



Sciences biologiques,
Écologie et Environnement
**CONFÉRENCES
JACQUES-MONOD**



Roscoff (France), Sept 11-15 2023

Sex unfolded: sex, asex, sexes
Le sexe dans tous ses états: sexe, asex, sexes

Sex unfolded
2023
sex
asex
sexes

TGACTAGA
AGTCCGCGTTA
GCTTAGAAAGCGAGATTCTAAGCTTCCGACGGACCCC
GTTTACCTGTATAGTTCCTCGGTCACTGGATT
CTGTACTCAGTTACCGCTGCGAGCCTCTAA
CTAAACCTCCGGCTTATCGGGTGTGCTAGTC
CATCTGTAAGGTCTGGATCCCATTTAAGGCTGACATC
GGGCGCCCATCCGTTACAGGTATGCCGGCTCTGGACCGCTATGGGTGGT
TATGCATGTCGACGGAAGGGTTACTTCAGCGTAACTTTTA
GTCTCGTGTGGGCTTCCTTCGGTTAAGAGAAATTCGGGTCTGAAGCAACA
GCCCTAAACGACTTCGCATCGGATTAATGATGAATAAGCTATGAAAACTCTCGAG

XX ♀ ♂ XY

$s_{ind} \approx 1.8 \frac{(N_e U)^2}{(N_e R)^3}$

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Conference report

Rapport sur la conférence

RESUME EN FRANCAIS

L'objectif de la conférence était de réunir des chercheurs travaillant sur différents aspects de l'évolution des systèmes génétiques (évolution du sexe, asexualité, conflits sexuels, chromosomes sexuels) afin d'évaluer l'état actuel du domaine et de discuter des questions en suspens. En particulier, des progrès importants ont été réalisés ces dernières années grâce à de nouveaux outils méthodologiques (tels que la génomique/bioinformatique, l'évolution expérimentale) et à la poursuite des travaux théoriques multilocus. Ces différentes approches étaient représentées parmi les participants à la conférence, avec des théoriciens et des empiristes travaillant sur une variété de sujets et de systèmes biologiques. Nous avons construit un programme mettant particulièrement l'accent sur l'extraordinaire diversité de situations chez les eucaryotes : les exposés ont porté sur les pucerons, les angiospermes, les fourmis, les branchiopodes, les algues brunes, les diptères, les vers plats, les poissons, les champignons, les isopodes, les acariens, les nématodes, les rotifères, les phasmes, les vertébrés. Cette diversité a été l'un des points forts de la conférence, largement apprécié par les participants. Un autre élément clé de la conférence a été les approches théoriques, qui ont été représentées dans environ 11 des 41 présentations orales. Le domaine évolue rapidement sur ce terrain théorique, et la présentation de ces nouvelles idées a constitué un autre point fort de la conférence. Les dernières avancées en génomique et transcriptomique ont été fortement représentées, dans environ 31 exposés, ce qui témoigne également des progrès rapides réalisés ces dernières années dans le domaine. L'obtention de données génomiques de haute qualité transforme très rapidement le domaine, et la vitalité de ces approches, y compris les développements très récents tels que les assemblages de haute qualité des chromosomes Y ou l'obtention de données transcriptomiques sur cellule unique, a été le troisième point fort de la conférence. Cette diversité d'approches a également été représentée lors des deux sessions de posters.

PROGRAM OVERVIEW

The conference took place in Roscoff from Sept 11th to Sept 15th. 115 participants attended the conference from 16 countries (see below). The program was structured into four overarching sessions dedicated to oral presentations (see below). These presentations encompassed a blend of talks by invited speakers (30 minutes each) and contributions from participants (15 minutes each), selected from submitted abstracts. The quality of the submitted abstracts was exceptionally high (making it challenging to select short talks), and included research done at major laboratories in the field. Ultimately, we sought to maintain a balanced representation across genders, geographical regions, model systems, laboratories, and career stages among the final speakers. Additionally, we ensured the poster sessions were engaging and dynamic. Ample opportunities for informal discussions were provided, including regular 30-minute coffee breaks, extended lunch breaks, evening gatherings in town, and an afternoon stroll and swim on Batz Island. These occasions allowed participants to mingle and sustain discussions for several hours following the scientific sessions, enriching their experience in the charming setting of Roscoff before their departure.

The different sessions corresponded to different aspects of the evolution of sex, sexes and asex:

Session 1: Reproducing without sex

Session 2: Recombination

Session 3: Sexual conflicts

Session 4: The evolution of sex chromosomes

PARTICIPANTS



Invited speakers

Each of the 25 invited speakers gave a 30 mn presentation.

Abbott Jessica Dept. of Biology, Lund, Sweden

Bachtrog Doris University of California, Berkeley, USA

Bast Jens Institute for Zoology, University of Cologne, Köln, Germany

Böhne Astrid Leibniz Institute for the Analysis of Biodiversity Change, Bonn, Germany

Connallon Tim Monash University, Victoria, Australia

Danchin Etienne Institut Sophia Agrobiotech, Sophia Antipolis, France

Delattre Marie Ecole Normale Supérieure de Lyon, Lyon, France

Giraud Tatiana Université Paris-Saclay, Gif-sur-Yvette, France

Glémin Sylvain UMR ECOBIO, Rennes, France

Haag Christoph Centre d'Ecologie Fonctionnelle et Evolutive, Montpellier, France

Kirkpatrick Mark University of Texas, Austin, Texas, USA

Lenormand Thomas Centre d'Ecologie Fonctionnelle et Evolutive, Montpellier, France

Lynch Michael Biodesign Institute, Arizona State University, Tempe, USA

Marais Gabriel CIBIO-InBIO, Universidade do Porto, Vairão, Portugal

Mercier Raphael Max Planck Institute for Plant Breeding Research, Cologne, Germany

Muralidhar Pavitra University of California Davis, USA

Muyle Aline Centre d'Ecologie Fonctionnelle et Evolutive, Montpellier, France

Otto Sally Dpt Zoology, University of British Columbia, Vancouver, Canada

Payseur Bret University of Wisconsin-Madison, USA

Reuter Max University College London, London, United Kingdom

Roze Denis Station Biologique de Roscoff, Roscoff, France

Schwander Tanja University of Lausanne, Switzerland

Teotónio Henrique Institut de Biologie de l'Ecole Normale Supérieure, Paris, France

VanDoninck Karine Université Libre de Bruxelles, Brussels, Belgium

Wright Stephen University of Toronto, Canada

Among these invited speakers, 8 were from outside Europe, 8 from Europe (not including France) and 9 from France; 10 invited speakers were female.

Other participants

91 non-invited participants from 14 countries attended the conference (16 countries including the invited speakers). From these 12 were from outside Europe (Canada, China, Japan, USA), 55 from Europe excluding France (Austria, Belgium, Czech Republic, Denmark, Germany,

Portugal, Spain, Switzerland, UK), and 24 were from France. Finally, 27 participants were PhD or master students.

16 contributed talks (of 15 mn each) were selected among the proposed abstracts (2 international / 12 European / 2 French; 9 female):

Baird Robert University of Edinburgh, UK
Bulankova Petre EMBL, Heidelberg, Germany
Coelho Susana MPI Tübingen, Germany
Cordaux Richard Université Paris Saclay, Gif-sur-Yvette, France
Darolti Iulia University of Lausanne, Lausanne, Switzerland
Darras Hugo Johannes Gutenberg University, Mainz, Germany
Janko Karel Liběchov, Czech Republic
Jaquiéry Julie Université de Rennes, Le Rheu, France
Johnston Susan University of Edinburgh, United Kingdom
Ma Wen-Juan Universiteit Brussel, Brussels, Belgium
McCaughey Michelle Emory University, Atlanta, USA
Mullon Charles University of Lausanne, Lausanne, Switzerland
Ross Laura University of Edinburgh, Edinburgh, UK
Sotero-Caio Cibele Wellcome Sanger Institute, Cambridgeshire, UK
Úbeda Francisco University of London, UK
Zhou Qi Zhejiang University, Hangzhou, China

72 participants presented posters during one of the two poster sessions.

Abdalahem Ammar France, **Abu Awad Diala** France, **Altmanová Marie** Czech Rep., **Bednarski Viktoria** Germany, **Boyer Lorelei** France, **Branco Catarina** Portugal, **Brandt Alexander** Switzerland, **Brazier Thomas** France, **Broquet Thomas** France, **Catalán Ana** Germany, **Clement Julie** France, **Coke-Schlachter Adriana** USA, **De Filippo Elsa** France, **Didukh Dmitrij** Czech Rep., **Defendini Hélène** France, **Dion-Côté Anne-Marie** Canada, **Flintham Ewan** Switzerland, **Fouqueau Louise** Austria, **Fyon Frédéric** France, **Gamble Tony** USA, **Gao Shan** Germany, **Gaudichau Emelyne** Switzerland, **Grewoldt Malte** Denmark, **Guiglielmoni Nadège** Germany, **Guiguen Yann** France, **Helleu Quentin** France, **Hitchcock Thomas** Japon, **Houtain Antoine** Belgium, **Hsiung Kevin** Germany, **Jayaprasad Suvratha** Germany, **Jecha Kristine** Switzerland, **Jeffries Daniel** Switzerland, **Kolesnikova Uliana** Germany, **Krueger-Hadfield Stacy** USA, **Ku Yu-Chia** Germany, **Lartillot Nicolas** France, **Lavanchy Guillaume** Switzerland, **Le Faou Ehouarn** Switzerland, **Lesaffre Thomas** Switzerland, **Letcher Brice** France, **Lipinska Agnieszka** Germany, **Illorente Bertrand** France, **Lucotte Elise** France, **Mackintosh Carl** UK, **Merel Vincent** Switzerland, **Nguyen Petr** Czech Rep. , **Nieuwenhuis Bart** Germany, **Óztoprak Hüsnü** Germany, **Pan Qiaowei** Switzerland, **Parée Tom** France, **Perrier Aurélien** France, **Pieszko Tymoteusz** UK, **Price Peter** UK, **Puixeu Gemma** Austria, **Rizos Iris** France, **Rovatsos Michail** Czech Rep. , **Ruzicka Filip** USA, **Saayman Xanita** France, **Sachdeva Himani** Austria, **Schlupp Ingo** USA, **Scott Michael** UK, **Scott Alison Dawn** Germany, **Smith Sophie Helen** Germany, **Soni Vivak** USA, **Stetsenko Roman** France, **Stöck Matthias** Germany, **Sudbrack Vitor** Switzerland, **Tenaguillo Ignacio** Spain, **Vasilikopoulos Alexandros** Belgium, **Veller Carl** USA, **Weyna Arthur** France, **Wilson Christopher** UK.

Two participants came as observers: **Jon Kaye** (USA) representing the *Gordon and Betty Moore Foundation* and **Vera Domingues** (UK) Senior editor for *Nature Ecology & Evolution*.

Financial support

We obtained financial support from Conseil Départemental du Finistère (1500€) and Région Bretagne (750€).

Scientific program

The goal of the conference was to gather researchers working on different aspects of the evolution of genetic systems (evolution of sex, asexuality, sexual conflicts, sex chromosomes) to assess the current state of the field and discuss open questions. In particular, this was the third CJM on the topic and important progress has been made over recent years thanks to new methodological tools (such as genomics/bioinformatics, experimental evolution) and continued multilocus theoretical work; furthermore, field work has continued to bring important insights about the diversity of reproductive systems and their ecological and biological correlates. These different approaches were represented among the participants of the conference, with both theoreticians and empiricists working on a variety of topics and biological systems. We built a program particularly emphasizing the extraordinary diversity across eukaryotes: the talks discussed Aphids, Angiosperms, Ants, Branchiopods, Brown algae, Diptera, Flatworm, Fishes, Fungi, Isopod, Mites, Nematodes, Rotifers, Stick insects, Vertebrates. This diversity was a highlight of the conference, widely appreciated by the participants. Another key feature of the conference were the theoretical approaches, which were represented in about 11 of the 41 oral presentations. The field is currently moving fast regarding new theoretical developments, and the presentation of these new ideas was another highlight of the conference. Last genomic and transcriptomic approaches were strongly represented, in about 31 talks, which also represents the rapid progresses made in recent years in the field. The obtention of extensive and high-quality genomic data is transforming the field very quickly, and the vitality of these methods, including very recent development such as the high-quality assemblies of Y chromosomes or the obtention of single cell transcriptomic data, was the third major highlight of the conference. This diversity of approaches was also represented during both poster sessions.

The conference started with an excellent keynote presentation by **Tanja Schwander** (University of Lausanne, Switzerland) former president of this Jacques Monod Conference. She presented genotype diversity in sexual and asexual *Timema* species, showing higher segregating polymorphism in asexuals compared to sexuals but more positively selected genes in sexuals. Transcriptomic studies highlighted dosage compensation in somatic tissue. Using markers for centromeric regions, centromere evolution was compared between sexuals and asexuals, highlighting the presence of both monocentric and holocentric chromosomes in asexual *Timema* species. **Cibele G. Sotero-Caio** presented the project Tree of Sex v2.0 of the Sanger institute, an initiative to gather reproductive data for all eukaryotic species across the tree of life. The phylogenetic coverage of this project could still be improved, this is why they presented this initiative at our conference. The database created is maintained and accessible through the server of the Sanger institute. The main goal of the project is to tackle scientific questions related to the evolution of reproductive modes, while the workshops aim to connect scientists in this field.

Session 1: Reproducing without sex

This session was opened by **Jens Bast** (University of Cologne, Germany), providing numerous new insights into the genomic evolution of asexual oribatid mite species: high haplotype divergence (Meselson effect), and evolvability through gene duplications, functional diversification between haplotypes, horizontal gene transfers and recent activities of transposons restricted to one haplotype. **Etienne Danchin** (Institut Sophia Agrobiotech, France) gave a very clear presentation on the diverse reproductive modes within the root-knot nematodes of the genus *Meloidogyne*, with the asexual species having emerged through hybridization, being polyploid with no signatures of meiotic recombination. The asexual species are plant parasites showing no genomic variation specific to a host-race, while being

virulent to different host species showing their adaptive potential. **Karine Van Doninck** reported on her latest research on bdelloid rotifers, presenting the spatiotemporal dynamics of DNA repair in the asexual species *Adineta vaga*. DNA repair in the somatic nuclei occurs within 24h following exposure to ionizing radiation, through non-homologous end-joining and break excision DNA repair mechanisms. In the germline however, DNA repair is delayed and taking place during oocyte maturation, through homologous recombination during a non-reductional meiosis I. A microevolution experiment further highlighted signatures of meiotic recombination in this ancient asexual species. **Karel Janko** (Liběchov, Czech Republic) presented, through a dynamic talk, the origin and evolution of parthenogenesis caused by interspecific hybridization in vertebrates, showing that parental subgenomes are transmitted intact, with hybrids inheriting and maintaining high levels of heterozygosity while accumulating some homozygosity in certain genomic regions. He also discussed the regulatory divergence between paternal genomes in the developmental programs transmitted. **Susana Coelho** (Max Planck Institute Tübingen, Germany) enthusiastically presented very interesting results on the independent emergence of asexuality in brown algae. Asexual lineages consistently showed a loss of phenotypic female traits like pheromone production and a change in expression of sexual traits, studying the importance of sexual conflict on gene expression changes following the loss of sex. **Michael Lynch** (Arizona State University, USA) gave a very broad overview on the evolutionary genomics of the model system *Daphnia*, providing unique insights into recombination dynamics, meiosis suppressor genes and contagious asexuality. **Christoph Haag** (Centre d'Ecologie Fonctionnelle et Evolutive Montpellier, France) presented very interesting results on contagious asexuality within laboratory settings, using two distinct model systems, *Daphnia pulex* and *Artemia parthenogenetica*, showing that newly arisen asexual lineages, through cross-mating between sexual females and rare males from asexual lineages, harbour signatures of loss of heterozygosity and lower fitness than the clones from the field. **Hugo Darras** (Johannes Gutenberg University, Germany) presented very original results from the yellow crazy ants, discovering that the males are a chimera of haploid cells coming from two divergent lineages when syngamy failed, while diploid queens or workers evolve when syngamy takes place. These results highlight the diversity of reproductive modes that can evolve, in this particular case due to a conflict between two lineages. This session ended with a talk by **Michelle A. McCauley** (Emory University, USA) presenting the results of three evolution experiments using the mixed-mating nematode *Caenorhabditis elegans* and its bacterial parasite *Serratia marcescens*, aiming at testing the “pluralistic approach” to the maintenance of sex. Her results provided evidence that the interaction between deleterious mutations and the coevolution with parasite was indeed broadening the conditions favoring outcrossing.

Session 2: The evolution of recombination

Raphaël Mercier (Max Planck Institute Cologne, Germany) presented exciting new results on the molecular mechanisms of recombination. In particular, his group identified several mutants of *Arabidopsis thaliana* that present greatly elevated numbers of crossovers; the analysis of these mutants suggests a new mechanistic model for crossover interference and heterochiasmy (difference of recombination rates between male and female meioses), based on the coarsening dynamics of the HEI10 protein. **Petra Bulankova** (EMBL, Germany) presented a new research project aimed at understanding the high rates of mitotic homologous recombination that she observed in diatoms by in vivo imaging (involving fluorescence in situ hybridization). **Bret Payseur** (University of Wisconsin-Madison, USA) gave a general overview of the work done in his lab on the genetic architecture of recombination rate variation at broad and fine genomic scales, using the house mouse as a model system. The results show that multiple loci are involved and that the genetic architecture of recombination rate variation differs between males

and females. Interestingly, results from island populations suggest that the effective population size may be an important determinant of recombination rate evolution, an observation that connects with theoretical predictions. **Susan Johnston** (University of Edinburgh, UK) presented recent results on recombination landscapes in birds (house sparrows in particular), showing important differences in the number and positions of crossovers between males and females (heterochiasmy), and showing that recombination rate variation is driven by many small-effect loci. **Marie Delattre** (ENS Lyon, France) presented the puzzling auto-pseudogamous system of *Mesorhabditis* nematodes, where males are produced by regular fertilization while females are produced by a form of automictic parthenogenesis. Interestingly, males are XY (while males in nematodes are generally XO) and regular fertilization always produces males due to a selective elimination of X-bearing sperm. Furthermore, automixis maintains heterozygosity due to the fact that recombinant chromosomes always co-segregate during meiosis. **Laura Ross** (University of Edinburgh, UK) presented the evolutionary enigma of paternal genome elimination (PGE): in many arthropod species (mealybugs in particular), the paternally inherited genome is not transmitted by males. Genomic and cytogenetic analyses show that this process (which involves a highly modified meiosis) can be incomplete and heterogeneous across the genome. This highly intriguing process still awaits an evolutionary explanation. **Henrique Teotónio** (ENS Paris, France) presented an exciting new system to test theories on the evolution of recombination using experimental evolution approaches, based on the *rec-1* mutant that affects the position of crossovers in *Caenorhabditis elegans*. The results obtained using this system suggest that the evolutionary fate of recombination modifiers are mostly driven by their local genomic effect, in agreement with theoretical predictions. **Francisco Úbeda** (Royal Holloway University of London, UK) presented theoretical work aimed at understanding the evolution of self-destructive recombination hotspots (as in the system based on PRDM9 found in many animal species). Several thought-provoking hypotheses were proposed, such as the idea that self-destructive hotspots may evolve in order to prevent the expansion on transposable elements. Finally, **Sylvain Glémin** (CNRS Rennes, France) presented the results of an impressive meta-analysis of recombination landscapes in flowering plants, showing the recombination rates are primarily driven by the physical size of chromosomes (due to a limited number of crossovers per chromosome), while the number of crossovers tends to correlate with chromosome size within species. Highly self-fertilizing species tend to exhibit higher numbers of crossovers, in agreement with the predictions of theoretical studies.

Session 3: Sexual conflicts

Using data on guppy, **Iulia Darolti** (University of Lausanne, Switzerland), offered a unique insight into the effects of allometry and cellular heterogeneity on perceived patterns of sex-biased gene expression and highlighted the power of single-cell RNA-sequencing in distinguishing between sex-biased genes that are the result of regulatory change and those that stem from sex differences in cell type abundance, and hence are a consequence rather than a cause of sexual dimorphism. **Tim Connallon** (Monash University, Victoria, Australia) made a very interesting and thought-provoking theoretical talk aiming at bridging the seemingly contradictory theories of dominance and empirical observations of faster-X evolution. **Wen-Juan Ma** (Vrije Universiteit Brussel, Belgium) reported on her detailed research on X chromosome meiotic drive in *Drosophila affinis*. These recent X drivers carry inversions and are enriched in differentially expressed transcripts, which target genes disrupting spermatogenesis during and immediately after meiosis. **Max Reuter** (University College London, UK) provided an excellent overview of his work on the fruit fly *Drosophila melanogaster* to characterise genome-wide sexually antagonistic variation. He highlighted the importance of sexual antagonism as a force maintaining heritable genetic variation for fitness.

Charles Mullon (University of Lausanne, Switzerland), on the contrary, highlighted with an outstanding talk (based on mathematical modelling and computer simulations) why there was a limited scope for elevated genetic polymorphism in sexually antagonistic traits. He concluded that sexually antagonistic selection was more likely to contribute to polymorphism when it was based on traits with large effect loci (rather than on quantitative traits). **Denis Roze** (SBR Roscoff, France) in an exceptionally didactic and brilliant talk explained, based on analytical work and simulations, how multilocus selective effects were combining to generate genome-wide selection pressure on recombination modifiers. **Mark Kirkpatrick** (University of Texas, USA), with an entertaining, and far-reaching talk, overviewed his research on sexually antagonistic selection in humans, based on genomic data from the contemporary UK Biobank population. New methods of analysis revealed pervasive and highly polygenic sex-antagonistic selection acting on both viability and fertility. These results highlighted the benefits of taking a polygenic perspective rather than focusing on individual SNPs. Finally, **Sally Otto** (University of British Columbia, Canada) explained how to expand classical population genetics theory to account for drift and selection in organisms with haploid-diploid life cycles. This is critical to better understand the evolution of many organisms with complex life cycles. Her results highlighted that (mal)adaptation could differ for haploid-diploid organisms compared to either fully haploid or diploid species.

Session 4: The evolution of sex chromosomes

Doris Bachtrog (University of California, USA) started the session with an intriguing and amazing talk on Y chromosomes in *Drosophila*. Instead of being gene deserts, she showed that they contained hundreds or thousands of genes, many of which are multi-copy, involved in spermatogenesis, perhaps meiotic conflicts, and highly variable within a species. This offers a completely renewed perspective on Y chromosomes, as being one of the most variable regions within genomes. Then, **Tatiana Giraud** (Université Paris-Saclay, France) provided a great overview of how, in anther-smut fungi of the *Microbotryum* genus, recombination suppression evolved and extended stepwise repeatedly on the mating-type chromosome, followed by degeneration. This work, based on extensive genomic data, highlights that sex antagonistic selection may not be the reason for the evolution of recombination suppression in these species. She then discussed alternative models to explain recombination suppression, based on the “lucky inversion” model. **Qi Zhou** (Zhejiang University, China) presented a fascinating example in soft-shell turtles, on how the transition from environmental (here temperature) to genetic sex determination could occur. She showed that this transition maybe initiated by silencing the temperature sensitive genes, followed by acquisition of a novel sex-determining gene and rewiring of the entire downstream cascades of sex determination. **Robert Baird** (University of Edinburgh, UK), in a very intriguing talk described how the bizarre reproductive strategy, observed in some flies, and called monogeny (where females produce offspring of exclusively one sex) could evolve. He showed that monogeny was associated with large sex-limited non recombining regions, showing evidence of “strata” and degeneration, features that are often observed on sex chromosomes. **Jessica Abbott** (Lund university, Sweden) summarized her research aimed at using experimental evolution to understand the evolution of sex chromosomes. She explained how she could study male and female-limited lines, using cleverly designed experiments using GFP-transformed hermaphroditic flatworms. She showed that the worms indeed responded to the sex-limited selection in a way generally consistent with expectations from other young sex chromosome systems. **Astrid Böhne** (Leibniz Institute for the Analysis of Biodiversity Change, Germany), made a fascinating panorama of sex chromosomes in fishes. Changes in sex determination systems are particularly frequent in fish, and the talk highlighted the hyperdiverse Cichlidae, characterized by an unprecedented high rate of sex chromosome turnover involving different chromosomes (but with a non-random

recruitment), and involving or not changes in heterogamety. **Richard Cordaux** (Université Paris Saclay, France), introduced us to the fascinating world of isopods where sex determination is hijacked by maternally inherited Wolbachia bacterial endosymbionts which can convert genetic males into phenotypic females. He detailed how the presence of these Wolbachia leads to a shift from chromosomal to cytoplasmic sex determination. But this is not the whole story as some population also show variation of sex determination, thanks to a large piece of the Wolbachia genome transferred to the nuclear genome of their isopod host, most probably on a B chromosome. This shows how bacterial endosymbionts can really mess up, and induce rapid evolutionary changes in sex determination. **Julie Jaquiéry** (Université de Rennes, France), talked about another unusual system, the aphids, alternating between clonal reproductive phases and a sexual generation with XX females and XO males. She documented a consistent enrichment of male-biased genes on the X chromosome across all races, and faster-X evolution regarding gene expression. The significance of these results is not yet elucidated but represent a great opportunity to test the theories of sex chromosome evolution. **Thomas Lenormand** (Centre d'Ecologie Fonctionnelle et Evolutive, France), presented recent and profoundly renewed theories for the evolution of sex chromosomes, that either involve constraints on the rate of reestablishment of recombination or regulatory evolution ensuring that recombination suppression is maintained on the long term. His talk outlined that the most important parameter determining whether sex chromosomes are stable or in a regime of turnover is the ease to evolve early dosage compensation. **Gabriel Marais** (Universidade do Porto, Portugal) told us about the efforts to assemble the full high quality reference genome of the dioecious plant *Silene latifolia*, and especially its giant Y chromosome. This amazing achievement opens the door for rapid and exciting progresses into understanding the evolution of *Silene* sex chromosomes. Finally, and as a follow-up to talk to the previous one, **Aline Muyle** (Centre d'Ecologie Fonctionnelle et Evolutive, France), explained how sexual dimorphism was emerging in the transition from hermaphroditism to dioecy in *Silene*. She showed that male-biased genes accumulate first during a transition to dioecy, later followed by female-biased genes, and unlike in other reports emphasizing drift as a major effect, she detected strong selective effects during this transition.

Conclusion and perspectives

The conference has met its initial objectives in providing a general overview of the latest developments of research on the evolution of sex, asex and sexes and establishing links between different research questions (e.g., B. Payseur or M. Lynch presentations linking most topics of the conference with an overview of the research that has been done on mice or *Daphnia*, respectively, T. Lenormand's presentation linking the evolution of gene expression and the evolution of recombination and sex chromosomes, or R. Mercier linking detailed molecular analysis of meiosis to the broad scale patterns of recombination across species and their evolutionary significance) and illustrating the power of recent methods combined with the explosion of high-quality genomic data. Many of the participants declared that a conference covering these different topics was extremely useful and timely, and that the overall quality of the presentations was outstanding. Moreover, each talk triggered many questions, and discussions continued during the different breaks. Many participants, including senior researchers who have attended many conferences in their career, found the quality of the conference exceptional. To quote one representative feedback from S. Wright (Toronto, Canada) who was also a participant to the two previous editions of this conference: "a stellar conference (...), the quality of the talks and discussion was so great. The three Roscoff meetings have been the conference highlights of my career". Invited speakers were present during all sessions and easily accessible; the poster sessions were both very interactive and many in depth discussions took place at the posters. All participants agreed that organizing another conference

on the same topic in a few years would be extremely useful. **Karine Van Doninck** agreed to become the president for this next conference, and **Sylvain Glémin** (CNRS Rennes) to be the vice-president.

Finally, we would like to stress that the CNRS staff for the Jacques Monod conferences (Nathalie Babic, Damien Landreau) have been extremely helpful during the preparation and the course of the conference.