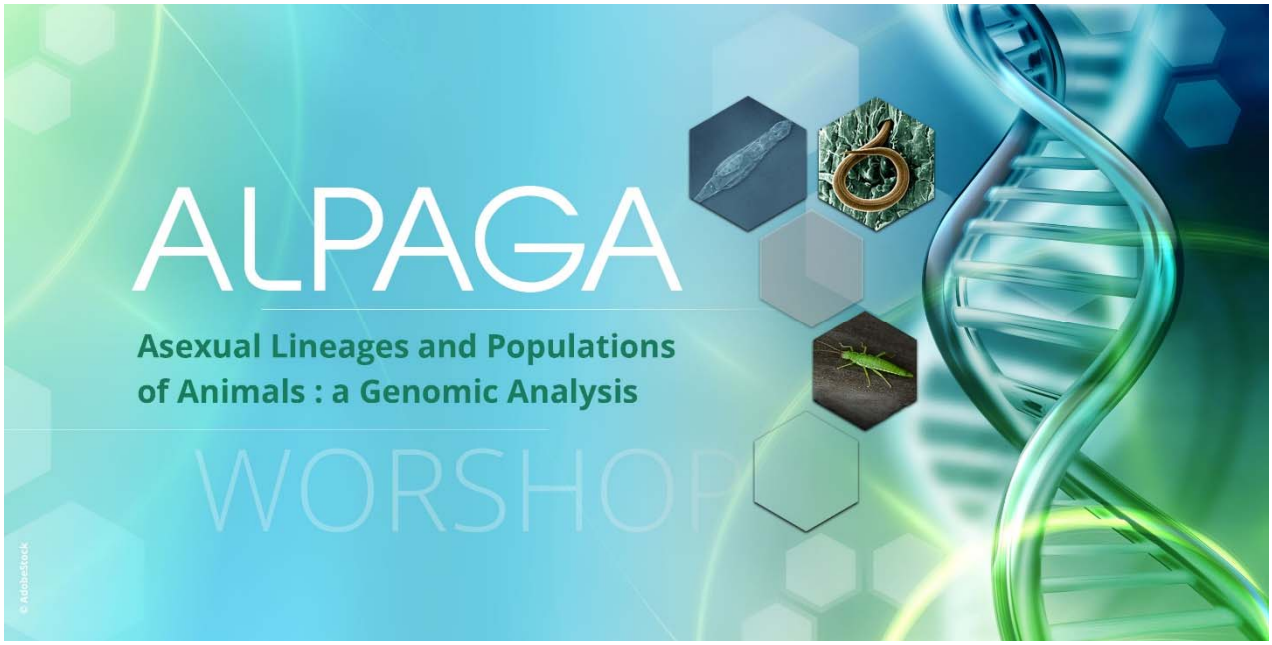
UNIVERSITÉ DE NAMUR

Genome evolution in asexual organisms



Abstract book

March 28, 29 & 30th 2017

University of Namur – Belgium

The ALPAGA worshop is supported by

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NARC NAMUR RESEARCH COLLEGE

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Table of contents

ALPAGA workshop program

Tuesday, March 28th - University of Namur – NARC room, rue de Bruxelles, 55

14h30-15h00	Arrivals – welcome package
15h00	Welcome and Introduction – **Karine Van Doninck** (host at UNamur)
Session 1: Asexual evolution: rare or common? – Chairman: Karine Van Doninck	
15h15-16h00	Local recombination suppression in an asexual springtail?" **Ken Kraaijeveld** (Vrije Universiteit Amsterdam, NL)
16h00-16h45	Automixis in Daphnia: A model for the evolution of clonality? **Christoph Haag** (CEFE-CNRS Montpellier, FR)
16h45-17h30	Contagious asexuality in Artemia **Thomas Lenormand** (CEFE-CNRS Montpellier, FR)
17h30-18h30	Belgian beers : informal discussions
18h30-19h30	Check-ins at the different hotels or B&B in Namur
19h45	Dinner in town at restaurant Grill des Tanneurs (this dinner is not covered by the workshop, price = 35€, drinks included)

Wednesday, March 29th – University of Namur – AGORA room, rue Godefroid, 5

Session 2: Evolutionary adaptation in asexuals – Chairman: Bernard Hallet	
9h00-9h45	Adaptive genome evolution in an asexual fungal plant pathogen **Michael F Seidl** (Wageningen University & Research, NL)
9h45-10h30	Evolutionary genomics of asexual fungi plant pathogens **Ronnie de Jonge** (Utrecht University, NL)
Coffee – tea break	
11h00-11h45	Gene expression and evolutionary rate changes after parallel evolution of asexuality in stick insects **Tanja Schwander** (Université de Lausanne, Switzerland)
11h45-12h30	C-value paradox revisited: Why is there so much intraspecific genome size variation in the monogonont rotifer Brachionus asplanchnoidis, and what are the consequences? **Claus-Peter Stelzer** (Universität Inssbruck, AU)
Lunch break	

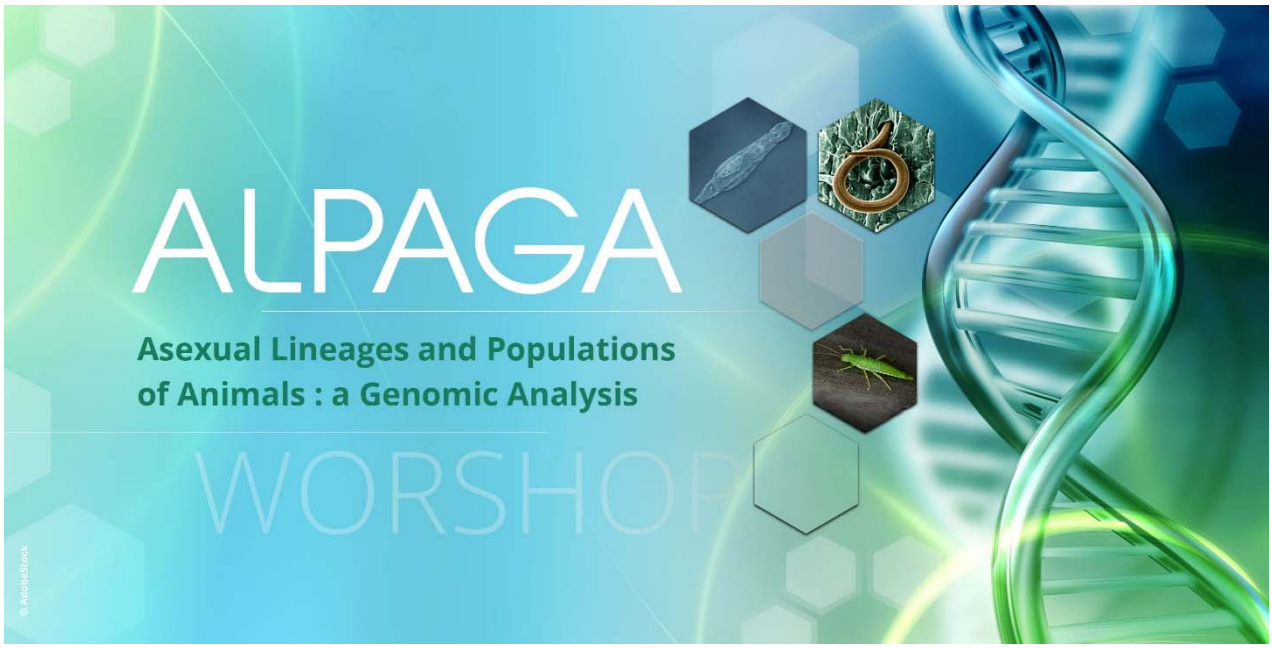
Session 3: Asexuality with hybridization – Chairman: Tanja Schwander	
13h30-14h15	Unorthodox reproductive systems in Cataglyphis desert ants **Serge Aron** (Université Libre de Bruxelles, BE)
14h15-15h00	Androgenesis in the Asian clam genus Corbicula **Lise-Marie Pigneur** (UNamur, Universite de Liège, BE)
Coffee – tea break	

Session 4: Ancient asexual scandals: do they exist and how do they persist? – Chairman: Jean-François Flot	
15h30-16h	Phylogenetic and genomic studies of ancient asexual darwinulid ostracods **Isa Schön** (Royal Belgian Institute of Natural Sciences, BE)
16h-16h30	Horizontal gene transfers among asexual bdelloid rotifers of the genus Adineta **Nicolas Debortoli** (Université de Namur, BE)
16h30-17h	Hybridization and polyploidy enable genomic plasticity without sex in the asexual root-knot nematodes **Etienne Danchin** (INRA – Sophia Antipolis, FR)
17h-17h30	Recent insights into ancient asexual mites **Jens Bast** (Université de Lausanne, Switzerland)
17h30-19h	Aperitive on the boat combined with a boat trip around Namur: Discussions
19h	Dinner on the boat (covered by the workshop budget): informal discussions

Thursday, March 30th – University of Namur – AGORA room, rue Godefroid, 5

Session 5: New tools to improve the assembly of heterozygous genomes – Chairman: Etienne Danchin	
9h00-9h30	Assembling heterozygous/polymorphic genomes: challenges and solutions **Jean-François Flot** (Université Libre de Bruxelles, BE)
9h30-10h00	BWISE: DBG-guided super-read assembly **Antoine Limasset** (INRIA Rennes, FR)
10h00-10h30	Alienomics **Jitendra Narayan** (Université de Namur, BE)
Coffee – tea break	
11h00-11h30	Oxford Nanopore technology : data and applications **Jean-Marc Aury** (Genoscope, France)
11h30-12h00	Horizontal gene transfer – population genomic approach in bdelloid rotifers – **Marie Cariou** (Université de Namur, BE)
12h-12h20	ALPAGA I: aim and objectives – **Etienne Danchin** (coordinator ALPAGA, INRA – Sophia Antipolis, FR)
12h20-12h40	ALPAGA II: aim and objectives Open discussion on the perspectives of ALPAGA II
Lunch break till 14h30: final discussions and perspectives ALPAGA	

The ALPAGA scientific committee & Chairs



Professor Karine Van Doninck

Workshop organizer

Affiliation

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Laboratory of Evolutionary Genetics and Ecology
Department of Biology - URBE
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Short CV

2003: PhD in Evolutionary Biology (VUB)
2003-2006: Postdoc in the laboratory of Prof. M.S. Meselson, Harvard University (MCB Dept), US
2006-2007: Marie-Curie IEF in the group of Dr. Y. Michalakis, IRD Montpellier (France)
Since Sept 2007: Professor at UNamur, head of the Laboratory in Evolutionary Genetics and Ecology

Keywords: Evolutionary genetics, ecology, asexual reproduction
Temporal and spatial dynamics of clonal lineages
Desiccation resistance, chromosome breakage, DNA repair and genome dynamics
Comparative genomics
Horizontal gene transfer, evolutionary genomics and adaptation
Oxidative stress
Androgenesis, phylogeography, ploidy variation and spermatogenesis
Invasive species and metagenomics

Professor Bernard Hallet

Affiliation

Biochemistry, Biophysics and Genetics of Microorganisms (BBGM)
Life Science Institute – Institut des Sciences de la Vie (ISV)
Catholic University of Louvain (UCL)

https://uclouvain.be/en/research-institutes/isv

Short CV

1993 : PhD in Molecular Biology (UCL)
1994-1998 :University of Oxford (UK) Biochemistry Dpt
2001 : Senior Research Associate at the FNRS (Fonds de la Recherche Scientifique)
2006 : Full-time Senior Lecturer (UCL)
2011 : Professor (UCL)

Keywords: Molecular Biology, Genetics, microbiology
- DNA and protein biochemistry, protein-ADN transactions
- DNA Transposition and site-specific recombination in bacteria
- DNA recombination, replication and repair
- Genome dynamics and Bacterial cell cycle

More recently: DNA repair and genome dynamics in the bdelloid rotifer Adineta vaga

Professor Tanja Schwander

Affiliation

University of Lausanne,
Department of Ecology and Evolution

Short CV

2013-
Assistant professor SNSF, Department of Ecology and Evolution, University of Lausanne

2010-2013:
NWO Veni Fellow, Centre for Ecological and Evolutionary Studies, University of Groningen

2009-2010
Short-term fellow at the Wissenschaftskolleg zu Berlin, Centre for Advanced Study

2007-2009:
FNS Postdoctoral fellow, Department of Biological Sciences, Simon Fraser University

2007 PhD University of Lausanne

Jean-François Flot, associate professor

Affiliation

Evolutionary Biology & Ecology
Department of Organismal Biology
Université libre de Bruxelles
Belgium

Short CV

University Paris7 – Denis Diderot (France)	BSc	Biochemistry	1998
University Paris7 – Denis Diderot (France)	MSc	Biochemistry	1999
University of the Ryukyus (Okinawa, Japon)	MSc	Marine Sciences	2003
Muséum National d'Histoire Naturelle (France)	PhD	Molecular Systematics	2008

Research interests
Phylogenetics; species delimitation; experimental evolution; genome dynamics; genome evolution; corals; amphipods; rotifers; xenacoelomorphs; coral reefs; groundwaters; "extreme" environments; microbial ecology; biodiversity; symbiosis; evolution of sexuality/asexuality; bioinformatics

Dr. Etienne Danchin
ALPAGA I coordinator

Affiliation

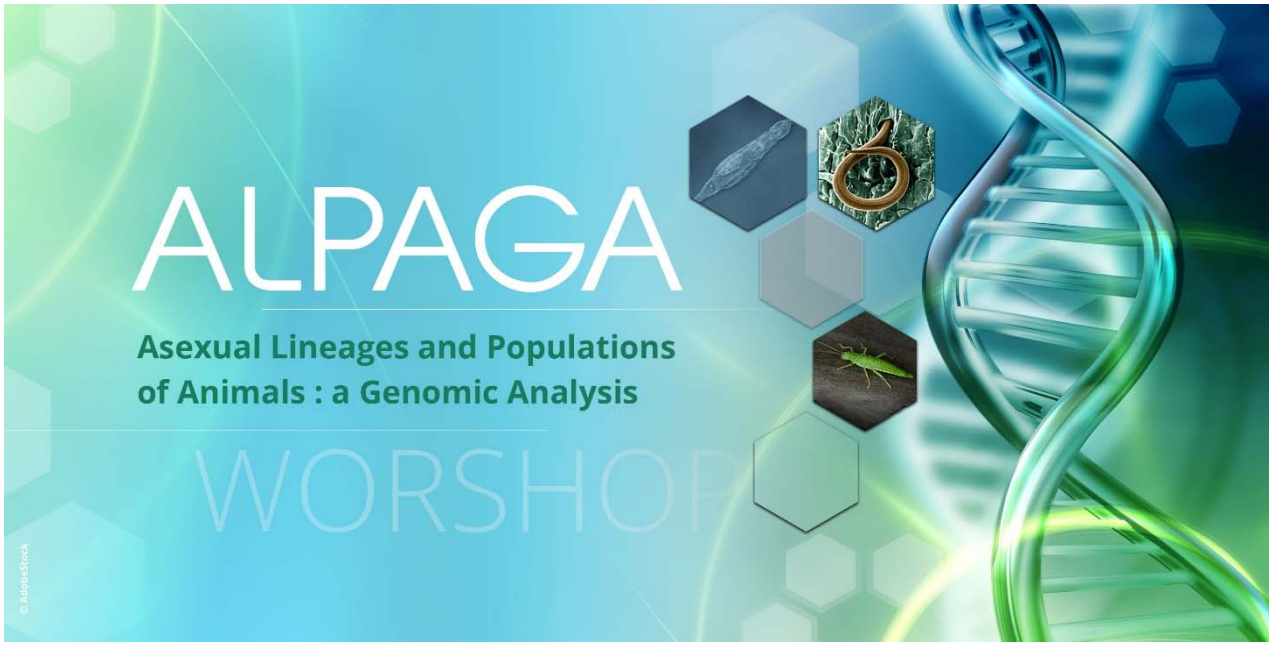
Institut Sophia Agrobiotech,
INRA, Universté Côte d'Azur,
CNRS,
400 route des Chappes,
06903, Sophia Antipolis, France.

Short CV

Current position: I am an INRA senior scientist in the laboratory of plant-nematode interactions, in Sophia Antipolis, France. As a principal investigator, I lead the researches in the domain of comparative and evolutionary genomics of plant-parasitic nematodes.

Background: After a PhD in bioinformatics, in which I studied evolutionarily conserved genome regions across bilaterian animals, I annotated and compared fungal genomes for their repertoires of carbohydrate-active enzymes. The aim was to correlate repertoire of enzymes with the ecology and life style of the fungi.

Scientific production: I currently have 56 accepted publications in peer-reviewed journals, including 3 in Nature, 3 in Nature Biotechnology, 1 in Genome Biology, 1 in Mol Biol Evol and 1 in PNAS. Over the 2004 – 2016 period, my papers received 6,522 citations yielding an h-index of 29.


ALPAGA
Asexual Lineages and Populations
of Animals : a Genomic Analysis
WORSHOP

ALPAGA
Asexual Lineages and Populations of Animals: a Genomic Analysis

In May 2013 was organized a Jacques Monod Conference on “recent advances on the evolution of sex and genetic systems”, in Roscoff, Brittany, France. Following the invitation of Prof. Tanja Schwander, several researchers interested in the evolution of reproductive modes presented and discussed their respective results. An informal discussion between different genome project leaders took place. This discussion mainly involved four European laboratories: (i) Drs. Etienne GJ Danchin and Philippe Castagnone from INRA in Sophia Antipolis, France, both involved in the genome sequencing and analysis of *Meloidogyne incognita*, a plant-parasitic nematode that represented not only the first published genome for a plant-parasitic animal but also the first for an animal that totally abandoned sexual reproduction [1]. (ii) Karine van Doninck from the University of Namur, the project leader for the genome sequencing of *Adineta vaga*, the first old asexual animal to be sequenced [2]. (iii) Isa Schön, from the Royal Belgian Institute of Natural Sciences, Brussels, working on the evolution of asexual ostracods and their sexual relatives. And (iv) Tanja Schwander, from the University of Lausanne co-organizer of the conference and project leader of evolutionary genomics analysis on sexual and asexual stick insects. During this discussion, we collectively thought that it would be timely and interesting to join forces, approaches and models to study the genomics of asexually-reproducing animals. We thus decided to build a consortium around this topic and to try to obtain funding to support this project.

By this time, we named our project GALA for “Genomics of Asexual Lineages of Animals”. This project gathered seven European laboratories combining different models of sexual and asexual animals as well as bioinformatics platforms. We identified as a priority the production of high quality reference genomes for asexual lineages of animals as well as for their sexual relatives. This appeared to us as a prerequisite to be able to identify singularities in the genome of asexuals and compare the results across the different animal lineages. We found that the “France Génomique” call for Big Sequencing Projects would be a good avenue for GALA. We decided to submit the GALA project with the seven European labs to this call, with Etienne Danchin as coordinator of the project and responsible for assembling the submission document. Although the project was not funded for the 2013 call, we received encouraging reviews and decided to continue our efforts and improve the project.

We organized a workshop in July 2014 that was hosted by Tanja Schwander in Lausanne, to present our different preliminary results as well as the questions we were interested in. At the end of this workshop we clarified the objectives of our project, discussed the methodology and defined the main work-packages to be included as well as who will coordinate which part. It was decided that Etienne Danchin would be the coordinator of the whole project and that we would resubmit a revised version of the project for the next France Génomique call (2015).

We collectively improved our sequencing plans and clarified the objectives and methodology of the whole project. Etienne Danchin was in charge of coordinating and assembling the new version of the manuscript. Our new project was named ALPAGA for "Asexual Lineages and Populations of Animals: a Genomic Analysis" and comprised 10 European labs combining forces in evolutionary biology, comparative genomics and bioinformatics. The project was accepted at the end of 2015 but we were asked to keep only 3 animal clades comprising asexual and sexual relatives out of the 7 clades initially present (Rotifers, Nematodes, Stick insects, Aphids, Ostracods, Mites and Parasitoid wasps). We decided to keep the nematodes the rotifers and the stick insects to maintain the maximal diversity of animal lineages and to make sure preliminary genomic data was already available.

In March 2016, a kick-off meeting took place at GENOSCOPE, in Evry, the French national genome-sequencing center, that will perform the sequencing effort for the different species, populations and isolates of sexual and asexual animals. We discussed at this occasion the sequencing strategy and scheduled the first main steps of the project. This officially launched ALPAGA-I.

Main objectives

Our main aim is to characterize animal genome evolution in the absence of sex and identify genomic features of asexually-reproducing animals that may allow them to compete with their sexual relatives and / or persist over evolutionary times, without the benefits of sex. We will compare the genomes of asexual and sexual species lineages across different animal clades to identify singularities associated to an asexual mode of reproduction. The preliminary goal of the project is to generate high quality reference genomes for asexual animals as well as their sexual relatives. This is a prerequisite to be able to address the main work packages detailed after. For this, we will use a hybrid approach, combining 3rd generation sequencing technology to obtain long reads and 2nd generation sequencing to correct errors and reach high genome coverage.

The genome data (from reference species, populations and isolates) generated during this project will be used to address the five following work packages.

WP1: Heterozygosity & Gene Conversion

Briefly, we will assess the levels of intra-genome, intra-population and inter-population heterozygosity at the whole genome scale for sexual and asexual species and compare whether there is any significant difference and trend in heterozygosity level between sexuals and asexuals. In the same trend, we will assess the propension for gene conversion in asexuals and sexuals. The rationale here is that gene conversion could slow down the accumulation of deleterious mutation.

WP2: Horizontal Gene Transfers

In the genomes of both the asexual root-knot nematodes [3] and the bdelloid rotifers [2], substantial amounts of horizontal gene transfers (HGT) of non metazoan origin have been observed. This is tempting to hypothesize that these HGT could generate plasticity in the absence of sex. However, it is not clear whether the prevalence of HGT is higher in these asexuals than their sexual relatives. Another possibility would be that evolution of asexuality is facilitated in lineages that are already prone to HGT. Here we will assess the proportion of HGT acquisitions in the different lineages of sexual and asexual animals analyzed in ALPAGA. We will compare these rates between asexuals and their asexual relatives and also with reference genomes from other animal lineages not closely related to asexuals.

WP3: Transposable Elements

Although movements of transposable elements (TEs) can generate genomic plasticity and thus promote adaptation in the absence of sex, they can also have highly deleterious effects. With contradicting theories and examples, it is unclear whether more or less TE load and potential activity should be expected in asexuals compared to sexuals. We will thus undertake a systematic annotation of TEs with the same standardized method for all the species and compare the TE load. Using Pool-Seq and RAD-Seq data from populations and isolates we will also assess whether these TE are active and potentially move within and between populations and isolates.

WP4: Copy Number Variations, Structural Variations

In the model nematode *C. elegans* and other species, the rate of copy number variation (CNV) per gene and per generation is several orders of magnitude higher than the rate of accumulation of mutation per gene per generation [4,5]. Whether gene copy number variations contribute significantly to the adaptability of asexual species remains unknown. We will assess this rate of CNV between the different sexual and asexual species as well as within and between the different populations and isolates and compare these rates to the rates of accumulation of mutations. In the bdelloid rotifer as well as in the root-knot nematode genomes, we have observed structural variations such as translocations and inversions that led to extensive synteny breakpoints, probably related to the absence of meiosis releasing the pressure for maintaining homologous chromosomes. The extant and consequences of these structural variations will be studied across the different sexual and asexual species.

WP5: Potential functional impact

In this work package, we will try to identify which genes could be affected by the different mechanism of genomic plasticity we will survey during ALPAGA (mutations, HGT, TE, CNV and structural variations). By performing functional annotations, and comparing gene expression levels, we will aim at predicting the functional impact of all these mechanism of genome plasticity. As a perspective, we will try to identify affected genes related to important function for the biology and ecology of the species under consideration. These findings will probably guide the biologists for further

References

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2. Flot J-F, Hespeels B, Li X, Noel B, Arkhipova I, Danchin EGJ, et al. Genomic evidence for ameiotic evolution in the bdelloid rotifer Adineta vaga. Nature. 2013;500: 453–457. doi:10.1038/nature12326

3. Paganini J, Campan-Fournier A, Da Rocha M, Gouret P, Pontarotti P, Wajnberg E, et al. Contribution of Lateral Gene Transfers to the Genome Composition and Parasitic Ability of Root-Knot Nematodes. PLoS ONE. 2012;7: e50875. doi:10.1371/journal.pone.0050875

4. Lipinski KJ, Farslow JC, Fitzpatrick KA, Lynch M, Katju V, Bergthorsson U. High Spontaneous Rate of Gene Duplication in Caenorhabditis elegans. Curr Biol. 2011;21: 306–310. doi:10.1016/j.cub.2011.01.026

5. Katju V, Bergthorsson U. Copy-number changes in evolution: rates, fitness effects and adaptive significance. Front Genet. 2013;4. doi:10.3389/fgene.2013.00273

ALPAGA workshop program & abstracts

Tuesday, March 28th

NARC room, rue de Bruxelles, 55

14h30-15h00	Arrivals – welcome package
15h00	Welcome and Introduction – **Karine Van Doninck** (host at UNamur)
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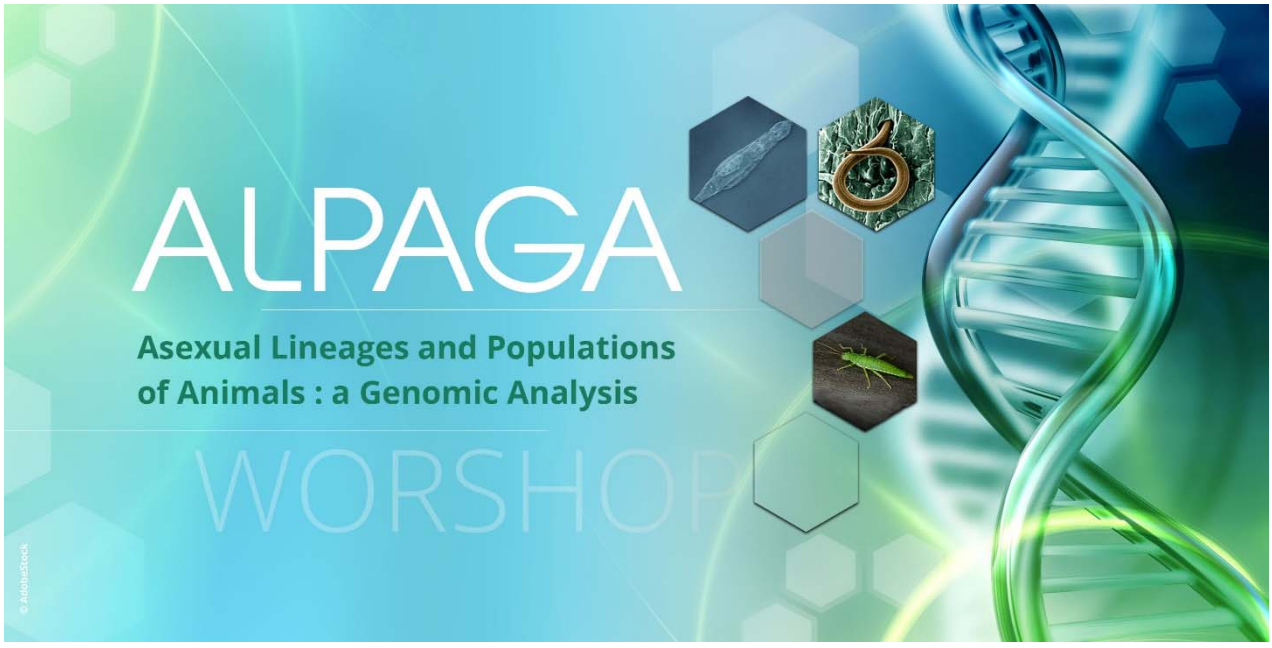

Dr Ken Kraaijeveld

Affiliation

Vrije Universiteit Amsterdam

Short CV

After studying the phenotypic consequences of asexual reproduction in parasitoid wasps at the University of Leiden, I am now examining the genomic consequences in the same system at the Vrije Univeristeit Amsterdam. Recently, I have also started invesstigating the genome of an asexual collembolan, for which a high quality reference genome is available in the lab.

Patchy recombination in the genome of an asexual springtail

Gradual accumulation of deleterious mutations through Muller's ratchet is often cited as an important contributor to the early demise of asexual lineages. Muller's ratchet is usually assumed to apply to all asexual taxa, regardless of how they achieve parthenogenesis. However, many parthenogens go through (partial) meiosis each generation, which may prevent the accumulation of deleterious mutations and provide an escape from Muller's ratchet. We examined the high-quality genome assembly of the asexual springtail *Folsomia candida*, in which parthenogenetic eggs are produced meiotically, for evidence of mutation accumulation. We found regions with signatures of reduced recombination on three of the seven chromosomes. These regions were characterized by palindromes, translocations, high densities of transposable elements and horizontally transferred genes. We suggest that meiotic recombination prevents the accumulation of deleterious mutations and transposable element insertions. However, structural genomic reorganizations may locally suppress meiosis. In such regions, Muller's ratchet then leads to the accumulation of deleterious genetic elements. This model predicts that Muller's ratchet is a local phenomenon, rather than an effect that impacts the entire genome of an asexual lineage equally.

Dr Christoph Haag

Affiliation

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Short CV

2000-2004: PhD, Univ. Basel and Fribourg, Switzerland
2004-2005: Post-Doc, Univ. Helsinki, Finland
2005-2007: Marie Curie Fellow, Univ. Edinburgh, Scotland
2007-2013: Group Leader, Univ. Fribourg, Switzerland
since 2013: Permanent Researcher (CR1) CNRS, HDR 2015

Research keywords: Evolution of Ageing, Genetic drift, Local adaptation, Breeding systems, Daphnia, Population Genomics, Asexuality, Automixis, Recombination, Meiosis.

Website: http://www.cefe.cnrs.fr/fr/recherche/ee/gee/800-c/3077-christoph-haag-2

Automixis in *Daphnia*: A model for the evolution of clonality?

Daphnia reproduce clonally throughout most of the year, except for the production of diapause stages, which is sexual. Until recently, clonal reproduction was thought to be mitotic ("apomictic parthenogenesis" in the animal literature), but recent findings show cytological vestiges of meiosis, suggesting that parthenogenesis is meiosis-derived. We investigated the occurrence of rare diapause stage production in female-only cultures. We carried out several experiments to verify the absence of rare males (which would be difficult to detect phenotypically in large-scale cultures). We then investigated offspring genotypes by RAD-sequencing, finding that they were neither produced by mating with rare males nor clonally, but rather by automixis. In automixis, two haploid products of a single meiosis fuse to restore diploidy (or certain steps of meiosis are skipped, which is genetically equivalent). This leads to a loss of heterozygosity compared to the mother, in a way that is similar to self-fertilization. However, the degree of heterozygosity reduction depends on the exact mode of automixis and on recombination. In particular, automixis by "central fusion" fully maintains maternal heterozygosity and is genetically indistinguishable from apomixis if recombination is fully suppressed. Central fusion can be achieved by fusing meiotic products that have been separated during meiosis I, or, equivalently, by skipping meiosis I. Interestingly, the latter is what is observed during clonal reproduction in Daphnia. Clonality may thus evolve through automixis by fixing central fusion and suppressing recombination.

Thomas Lenormand, Research director, CNRS

Affiliation

CEFE, Campus CNRS, Montpellier

Short CV

I am a CNRS research director at the Centre d'Ecologie Fonctionnelle et Evolutive in Montpellier, France. Since my PhD obtained in Montpellier in 1998, I have been mainly working in evolutionary and ecological genetics. I have been doing theoretical work on the evolution of sex, mating systems, dispersal, recombination, gene expression. I am also interested in theories of adaptation local adaptation and niche evolution, on the effect of mutations, on the process of speciation, and genetic conflicts. On a more empirical side, I have worked on a variety of animal systems (mice, mosquitoes, snails, artemia, daphnia), microbes (yeast, bacteria), and few plants (corn, thyme, Arabidopsis) and investigated host parasites (cestodes, phages, microsporidia) and microbiota interactions.

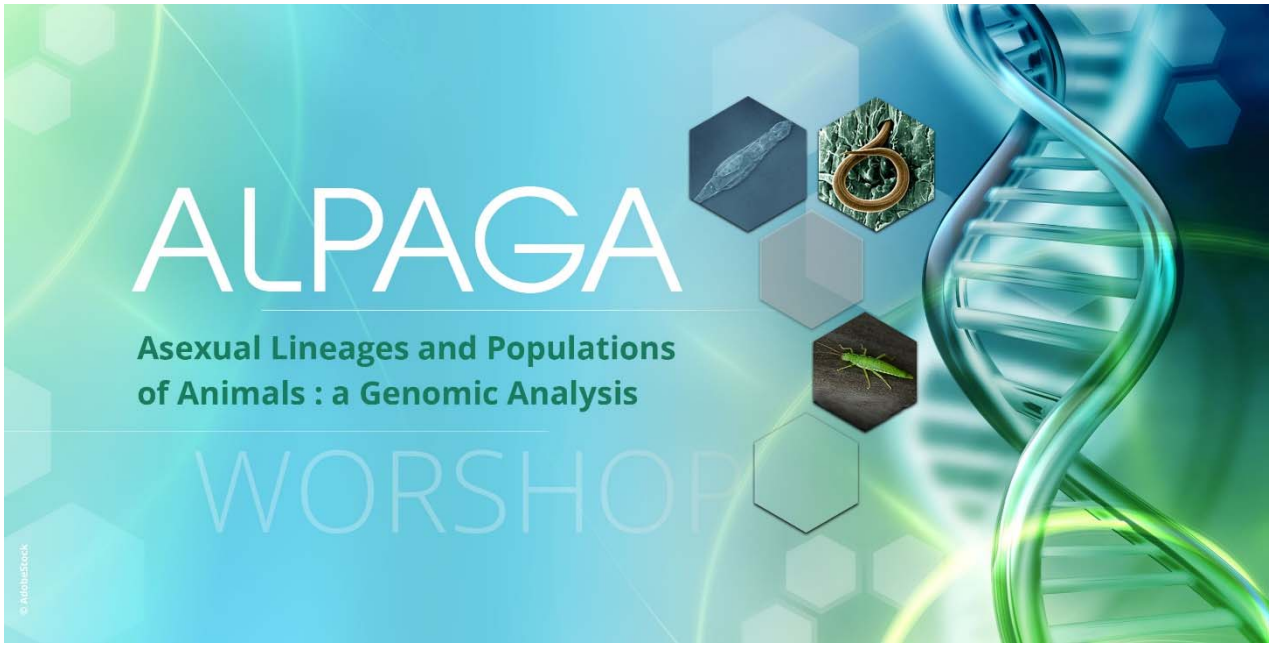
Contagious asexuality in Artemia

Artemia parthenogenetica has been known to reproduce by parthenogenesis for more than a century. Its mode of reproduction has been intensely studied using cytological techniques for decades. Today, however, the reproductive system in this group remains largely unknown and controversial. Different modes of automixis have very different genetic and evolutionary consequences, but can be particularly difficult to tease apart. In this presentation, I will summarize what is known and show that diploid *A. parthenogenetica* asexuals reproduce through central fusion automixis, with non-zero rates of recombination. Further, I will show that new asexuals originate by contagious asexuality through the crosses of “rare males” with related sexual species from central Asia. Using genomic data, I will discuss the phylogenetic context of these groups as well as puzzling patterns of recombination in closely related sexuals. Then, I will show how these crosses can be used to engineer new asexual genotypes and even develop introgression of part of asexual genomes in sexual background. These experiments allow tracking the genetic basis of asexuality. Because *A. parthenogenetica* harbors steep within-chromosome gradients of heterozygosity (due to its mode of automixis), it also offers a new avenue for contrasting the genomic consequences of asexuality and inbreeding. Overall, I will try to settle the century-old controversy over *A. parthenogenetica* reproduction, and show that it is a very powerful model to study the genomic consequences of asexuality.

Wednesday, March 29th

AGORA room, Business & Learning Center, rue Godefroid, 5

Session 2: Evolutionary adaptation in asexuals – Chairman: Bernard Hallet	
9h00-9h45	Adaptive genome evolution in an asexual fungal plant pathogen **Michael F Seidl** (Wageningen University & Research, NL)
9h45-10h30	Evolutionary genomics of asexual fungi plant pathogens **Ronnie de Jonge** (Utrecht University, NL)
Coffee – tea break	
11h00-11h45	Gene expression and evolutionary rate changes after parallel evolution of asexuality in stick insects **Tanja Schwander** (Université de Lausanne, Switzerland)
11h45-12h30	C-value paradox revisited: Why is there so much intraspecific genome size variation in the monogonont rotifer Brachionus asplanchnoidis, and what are the consequences? **Claus-Peter Stelzer** (Universität Inssbruck, AU)
Lunch break	



Michael F Seidl, assistant Professor

Affiliation

Laboratory of Phytopathology
Wageningen University & Research
Wagenningen, The Netherlands

Short CV

2016-present:	Assistant Professor (Tenure track) at the Laboratory of Phytopathology, Wageningen University, The Netherlands
2015-2016:	NWO VENI post-doctoral research fellow at the Laboratory of Phytopathology, Wageningen University, The Netherlands
2013-2015:	Post-doctoral research fellow at the Laboratory of Phytopathology, Wageningen University, The Netherlands
2012-2013:	Post-doctoral research fellow at Theoretical Biology and Bioinformatics Group, Utrecht University, The Netherlands
2008-2012:	PhD, Theoretical Biology and Bioinformatics Group, Utrecht University, The Netherlands
2006-2008:	Diplom Biol. (Univ) – *cum laude*, Julius-Maximilians-Universität Würzburg, Germany

Adaptive genome evolution in an asexual fungal plant pathogen

Sexual reproduction has been observed in nearly all branches of the eukaryotic tree of life. It is considered an important mechanism for establishing genomic variation by combining genetic information from genetically different parents. Before genetic information is transferred to the progeny, meiotic recombination generates novel combination of existing alleles. Therefore, meiotic recombination is an important driver for rapid adaptation to novel or changing environments. However, in a considerable number of eukaryotic lineages, no sexual cycle has been observed. For example, in around 20% of all fungi, a diverse group of organisms that contain numerous pathogens of animals and plants, a sexual cycle has never been described, and thus these asexual lineages are often considered to be limited in their adaptive capacity.

Pathogens and their hosts are engaged in everlasting co-evolutionary arms races where hosts utilize their surveillance system to detect invaders and mount appropriate defences, involving detection of invasion patterns by immune receptors, whereas pathogens secrete so-called effector molecules to support host colonization and counteract immune responses. This tight interaction exerts strong selection pressure on both partners and incites rapid genomic diversification.

Verticillium dahliae is a soil-borne fungal pathogen that infects susceptible hosts through their roots and colonizes the water-conducting xylem vessels, leading to vascular wilt disease. Despite its presumed asexual nature, *V. dahliae* is a highly successful pathogen that causes diseases on hundreds of plant hosts, including important crop species such as tomato, olive and cotton. Using comparative genomics, we recently established that transposable elements are major drivers of adaptive genome evolution in this asexual plant pathogen. We show that highly variable lineage-specific (LS) regions evolved by genomic rearrangements that are mediated by erroneous double-strand repair, often utilizing transposons. We furthermore show that recent genetic duplications are enhanced in LS regions and that LS regions are enriched in active transposons, which contribute to local genome plasticity. Additionally, we interrogated the genome of *V. dahliae* and related *Verticillium* species for traces of genes derived from horizontal gene transfer (HGT), the exchange of genes over species barriers. While the overall abundance of HGT in *V. dahliae* is limited compared with other asexual lineages, we identified multiple HGT-derived genes that play significant role in *V. dahliae* virulence. In summary, our research highlights that asexual organisms can be as persistent as organisms with conventional sexual cycles through the use of other mechanisms to foster adaptation, such as genomic rearrangements and HGT.

Dr. Ir. Ronnie de Jonge, Assistant professor in Plant-Microbe interactions

Affiliation

Utrecht University, The Netherlands

Short CV

EDUCATION / QUALFICATIONS / PROFESSIONAL HISTORY

2002: VWO, Athenaeum degree (Goes, The Netherlands)
2005: B.Sc. Biology, Wageningen University (Wageningen, The Netherlands)
2007: M.Sc. Plant Biotechnology, Wageningen University (Wageningen, The Netherlands)
2012: Ph.D. Plant pathology, dissertation entitled: "The role and evolution of fungal effectors in plant pathogenesis", Wageningen University, (Wageningen, The Netherlands), *cum laude (top 2%)*
2012: Postdoc – Lab of Prof. Yves Van de Peer, Bioinformatics and Evolutionary Genomics, VIB (Ghent, Belgium)
2013: Awarded Hugo R. de Vries price for best thesis in the field of botany (Wageningen, The Netherlands)
2015: Assistant professor – Plant Microbe Interactions, Faculty of Science, Department of Biology, Utrecht University (Utrecht, The Netherlands)
2015: Awarded FWO Postdoctoral Fellowship, Lab of Prof. Yves Van de Peer, Bioinformatics and Evolutionary Genomics, VIB (Ghent, Belgium)

ACADEMIC ACTIVITIES (LAST 4 YEARS)

2013 Mar 27th Fungal Genetics Conference, Asilomar USA (presented poster)
2013 Mar Invited presentation "Chromosome reshuffling drives evolution of virulence in an asexual pathogen" at USDA/USDA, Fargo ND, USA
2013 Apr Invited plenary presentation at the ALW Meeting Experimental Plant Sciences, Lunteren, NL as part of the Hugo de Vries price ceremony.
2013 Jun International Conference on Genomics in Europe, Ghent, BE (invited talk)
2014 Dec Institute of Life Sciences (ILV) Symposium, Louvain-la-Neuve, BE (invited talk)
2014 Mar Green Life Sciences (GLS) seminar, Amsterdam, NL (invited talk)
2015 Jan Invited presentation "Identifying the genomic blueprints of sugarbeet pathogenicity" at USDA/USDA, Fargo ND, USA
2016 Jun Selected presentation "Illuminating the missing links in cercosporin toxin biosynthesis and auto-resistance" at the EMBO Fellows meeting (Heidelberg, Germany)
2016 Sep Selected presentation "The root microbiome and plant health" at the Functional Metagenomics Meeting (Trondheim, Norway)
2016 Dec Invited presentation "The root microbiome and plant health" at Wageningen University, Wageningen (The Netherlands)
2017 Jan Invited GELIFES seminar "The root microbiome and plant health" at Groningen Institute for Evolutionary Life Sciences, Groningen (The Netherlands).

Ancient duplication and horizontal transfer of a toxin gene cluster reveals novel mechanisms in the cercosporin biosynthesis pathway

Ronnie de Jonge[1,2,3,4,†,*], Malaika K. Ebert[5,6,7 †], Callie R. Huitt-Roehl[8], Paramita Pal[8], Jeffrey C. Suttle[5], Jonathan D. Neubauer[5], Wayne M. Jurick II[9], Gary A. Secor[6], Bart P.H.J. Thomma[7], Yves Van de Peer[1,2,3,10], Craig A. Townsend[8], & Melvin D. Bolton[5,6,*]

[1]Department of Plant Systems Biology, VIB, Ghent, Belgium. [2]Department of Plant Biotechnology and Bioinformatics, Ghent University, Ghent, Belgium. [3]Bioinformatics Institute Ghent, Ghent University, B-9052 Gent, Belgium. [4]Plant-Microbe Interactions, Department of Biology, Faculty of Science, Utrecht University, Utrecht, The Netherlands. [5]Northern Crop Science Laboratory, United States Department of Agriculture, Fargo, ND, United States. [6]Department of Plant Pathology, North Dakota State University, Fargo, ND, United States. [7]Laboratory of Phytopathology, Wageningen University, Wageningen, the Netherlands. [8]Department of Chemistry, The Johns Hopkins University, Baltimore, MD, United States. [9]Food Quality Laboratory, United States Department of Agriculture, Beltsville, MD, United States. [10]Department of Genetics, Genomics Research Institute, University of Pretoria, Pretoria, South Africa.

Cercospora species have a global distribution and are best known as the causal agents of leaf spot diseases of many crops. Cercospora leaf spot (CLS) is an economically devastating disease of sugar beet caused by *C. beticola*. The *C. beticola* genome encodes 63 biosynthetic gene clusters, including the cercosporin toxin biosynthesis (*CTB*) cluster. Studies spanning nearly 60 years have shown that cercosporin is photo-activated, critical for disease development, and toxic to most organisms except *Cercospora* spp. themselves, which exhibit cercosporin auto-resistance. We show that the *CTB gene cluster* has experienced an unprecedented number of duplications, losses, and horizontal transfers across a spectrum of plant pathogenic fungi. Although cercosporin biosynthesis has been widely assumed to rely on the eight gene *CTB* cluster, our comparative genomic analysis revealed extensive gene collinearity adjacent to the established cluster in all *CTB* cluster-harboring species. We demonstrate that the *CTB* cluster is larger than previously recognized and includes the extracellular proteins fasciclin and laccase required for cercosporin biosynthesis and the final pathway enzyme that installs the unusual cercosporin methylenedioxy bridge. Additionally, the expanded cluster contains CFP, which contributes to cercosporin auto-resistance in *C. beticola*. Together, our results give new insight on the intricate evolution of the *CTB* cluster.

Professor Tanja Schwander

Affiliation

University of Lausanne, Department of Ecology and Evolution

Short CV

2013-
Assistant professor SNSF, Department of Ecology and Evolution, University of Lausanne

2010-2013:
NWO Veni Fellow, Centre for Ecological and Evolutionary Studies, University of Groningen

2009-2010
Short-term fellow at the Wissenschaftskolleg zu Berlin, Centre for Advanced Study

2007-2009:
FNS Postdoctoral fellow, Department of Biological Sciences, Simon Fraser University

2007 PhD University of Lausanne

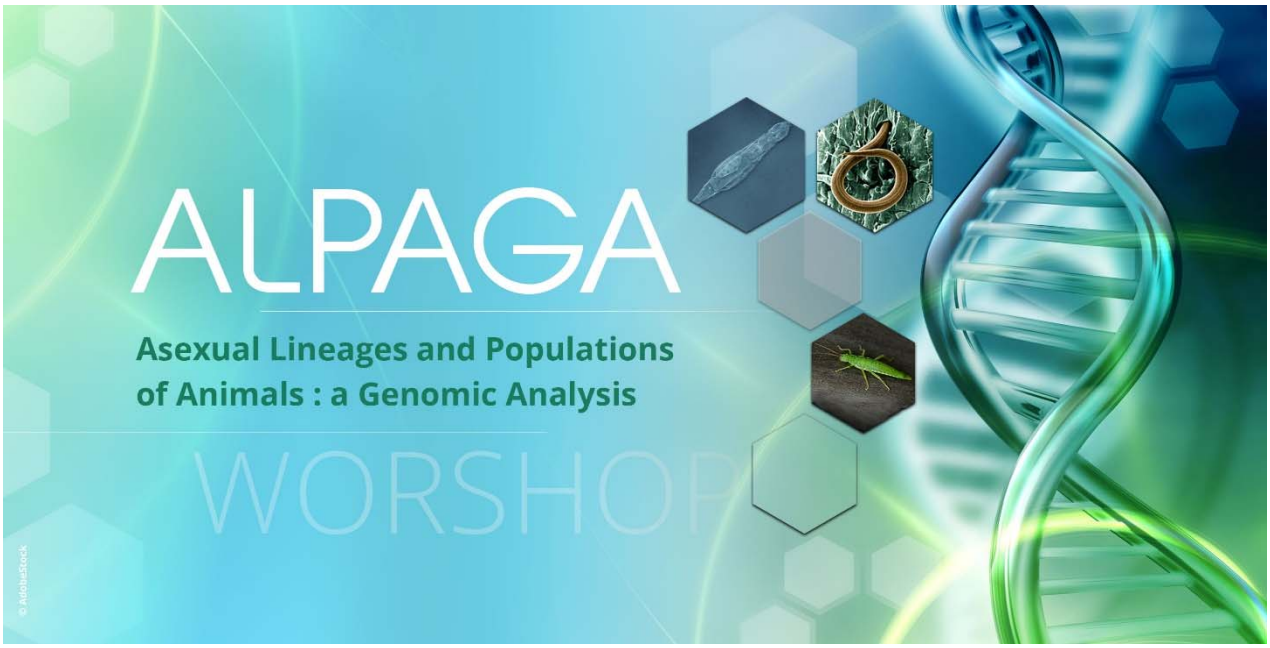
Gene expression and evolutionary rate changes after parallel evolution of asexuality in stick insects

Asexual reproduction has evolved repeatedly in ancestrally sexual populations, with significant consequences for population dynamics and the evolutionary fate of lineages. We generated whole-body and tissue-specific transcriptomes of independently evolved asexual stick insect lineages and their sexual relatives, to test for predicted consequences of asexuality as well as for signatures of convergent gene expression changes. As expected given the reduced effectiveness of selection under asexuality, we find evidence for deleterious mutation accumulation and high allelic divergence in asexuals. Although many genes are differentially expressed between sexual and asexual females, there is no convergence across independent transitions to asexuality at the gene level. Furthermore, we find that asexual females feature masculinized transcriptomes relative to sexual females, with higher expression of male-biased genes and lower expression of female-biased genes. We argue that these changes are most likely due to the decay of sexual traits in asexual females and to shifts of gene expression optima in females following transitions to asexuality.

Wednesday, March 29th

AGORA room, Business & Learning Center, rue Godefroid, 5

Session 3: Asexuality with hybridization – Chairman: Tanja Schwander	
13h30-14h15	Unorthodox reproductive systems in Cataglyphis desert ants **Serge Aron** (Université Libre de Bruxelles, BE)
14h15-15h00	Androgenesis in the Asian clam genus Corbicula **Lise-Marie Pigneur** (UNamur, Université de Liège, BE)
Coffee – tea break	



Serge Aron, Research Director of the Belgian NFSR

Affiliation

Evolutionary Biology and Ecology
Université Libre de Bruxelles

Short CV

Research Director at the Belgian FRS-FNRS and Head of the service *Evolutionary Biology & Ecology* at ULB.

My sphere of interests concerns the evolution of reproductive strategies, through detailed analyses of mating systems, dispersal strategies and population/colony genetic structure, using ants as biological models. These works are based on a combination of ecological and behavioural studies under natural and lab conditions, as well as on molecular analyses involving genotyping of microsatellite marker loci, flow cytometry analyses, fluorescent sperm marking, and *in situ* hybridisation.

The evolution of unorthodox reproductive systems in *Cataglyphis* desert ants.

With a few rare exceptions, the vast majority of animals reproduce sexually. Some species have, however, evolved alternative modes of reproduction by shifting from classical bisexuality to unorthodox reproductive systems, like parthenogenesis, gynogenesis, or hybridogenesis. Desert ants of the genus *Cataglyphis* provide remarkable examples of eccentric reproductive strategies.

Queens of several species conditionally use sexual and asexual (parthenogenetic) reproduction for the production of nonreproductive (workers) and sexual (queens and males) offspring, respectively. Other species have evolved hybridogenesis at the social level. Under social hybridogenesis, populations are characterized by the co-existence of two genetic lineages. Hybrid mating between queens and males originating from different genetic lineages results in the production of sterile workers, whereas new queens and males (the ‘‘germline’’) are produced asexually by parthenogenesis. As a consequence, only maternal genes are perpetuated across generations. This reproductive system leaves males with null fitness since they transmit their genes to nonreproductive workers only. Yet, the widespread distribution of social hybridogenesis in *Cataglyphis* supports that this strategy has been evolutionarily conserved. Finally, phylogenetic inferences show that multiple mating is ancestral in the genus. Polyandry sets the stage for sperm competition. Indeed, sperm production covaries with female (queen) mating frequency, and sperm cooperation occurs in the most polyandrous *Cataglyphis* species.

Lise-Marie PIGNEUR, PhD

Affiliation

University of Liège (Ulg)
University of Namur (UNamur)

Short CV

PhD (in 2011) from the reserarch unit in environmental and evolutionary biology at the University of Namur with Prof. Jean-Pierre Descy and Prof. Karine Van Doninck (Laboratory of Evolutionary Genetics and Ecology, LEGE). Thesis title : « Phylogeny, phylogeography and impact of invasive androgenetic clams *Corbicula* spp. ».

Post-Doctoral researcher (2012-2016) jointly in the Laboratory of Conservation Genetics (University of Liège) with Dr Johan Michaux and in the LEGE with Prof. K. Van Doninck, including a 6-months research internship at UMR AGIRs, CIRAD, Montpellier. FNRS Fellow « Chargée de recherches », project « Invasive mammals ».

Since January 2017, I am a freelance scientist, working mainly on conservation genetics projects in collaboration with Dr J. Michaux.

Androgenesis in the Asian clam genus Corbicula

Androgenesis, also known as “all-male asexuality”, is a unique mode of reproduction that results in offspring that carry nuclear chromosomes from the paternal lineage only. This strict paternal nuclear inheritance is particularly rare throughout the plant and animal kingdoms. However the clam genus Corbicula harbours several androgenetic lineages with widespread distribution. Moreover the cytological mechanisms underlying androgenesis are well described in Corbicula. Androgenetic Corbicula clams are hermaphrodites that produce offspring after fertilization of oocytes by a biflagellate, unreduced sperm. The oocyte then undergoes an abnormal meiosis with all nuclear chromosomes being discarded as two polar bodies but with the entire nuclear genome coming from the sperm. Besides androgenetic lineages, sexual species are also found within this genus and can occur in sympatry with androgens. Interestingly, Corbicula clams are successful exotic invasive species in several regions and all the invasive lineages seem to be androgenetic.

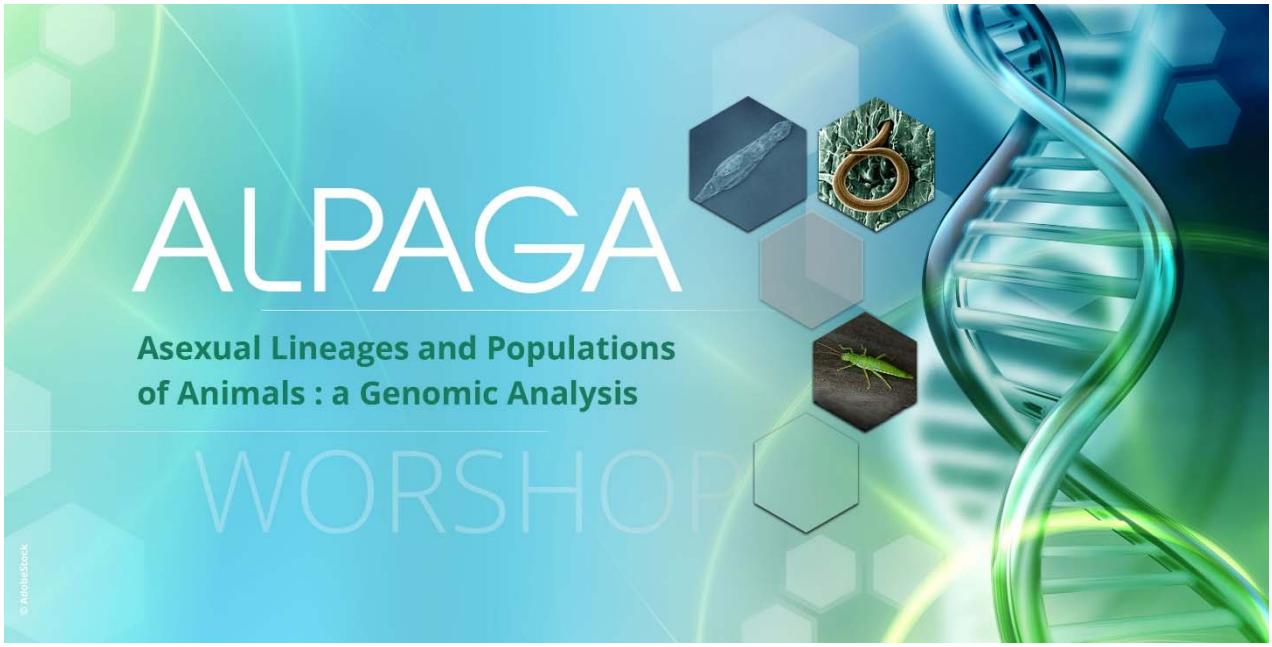
By analyzing patterns of allele sharing at three different nuclear markers in Corbicula individuals collected across most of their worldwide distribution, we identified three distinct genetic pools containing androgenetic lineages. Moreover, while one sexual species formed a distinct fourth genetic pool, the other sexual lineages clustered with the androgenetic ones. It remains unclear whether androgenesis originated only once in Corbicula, however our new data suggests that androgenetic Corbicula lineages emerged multiple times in separate geographic regions where sexuals are found.

Since androgenetic clams are distinguishable from sexuals by unreduced sperm, we also investigated the cytological mechanisms underlying spermatogenesis in Corbicula by following the DNA content variation of male germ cells throughout gametogenesis. We compared androgenetic and sexual Corbicula lineages, with a particular focus on Corbicula sandai which is closely related to androgenetic lineages and found in sympatry with them in Lake Biwa (Japan). We found that C. sandai males produced about 50% of unreduced sperm through an apomictic mode of reproduction in which the first meiotic division is probably disrupted and therefore causing androgenesis to emerge. The frequency of unreduced sperm in C. sandai moreover suggests that the switch to androgenesis might be simple and that new androgenetic lineages could frequently originate from this "sexual" species.

Wednesday, March 29th

AGORA room, Business & Learning Center, rue Godefroid, 5

Session 4: Ancient asexual scandals: do they exist and how do they persist? – Chairman: Jean-François Flot	
15h30-16h	Phylogenetic and genomic studies of ancient asexual darwinulid ostracods **Isa Schön** (Royal Belgian Institute of Natural Sciences, BE)
16h-16h30	Horizontal gene transfers among asexual bdelloid rotifers of the genus Adineta **Nicolas Debortoli** (Université de Namur, BE)
16h30-17h	Hybridization and polyploidy enable genomic plasticity without sex in the asexual root-knot nematodes **Etienne Danchin** (INRA – Sophia Antipolis, FR)
17h-17h30	Recent insights into ancient asexual mites **Jens Bast** (Université de Lausanne, Switzerland)
17h30-19h	Aperitive on the boat combined with a boat trip around Namur: Discussions
19h	Dinner on the boat (covered by the workshop budget): informal discussions



Prof. Dr.Isa Schön

Affiliation

Royal Belgian Institute of Natural Sciences (RBINS)
OD Nature, ATECO group, Freshwater Biology
Vautierstraat 29
1000 Brussels, Belgium.
isa.schoen@naturalsciences.be

Phone: 0032 262 74312

Short CV

- Team leader of Freshwater Biology (since June 2015)
- Visiting professor for Molecular Ecology at University of Hasselt, Belgium (since 2011)
- Principal Investigator at the RBINS (since 2009); post-doc at the RBINS (1997-2008) & Leeds University (1995-1996); Marie Curie (1999-2000) & BASF postdoc (1997-1998) fellow
- More than 200 publications & 1700 citations; h-index Google scholar: 24
- **Schön I.**, Martens K. & Van Dijk P. (eds.) 2009. *Lost sex. The evolutionary biology of parthenogenesis*. 615 pp., 27 chapters and 96 figures. Springer Academic Publishers.
- Relevant projects: **LATTECO** – BRAIN pioneer project (2015-2018), 2 partners, coordinator. **SEXASEX** - EU Marie-Curie Research and Training network (2004-2008; 7 PhD students and 5 Post-docs; 9 European partners); PI for the RBINS.

Phylogenetic and genomic studies of ancient asexual darwinulid ostracods

A few animal groups seem to defy the evolutionary theory that obligate asexuals are doomed to early extinction and limited to the short-lived twigs of the tree of life. These are the so-called ancient asexual scandals. However, ancient asexuality is not easy to prove as most evidence is negative, as for example the absence of males, meiosis and (sexual) recombination. The case of the Darwinulidae (Ostracoda, Crustacea) has been debated for several years (Martens & Schön 2009) but has so far remained inconclusive. Fossil data show that the family might have been asexual for more than 200 million years (myr) (Martens et al. 2003) and the type species, *Darwinula stevensoni*, for at least 20 myr (Straub 1952). However, the discovery of three males (Smith et al. 2006) in one of the c. 30 darwinulid species has cast doubt on the ancient asexual status of this group. The functionality of these males could never be tested and no males have been found since. Therefore, a molecular approach had to be sought for testing the ancient asexual status of the Darwinulidae.

Here, we analyze DNA sequence data from three nuclear regions (two coding genes and ITS) and the mitochondrial COI gene in more than 20 darwinulid species from different localities and habitats around the world. Our dataset also includes the Japanese *Vestalenula cornelia*, the species where the males have been found, and is supplemented by DNA sequence data from sexual ostracods. Applying maximum-likelihood frameworks (PAML) for examining substitution patterns at individual codon sites and data monkey for analyses on a per site basis both reveal elevated dN/dS ratios for two nuclear darwinulid coding genes and darwinulid COI as evolutionary theory would predict for long-term asexuals. We do not find any evidence for the so-called Meselson effect, nor do statistical tests show signatures for recombination within darwinulid species, also not in *V. cornelia*. We also use our DNA sequence data to reconstruct the evolutionary history of the Darwinulidae in a phylogenetic framework.

Because of their small size, limited DNA quantity and distant evolutionary relationship to other crustaceans and arthropods, the application of genomics to darwinulid ostracods has only just started. Constructing a low coverage genomic library of *D. stevensoni* has been a first step. We will present preliminary results of sequencing and analysing selected cosmids (in collaboration with Irina Arkhipova, Woodshole, USA) for retro- and DNA transposons. Comparing different cosmids with homologue single nuclear genes will furthermore provide a first glimpse of the genomic structure of *D. stevensoni*.

Additionally, ongoing genomic projects will be briefly presented: (1) *de novo* transcriptomic and metagenomic analyses of *D. stevensoni* from different geographic populations (Belgian BRAIN pioneer project LATTECO) and (2) *de novo* whole genome sequencing of non-marine ostracods with different reproductive modes (Swiss Sinergia project “Genome evolution under sexual and asexual reproduction”, in collaboration with Tanja Schwander, University of Lausanne).

Nicolas Debortoli, PhD student

Affiliation

University of Namur, LEGE lab

Short CV

I have always been interested in organisms that have chosen alternative strategies to survive and diversify. I have therefore studied biology at the University of Namur (Belgium) and I specialized in molecular ecology and evolution during my master degree. I wrote a master thesis in the Laboratory of Evolutionary Genetics and Ecology (LEGE) about the genetic diversity of the asexual bdelloid rotifers at the local scale. Then, I went to Stanford University for a 5 months internship on dependent-lineage harvester ant populations. My PhD thesis aims at understanding how degenerate tetraploidy and desiccation enable bdelloid rotifers to survive, disperse and diversify in the absence of sexual reproduction. I therefore used several approaches from comparative genomics to population genetics to study (1) the bdelloid communities' spatio-temporal dynamics; (2) understand the mechanisms underlying molecular adaptation and survival of bdelloid rotifers.

Horizontal gene transfers among asexual bdelloid rotifers of the genus *Adineta*

Debortoli N[1,2], Li X[1,2], Tang CQ[3], Hespeels B[1,2], Fontaneto D[4], Flot J-F[5] and Van Doninck K[1,2]

1 University of Namur, Department of Biology, URBE, Laboratory of Evolutionary Genetics and Ecology, 5000 Namur, Belgium

2 Namur Research Institute for Life Sciences (NARILIS), 5000 Namur, Belgium

3 Division of Biology, Imperial College London, Silwood Park Campus, Ascot, Berkshire SL5 7PY, UK

4 Institute of Ecosystem Study, National Research Council, Largo Tonolli 50, 28922, Verbania Pallanza, Italy

5 Max Planck Institute for Dynamics and Self-Organization, Biological Physics and Evolutionary Dynamics, Bunsenstraße 10, 37073 Göttingen, Germany

Bdelloid rotifers have survived and diversified into more than 400 morphospecies over the past 40 My through asexual reproduction. The first genomic data suggested that chromosome pairing, and thus conventional meiosis, is impossible within the bdelloid rotifer *Adineta vaga*. Hence, their persistence and diversification as ancient asexuals is puzzling and suggest that they have developed alternative mechanisms to evolve and diversify. Moreover, the genome of *A. vaga* comprises 8-10% of genes of putative non-metazoan origin, indicating that horizontal transfers are frequent within this group and may eventually promote exchanges among bdelloid individuals as well. Using a population genetic approach combining nuclear and mitochondrial markers, distinct species delineation methods (GMYC and Haplowebs) and genomics, we demonstrate for the first time inter-individual genetic transfers within a bdelloid rotifer lineage.

Our results indicate the existence of 6 distinct species in which individuals reproduce clonally. However, two distinct patterns suggesting inter-individual genetic transfers were observed: (1) seven individuals were assigned to different species depending on the marker considered and (2) three cycles of allele-sharing in a [A||B, B||C, C||A] fashion were reconstructed. Comparison of genomic regions of three allele-sharing individuals further revealed signatures of genetic exchanges and gene conversion, scattered among regions evolving asexually. Our hypothesis is that desiccation could promote horizontal gene transfers since it occurs frequently in the semi-terrestrial habitats bdelloids inhabit, and during prolonged desiccation DNA double-strand breaks accumulate that are repaired upon rehydration. However, additional data need to be obtained to totally exclude forms of non-meiotic recombination such as parasexuality or some other unknown mechanism.

Dr. Etienne GJ Danchin

Affiliation

Institut Sophia Agrobiotech, INRA,
Universté Côte d'Azur,
CNRS,
400 route des Chappes,
06903, Sophia Antipolis,
France.

Short CV

Current position: I am an INRA senior scientist in the laboratory of plant-nematode interactions, in Sophia Antipolis, France. As a principal investigator, I lead the researches in the domain of comparative and evolutionary genomics of plant-parasitic nematodes.

Background: After a PhD in bioinformatics, in which I studied evolutionarily conserved genome regions across bilaterian animals, I annotated and compared fungal genomes for their repertoires of carbohydrate-active enzymes. The aim was to correlate repertoire of enzymes with the ecology and life style of the fungi.

Scientific production: I currently have 56 accepted publications in peer-reviewed journals, including 3 in Nature, 3 in Nature Biotechnology, 1 in Genome Biology, 1 in Mol Biol Evol and 1 in PNAS. Over the 2004 – 2016 period, my papers received 6,522 citations yielding an h-index of 29.

Hybridization and polyploidy enable genomic plasticity without sex in the asexual root-knot nematodes

Root-knot nematodes (Meloidogyne spp) exhibit a diversity of reproductive modes ranging from obligatory sexual to fully asexual reproduction, with intermediated able to switch between sexual and asexual reproduction. Intriguingly, the most widespread and devastating species to global agriculture are those that reproduce asexually, without meiosis. To disentangle this surprising parasitic success despite the absence of sex and genetic exchanges, we have sequenced and assembled the genomes of three obligatory ameiotic asexual Meloidogyne. We have compared them to those of relatives able to perform meiosis and sexual reproduction. We show that the genomes of ameiotic asexual Meloidogyne are large, polyploid and made of duplicated regions with a high within-species average nucleotide divergence of ~8%.

The genome of the sexual meiotic relative, in contrast, is diploid and does not exhibit duplicated genome regions with high nucleotide divergence. In the ameiotic asexuals, phylogenomic analysis of the genes present in the duplicated regions suggests that they originated from multiple hybridization events and are thus homoeologs. We found that up to 22% of homoeologous genes pairs were under positive selection and these genes covered a wide spectrum of predicted functional categories. To biologically confirm functional divergence, we compared expression patterns of homoeologous gene pairs across developmental life stages using a RNAseq approach in the most economically important asexually-reproducing nematode, *Meloidogyne incognita*. We showed that >60% of homoeologous gene pairs display diverged expression patterns. These results suggest a substantial functional impact of the hybrid genome structure. Contrasting with high within-species nuclear genome divergence, mitochondrial genome divergence between the three ameiotic asexuals was very low, signifying that these putative hybrids share a recent common maternal ancestor. Transposable elements (TE) cover a ~1.7 times higher proportion of the genomes of the ameiotic asexual Meloidogyne compared to the sexual relative and might also participate in their plasticity.

The intriguing parasitic success of asexually-reproducing Meloidogyne species could be partly explained by their TE-rich composite genomes, resulting from allopolyploidization events, and promoting plasticity and functional divergence between gene copies in the absence of sex and meiosis.

Dr. Jens Bast

Affiliation

University of Lausanne
Department of Ecology and Evolution

Short CV

I am a postdoctoral researcher at the University of Lausanne in the group of Tanja Schwander. My interest focuses on the evolution of reproductive modes. I elucidate, if predicted causes and consequences of (a)sexuality are found in nature using mostly genomic tools. Current and previous work involved for example identifying transposable element dynamics in natural and artificial systems and comparing rates of evolution between sexual and asexual species. Since my studies at the University of Göttingen in the animal ecology group of Stefan Scheu I am fascinated by oribatid mites.

Recent insights into ancient asexual mites

The question of why sex is maintained in nature still remains elusive. One possibility to identify the advantages of sexual reproduction over strict asexuality is to investigate the peculiarities that allowed some animal species to exist over evolutionary time without sex. Here, I discuss recent findings and ongoing genomic work on oribatid mites that are a potentially very powerful animal model system.

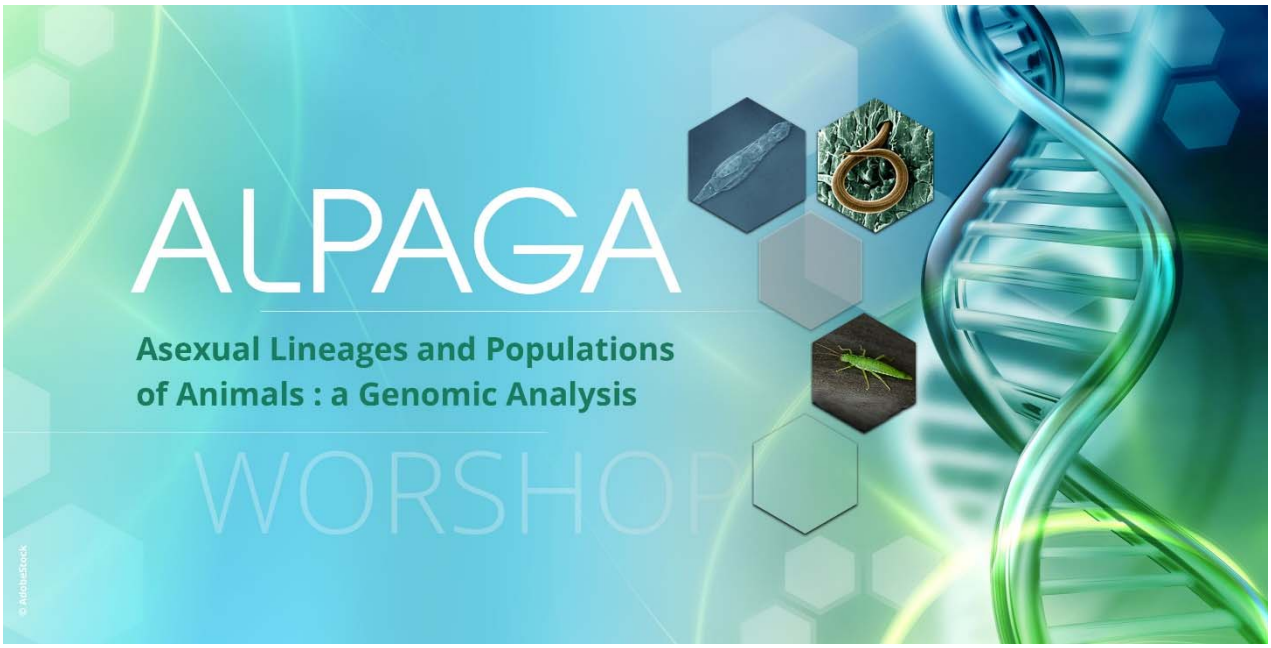
Oribatid mites are small, specious, geographically widespread decomposers that can reach high population densities in forests. Within this group, sex was lost several times up to tens of millions of years ago, followed by extensive radiation of asexual clades. Using these 'evolutionary replicates' we showed that I) transposable elements do not accumulate in asexual arthropods, both in old oribatid mites and other, younger taxa.

Further, we provided evidence that II) purifying selection acts more effectively in asexual oribatid mites as compared to sexuals. I speculate which mechanisms might potentially generate these patterns, but remain to be investigated. Finally, I discuss the problems encountered during the generation of genomic resources of two closely related sex-asex oribatid mite species pairs.

Thursday, March 30th

AGORA room, Business & Learning Center, rue Godefroid, 5

Session 5: New tools to improve the assembly of heterozygous genomes – Chairman: Etienne Danchin	
9h00-9h30	Assembling heterozygous/polymorphic genomes: challenges and solutions **Jean-François Flot** (Université Libre de Bruxelles, BE)
9h30-10h00	BWISE: DBG-guided super-read assembly **Antoine Limasset** (INRIA Rennes, FR)
10h00-10h30	Alienomics **Jitendra Narayan** (Université de Namur, BE)
Coffee – tea break	
11h00-11h30	Oxford Nanopore technology : data and applications **Jean-Marc Aury** (Genoscope, France)
11h30-12h00	Horizontal gene transfer – population genomic approach in bdelloid rotifers – **Marie Cariou** (Université de Namur, BE)
12h-12h20	ALPAGA I: aim and objectives – **Etienne Danchin** (coordinator ALPAGA, INRA – Sophia Antipolis, FR)
12h20-12h40	ALPAGA II: aim and objectives Open discussion on the perspectives of ALPAGA II
Lunch break till 14h30: final discussions and perspectives ALPAGA	



Jean-François Flot, associate professor

Affiliation

Evolutionary Biology & Ecology
Department of Organismal Biology
Université libre de Bruxelles
Belgium

Short CV

University Paris7 – Denis Diderot (France)	BSc	Biochemistry	1998
University Paris7 – Denis Diderot (France)	MSc	Biochemistry	1999
University of the Ryukyus (Okinawa, Japon)	MSc	Marine Sciences	2003
Muséum National d'Histoire Naturelle (France)	PhD	Molecular Systematics	2008

Research interests

Phylogenetics; species delimitation; experimental evolution; genome dynamics; genome evolution; corals; amphipods; rotifers; xenacoelomorphs; coral reefs; groundwaters; "extreme" environments; microbial ecology; biodiversity; symbiosis; evolution of sexuality/asexuality; bioinformatics

Assembling heterozygous / polymorphic genomes: challenges and solutions

One of the main challenges hindering the assembly of non-model organisms is heterozygosity: as most assemblers were designed with the human genome in mind (the heterozygosity of which is a mere 0.1 percent), they often fail when applied to the genomes of species with larger effective population sizes (in which heterozygosity commonly reaches 1 to 6 percents). Solving this problem requires first redefining the assembly problem: should we aim to reconstruct a single haploid sequence or should we rather aim to reconstruct the various haplotypes? The second option is clearly more appealing, as it does not assume that the genome is organized in pairs of colinear homologous chromosomes; besides, comparing the haplotypes among themselves makes it possible to perform "1-genome population genomics" and gain unique insights into the genome dynamics of the organism under scrutiny. Very few programs are able to deal with heterozygous genomes: after reviewing the different options available, I will compare their performance and highlight their respective strengths and limitations.

Antoine Limasset

Affiliation

Université Rennes 1/IRISA/INRIA

Short CV

B.Sc and M.Sc in Computer Science (ENS Cachan and ENS Rennes).
Ongoing PhD in computer Science at Université Rennes 1/IRISA/INRIA on the subject : “New approaches for the exploitation of high throughput sequencing data”.
Working on data structure, De Bruijn graph and graph alignment.
Ongoing project with Jean-Francois Flot on heterozygous assembly.

Assembly of heterozygous genomes with high order De Bruijn graph

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1. Introduction

Heterozygous genome assembly constitutes a complex task for which no satisfying solution exists at the present time. Phasing chromosomes in diploid or polyploid species or in metagenomes is still an open problem, despite the emergence of new long-read technologies and other dedicated approaches. In particular, intraspecies or inter-species variations are usually discarded and/or result in highly fragmented assemblies. Several approaches tried to produce phased contigs using regular or paired-end short reads. On such genomes, String graph approaches like MIRA[1] produce large contigs but are intractable on large genomes. De Bruijn graph approaches (Spades[2], platanus[3], discovarDenovo[4]) are limited to very high or very low heterozygosity rates since they produce unsactisfactory fragmented contigs in the intermediary rates.

2. BWISE, a high order De Bruijn graph assembler

In this work we propose a novel de Bruijn graph-based assembler called BWISE that performs the construction of a very high order De Bruijn graph. This assembly fully takes advantage of read lengths and paired-end relationships between reads. Thereby correct paths are allowed to be determined resolving haplotypes and genomic repeats.

Results on simulated datasets show that BWISE is able to produce order of magnitude longer contigs than state of the art methods on highly heterozygous genomes. We also show that BWISE is comparable to state of the art assemblers for ”regular” haploid genomes, and has the potential to scale up to very large genomes as the human one.

Beyond paired-end reads, the proposed framework allows in principle the integration of long-range information (mate pairs, 3Cseq/Hi-C, 10X, Single Molecule Real-Time (SMRT) as well as Nanopore reads) to determine accurate long paths in the assembly graph, with the ultimate goal of generating a single high-quality contigs per chromosome.

References

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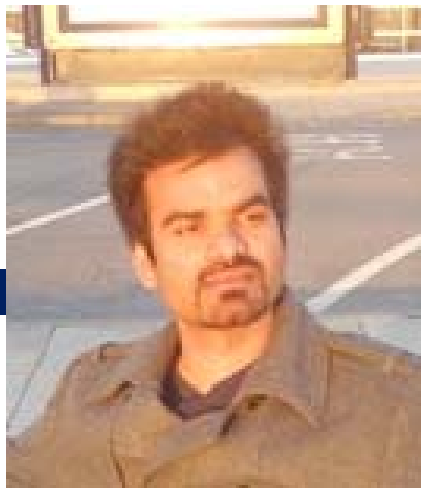
Jitendra NARAYAN, Post-doctoral researcher



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Short CV

2015: PhD in Bioinformatics (AU, UK)
Since Sept 2016- : Postdoc in the laboratory of Prof. Karine Van Doninck, Namur University, Belgium

Keywords:

- Evolutionary genetics,
- Chromosome breakage
- DNA repair and genome dynamics
- Comparative genomics
- Horizontal gene transfer
- evolutionary genomics and adaptation
- Metagenomics, NGS, Synteny

Alienomics v0.1: A parametric tool to distinguish, within assembled genome data, contaminants from horizontally transferred alien genes

Jitendra Narayan, Nicolas Debortoli & Karine Van Doninck

The growing number of genomic data generated for non-model organisms is tremendous but these new datasets are very different from the inbred, haploid model organisms cultured in laboratories. Organisms sampled in the wild cannot always be cultured or washed extensively and therefore are not isolated free of environmental contaminants. Genomic DNA extracted from those samples may include DNA from organisms attached to the individual or recently ingested. This type of problem is also characteristic of metagenomics samples that differ greatly in nucleotide compositional biases. While tools have been developed to filter contaminants or extract subsets of single species genomes from mixed DNA sequences, the difficulty becomes more complex when the target genome contains horizontally transferred genes (HTG).

In order to distinguish in the genomic dataset contaminants from horizontally acquired alien genes, we have developed a post assembly tool “Alienomics” to filter out contigs of contaminants (CC) while keeping contigs of interest with horizontally transferred genes. Gene prediction analysis, similarity searches (megaBLAST scores) and biological indicators (GC%, presence of introns, coverage, taxonomy, rRNA and tetra-nucleotide frequencies) are used to distinguish between CC and HTG. Moreover, a scoring system has been implemented to filter out non-relevant candidates and users can upload their reference genomes or any genome of interest that can improve the filtration process. This tool should rescue error prone and misreported assemblies and report reliable levels of HTG. We tested the tool, still in development, on an in-silico generated sample of contigs with distinct compositions and complexities and show that it outperforms other tools and reliably separated the CC from HTG.

Jean-Marc Aury, Head of a bioinformatic group, Genoscope

Affiliation

CEA/Genoscope, France

Short CV

Jean-Marc Aury is a Genoscope engineer since 2003.

He was focused on eukaryotic genome analysis, and was a main actor of several genome projects, like paramecium, grape, banana, cocoa and oak.

He is now the team leader of a bioinformatics group (23 members) which focusses on data production in the Institut de Génomique, genome assembly and gene prediction in eukaryotic genomes.

Oxford Nanopore technology: data and applications

Oxford Nanopore Technologies Ltd (Oxford, UK) have recently commercialized MinION, a small and low-cost single-molecule nanopore sequencer, which offers the possibility of sequencing long DNA fragments. The Oxford Nanopore technology is truly disruptive and can sequence small genomes in a matter of seconds. It has the potential to revolutionize genomic applications due to its portability, low-cost, and ease of use compared with existing long reads sequencing technologies. The MinION sequencer enables the rapid sequencing of eukaryotic genomes, and combined with existing assembler algorithms, near complete genome assemblies can be generated. Here, we resequenced the genome of the Saccharomyces cerevisiae S288C strain to evaluate the performance of nanopore-only assemblers. Then we de novo sequenced and assembled the genomes of 21 isolates representative of the S. cerevisiae genetic diversity using the MinION platform as well as larger eukaryotic genomes.

Marie Cariou,
Post-doctoral researcher

Affiliation

University of Namur

Short CV

During my PhD at the University of Lyon, under the supervision of Sylvain Charlat and Laurent Duret (2011-2015), I studied the impact of an endocellular bacteria, Wolbachia, on the evolution of its Arthropod hosts.

More specifically, I looked for effects of these maternally transmitted symbionts on host mitochondrial genomes, to which they are linked within the cytoplasm, at a global scale, among hundreds of species from French Polynesia.

Since september 2015, I work as a Post-doctoral researcher at the University of Namur, with Pr. Karine van Doninck, on the evolution of Bdelloid rotifers genomes. My project focuses on the detection and quantification of horizontal tranfers within and between species. I am generally interested in studying the evolution of genomes and on processes that shape this evolution at the scale of populations and species.

Species tree, frequent HGT and gene conversions in Bdelloid Rotifers

The vast majority of animals reproduce sexually, i.e. with recombination of genetic material between generations. This genetic mixing is thought to favor the persistence of sexual lineages despite a theoretical advantage of asexuals regarding colonization capacity and population growth. In this context Bdelloid Rotifers, a highly diversified group of animals evolving asexually for millions of years, appears as a puzzle but also as an outstanding model to better understand long-term evolution in the absence of sexual reproduction.

The sequencing of the first Bdelloid Rotifer genome (Flot et al. 2013) revealed a peculiar organization, characterized by a degenerate tetraploidy, numerous rearrangements and the absence of homologous chromosomes. This structure, incompatible with meiosis, likely testifies the long asexual evolution of this genome. Besides, population genetic studies suggest that Bdelloids might exchange DNA within and between species, which likely plays a major role in their evolutionary history (Debortoli et al. 2016).

To better understand the dynamics of gene conversion and horizontal genetic transfers on these asexually evolving genomes and their importance in the success of Bdelloids, we are generating genomic data (RAD sequencing) from a large number of species distributed across the four existing families. We will show how methods involving the reconciliation of gene and species trees can help resolving species phylogeny of Bdelloids despite asexuality, polyploidy, gene conversions, transfers and losses. The resolution of the species tree is indeed a requirement for further study of the dynamics of horizontal transfers, which might play a key role in their evolution.

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Short CV

Current position: I am an INRA senior scientist in the laboratory of plant-nematode interactions, in Sophia Antipolis, France. As a principal investigator, I lead the researches in the domain of comparative and evolutionary genomics of plant-parasitic nematodes.

Background: After a PhD in bioinformatics, in which I studied evolutionarily conserved genome regions across bilaterian animals, I annotated and compared fungal genomes for their repertoires of carbohydrate-active enzymes. The aim was to correlate repertoire of enzymes with the ecology and life style of the fungi.

Scientific production: I currently have 56 accepted publications in peer-reviewed journals, including 3 in Nature, 3 in Nature Biotechnology, 1 in Genome Biology, 1 in Mol Biol Evol and 1 in PNAS. Over the 2004 – 2016 period, my papers received 6,522 citations yielding an h-index of 29.

ALPAGA I: aims and objectives

Here I will briefly present the ALPAGA-I project (for Asexual Lineages and Populations of Animals: a Genomic Analysis). This project's main aim is to characterize animal genome evolution in the absence of sex and identify genomic features of asexually-reproducing animals that may allow them to compete with their sexual relatives and / or persist over evolutionary times, without the benefits of sex. We will compare the genomes of asexual and sexual species lineages across different animal clades to identify singularities associated to an asexual mode of reproduction. The three animal clades selected for ALPAGA I are the root-knot nematodes, the rotifers and the stick insects. Each of these groups of animals comprise asexually-reproducing species as well as sexual relatives.

The preliminary goal of the project is to generate high quality reference genomes for asexual animals as well as their sexual relatives. For this, we will use a hybrid approach, combining 3rd generation sequencing technology to obtain long reads and 2nd generation sequencing to correct errors and reach high genome coverage. We will also use Pool-seq and RAD-seq approaches on different populations and isolates of sexual and asexual species to measure variations within and between the samples. This sequencing effort is a prerequisite to be able to address the main work packages of the project. Briefly, in ALPAGA-I we will study the levels of heterozygosity and rates of gene conversion, the prevalence of horizontal gene transfers, the load of transposable elements and their mobility, gene copy number variations as well as the possible functional consequences associated to these mechanisms of genomic plasticity. In the framework of this project we will have the occasion to compare different lineages of animals that have developed the ability to survive without sex and at different times.

ALPAGA II: AIMS AND OBJECTIVES

Open discussion on the perspectives of ALPAGA

List of participants

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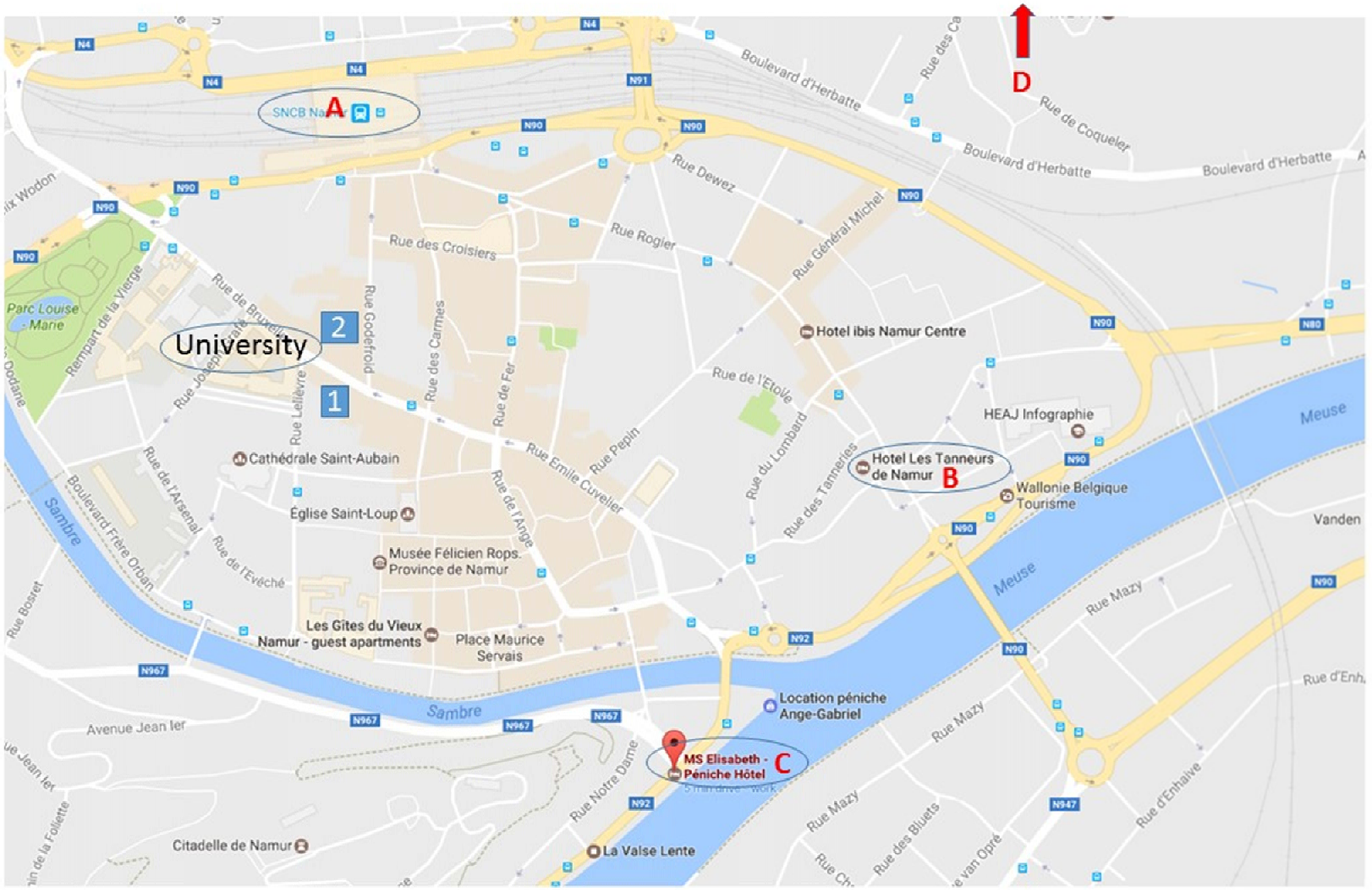

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B: Hotel Les Tanneurs

C: Boat (Ms Elisabeth)

D : B&B
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ALPAGA Workshop venues

1: ADRE, NARC room
Rue de Bruxelles, 55
On 28 March

2: Business & Learning Center
Rue Godefroid, 5
On 29 & 30 March

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