels of organisation has been integrated that the key mechanisms related to the development, adaptation or tolerance to stressors can be demonstrated. Integration is necessary for (1) managing, organising and structuring these metadata in order to improve use, (2) developing an integrated environment for extracting interpretable information more easily, (3) filtering the relevant relationships between the data to create a data hierarchy, (4) identifying significant relationships between heterogeneous data, and (5) delivering a knowledge map to users with which they can interact via a customisable interface.

Challenge: Integrate various levels of organisation

The standard nature of “omics” data, supported by modelling applied to these data, can help integrate various levels of organisation (cell - organ - organism - population/community - lot - land/territory) for defining functional determinants in the optimisation of ecosystem services.

In the same way, this should enable series of more reductionist approaches to follow suit, covering the influence of farming practices or climate factors on agroecosystem functioning, towards a more holistic vision, and to define more effective leverage for action. The principles defined thanks to these integrated approaches can be validated, monitored and adjusted within certified workshop areas or certain long-standing research units benefiting from monitoring of their development and their data over time, and in particular genomics data collected being free to access.

The development of data analysis, modelling and knowledge representation methods has become essential for optimising “omics” data use. To rise to this challenge, a multidisciplinary research theme (involving mathematicians, statisticians, genomics specialists, genetics specialists, physiologists and agronomists), could cover the rolling out of general methods (mathematical, exploratory or predictive statistics, information technology) for the integration of “omics” data meeting the previous five criteria, and which must be able to be adjusted when it comes to integrating “omics” data at different levels of organisation considered to be biological systems in their own right: the individual (from the cell to the whole organism), the holobiont (interactions with the microbiota), the seed production area, populations and species making up the agroecosystem.

Our ability to predict the response (phenotype) of an organism within its agroecosystem faced with a changing environment from the omic data produced, involves the development of an environment propitious to optimal data integration.

3) Comparing “omics” data for the more effective use of knowledge between lines/races or species

At intra-specific or population scale (i.e. genotypes representing the diversity of a species), integration of “omics” data for a set of agronomic characteristics among a few representatives (lines) of a species, could enable imputation/inference to the population as a whole in order to predict the potential phenotypic response of a race /line in a given environment. This is (partly) the area of genomic selection which must be generalised to all “omics” resources available without restricting it to the use of structural genomic variations (SNP data) for example. At the inter-specific scale, the integration of “omics” data, for all characteristics of interest of a species, taken as a model (or pivot) for a botanical family (for example peas for pulses or wheat for cereals), must enable imputation/inference of the phenotypic response to species similar to that family.

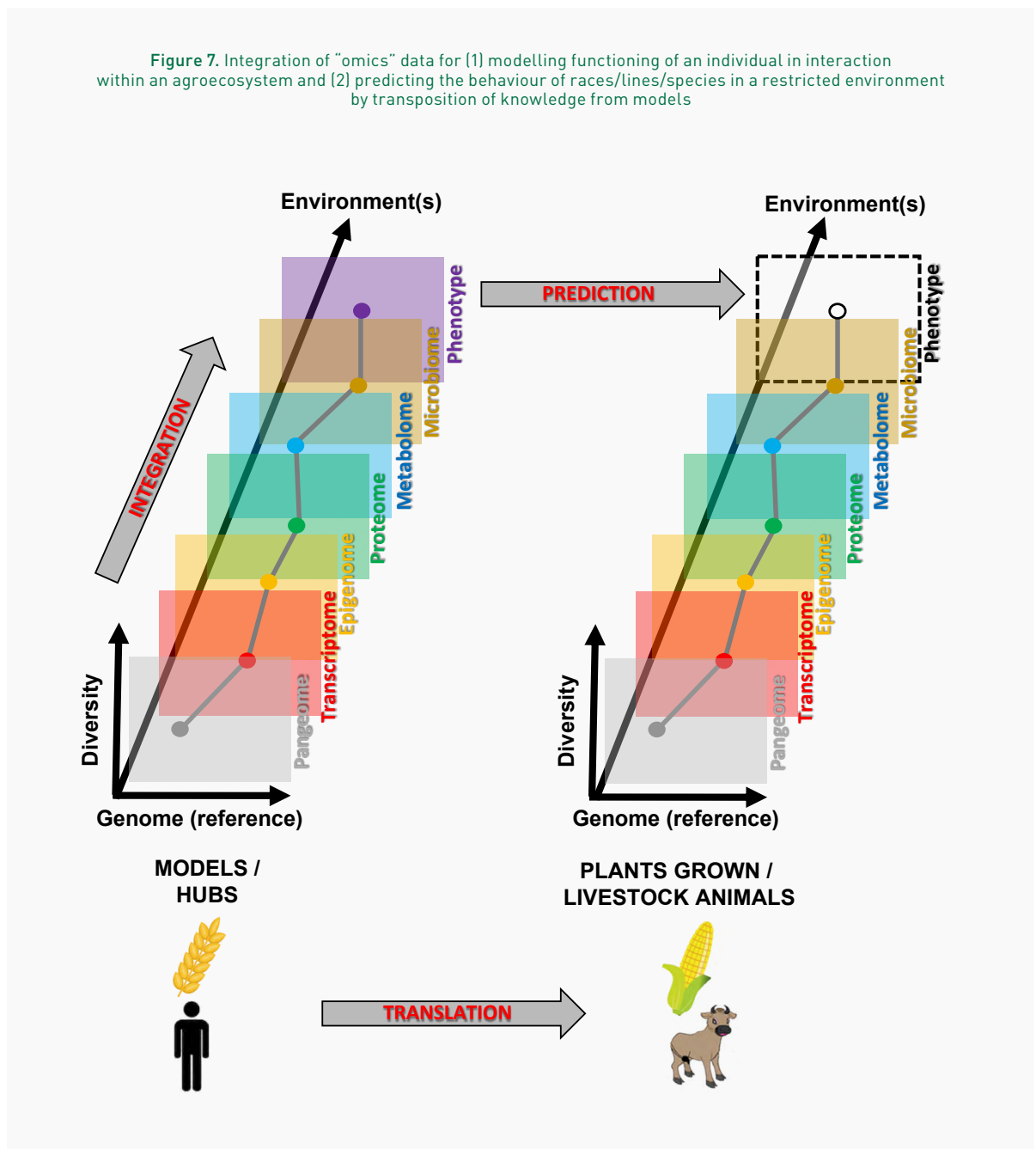
In angiosperms (beyond major botanical families such as cereals and pulses), integration of “omics” data in that way is used to transfer knowledge acquired from models to agronomic species of interest, for example by transferring knowledge acquired with *Arabidopsis thaliana* to cereals, an objective that was difficult to obtain until recently.

In this context, a research theme could consist in the development of comparative "omic" methods and approaches between lines/races or species to model gene regulation and function within a race/line by integrating the "omics" knowledge from models.

Finally, the convergent change in "omics" variations at intra-specific or inter-specific scale can be used to identify changes within "omic" regulation circuits in a very specific manner during changes in a group of

racelines or species having acquired new phenotypes, compared to a group of races/lines or species not exhibiting this trait (Evo-Devo literally for Evolutionary Developmental Biology). This evolving dimension of comparative "omics" must be used henceforth to generalise these Evo-DEvo approaches for more effective characterisation of the molecular mechanisms of numerous functionalities targeted in agroecology.

Figure 7. Integration of "omics" data for (1) modelling functioning of an individual in interaction within an agroecosystem and (2) predicting the behaviour of races/lines/species in a restricted environment by transposition of knowledge from models



► Area 2:

Dynamic characterisation of intra- and interspecific functional diversity of organisms found in an agroecosystem

1) Cultivating plant diversity

In an agroecosystem, the performance of plants grown and their adaptation to low levels of inputs (phytosanitary products, synthetic fertilisers, water intake etc.) and to climatic extremes (thermal and hydric fluctuations) seems to be influenced by the levels of diversity introduced or promoted (micro-organisms) in this agroecosystem. However, the added value of diversity, genetic diversity in particular, remains to be demonstrated, or consolidated, along with the conditions in which this diversity is expressed.

It is also essential to move beyond the descriptive approach and to develop research into the genetic and ecological mechanisms involved in the functioning of complex coverages. The knowledge thus acquired can be used to define effective levels of diversity for improving the expected services. These studies should be applied

at various levels of organisation (cellular, organ, whole plant, populations, communities). The phenotypic character approaches shall be correlated with genomic and molecular approaches.

The genetic leverage that is the improvement of plants, has generally given rise to little-diversified service cover crops, at least in Northern countries. Complementary to species diversity, the introduction of plant cultivated intra and/or inter-specific genetic diversity in agroecosystems is an area for action that is little explored. It is therefore a question of defining new selection criteria for the improvement of complex seed production areas with production and ecosystem service supply objectives, and new methodologies for selecting varieties on the basis of their behaviour in a mixture, and not exclusively on the basis of their individual behaviour.

Challenge: Define the influence of the introduction of genetic and species diversity in cultures to compensate for production variability faced with climate hazards, lower the impact of bioaggressors and invasions or even maintain greater soil fertility

Having broken ties with conventional agriculture, agroecology considers an agroecosystem in its entirety and in the long-term, requiring characterisation of the dynamics of the functional intra- and inter-specific diversity of the organisms in the agroecosystem. This diversity must be envisaged at the different levels of organisation of living things. Genomics tools are used to study precisely the expression and the influence of this diversity on functioning at different levels, ranging from the individual to the complex agroecosystem.

Therefore genomics is used to support and accelerate the switch to a taxonomic approach, characterised by a catalogue of the presence and abundance of organisms in an agroecosystem, towards a functional approach of the sort agroecology seeks to develop. The latter considers organisms as a support for general functions, the determinants of which are identified, at the origin of production of goods or services for human populations.

2) Managing complex agroecosystems without reducing them to their components

Complex seed production areas require the interactions between the plants of the seed population but also their interactions with related organisms to be taken into account. Aerial and underground interactions (architecture, root development and morphology, exsudates, signalling, effect on the biotic and abiotic properties of the rhizosphere, etc.) are considered to improve production (quality and quantity), plant health and the expected services of the agroecosystem. Identification of the characteristics of friendly interactions (with micro-organisms, microfauna, beneficials, other varieties of the same species, other cultivated plants, non-cultivated plants etc.) among cultivated plants is an important area of research, as is the development of medium and high-throughput phenotyping methods for some of these characteristics. All of these research areas should be positioned by considering the management practices applied in the agroecosystem and the abiotic parameters to define genetic and agronomic levers, including new and favourable agricultural practices (production, plant health, ecosystem services).

3) Studying traditional agroecosystems to reintroduce diversity

With this outlook, studying traditional agroecosystems in countries located in or near to cultivated species domestication areas, especially in the South, can provide valuable information when looked at from a genomics perspective. For example, maize-bean intercropping in central America or sorghum-cowpea in West Africa have been used for some time and in various forms. The varieties/populations were selected by farmers on the basis of their ability to be used in intercropping, often in conditions of high environmental stress with low levels of inputs. Genetic typing of these populations could be used to approach chromosome regions that are important for the characteristics promoting intercropping, characteristics potentially lost in the pool of our modern varieties.

The same applies for the related microbiota recruited by the species in combination. This microbiota observed in these traditional agroecosystems, spread by traditional seed exchange, should be closer to that recruited initially during domestication of the species, than that associated with modern varieties. In effect, modern seed exchange phytosanitary practices (pesticide treatments), especially between continents, and the methods of selection of modern varieties minimising nutritional or sanitary pressure could have brought about the change in the original microbiota.

Exploration of this microbiota through genomic and metagenomic approaches and exploration of plant genetic characteristics promoting recruitment could be used to optimise the corresponding biological interactions and thus reduce the use of synthetic inputs.

Therefore, studying plant genetic diversity would make it possible to confirm whether the modern varieties, selected in low stress conditions (fertiliser, pesticides, water etc.), led to the counter-selection of plant characteristics contributing to the recruitment of microbial populations favourable to the nutrition and health of the host plant. After identification, these plant characteristics could be reintroduced in plant selection programmes.

4) Protecting and maintaining soil diversity

Soils represent one of the main reservoirs of the planet's biodiversity with eukaryotes, bacteria and archaeobacteria. All of these organisms represent an extremely high biomass (around 5 tons for one hectare of pasture. Despite their abundance and their diversity, telluric microflora (archaeobacteria, bacteria and fungi) were underestimated for a long time as they were difficult to study. These difficulties are inherent to the microscopic size of these organisms (around a micrometre for bacteria) and to the opaque nature of the heterogeneous structure of soils. Analysis of microbial diversity therefore required methodological developments. DNA extraction directly from the soil (1990-2000) made it possible to analyse all microbial communities (meta-communities) and their genomes (metagenome).

Analysis of these genomes is facilitated by the highly significant reduction in sequencing costs in favour of technological developments recorded during major sequencing projects (e.g., human genome, gut microbiota genome). We thus realise today the immensity of soil microbial diversity with 104 to 107 species of bacteria per gram of soil, many of which remain to be identified (as an example, 75% of new bacterial species were described in 2012).

Beyond taxonomic diversity, these metagenomics approaches, combined with a functional analysis, should make it possible to identify new genes of function and to access better understanding of the biological functioning of soils in interaction with plants (and animals). It is a major challenge as the biological functioning of the soil-plant system (animals) is at the origin of ecosystem services essential to humankind. Despite its importance, biodiversity and soils more generally are exposed to threats, and it is therefore essential to further understand this biodiversity to protect it and increase its value. With this in mind, major biogeography projects have been launched applying molecular methods to characterise biodiversity on large spatial scales.

► Area 3: Optimisation of friendly plant-micro-organism interactions

The plant rhizosphere is colonised by a myriad of micro-organisms. Plant-bacteria interactions lead to variable effects and associations range from symbiosis, which leads to the establishment of a specialised host organ, to more or less intimate associations (e.g. plant growth-promoting rhizobacteria, PGPR). The specificity of microbial recruitment in the rhizosphere is controlled by plant and microbe characteristics.

The composition of the rhizodeposits established by plants varies according to the plant genotypes, and the telluric microbial populations respond differently to the organic compounds (sugars, amino acids, organic acids) they contain. Rhizodeposits set up complex and subtle molecular communication also contributing to recruitment of the rhizosphere microbiota and regulation of activities.

Conventional agricultural systems minimise biotic interactions, in particular those between plants and micro-organisms. Current cultivars could have lost characteristics involved in positive feedback loops between plants and micro-organisms during selection processes conducted in most artificialised situations (inputs). For instance, the application of nitrogen fertiliser reduces the ability of pulses to use nitrogen-fixing symbiosis and phosphate fertilisation has a negative impact on moss mycorrhization. Furthermore, simplification of rotations comes with a reduction in the rhizodeposits' variety.

Agroecology represents a major change of paradigm as it places biodiversity and biotic interactions at the heart of its methods. Knowledge of plant-micro-organism interactions in the rhizosphere thus represents a central challenge for reducing the use of fertilisers and pesticides.

Challenge: Characterise a group of organisms linked by friendly interactions within an agroecosystem, example of the holobiont

The term holobiont (from the Greek *holos*, "whole", and *bios* "life") describes the entity comprising a host organism (human, animal or plant) and the cohort of organisms closely related to it, especially micro-organisms such as bacteria, viruses and archaeobacteria, protists and microscopic fungi, making up the microbiota. This holobiont generally exhibits higher performance than that of the host when taken separately and without its microbiota. Concerning plants, the holobiont includes the microbiota colonising its various organs (seed, root, stem, leaf, flower, fruit) epiphytically or endophytically. Concerning animals and humans, the holobiont includes the gut, respiratory, skin, vaginal and breast microbiota... Identification of the host's genetic characteristics and those of the microbes involved in the positive feedback loops between the

holobiont host and microbiota represent a significant challenge to which genomics must contribute.

The functional microbiota combined with a host genotype can thus be compared in various types of soils (exhibiting varied microbial diversity) or under the effect of various farming practices for plants and in different environments or under the effect of livestock farming practices in the case of animals. In the same way, the host genotypes can be studied for their potentially variable mechanisms and capacities for recruitment of the related microbiota. Genomic approaches are valuable for decrypting interactions within the holobiont, their regulations, their functional roles and their responses to changes in the environment.

1) The rhizosphere microbiota at the service of plant growth and health

Modulation of host plant growth and health by the rhizosphere microbiota is a significant challenge in agroecology and enables, in the case of nitrogen-fixing symbiosis, an almost total decrease in the use of nitrogen fertilisers in pulses and soil nitrogen enrichment. More generally, beneficial microbiota populations (PGPR or others) contribute to:

- ▶ plant nutrition via nutrient provision (N, P, Iron etc.), nitrogen fixation by bacteria (except for specialised organs in which case the term referred to is symbiosis);
- ▶ plant growth and development via the production of phytohormones (auxine, cytokinine, ethylene);
- ▶ plant health via the reduction in root infections by antagonism against plant pathogens (antibiosis, nutrient competition) and via the induction of plant defence reactions.

New growth biostimulants and/or biocontrol could represent precious beneficials, however research into their mechanism of action and their efficacy using genomics approaches must be undertaken.



2) Plant and microbial genomics for optimising beneficial interactions in agroecology

Over the last few years, genomics and metagenomics have significantly changed the study of the diversity of the microbiota found in the rhizosphere. They both have opened up new research perspectives for the identification of new functions involved in rhizosphere interactions, and also for research aiming to characterise general functions managed by the microbiota, beyond individual and specific functions. In addition to the methods to evaluate the positive effects of rhizosphere microbiota, genomics can be used to process complex data characteristic of agroecology systems.

In order to understand the complex environment between plants and soil micro-organisms, it would be especially important to identify the molecular and genetic determinisms of recognition between the plant and its micro-organisms, in order to be able to ensure inter-organism mutual exchanges are efficient. These methods of action of microbiota in interaction with the roots should be explored in contrasting agronomic conditions (minerals, access to water etc.). Indeed, the effects of micro-organisms, including secondary micro-organisms, on plant nutrition, should be estimated holistically. Research should take account of the parameters related to microbiota functioning, in particular its nutrition in contrasted mineral conditions. Beneficial bacteria in a specific type of soil (e.g. nitrogen fixation) can be ultimately harmful to the plant in a nitrogen-rich soil with low phosphate levels (potential competition for phosphorus).

Generally, when studying microbial and plant characteristics, it is important to not only take those beneficial to the growth and health of the host plant into account but to also take account of those involved in the ecosystem functions and services expected of the agroecosystem (climate regulation: soil carbon storage, reduction in greenhouse gas emissions, water biofiltration, etc.).

Genomics and metagenomics studies are also appropriate for identifying plant and microbial characteristics and the mechanisms involved in the recruitment and expression of beneficial population activities.

3) Characterising and highlighting plant characteristics involved in interactions

The identification and the characterisation of plant characteristics, including recruitment characteristics involved in beneficial interactions with the rhizosphere microbiota, and their introduction in modern cultivars is an excellent opportunity for better showcasing photosynthates specific to rhizodeposits, for plant nutrition and health, in situations where low levels of synthetic inputs are used (synthetic pesticides, fertilisers).

In order to better understand plant and microbial characteristics involved in positive feedback loops, the first strategy aims to introduce preisolated beneficial plant characteristics in plants to promote (i) recruitment of beneficial microbial function genes from telluric microbial populations and (ii) the plant's ability to respond to beneficial activities resulting from these genes.

It also involves creating value around the facilitation and complementarity processes among cultivated plants and the competition processes among cultivated and adventitious plants while maintaining them at a sufficient level so they provide the expected services (pollination in particular) where applicable. The choice of plant intercropping to promote biodiversity, or beneficial populations and activities must be made over time and in space (rotation). Genomics tools, the possibility of processing big data and modelling are essential in this context.

4) Characterising and highlighting the microbiota adapted to plants

The question of creating value around these plant characteristics in soils which do not exhibit the same taxonomic diversity must also be considered on the basis of a possible core functional microbiota associated with the plant genotype. Research on identification of the core functional microbiota associated with agronomic species genotypes must be continued by using the plant genetic resources of these species and by testing the genericity of the functional microbiota associated with these plant genotypes in different soils. Genomics tools and high-throughput tools in particular are especially useful.

Non-symbiotic microbial strains inoculated in the rhizosphere exhibit low competitiveness, faced with the resident telluric microbiota. The strategy to transmit bacteria to the seed by inoculating the flowers requires in-depth knowledge of the mechanisms of floral colonisation and transmission to the seed.

► Area 4: Genomics at the service of the ecological transition in livestock farming

Concerning livestock farming in particular, Dumont *et al.* (2013)³ propose five major objectives to support the transition towards agroecology systems which protect both animals and the environment and which put the available biomasses, effluents and animal products to the best use:

- reduce inputs required for animal production by increasing the efficacy of use of limiting resources (nitrogen, phosphorus etc.) and by reducing the use of human food resources;
- reduce pollutant discharge in livestock farming systems, especially by optimising the efficiency of feed resources and by reusing waste;
- adopt livestock farming practices which protect animal health and well-being while reducing drug and hormone inputs by mobilising the animals' adaptive capacity;
- promote the diversity of resources and the complementarity of varied animal profiles within livestock farming systems to reinforce their resilience;
- develop coverage management practices (permanent pasture, agroforestry etc.) contributing to preserving the biodiversity of agroecosystems and ensuring the provision of ecosystem services.

Genomics approaches are useful when mobilised to serve these five objectives, as an example:

- genomic selection to increase the originality of breeding stock;
- nutrigenomics to study the digestive and metabolic use of feed components and the genesis of pollutant discharge;
- microbial genomics and metagenomics to understand the role of the intestinal microbiota in the production of methane and nitrogenous waste among ruminants;
- the combination of descriptive "omics" approaches to characterise the genetic and functional diversity of livestock farming system elements;
- functional genomics approaches to understand the regulation of major functions and animals' adaptive capacities;
- epigenetics to clarify the impact of biotic and abiotic environmental factors on genes and phenotypes.

³ Dumont B., Fortun-Lamothe L., Thomas M., Jouven M., Tichit M., 2013. Prospects from agroecology and industrial ecology for animal production in the 21st century. *Animal* 7: 1028–1043.

1) Reintroducing diversity within herds

Among the five agroecology objectives applied to livestock farming, the objective concerning value-creation for animal profile diversity within livestock is undoubtedly the most far removed from practices and research conducted to date. It is a question of finding sustainable management methods (intended and controlled) for a variety of species or intraspecies varied genetic profiles within the same system. This approach is only in the early stages and is coming up against farmers' needs to have a simplified management system and controlled numbers of lots for slaughter.

However, some benefits can be hoped to be reaped, especially for managing herd health. For example, mixed grazing of various herbivore species can reduce the parasite load in meadows by the dilution effect of pathogens specific to each and improve the use of grazing resources. The reality of the expected effects of intra-herd animal profile diversity on the resilience of production systems and their overall efficiency remains yet to be demonstrated (beyond theoretical simulations).

The contribution of genomics, especially by the intricate characterisation of the various genetic profiles and their responses to changes in the environment, may, in the long-term, make it possible to put forward selection strategies for mixed race/line populations or for use in cross-breeding in order to better answer to the needs of systems with low input levels.



2) Robust animals faced with an unpredictable environment

The agroecological challenges for livestock farming require knowledge on the interactions between the animal and its environment (food resources, housing, climate, other animals of the same species, other animal species, humans, pathogens, microbiota etc.). Answers should also come from research into more efficient animals for transforming food resources and which are able to express their production potential within a wide range of climate conditions and livestock farming systems, and also exhibiting increased adaptability (climate, pathogens, economic contingencies).

Faced with climate change, the sustainability of production systems requires animals resistant to climate stress and its consequences (heat, humidity, variability in food resource availability etc.). It is all the more crucial in tropical countries and for production systems with low inputs (food, energy, water, and medicines).

The search for greater robustness is becoming a priority in a context in which housing conditions are changing with more of a "connection to the land", causing increased exposure to climate hazards and potentially to pathogens.

These objectives require developing knowledge on the plasticity of the genome and its relationships with animal adaptation capacities. In concrete terms, it involves better characterising the notions of animal robustness and resilience capacity, and in a broader sense, those of livestock farming systems. Adaptation to heat and resistance to diseases are key elements in the exploratory field. It has in effect been shown that even subclinical states lead to decreased performance. New characters are introduced in selection programmes to improve animal robustness within a varied range of livestock farming systems, enabling the procreation and dissemination of new genotypes.

Access to increasingly high-performance functional exploration techniques in the field of animals, in particular based on "omics" approaches and modelling approaches, opens up new perspectives for investigation into understanding the functional relationships between the animal's phenotype, its genotype and the environment in which it is expressed, in more detail.

In this context, research in animal sciences (nutrition, reproduction, neurosciences and ethology, physiology of adaptation, animal health, genetics and genomics, economy and sociology) should promote interdisciplinarity, integrate statistics and modelling, to be more systemic and predictive and ultimately identify levers for the development of production systems compatible with agroecology.

Genetic selection, using “omics” data, allows for the integration of different levels of organisation and for “nested” responses from the individual through to the livestock farming systems, including interactions between the organisms and their environment. It is not a question of selecting a “standard” animal for agroecology systems, but of preserving sufficient intra- and interpopulation genetic diversity, and encouraging, in addition to widely disseminated races/lines, the use of races with performances suited to local and sustainable production, animals with varied profiles and adapted to the diversity of livestock farming environments and practices.

Genomic selection facilitates evolutions and provides for genetic improvement with smaller numbers of phenotyped animals in each livestock farming system than with selection per performance and pedigree.

“Omics” tools can also be used to study epigenetic regulations associated with variations in the environment on the expression of animal genetic potential. They can be used to entertain the dissociation of certain genetic antagonisms between animal aptitudes (production/reproduction; production/health etc.) in order to improve animal robustness. They enable in particular better understanding of the effect of events during the perinatal period, which are little known and could be used as levers to optimise livestock farming conditions enabling animals to fully express their production potential.

These approaches could add to techniques of genetic selection and dissemination of genetic progress specific to certain environments, innovative practices for environment and animal coadaptation.

Livestock farming system development and diversification, and globalisation of animal and product trade, also lead us to consider genotype x environment interactions in the prediction of genetic values, and to directly evaluate the performances of animals in low input systems, especially food and medicines, which until recently was still not possible in these systems. By disconnecting the calculation of the genetic value of candidates for selection from obtaining phenotypes, genomic assessment is used for selection in a given environment, by targeting production in another, on the condition the effects in each farming environment are fully known.

Challenge: Address the complexity of the networks of interaction and regulation among and between organisms within agroecosystems

Agroecology considers an agroecosystem as a whole and includes interactions between wild and domestic organisms, under the effect of human activities. Genomics could provide for deconvolution of complexity through the construction of networks of interactions. Genomics also allows for translational approaches between wild/cultivated/farmed organisms, to model, and in the long-term, to predict how their interactions are likely to contribute to their adaptation to the environment, to plant and animal agricultural production (health, productivity and product quality) and to the supply of ecosystem services in a situation where inputs are little used or where there are no synthetic inputs (fertiliser, pesticides, veterinary products etc.).

3) Towards better food efficiency

Efforts are also to be continued in improving food efficiency in order to decrease the consumed biomass/produced biomass ratio. Animals' adaptation capacity to value creation for grass for ruminants, for lower quality feed for monogastric animals while minimising discharge into the environment are also priorities to follow. Metagenomic and nutrigenomic approaches and additional research on plant production (crop co- and by-product value creation, replacement of soya etc.), could contribute to the food efficiency objectives, especially through the characterisation of animal genotype x microbiota x food resource interactions.

RECOMMENDATIONS

Meeting set objectives and services in a context of global change: summary in pictures

As part of our reflections and discussions between genomics and agroecology researchers, which led to the creation of the prospective part of this journal, we have identified cognitive and methodological obstacles with respect to important challenges for agroecology, which genomics could help remove.

Spanning several challenges, genomics could help optimise the performances and services expected of value creation for biodiversity, characterise the functions ensured by living beings in agroecosystems, define early events in order to foresee and promote adult phenotypes or determine interactions between organisms that are beneficial to the functioning and sustainability of agroecosystems (conservation, production, restoration, protection etc.).

The figures below alone cannot replace any form of discussion, but they summarise the pathways involving genomics that can be followed to reach the objectives and produce the services expected of agroecosystems in a context of global change.



Figure 8. Demonstration and characterisation of the added value of diversity cultivated in agroecosystems (species associations, varietal mixtures, crop rotations etc.) to define optimal methods of introduction of the said diversity to improve crop productivity, stability and health and services expected in the context of a low-input environment

Aims

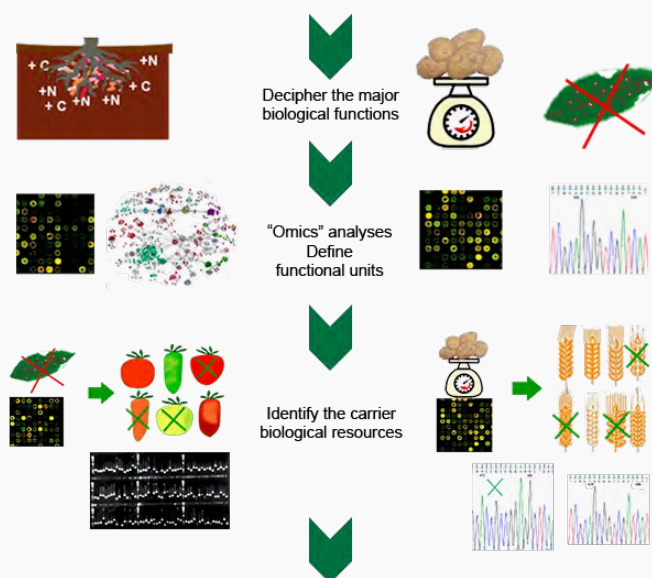
Productivity, plasticity and health of crops

Expected functions and services
Reduced or no inputs, pesticides and GHGs - increased organic matter sequestration

Leverage
Optimize functions by favoring carrier organisms



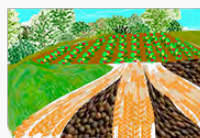
ACTIONS



Disseminate information



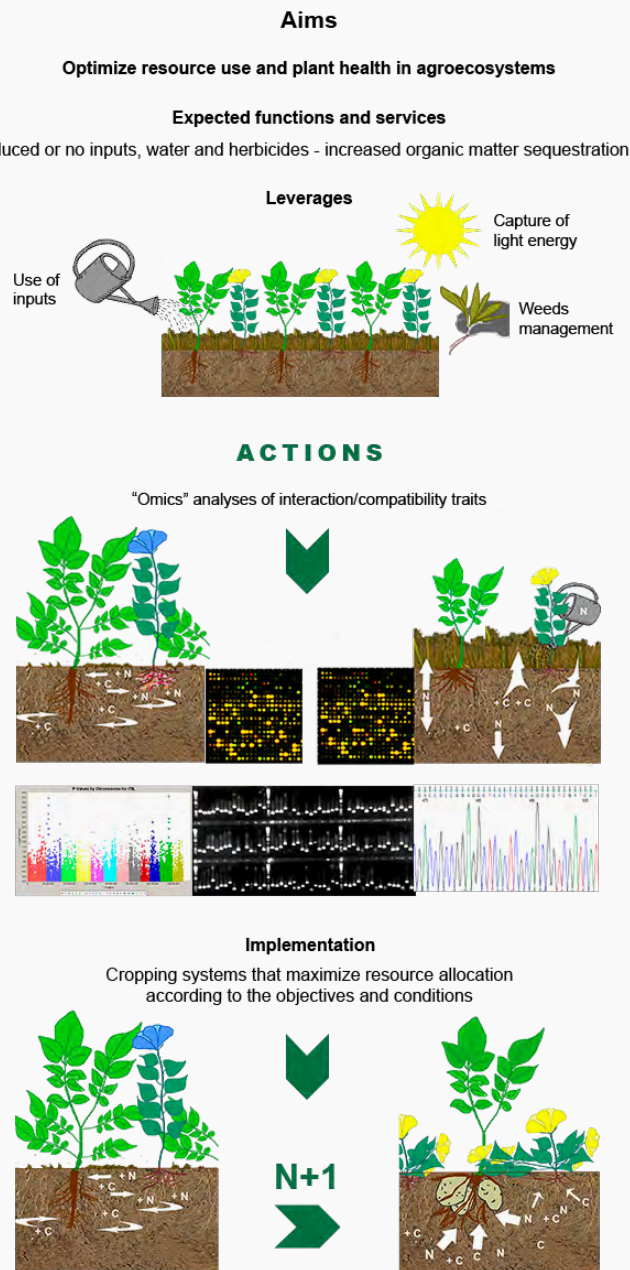
Crop systems adapted to constraints



- ▶ Describe the added value on the functioning of related plants (use of resources, resilience to stress, protection from stressors and immunity etc.).
- ▶ Look for characters and combinations of agronomic characters promoting beneficial interactions between plants, especially those promoting the recruitment of related organisms: aptitude for association and use of the association.

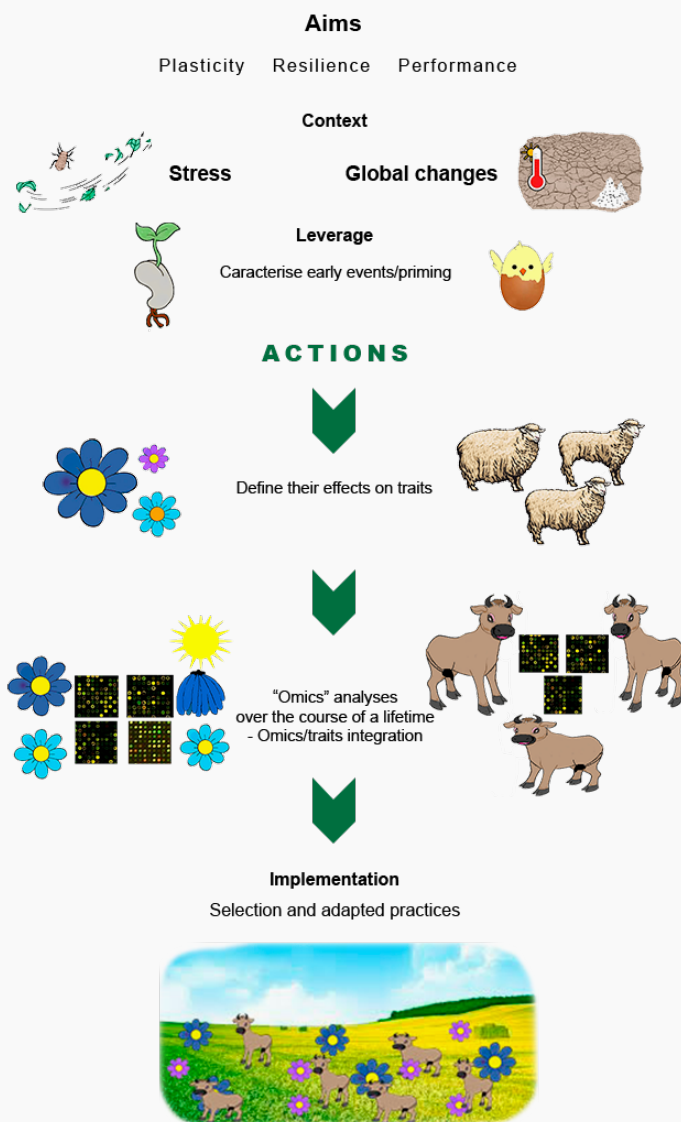
- ▶ Identify genes and underlying networks of genes for characteristics of aptitude.
- ▶ Research the positive allelic variation of these genes in the natural diversity of associated species to include it in programmes to improve the said species.

Figure 9. Contribute to the move from the straightforward description of taxonomic diversity of organisms in an agroecosystem to that of optimisation of functional biodiversity ensuring the services expected from the agroecosystem



- ▶ Characterise the diversity of functions fulfilled by crop-related organisms.
- ▶ Identify the main functions fulfilled by these organisms.
- ▶ Define operational, functional units.
- ▶ Characterise the biological resources for their support for these essential functions.
- ▶ Optimise these contributions by identifying the genotypes and technical routes promoting the presence and activities of organisms supporting the expected functions and services of the agroecosystem.

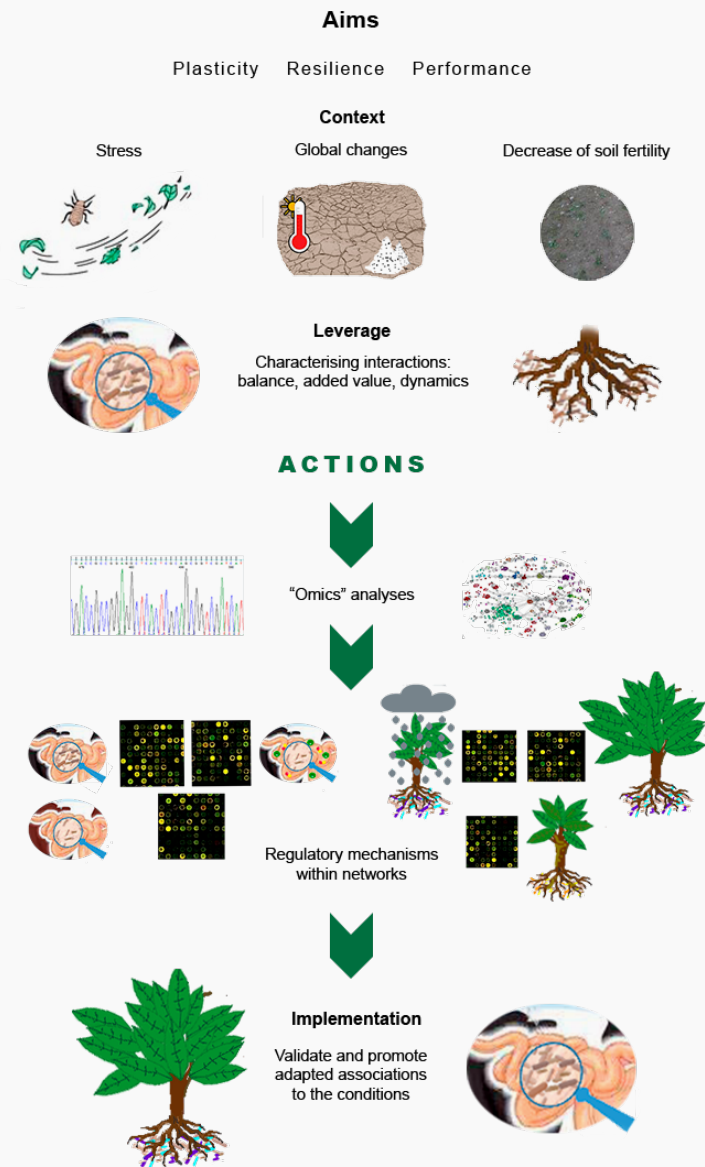
Figure 10. Early events and phenotype construction



► For animals, the combination of "omics" applications can also be used to study and further understanding of the effect of early events (reproduction conditions, farming experiences-practices during the perinatal period) on phenotype construction (Notion of DOHAD = Developmental Origins of Health and Disease) including behaviours.

► For plants, studies can be carried out from the germination stage (Priming).

Figure 11. Characterise and create value for the holobiont for the sustainable optimisation of agroecosystem functioning



- ▶ Characterise organism recruitment by cultivated/farmed organisms.
- ▶ Describe the influence of recruitment on the health and performance of cultivated/farmed organisms and environmental performance (productivity, product quality, ecosystem services).

- ▶ Decipher the networks of genes at work within the holobiont and their interactions.
- ▶ Promote the recruitment of beneficial populations by the introduction of specific species and their associations.



GENERAL CONCLUSION

Managing research through “a projective vision” and not through projects!

Around one hundred French teams received funding from the ANR over the last ten years on almost 40 genomics projects. Their approaches and results are of significant interest to agroecology. On the basis of the analysis of these projects presented in this journal, and of future challenges, the different and shared angles of approach between genomics specialists and agroecologists have highlighted priority genomics research areas likely to have a strong impact for agroecology and its application, as much for plant production as for animal production.

The move towards more integrated approaches in agronomics was based on a conceptual change in the relationship with the living world among the technical sciences. It involved building on diversity and dynamics as advantages of agroecosystem functionalities rather than seeking to stabilise and homogenise the living world, at the risk of reifying them and building simplified artefacts, giving priority to the technique and to application of technologies. The concepts of genetics and agronomic thinking therefore have the resources to join with functional ecology, the latter having developed when information technologies were first used to avoid reducing complexity through data analysis and modelling methods.

Genomics and metagenomics also placed technologies at the service of scientific thinking (and not the reverse), at least for some, by addressing the reification of living things (that these technologies also allow for up to a point, which is yet unknown) to study the dynamics and interactions which are the very source of life and of the diversity of all its forms. The concepts of agroecology should be able to rely on and pool resources with the genomics approaches we have showcased in this journal, and to contribute together to the design of a resolutely modern and sustainable agriculture, which respects living things and the environment, and of those who manage and lead it for the benefit of human societies.

It was repeated throughout the document that the very essence of agroecology, which envisages the agroecosystem as a whole and all interactions between its biological components and its environment, requires multi- and inter-disciplinary approaches and multi-year time steps. This journal also revealed throughout that the premise to all interaction was the appropriation of concepts and vocabulary and lastly, of a certain manner of approaching research and defining its objectives by the members of each community.

Thus are the objectives (giving priority to interactions and relations, navigating between levels of organisation, seeing diversity as an advantage, etc.), and the vision lighting the way to reach them, which must be highlighted to bring together a wide range of disciplines to contribute to the agroecological transition. The projects of a few years, bringing together a small group of teams, have only laid the first stones, but if the cornerstone and the plumb line of the successive GCPs are essential for building a wall, we first and foremost need an architectural vision to make an edifice that is sustainable and pleasant to live in!



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