9th IDEEV Day
10/18/2017

Ex-IMAGIF auditorium Gif-sur-Yvette

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9th IDEEV Day

Auditorium ex IMAGIF, Gif-sur-Yvette CNRS Campus

October the 18th of 2017

Acknowledgements

Program

9h15-9h30

    Accueil café

9h30-9h40

    Capy Pierre

    Introduction

Session Evolutionary genomics (Chairman : Arnaud Le Rouzic)

9h40-10h25

    Philippe Hervé

    What can be done for very deep phylogenetic inference ?

10h25-10h45

    Torruella Guifre

    Phylogenomic analysis of *Paraphelidium tribonemae* (Aphelida, Opisthosporidia, Opistho-
konta)

10h45-11h05

    Pause

11h05-11h25

    Odorico Andréas

    Modelling evolutionary interactions between genetic architecture complexity and epigenetic
heredity

11h25-11h45

    Giraud Tatiana

    Evolutionary strata on young mating-type chromosomes despite the lack of sexual antago-
nism

Session Evolutionary Ecology (Chairman : Pierre Gérard)

11h45-12h05

    Cornille Amandine

    PomFlux project : Anthropogenic factors and consequences of gene flow in apples.

12h05-12h25

Chole Hanna

Social contact as a reinforcement in olfactory learning in honeybees

12h30-14h15

Déjeûner / Posters

14h15-14h35

Constance Pierre

Evolution of brain and behavior in the blind cavefish *Astyanax mexicanus* : consequences of a mutation in the MonoAmine Oxidase (MAO)

14h35-14h55

Ressayre Adrienne

Consequences on phenology and morphology of divergent selection experiments for flowering time in maize

Session Host-Pathogen interactions (Chairman : Fanny Hartmann)

14h55-15h40

Huguet Elisabeth

Impact of bracoviruses on host and non host lepidopteran genomes

15h40-15h55

Pause

15h55-16h15

Genissel Anne

Dissecting complex traits using genome-wide association studies in the fungal pathogen *Zymoseptoria tritici*

16h15-16h35

de la Vega Ricardo

Distinct genomic footprints of host range expansion and host specialization in a plant castrating fungi

16h35-16h55

Kobmoo Noppol

Adaptation genomics of the zombie-ant fungus Ophiocordyceps unilateralis complex

16h55-17h15

Kroymann Juergen

Positive selection driving host plant adaptation in a lepidopteran herbivore

Communications : Oral & Poster

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Social contact as a reinforcement in olfactory learning in honeybees

Honeybees' foraging behavior critically depends on individual learning by foragers of floral cues, among which odors play a prominent role. Foragers thus learn to associate floral odors with sugar reinforcement from flower nectar. In the Lab, this process is studied using the Pavlovian conditioning of the proboscis extension response (PER), in which an odor (CS) is associated with sucrose solution (US). This learning has been studied for 50 years and its neural bases are nowadays partially unraveled. Interestingly, olfactory learning about floral resources is not limited to the foraging situation, and honeybee workers can learn chemosensory information directly from successful foragers within the hive. Previous work attributed this learning to a simple classical association between the floral scent adsorbed on the returning foragers' body and a sugar reward given by this forager via trophallaxis. However, nectar transfer is not performed during all dual interactions with returning foragers, suggesting that other mechanisms may be involved in this transmission. Here, we determined whether social cues may be involved in this transmission, i.e. can interaction with another forager represent an appetitive reinforcement for bees ? Our recent data supports this hypothesis. We found that simple antennal contact with a fed nestmate, in absence of any sugar stimulation, can induce PER in harnessed worker bees. In addition, bees can learn to associate an odor CS with this antennal contact with a nestmate. After such association, the odor alone triggers the PER. This suggests that simple social contact can act as an appetitive US in honeybees. We currently study the mechanisms implied in this new conditioning focusing on the physical nature of this social US. Our current data suggest the implication of antennal movements produced by the US nestmate.

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PomFlux project : Anthropogenic factors and consequences of gene flow in apples.

This project aimed at understanding genomic processes underlying the adaptation of apples and also anthropogenic factors influencing crop-to-wild gene flow in apples. The PomFlux project allowed (1) to assess the genetic diversity and structuring of French populations of wild apple trees, revealing the existence of different genetic groups in France, (2) to reveal high levels of introgression (i.e. incorporation of genetic material by hybridization) of the wild apple populations by the cultivated apple, (3) to show that this genetic pollution depends on the degree of anthropisation of the region and on the intensity of the cultivation of the apple tree, (4) to identify pure populations of wild apple trees, not introgressed by the cultivated apple tree, from the different large genetic groups existing in France, to establish conservatory orchards of wild apple trees that could be used for the reintroduction of wild apple trees in forest and agrosystems, (4) to show that the seedling company of wild apples provide at best only hybrids, (5) promulgate a decree regulating the re-establishment of wild apple trees to avoid reintroduction of hybrid individuals, (6) conservatory orchards are under construction.

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De novo assembly of the Rosy Apple Aphid Genome from a Single Linked-Read Library

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Since the foundation of modern evolutionary theory, scientists have tried to understand how species adapt to their environment. In this context, studying the mechanisms of adaptation of crop parasite during crop domestication is particularly relevant, with frequent host shifts involving adaptation to new hosts following anthropic environmental changes. The Rosy Apple Aphid, *Dysaphis plantaginea*, is causing major economic losses every year in apple production and is an outstanding model for unraveling the evolutionary processes involved in pest insect emergence and adaptation in the context of fruit tree domestication. Our project will use high-throughput sequencing to investigate this issue. As a first step, we are currently assembling de novo a genome of *D. plantaginea* using a new sequencing technology, the 10X-Genomics Chromium, a linked-read sequencing technology. Linked-Read sequencing technology has recently been employed successfully for de novo assembly of human and plant genomes, however the utility of this technology for insect genomes has been unexplored so far. We are therefore currently evaluating the technology for this purpose by sequencing the 400 Mb diploid Rosy Apple Aphid genome (*D. plantaginea*) genome with a single Linked-Read library.

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SHiNeMaS : A database dedicated to seed lots history, phenotyping data and field practices

Introduction

In 2005, a collaboration started between the French National Institute for Agricultural Research (INRA) and the farmer organization Réseau Semences Paysannes (RSP). The aim was : (1) to study on-farm management of crop diversity[1], (2) to develop population-varieties adapted to organic and low inputs agricultures in the context of a participatory plant breeding program involving farmers, NGOs´ faciltators and researchers [2]. In this project, researchers needed to map the history of the population-varieties using the network formalism. In addition to the diffusion among farms, they wanted to document the other steps of life cycle of the seed lot like the reproduction, the selection, and the cross steps. Data characterizing the different seed lots were produced at each step like phenotyping and cultural practices data. All this information needed to be centralized and stored. Thus, we developed SHiNeMaS (Seeds History and Network Management System) a database with its web interface, dedicated to the management of the history of seed lots and the associated data.

Data management

SHiNeMaS has been developed to be a flexible tool and to support multiple agronomic species. The schema of the database is organized around the seed lot. It manages several types of relations between seed lots : multiplication, cross, intra-varietal selection, seed lot mixture and diffusion. For each type of event the user can define the measured variables such as traits, practices, etc., and how they were measured. The stock information of the seed lots is also stored in the database. SHiNeMaS provides interfaces to massively load data in tabulated format, or to individually load data through the web interface. A file format was designed for each type of event, and contains the minimum information to describe the concerned event. SHiNeMaS also provides tools to correct data already recorded.

Tools

A tool was developed in SHiNeMaS to provide a helpful assistant to the creation of the files used for massive data loading. SHiNeMaS also provides query interfaces to retrieve and extract data. The user can access to the profile of a seed lot or a population-variety.

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Beyond B-class genes : towards genetic pathways controlling petal formation in the Ranunculaceae *Nigella damascena.*

The Ranunculaceae is a remarkable group to analyze the genetics of petal development, because they consist of species with a large variety of color, size and form of perianth. *Nigella damascena* presents a rare perianth architecture dimorphism. The [P] morph presents usually five petaloid sepals and eight petals. In contrast in the [T] morph, petals are absent and the perianth is composed of a single type of sepaloid organs, the tepals. The latter phenotype is caused by the inactivation of a single B-class gene, the NdAP3-3 gene that is highly expressed in the petal of the [P] morph. In order to characterize the mechanisms that control petal identity and development, we implemented in the two morphs (i) a comparative transcriptome analysis at early floral stages and (ii) a comparative study of the expression patterns of all B-class genes during development. Based on an RNA-seq resource that was produced from floral buds harvested 1 and 4 days after bolting, we found more than 600 genes that are differentially expressed between the two morphs and potential members of the genetic pathway controlling petal formation. Among them, a candidate subset was validated by confirming the genes deregulation using quantitative PCR experiments made on floral buds of [P] and [T] morph plants from genetically distinct populations. Analysis of the B-class gene expression indicated that their transcripts accumulate during floral maturation, and have different expression dynamics in the two morphs. Further investigation of the candidate genes function and regulation by the B-class genes is currently under way, to gain a better insight into the B-class gene network, particularly that of NdAP3-3, operating in *Nigella damascena* petal development.

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Comparative genomics of Cuban (*L. dentata* and *L. holguinensis*) and mexican (A. mexicanus) cavefish

Cave animals are found in many taxa. They often share biotic and abiotic environmental characteristics, in particular the absence of light. These animals often share also similar phenotypic traits like eye loss, depigmentation and enhanced non-visual sensory organs. Here, we investigate the genomic changes related to the absence of light. We focused on cavefish from Mexico (*Astyanax mexicanus*) and from Cuba (*Lucifuga spp.*). First, in *Lucifuga spp.*, we looked for loss of function and deleterious mutations in genes known to be involved *A. mexicanus* phenotypic changes. These mutations were not found, suggesting no parallel evolution of these genes in Cuban and Mexican cavefish. We also looked for loss of function mutations in opsin genes. We found such mutations, whereas there are rare in *A. mexicanus* and *L. holguinensis* and more frequent in *L. dentata*. The frequencies of loss of function mutations in opsin genes in *A. mexicanus* and *L. holguinensis* suggest that these fish settled in caves recently, i.e. about 20,000 years ago, or less, in accordance with other dating approaches, whereas *L. dentata* probably involved in caves for a longer period of time. These results are congruent with a more troglomorphic morphology of *L. dentata* than *L. holguinensis*.

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Dissecting complex traits using genome-wide association studies in the fungal pathogen *Zymoseptoria tritici*

The nature of the evolutionary dynamics between plant and their pathogens remain poorly understood. We want to address this question in the plant pathogen *Zymoseptoria tritici*, which is the main pathogen of bread wheat. Towards this goal our first aim is to dissect the genetic basis of the disease symptoms using natural population samples of the fungus. We performed association genetics (whole genome and within candidate regions) to identify significant genetic variants associated with the disease. Second generation sequencing data were used to test for significant phenotype-genotype associations using SNPs, short indels and also structural variants (chromosomal rearrangements). Our phenotypic measurements corresponded to : (1) ability of the pathogen to develop at early stage after inoculation using fluorescent microscopy, (2) asexual multiplication of the pathogen with 21 days after inoculation. Our results show that : (1) early and late development of the pathogen in the host is not necessarily correlated, (2) SNPs in coding regions of effector gene and other regulatory variants contribute to the disease. We then discuss hypotheses to explain the maintenance of non virulent alleles at intermediate frequency in wheat fields.

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Evolutionary strata on young mating-type chromosomes despite the lack of sexual antagonism

Sex chromosomes can display successive steps of recombination suppression known as "evolutionary strata", which are thought to result from the successive linkage of sexually antagonistic genes to sex-determining genes. However, there is little evidence to support this explanation. Here we investigate whether evolutionary strata can evolve without sexual antagonism using fungi that display suppressed recombination extending beyond loci determining mating compatibility despite lack of male/female roles associated with their mating types. By comparing full-length chromosome assemblies from five anther-smut fungi with or without recombination suppression in their mating-type chromosomes, we inferred the ancestral gene order and derived chromosomal arrangements in this group. This novel approach shed the first light on the chromosomal fusion underlying the linkage of mating-type loci in fungi and provided the first evidence for multiple clearly resolved evolutionary strata over a range of ages (0.9 to 2.1 million years) in mating-type chromosomes. Several evolutionary strata did not include genes involved in mating-type determination, and their existence despite the lack of sexual antagonism calls for a unified theory of sex-related chromosome evolution, incorporating, for example, the influence of partially linked deleterious mutations and the maintenance of neutral rearrangement polymorphism due to balancing selection on sex and mating type.

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Impact of bracoviruses on host and non host *lepidopteran* genomes

Bracoviruses are mutualist viruses associated with over 17000 species of Braconid parasitoid wasps, that develop during their larval stages within lepidopteran hosts. Bracoviruses are present in wasp genomes as proviruses, which serve as template for the production of double stranded circular viral DNA carrying virulence genes that are packaged and injected into lepidopteran hosts at the same time as wasp eggs. Bracoviruses act by manipulating caterpillar immune defenses and development, thereby enabling wasps to survive in an immune-competent host. Bracovirus circles do not however contain genes coding for replication and particle production hence impeding viral replication in caterpillar hosts during parasitism.

Here, recent data describing the molecular impact of bracoviruses on host and non host lepidopteran species will be presented.

In the interaction involving the Braconid parasitoid wasp Cotesia congregata, its associated Cotesia congregata Bracovirus (CcBV), and the caterpillar host Manduca sexta, a high throughput transcriptomic approach allowed to obtain a functional map of the bracovirus (Chevignon et al. 2014). Moreover these data also allowed to visualize the global impact of parasitism on M. sexta immune gene regulation 24h post oviposition (Chevignon et al. 2015). Results showed that BV virulence genes posses regulatory sequences and gene structures likely to facilitate expression within an insect host.

Our investigation of the fate of CcBV circles during parasitism of M. sexta revealed that certain circles could integrate into M. sexta hemocyte genomic DNA (Chevignon et al. in preparation). The identification of this integration process at the genome scale, allowing BV circle persistence throughout parasitism, questions its functional role in parasitism success. Furthermore, this integration process could serve as a basis to understand how BVs mediate horizontal gene transfer.

Indeed CcBV DNA sequences have been found to be present in the genomes of several non host lepidopteran species (Gasmi et al. 2015). The integrated CcBV sequences can harbour genes that are expressed in the non host lepidopteran and that present evidence of purifying selection suggesting the transferred sequences are functional. In point of fact, certain BV genes integrated in caterpillar pest species do appear to play a functional protective role against other pathogenic viruses (baculoviruses) present in nature. In the future, it will be of great interest to investigate the extent of these horizontal gene transfers in the field.

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Evolution of acoustic communication in the blind cavefish *Astyanax mexicanus*

Acoustic communication is an essential feature to exchange information related to social cohesion, coordination (i.e. : alarm calls, mother-youth interaction, sexual selection) and survival, in many vertebrates. In fish, behaviours like territory defence, reproduction, as well as speciation processes involve acoustic functions. However, little is known on how acoustic communication evolved. The physiological, morphological and behavioural adaptations reported in the blind cavefish (CF) compared to its river-dwelling surface fish (SF) ancestor, makes *Astyanax mexicanus* a good model to investigate the evolution of acoustic communication. We hypothesized that acoustic communication evolved in CF to compensate for the lack of visual modality in the dark. Combining biophysics, neuroscience and evolutionary biology, this original study aims at 1) characterising the Astyanax sound repertoire, 2) investigating qualitative and quantitative acoustic differences between SF and CF, 3) deciphering behavioural and environmental contexts promoting sounds and thus, acoustic communication, 4) exploring sound production mechanisms and 5) identifying acoustic signatures in independent CF populations. Based on promising results of acoustic and video recordings conducted in our laboratory and in the CF natural environment (6 different Mexican caves), this pioneer project can provide major knowledge on neurobiological basis of adaptive evolutionary mechanisms allowing the survival of species exposed to drastic environmental changes.

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PhenoMaRa : Phénologie du maïs et ravageurs associés, Rôle des habitats sauvages

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En France deux lépidoptères foreurs de tige sont des ravageurs majeurs des cultures de maïs, la sésamie (*Sesamia nonagrioides*) et la pyrale (*Ostrinia nubilalis*). Les plantes peuvent échapper aux attaques d'herbivores par un décalage des cycles de vie des plantes et des herbivores. L'équipe BASE de l'UMR GQE, dispose de lignées de maïs précoces et tardives obtenues à l'issue de 20 ans de sélection divergente pour la date de floraison (liée à la durée du cycle). Deux aspects du développement de la sésamie restent mal documentés et sont essentiels pour appréhender l'incidence de la phénologie de la plante sur l'impact du ravageur. Il s'agit d'une part de la réponse phénologique de l'insecte aux températures et au stade de développement des plantes, et d'autre part du rôle des habitats sauvages comme réservoir d'infestation de la sésamie.

Dynamique de population des ravageurs (poster 1, J. Legrand *et al.*) : Afin de développer et de calibrer un modèle mathématique pour la dynamique de population des insectes, les données et modèles phénologiques existants (suivi de vols, développement en fonction des températures) ont été rassemblées. La spécificité du modèle développé est de prendre en compte la dynamique du développement de la plante et son rôle sur le développement des insectes. Par ailleurs un premier suivi de l'infestation des lignées de maïs précoces et tardives par la pyrale du maïs a été réalisé, et une infestation de sésamie a été quantifiée sur une parcelle expérimentale de maïs dans les Landes.

Rôle des habitats sauvages (poster 2, L. Kaiser *et al.*) : dans l'objectif de savoir si une population de sésamie passe réellement de plantes sauvages au maïs au cours de son cycle de développement, nous avons poursuivi une campagne de collecte sur plante sauvages, initiée par l'équipe DEEIT de l'UMR EGCE. Des études antérieures ont montré l'existence de populations de sésamies sur plantes sauvages en Camargue où le maïs est peu cultivé. Nous avons prospecté des régions où le maïs est abondant et sujet aux attaques de sésamie (Landes, Pyrénées Atlantiques et Deux Sèvres). Un inventaire des insectes se nourrissant de plantes sauvages connues comme hôtes de la sésamie a révélé la rareté de celle-ci, suggérant que l'espèce reste dans le maïs d'une année à l'autre. L'ensemble de ces données seront complétées et utilisées pour mieux comprendre les relations entre le cycle de vie de l'insecte et celui du maïs.

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Adaptation genomics of the zombie-ant fungus *Ophiocordyceps unilateralis* complex

Identifying genes underlying adaptation allows elucidating the biological functions targeted by natural selection. Looking for footprints of positive selection in the form of differentiation outliers, rapid changes in amino-acids and identifying species-specific genes have proven powerful for the detection of genes involved in host specialization in plant pathogenic fungi. Here we used an evolutionary population and comparative genomic approach for unravelling population structures and identifying genes underlying host adaptation in the *Ophiocordyceps unilateralis* sensu lato complex of fungal cryptic species manipulating ant behavior. The population genomics highlight a high differentiation between three closedly related species witout evident outlier, suggesting a relatively ancient divergence. By comparing the genomes of three closely related species from Thailand and a more distant taxon from the USA associated to distinct ant host species, we found that species-specific genes were enriched in pathogenesis functions, and mostly in heat-labile enterotoxins. Furthermore these genes were over-represented among those with significant footprints of positive selection, other categories of genes suspected to be important for virulence and pathogenicity in entomopathogenic fungi (e.g., chitinases, lipases, proteases, core genes of secondary metabolites) were much less represented, although a few candidates were found to evolve under positive selection.

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Positive selection driving host plant adaptation in a lepidopteran herbivore

Antagonistic chemical interactions between herbivorous insects and their host plants are often thought to co-evolve in a stepwise process, with an evolutionary innovation on one side being countered by a corresponding advance on the other. More than 20 million years ago ermine moths shifted towards new host plants from the order Brassicales. Key for successful adaptation to the new hosts was the emergence of an enzymatic function that enabled the insects to overcome a highly diversified secondary metabolite-based plant defense system. This insect counteradaptation evolved in an ancient gene cluster, and involved several gene duplications with subsequent functional specialization. Analyses of nucleotide substitution patterns indicate a strong contribution of positive selection during the evolution of this counteradaptation, but neither neofunctionalization nor resolution of adaptive conflict appear to be fully compatible with both, diversification in enzyme function and pattern of positive selection. This study highlights the importance of investigating both, function and evolution of key genes for understanding processes of host plant adaptation in herbivorous insects.

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Modelling evolutionary interactions between genetic architecture complexity and epigenetic heredity

Studying the impact of epigenetic heredity on evolution is a major topic in modern evolutionary biology. Here, we investigate the impact of non-genetic inheritance on gene regulatory network evolution. We modified a classical gene network model by allowing maternal transmission of gene expression, and studied its evolutionary properties through individual-based simulations. Our results show that the way gene networks respond to directional selection (adaptation) is not substantially different when gene expression levels are fully, partially or not inherited. Nevertheless, simulations suggest that non-genetic inheritance affects the robustness to genetic (mutational) and environmental disturbances (i.e. genetic and environmental canalizations). These effects are magnified when the developmental process is constrained by the need to reach a stable equilibrium in gene expression rapidly. Therefore, the effect of non-genetic inheritance might not be found in evolutionary trajectories themselves, but rather in the long-term consequences on the emergent properties of complex genetic architectures.

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Evolution of adoption of variety mixtures and low-input multi-resistant bread wheat varieties since two decades in France : increased use of these agroecological levers

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Biodiversity-based agriculture has been proposed as a way to reduce the widespread use of agro-chemical inputs in current cropping systems. This reduction target can be achieved by relying on many agroecological levers, such as the increased use of variety mixtures or/and low-input multi-resistant varieties. The degree of adoption of these agroecological levers by farmers over the long term has seldom been the subject of analyses.

Based on systematic surveys conducted by FranceAgriMer at a yearly time step and at a district scale, we focused on the temporal evolution of areas and relative acreages of variety mixtures and low-input multi-resistant bread wheat varieties since the 1990s, furthermore relying on expert knowledge to define the set of multi-resistant varieties. We performed principal component analyses associated with a clustering algorithm to group districts characterized by a similar temporal evolution of areas or relative acreages for each agroecological lever over time. Overall, we highlight a substantial increase of areas sown with variety mixtures and low-input multi-resistant bread wheat varieties in France since the early 1990s, suggesting an increasing degree of adoption of these levers. Moreover, the speed and the degree of adoption of these two levers differed from one to the other and was spatially structured. Large areas sown with variety mixtures were observed only since 2010 and mainly in Western-Central France, while low-input multi-resistant bread wheat varieties were largely adopted since the early 2000s in Northern and Western France, as well as in the Paris Basin. Future studies should focus on the potential multiple causes of these evolutions.

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What can be done for very deep phylogenetic inference ?

The inference of ancient evolutionary events, such as the early diversification of animals, eukaryotes or archaea, appears to be highly controversial. Different phylogenetic hypotheses are proposed depending on the datasets considered or on the inference methods used. For instance, Ctenophora-sister hypothesis is supported by site-homogeneous models of sequence evolution while Porifera-sister hypothesis by site-heterogeneous models. These debates about relatively recent events raise doubts about our ability to infer one of the most ancient event, the root of the universal tree of life. Testing the accuracy of the phylogenetic method is difficult because the evolutionary process is unknown, limiting the usefulness of simulations, and because the true phylogeny is generally unknown. I will use empirical datasets for which phylogenetic relationships are known with a high level of confidence and will exacerbate the possibility of reconstruction artefacts, either by modifying taxon sampling or by selecting the fastest evolving positions. This approach allows to compare the accuracy of the most commonly used phylogenetic methods. Finally I will discuss the question of the rooting of the tree of life.

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Evolution of brain and behavior in the blind cavefish *Astyanax mexicanus* : consequences of a mutation in the MonoAmine Oxidase (MAO)

The fish *A. mexicanus* comes in 2 morphotypes : a river-dwelling surface morph (Surface fish, SF), and a cave-adapted morph living in the darkness of Mexican caves. Cavefish (CF) present complex behavioral changes : increased locomotor activity, loss of the aggressive behavior, schooling and sleep. This corresponds to the "cavefish behavioral syndrome". We aim at understanding the genetic and neural bases of the behavioral adaptation of *A. mexicanus* to the cave environment.

Our group has previously described a point mutation in the CF gene encoding Monoamine Oxidase(MAO), the serotonin degrading enzyme. This mutation causes a two-fold reduction of the MAO activity, and increased brain serotonin level. As accumulated evidences suggest that changes in neuro-modulatory systems generate significant variations in complex behaviors, we address the following question : what are the consequences of this MAO mutation at the level of the serotonergic system and the behavior in CF ? We thus compared brain serotonin level of SF, CF, and CF without the mutation. We analyzed levels of monoamines and their metabolites in the brain of 5 month-old fish by HPLC. The level of serotonin in the brain of the CF without the mutation is the same as in SF brain. Thus, the difference in the level of serotonin between CF and SF is only due to the MAO mutation.

Next we generated a phylogeographic map of MAO mutated alleles in various caves and rivers, by genotyping 156CF and 178SF, caught in the wild. The MAO mutated allele was found in 5 different caves of the Sierra de El Abra, but not in other, independently-evolved caves located in other Sierras. Our data suggest that the mutation was probably selected in the cave environment. Finally, the mutation seems to be more frequent in caves that are rich organic materials, i.e., where food seems more abundant. We therefore compared food intake in CF and CF without the mutation. The CF with the mutation eat less than the CF without the mutation. We hypothesize that this reduced appetite induced by the mutation could increase the longevity of the fish in caves, where the mortality induced by environmental causes (predation, parasitism, temperature variation. . .) is probably less important than in rivers.

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Hide and seek : The complex evolutionary history of green secondary plastids

Photosynthesis in eukaryotes arose from the endosymbiosis between a cyanobacterium and a heterotrophic host. This primary endosymbiotic event gave rise to Archaeplastida, a supergroup composed of glaucophytes, Viridiplantae (Green algae and land plants) and Rhodophyta (red algae). In their turn, red and green algae established secondary endosymbioses spreading the ability to photosynthesize to other eukaryotic groups. During endosymbiosis, multiple genes of the alga were relocated to the host nucleus (Endosymbiotic Gene Transfer, EGT). Through the phylogenetic analyses of 85 EGT genes, we showed that extant phyla with green-alga derived plastids (chlorarachniophytes and euglenids) likely carried a red plastid that was later replaced by a green one. We propose that the former red plastid might have helped to establish the secondary endosymbiosis with a green alga.

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Consequences on phenology and morphology of divergent selection experiments for flowering time in maize

Two ongoing Divergent Selection Experiments (DSEs) for flowering time in maize are driven on the Plateau de Saclay since 1993. During the course of these experiments undertaken within two inbred lines (F252 and MBS847), early and late populations that display contrasted flowering time have been produced throughout 21 generations of reccurent selection for earliness in early populations and lateness in late populations. Each DSE is characterized by (i) a very narrow genetic basis (four selfed plants originated from a commercial seed lot of a maize inbred line), (ii) a large number of plants (1000) evaluated at each generation in each population (Early or Late population), (iii) the small sample size of the selected individuals at each generation (the 10 most early respectively late plants are selfed within each early respectively late populations) and (iv) selfing of the selected plants to produce the next generation. Stochastic simulations indicate that such experimental setting promote the fixations of favorable variants (early mutations in early populations and late mutations in late populations) while reducing the fixation of neutral variants. Using plants belonging to early and late populations of DSEs, we are investigating (i) the causes of the differences in flowering time trying to understand whether changes in flowering time were achieved through changes in growth rates and/or developmental timings (heterochrony of development) and (ii) the morphological consequences of phenology changes.

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Distinct genomic footprints of host range expansion and host specialization in a plant castrating fungi

Elucidating the genetic and genomic processes associated with the host range of plant pathogens is important for understanding the evolutionary mechanisms of adaptation, it is also crucial for understanding emerging diseases, that often occurs via host shifts. Using a unique set of 38 near chromosome-size assemblies from 19 closely related species from the *Microbotryum* species complex under a comparative genomics framework, in this talk I will show that host specialization and host range expansion have left different genomic signatures after a polyploidization event. While species with strong host specificity show high rates of differential losses of pathogenicity related genes, the sole lineage of anther smut fungi that has evolved the capacity to infect several hosts shows the highest retention rate of polyploid duplicates. I propose that the reductive genome evolution of host specific species reflects the co-evolution driven fine tuning of the host pathogen interaction, whereas the more generalistic strategy would have selected for divergent evolution and higher retention of gene duplicates.

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ThaliaDB, a tool for data management and genetic diversity data exploration

Diversity and association genetics studies lead to manipulate a large number of individual, lines, clones and/or populations. Moreover, emergence of high-throughput technologies for both genotyping and phenotyping generates a large amount of data. These data need to be stored and managed in order to make requests and to organize datasets to perform genetic diversity data exploration and association genetics analysis. The new version of ThaliaDB, V3.1, is developed for scientists to facilitate their data management and analysis. The database holds genetic resources data, seed lots, samples, genotyping and elaborated phenotyping datasets. It is well adapted for data that are useful to apply GWAS methods. It can manage high-throughput results coming from different projects and experiments and propose several views and options to explore these data and to give access to them for reuse. This Web tool offers to users a Select (Data view) mode and an Admin (Data administration and loading) mode. Data confidentiality is maintained using user accounts and specific levels of rights can be set on data. It enables data extraction in CSV format. A version exists today in our lab with maize data produced from projects of A. Charcosset's GQMS team and theirs partners. Perspectives are to test this new version for tomato, wheat and poplar. The software is currently in improvement with funding of Amaizing, Investment for the future, project. It is developed in Python under Framework Django, running under PostGreSQL and MongoDb databases. Contact : delphine.steinbach@inra.fr for more information and collaboration.

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Phylogenomic analysis of *Paraphelidium tribonemae* (Aphelida, Opisthosporidia, Opisthokonta)

Aphelids are a poorly known group of parasitoids of algae that have raised considerable interest due to their pivotal phylogenetic position in the holomycotan branch of the opisthokonts. Based on 18S rRNA genes, they form a monophyletic group with Rozellosporidia (Cryptomycota) and the highly derived Microsporidia. This clade has been re-classified as the Opisthosporidia, which constitute the sister group to the fungi. Despite their huge diversity, as revealed by molecular environmental studies, only four genera have been described and we still lack genome or transcriptome data. Here we present the first transcriptome for one aphelid representative, the recently described *Paraphelidium tribonemae.*

Aphelids cannot be cultured axenically. Therefore, the transcriptomic data from *Paraphelidium tribonemae* had to be cleaned from host and bacterial contamination using strict criteria. Our phylogenomic analyses using a concatenated supermatrix approach show that aphelids represent the earliest-branching lineage within the Opisthosporidia. We have carried out a comparative gene-content analysis with Rozella allomycis (Cryptomycota), microsporidian and other opisthokont genomes. We have detected genes involved in chitin cell-wall synthesis, suggesting this is an ancestral character to Opisthosporidia and Fungi. Aphelids also contain genes involved in the degradation of algal cellulose, attesting at the molecular level for an active mechanism of algal wall perforation. Also, the presence of electron transport chain complex I genes and a standard metabolism gene repertoire, which are missing in Rozella, argue for a less specialized parasitic lifestyle in aphelids, in agreement with their more basal phylogenetic position. Finally, the characterization of its repertoire of myosin molecular motors reveals that aphelids and nuclearids have similartiries with both holozoans and fungi, thus retaining many similarities with the ancestral opisthokont set. The availability of *P. tribonemae* transcriptomic data will be useful to address broader questions related to the evolution of parasitism in the Opisthosporidia and osmotrophy in Fungi.

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