



## 22<sup>nd</sup> national congress on transposable elements

July 8-10, 2019

Lyon

### Organizing committee

Fabienne Rogowsky (IGFL, ENS de Lyon)

Frédéric Brunet (IGFL, ENS de Lyon)  
 Nelly Burlet (LBBE, UCBL1)  
 Marie Fablet (LBBE, UCBL1)  
 Zofia Haftek-Terreau (IGFL, ENS de Lyon)  
 Annabelle Haudry (LBBE, UCBL1)  
 Cristina Vieira (LBBE, UCBL1)  
 Jérémy Just (RDP, ENS de Lyon)  
 Emmanuelle Lerat (LBBE, UCBL1)  
 Rita Rebollo (INRA/INSA)

### Gestion

Fatiha Berriche Doudou (IGFL, ENS de Lyon)  
 Aurélie Hazan (DR7, CNRS Villeurbanne)

### Scientific committee:

Mohammed Bendahmane (RDP, ENS de Lyon)  
 Matthieu Boulesteix (LBBE, UCBL1)  
 Frédéric Brunet (IGFL, ENS de Lyon)  
 Marie Fablet (LBBE, UCBL1)  
 Annabelle Haudry (LBBE, UCBL1)  
 Cristina Vieira (LBBE, UCBL1)  
 Jérémy Just (RDP, ENS de Lyon)  
 Emmanuelle Lerat (LBBE, UCBL1)  
 François Mallet (HCL\_Biomérieux)  
 Magali Naville (IGFL, ENS de Lyon)  
 Rita Rebollo (INRA/INSA)  
 Jean-Nicolas Volff (IGFL, ENS de Lyon)

#CNET2019

Lyon, July 2019

To all CNET participants,

We welcome you to the 22<sup>nd</sup> national conference on transposable elements in Lyon. We hope you will enjoy the seminars, scientific discussions and of course, Lyon. This is the 22<sup>nd</sup> time the French community gathers to discuss all aspects of TE biology and their impact on host genomes. We are planning to submit a small meeting report to Mobile DNA, including a brief historical view of the CNET. For this, we would like to build a French TE graphical network in order to show how the TE community came to be in France. Hence, could you please fill in your own information on the spreadsheet accessible through the QR code below. You only need to write down your name, the name of your PhD supervisor and your post-doc supervisor. One row per interaction. We only ask you to write down the interactions that are TE related.

Thank you very much for your time, enjoy the conference,

The organizing committee



*First attempt at a TE network*

# Schedule

Monday, July 8<sup>th</sup> 2018

**12:00 – 13:30**    **Lunch buffet & Participant registration**

**13:30 – 13:40**    **Welcome remarks**

**13:40 – 17:30**    **Session #1 – Chair : Emilie Brasset**

- ✚ 13:40 – 14:30. Transcriptional control of immune-responsive genes by DNA methylation and demethylation and its relevance in antibacterial defense. **Invited speaker: Lionel Navarro** (Institut de Biologie de l'Ecole Normale Supérieure, Paris, France).
- ✚ 14:30 – 14:50. Ty1 integrase bipartite nuclear localization signal promotes retrotransposon targeting to tRNA genes. **Amna Laidin** (Institut de Recherche Hôpital St. Louis, Paris, France).
- ✚ 14:50 – 15:10. An indirect Regulation of LINE-1 elements by miRNAs in mouse embryonic stem cells. **Constance Ciaudo** (Institute of Molecular Health Sciences, ETH, Zurich, Suisse).

**15:10 – 16h10**    **Coffee Poster session**

- ✚ 16:10 – 16:30. The NuRD subunits mediate piRNA-guided heterochromatin formation in metazoans. **Séverine Chambeyron** (Institute of Human Genetics, Montpellier, France).
- ✚ 16:30 – 16:50. Trapping a somatic endogenous retrovirus into a germline piRNA cluster immunizes the germline against further invasion. **Marianne Yoth** (Genetics reproduction and development, Clermont-Ferrand, France)
- ✚ 16:50 – 17:10. Modes of somatic genome alterations by mobile elements in adult intestinal stem cells. **Kasia Siudeja**. (Institut Curie, Paris, France).
- ✚ 17:10 – 17:30. Insertional mutagenesis using TC1-mariner transposon impala is influenced by chromatin modifications in the wheat fungal pathogen *Zymoseptoria tritici*. **Marc-Henri Lebrun** (Biologie Gestion des Risques en agriculture, Thiverval-Grignon, France).

Tuesday, July 9<sup>th</sup> 2019

**9:00 – 12:10**    **Session #2 – Chair : Severine Chambéryon**

- ✚ 9:00 – 9:50. The rapid evolution of small RNA pathways and DNA methylation targeting transposons in arthropods. **Invited speaker: Frank Jiggins** (Dpt. of Genetics, Cambridge University, Cambridge, UK).
- ✚ 9:50 - 10h10. Repeat sequences in genome organization. **Geneviève Fourel** (Laboratoire de biologie et modélisation de la cellule, Lyon, France).
- ✚ 10:10 – 10h30. Role of transposable elements in the control of sexual genes in teleost fish. **Corentin Dechaud** (Institut de génomique fonctionnelle de Lyon, Lyon, France).

**10:30 – 11h10**    **Coffee Poster session**

- 🚦 11:10 – 11:30. TBD
- 🚦 11:30 – 11:50. Distribution and evolution of Tc1-mariner superfamily in plants. **Maryem Bouallegue** (Laboratoire Biochimie et Biotechnologie, Tunis, Tunisie).
- 🚦 11h50 - 12h10. Exploratory analysis of transposable element expression in mouse early embryo. **Federico Ansaloni** (International School for Advanced Studies, Trieste, Italy)
- 🚦 12h10 - 12h30 : New England Biolabs. **Morgane Moreau & Nicolas Doll**.

**13:00 – 14:00** Lunch Break CROUS Descartes

**14:00 – 17:00** Session #3. Chair: Anna-Sophie Fiston-Lavier

- 🚦 14:00 – 14:50. Living with a million-year long infection. **Invited speaker: George Kassiotis** (The Francis Crick Institute, London, UK).
- 🚦 14:50 – 15:10. Insertion sequence massive expansion, gene expression and pseudogenization: insights into the transcriptome of the rice weevil's primary endosymbiont *Sodalis pierantonius*. **Mariana Ferrarini** (BF2i, INRA/INSA de Lyon, Lyon, France)
- 🚦 15:10 – 15:30. Characterizing the host range of SXT ICEs, vectors of antibiotic resistance genes in aquatic environments, by the innovative approach of epicPCR. **Xavier Bellanger** (Laboratoire de Chimie Physique et Microbiologie pour les Matériaux de l'Environnement, Villers-les-Nancy, France)
- 🚦 15:30 – 15:50. Transposable element domestication in Vertebrates: Functional and evolutionary study of a gene family derived from Harbinger transposons. **Ema Etchegaray** (Institut de génomique fonctionnelle de Lyon, Lyon, France).

**15:50 – 16:20** Coffee Poster session

**16:20 – 18:00** Session #4. Chair: Aurélie Hua Van

- 🚦 16:20 – 16:40. Hominoid-specific regulatory sequences and their controllers shape human genome regulation. **Julien Pontis** (Ecole polytechnique fédérale de Lausanne, Lausanne, Suisse)
- 🚦 16:40 – 17:00. Tc1/mariner phylogeny and the unexplored world of pogo elements. **Mathilde Dupeyron** (Center for ecology and conservation, University of Exeter, Cornwall, United Kingdom).
- 🚦 17:00– 17:20. The role of Piwi pathway genes and histone modification in transposable element misregulation of *Drosophila* hybrids. **Maria Pilar Garcia Guerreiro** (Universitat Autònoma de Barcelona, Barcelona, Spain)

**18:00 – 19:30** Guided tour ***Le vieux Lyon et ses traboules***. Meeting point at Métro Vieux Lyon (av. Adolphe Max 69005)

**19:30 – 23:00** Gala dinner (Sainte Russie, 12 rue de la Juiverie, 69005)

Wednesday, July 10th 2019

**9:30 – 12:40** Session #5 – Chair : Pili Garcia Guerreiro

- 🚦 09:30 – 10:20 The role of natural transposable element insertions in stress response. **Invited speaker: Josefa Gonzalez** (Instituto de Biología Evolutiva, Barcelona, Spain)

- ✚ 10:20 – 10:40. Transposable element distribution along high-quality chromosome-level assembly reveals recent rose genome history. **Jeremy Just** (Laboratoire Reproduction et Développement des Plantes, Lyon, France)
- ✚ 10:40 – 11:00. Genomic impact of TEs in *Oryza*. **Oliver Panaud** (Laboratoire de Génome et Développement des Plantes, Perpignan, France)

**11:00 – 11:20** Coffee

- ✚ 11:20 – 11:40. Transposable elements found in conserved noncoding elements of *Drosophila* genome. **Annabelle Haudry** (Laboratoire de Biométrie et Biologie Evolutive, Lyon)
- ✚ 11:40 – 12:00. Investigating the effects of genomic transposable element proliferation on diversification rates of Corydoradinae catfishes. **Ellen Bell** (University of East Anglia, Norwich, United Kingdom)
- ✚ 12:00 – 12:20 The siRNA and piRNA pathways interplay and modulate transposable element transcription upon viral infection in *Drosophila*. **Marie Fablet** (Laboratoire de Biométrie et Biologie Evolutive, Lyon, France)

**12:20 – 12:30** Awarding prizes, summary and closing address

**13:00 – 14:00** Lunch Break CROUS Descartes

**14:00** Start of the 1<sup>st</sup> Mobil-ET bioinformatic days

## Poster presentation

- ✚ Misexpression of genes and transposable elements in *Drosophila arizonae* and *D. mojavensis* hybrids. **Cecilia Artico Banho**, Claudia Carareto, Cristina Vieira.
- ✚ Transposable Elements as agents of adaptation in the invasive species *Drosophila sukuii*? **Vincent Mérel**, Marie Fablet, Matthieu Boulesteix, Arnaud Estoup, Patricia Gibert, Cristina Vieira
- ✚ The evolutionary depth of Sireviruses transposable elements in plants. **Julie DAZENIERE**, Alexandros Bousios.
- ✚ Assessing the potential roles of DNA methylation in the excision of Internal Eliminated Sequences in the ciliate *Paramecium tetraurelia*. **Suzanne Marques**, Eric Meyer.
- ✚ Comparative Analysis of Transposable Element Dynamics and Gene Association Preference in Aphids. **Tobias Baril**, Alex Hayward, Mathilde Dupeyron, Chris Bass, Kumar Saurabh Singh
- ✚ How to deal with environmental changes: molecular characterization of mechanisms on invasive species model. **Pierre Marin**.
- ✚ Optimizing the de novo annotation of transposable elements in large, TE-rich genomes. **Maud Fagny**, Véronique Jamilloux, Johann Joets, Clémentine Vitte.
- ✚ Transposable element dynamics and regulation in a major crop pest: *Sitophilus oryzae*. **Caroline Blanc**, Théo Chancy, Agnès Vallier, Séverine Balmand, Clément Goubert, Mariana Galvao Ferrarini, Elisa Dell'Aglio, Nicolas Parisot, Abdelaziz Heddi, Cristina Vieira, Rita Rebollo.

- ✚ The epigenetic and evolutionary importance of palindromic motifs in the regulatory region of LTR retrotransposons. **Elias Primetis**, Alexandros Bousios.
- ✚ High frequency horizontal transfer in Jockey families (Order LINE) in Drosophilids. **Izabella Tambones**, Annabelle Haudry, maryanna simao, Claudia Carareto.
- ✚ Transcriptional abundance and diversity of transposable elements within a species rich group of armoured catfish (Corydoradinae). **Christopher Butler**, Ellen Bell, Tracey Chapman, Martin Taylor.

---

# Transcriptional control of immune-responsive genes by DNA methylation and demethylation and its relevance in antibacterial defense

Lionel Navarro

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

## Abstract

In plants, small non-coding RNAs can guide DNA methylation of transposable elements (TEs) as well as repeat. This phenomenon is referred to as RNA-directed DNA methylation (RdDM) and contributes to the transcriptional repression of some developmentally and stress-regulated genes that carry TE-derived repeats in their vicinity. We have previously shown that the RdDM pathway negatively regulates the Arabidopsis immune response raised against a phytopathogenic *Pseudomonas syringae* strain. Accordingly, we have identified a subset of defense genes that are targeted and repressed by RdDM, presumably to prevent trade-off effects that would be caused by their constitutive expression and/or sustained induction. Some of these genes are also concomitantly demethylated in their promoters through an active DNA demethylation process, which often targets TE/repeat-boundaries. The latter process ensures the rapid and pervasive induction of these defense genes upon pathogen detection. Here, I will present the extent to which the Arabidopsis active demethylase ROS1 reprograms the Arabidopsis transcriptome during antibacterial defense. I will also report on the detailed mechanisms by which ROS1 facilitates the transcriptional activation of specific immune receptors. Finally, I will provide evidence that modulation of active demethylation activity is essential to fine-tune the plant immune response in nature, presumably to promote adaptation to specific environment.

---

# Ty1 integrase bipartite nuclear localization signal promotes retrotransposon targeting to tRNA genes

Amna Laidin<sup>\*1</sup>, Christine Conesa<sup>2</sup>, Camille Grison<sup>1</sup>, Indranil Adhya<sup>2</sup>, Amandine Bonnet<sup>1</sup>, Rachid Menouni<sup>1</sup>, Hélène Fayol<sup>1</sup>, Noé Palmic<sup>1</sup>, Joël Acker<sup>2</sup>, and Pascale Lesage<sup>1</sup>

<sup>1</sup>Genome and Cell Biology of Diseases – Institut de Recherche Hôpital St. Louis, INSERM U944, CNRS UMR 7212, Université Paris Diderot Sorbonne Paris-Cité – 1 Avenue Claude Vellefaux, 75475 Paris cedex 10, France

<sup>2</sup>Biologie des Génomes – I2BC, Université Paris-Saclay, CNRS, CEA UMR 9198, Bât. 430, F-91405 Orsay – Bâtiment 21, 1 avenue de la Terrasse, 91198 Gif/Yvette cedex, France

## Abstract

Long terminal repeat (LTR) retrotransposons are genomic parasites related to retroviruses and contribute to host genome stability, expression and evolution. The Ty1 LTR retrotransposon of budding yeast preferentially integrates upstream of RNA polymerase III (Pol III)-transcribed genes. This targeting requires an interaction between the AC40 subunit of Pol III and Ty1 integrase (IN1). Here, we show that AC40-IN1 interaction depends on a short motif in IN1 bipartite nuclear localization signal (NLS). Single amino acid mutations in this motif compromise IN1 recruitment at Pol III-transcribed genes and Ty1 integration preference for these genes. When IN1 NLS is introduced in the Ty5 retrotransposon in place of the sequence responsible for Ty5 targeting into heterochromatin, Ty5 targets Pol III-transcribed genes. This work reveals that IN1 NLS can provide Ty1 integration site selection to another retroelement.

**Keywords:** retrotransposon, Ty1, Integration targeting, RNA polymerase III

---

<sup>\*</sup>Speaker



---

# An indirect Regulation of LINE-1 elements by miRNAs in mouse embryonic stem cells

Rajika Arora , Maxime Bodak , Jian Yu , and Constance Ciaudo\*<sup>1</sup>

<sup>1</sup>Institute of Molecular Health Sciences ETH (IMHS ETH) – HPL G 32.1 Otto-Stern-Weg 7 CH-8093 Zurich, Switzerland

## Abstract

Mechanisms regulating LINE-1 transposition include DNA methylation in somatic cells and Piwi-interacting RNA (piRNA) pathway in the germline. During the blastocyst stage of mouse embryonic development however, both these pathways are inactivated leading to a critical window necessitating alternate means of L1 regulation. We previously observed an increase in L1 transcript and protein levels in mouse embryonic stem cells (mESCs) deprived of microRNAs (miRNAs). Curiously, the fold change in L1 expression levels in the miRNA KO mESCs did not translate into a similar increase in transposition rates, suggestive of an extra layer of regulation in keeping these mobile elements in check. Analysis of AGO2 CLIP-seq data from mESCs did not reveal a direct interaction between miRNAs and L1 mRNA, suggesting an indirect regulation of L1 expression by one or several miRNA target genes. Integrative analysis of transcriptomic and proteomic data from several miRNA mutant mESCs reported a consistent upregulation of the RNA helicase MOV10, a known regulator of L1 mRNA stability in cancer. We were able to demonstrate that Mov10 is directly regulated by miRNAs. Moreover, upon miRNAs depletion MOV10 is relocalized in the cytoplasm of mESCs, where it interacts with L1 RNA and protein to create L1-RNP condensates. Interestingly, unlike in cancer cells, these L1-RNP condensates do not appear to be stress granules (SGs), P-bodies or autophagosomes. In addition, while accumulation of L1 RNP and MOV10 in condensates is not a consequence of L1 mRNA upregulation, over-expressing MOV10 by transient transfection along with L1 mRNA upregulation leads to *de novo* condensate formation. On the other hand, siRNA mediated knockdown of MOV10 in *Dicer*-KO cells causes dissolution of L1-RNP condensate formation. We are currently investigating the molecular composition of these condensates and their role in regulating retrotransposition.

**Keywords:** LINE, 1, RNA interference, mouse embryonic stem cells, microRNAs

---

\*Speaker

---

# The NuRD subunits mediate piRNA-guided heterochromatin formation in metazoans

S  verine Chambeyron<sup>\*1</sup>

<sup>1</sup>IGH CNRS Montpellier University – IGH UMR9002 – 141 rue de la Cardonille 34396 Montpellier, France

## Abstract

In eukaryotes, trimethylation of lysine 9 on histone H3 (H3K9me3) is associated with the transcriptional silencing of transposable elements (TEs). In *Drosophila* ovaries, this heterochromatic repressive mark is thought to be deposited on TE genomic loci after the initial recognition of their nascent transcripts by PIWI-interacting RNAs (piRNAs) that guide a piRNA-induced transcriptional silencing (piRITS) nuclear complex the composition and mechanisms of action of which are still elusive. Here, we identify chromatin factors as part of the piRITS complex in *Drosophila*. We show that the piRNA-dependent H3K9me3 deposition by the Eggless/SetDB1 histone methyltransferase requires at least three Nucleosome Remodeling and histone Deacetylase (NuRD) subunits. Moreover, we found that the mouse NuRD subunit CHD5 also interacts with the MIWI2 PIWI protein in mouse embryonic testes, suggesting a conserved mechanism for the repressive role of NuRD in metazoan piRITS complexes.

**Keywords:** piRNA, heterochromatin, transposable element

---

<sup>\*</sup>Speaker

---

# Trapping a somatic endogenous retrovirus into a germline piRNA cluster immunizes the germline against further invasion

Marianne Yoth<sup>\*†1</sup>, Céline Duc<sup>2</sup>, Silke Jensen<sup>1</sup>, Nolwenn Mounié<sup>3</sup>, Casey M. Bergman<sup>4</sup>,  
Chantal Vaury<sup>1</sup>, and Emilie Brasset<sup>‡1</sup>

<sup>1</sup>GReD, Université Clermont Auvergne, – GReD UMR CNRS 6293, INSERM U1103 – Faculté de Médecine, 63000 Clermont-Ferrand, France., France

<sup>2</sup>UFIP UMR-CNRS 6286, Epigénétique: prolifération et différenciation – UFIP UMR-CNRS 6286 – Faculté des Sciences et des Techniques, 2 rue de la Houssinière 44322 Nantes, France

<sup>3</sup>GReD, Université Clermont Auvergne, – GReD UMR CNRS 6293, INSERM U1103 – Faculté de Médecine, 63000 Clermont-Ferrand, France

<sup>4</sup>Department of Genetics and Institute of Bioinformatics, – University of Georgia, 120 E. Green St., Athens, Georgia, 30602, USA., Georgia

## Abstract

### Background

For species survival, the germline must faithfully transmit genetic information to the progeny. Transposable elements (TEs) constitute a significant threat to genome stability due to their mobility. In the metazoan germline, their mobilization is limited by a class of small RNAs called PIWI-interacting RNAs (piRNAs) produced by dedicated genomic loci called piRNA clusters. Although the piRNA pathway is an adaptive genomic immunity system, it remains unclear how the germline gains protection from a new transposon invasion.

### Results

To address this question, we analyze *Drosophila melanogaster* lines harboring a deletion within flamenco, a major piRNA cluster specifically expressed in somatic follicular cells. This deletion leads to derepression of the retrotransposon ZAM in the somatic follicular cells and subsequent germline genome invasion. In this mutant line, we identify de novo production of sense and antisense ZAM-derived piRNAs that display a germinal molecular signature. These piRNAs originated from a new ZAM insertion into a germline dual-strand piRNA cluster and silence ZAM expression specifically in germ cells. Finally, we find that ZAM trapping in a germinal piRNA cluster is a frequent event that occurs early during the isolation of the mutant line.

### Conclusions

---

<sup>\*</sup>Speaker

<sup>†</sup>Corresponding author: Marianne.YOTH@uca.fr

<sup>‡</sup>Corresponding author: emilie.brasset@uca.fr

Transposons can hijack the host developmental process to propagate whenever their silencing is lost. Here, we show that the germline can protect itself by trapping invading somatic-specific TEs into germline piRNA clusters. This is the first demonstration of "auto-immunization" of a germline endangered by mobilization of a surrounding somatic TE.

**Keywords:** Transposable elements, piRNAs, piRNA cluster, genome stability, inheritance, *Drosophila*, germline

---

# Modes of somatic genome alterations by mobile elements in adult intestinal stem cells

Kasia Siudeja<sup>\*1</sup>, Marius Van Den Beek<sup>1</sup>, Nick Riddiford<sup>1</sup>, and Allison Bardin<sup>†1</sup>

<sup>1</sup>Institut Curie – Institut Curie UMR 3215/ U934 – 26 rue d’Ulm - 75005 Paris, France

## Abstract

Transposable elements (TE) are a threat to the stability of genomes in which they reside. Although activation of transposons has been linked with aging and numerous diseases, relatively little is known about the real contribution of the mobile genome to somatic genetic variation and its potential effects on somatic cells and tissues. Recent work aimed to identify somatic TE insertions mostly focused on the nervous system and showed conflicting results likely due to technical limitations in detecting rare somatic variants.

Using our recently established model system, whole genome sequencing approaches and stringent bioinformatics analysis we find strong evidence for frequent involvement of transposable elements in somatic genetic variation in the adult *Drosophila* intestinal stem cells (ISCs). De novo somatic insertions are detected along the genome frequently affecting coding regions, including genes relevant for stem cell and tissue physiology. Furthermore, TE insertions are found at breakpoints of somatic structural variants (deletions, translocations, duplications) and TE sequences mediate Non-Allelic Homologous Recombination leading to genomic deletions.

Thus, we reveal complex mechanisms by which the somatic mobile genome contributes to genetic instability of adult stem cells. Moreover, using this model system, we are currently dissecting the mechanisms that protect stem cells genomes from the somatic transposition.

**Keywords:** somatic transposition, *Drosophila*

---

<sup>\*</sup>Speaker

<sup>†</sup>Corresponding author: [allison.bardin@curie.fr](mailto:allison.bardin@curie.fr)

---

# Insertional mutagenesis using TC1-mariner transposon *impala* is influenced by chromatin modifications in the wheat fungal pathogen *Zymoseptoria tritici*

Marc-Henri Lebrun<sup>\*1</sup>, Anais Pitarch<sup>1</sup>, Camille Delude<sup>2</sup>, Marie Dufresne<sup>3</sup>, and Gabriel Scalliet<sup>2</sup>

<sup>1</sup>BIOlogie GEstion des Risques en agriculture (BIOGER) – Institut National de la Recherche Agronomique : UMR1290, AgroParisTech – Campus AgroParisTech BP01 F-78850 Thiverval-Grignon, France

<sup>2</sup>Syngenta Crop Protection AG (Syngenta) – CH-4332 Stein,, Switzerland

<sup>3</sup>Institut des Sciences des Plantes de Paris-Saclay (IPS2) – Institut National de la Recherche Agronomique : UMR1403, Université Paris-Sud - Paris 11, Université Paris Diderot - Paris 7, Université d'Évry-Val-d'Essonne, Centre National de la Recherche Scientifique : UMR9213 – Institute of Plant Sciences - Paris-Saclay Bâtiment 630, rue de Noetzelin Plateau du Moulon - Gif-sur-Yvette Cedex, France

## Abstract

A novel tool for insertional mutagenesis in *Zymoseptoria tritici* was developed using fungal *TC1-mariner* transposon *impala*. ATMT excision vectors containing an autonomous copy of *impala* inserted in the promoter of *A. nidulans* nitrate reductase gene were constructed, and introduced in a *Z. tritici* Nial<sup>-</sup> mutant. We selected a transformant with an *impala* vector inserted in chromosome 1. *impala* excision events were selected by recovering nitrate-utilizing revertants. Most revertants (80%) had a single copy of *impala* inserted at a new genomic location. *impala* was inserted in all core chromosomes without "hot spots", but displayed a preference for chromosome 1 (40% of insertions). This bias is likely due to preferential insertion of *impala* on the same chromosome as donor copy. *impala* was rarely inserted in accessory chromosomes (1/10 of expected insertions). Similarly, we found only few insertions of *impala* in native transposons (1%), although they are abundant (24%). At the gene level, *impala* preferentially inserted near transcriptional start sites (TSS, 72%) of expressed genes. Since accessory chromosomes and transposons are characterized by their enrichment in repressive chromatin marks, we hypothesized that *impala* insertion pattern could be influenced by chromatin modifications. *Z. tritici* histone deacetylases were inhibited with trichostatin A (TSA) to open chromosomal regions with hypo-acetylated histone repressive marks. TSA increased *impala* excision rate (2-fold), as well as the frequency of insertions in native transposons (5-fold). In addition, TSA abolished the bias toward insertions in chromosome 1. However, TSA did not increase the insertion rate of *impala* in accessory chromosomes. These experiments showed that inhibition of histone deacetylases modified *impala* insertion pattern, suggesting that its insertion is dependent on chromatin status of its target site. Overall, *impala* is active in *Z. tritici*. Its integration bias toward promoter/TSS of expressed genes makes it suitable for insertional mutagenesis.

---

<sup>\*</sup>Speaker

**Keywords:** TC1, mariner, insertion pattern, chromatin, mutagenesis, fungi

---

# The rapid evolution of small RNA pathways and DNA methylation targeting transposons in arthropods

Frank Jiggins

Dpt. of Genetics, Cambridge University, Cambridge, UK

## Abstract

In the *Drosophila* germline, small RNA molecules termed PIWI-interacting RNAs (piRNAs) silence transposable elements (TEs), protecting the germline from genomic instability and mutation. In the soma, TEs are silenced by another class of small RNAs called siRNAs. We have found that this difference between the germline and soma is a recent evolutionary quirk of *Drosophila*, and analysis of 20 species across the arthropod phylum suggests that somatic piRNAs targeting TEs and messenger RNAs are common among arthropods. The presence of an RNA-dependent RNA polymerase in chelicerates (horseshoe crabs, spiders and scorpions) suggests that arthropods originally used a plant-like RNA interference mechanism to silence TEs. In mammals and plants, cytosine methylation plays an important role in silencing TEs. This DNA methylation machinery is missing from *Drosophila*, but in other arthropods TEs are targeted by methylation.



---

# Repeat sequences in genome organization

Raphaël Mourad , Magali Naville , Cédric Vaillant , Nikita Vassetzky , Claire Vourch ,  
Eric Gilson , and Geneviève Fourel\*<sup>1</sup>

<sup>1</sup>INSERM (INSERM) – ENS de Lyon – ENS DE LYON LBMC CNRS UCBL UMR 5239 U 1210  
Équipe Gandrillon 46 Allée d'Italie 69007 LYON, France

## Abstract

There has been growing awareness over the past three decades that gene regulation in Eukaryotes largely depends on genome organization in the nucleus. Partitioning of genomes into an active and a repressed fraction, called euchromatin and heterochromatin, are prominent features of all Eukaryotes. The latter appears more compact in microscopy, nucleosomes are better positioned and DNA within is less accessible to trans-factors, hence heterochromatin is also dubbed "closed chromatin". Euchromatin is more prevalent in single cell Eukaryotes and in mammalian early embryo whereas heterochromatin progressively gains weight in evolution and in development up to a 50-50 partitioning in a typical mammalian differentiated cell (1), suggesting a key role for heterochromatin in differentiation.

The HiC technique (2) further showed that chromatin domains assembled into heterochromatin and euchromatin build up two separate compartments in the nucleus, called A and B compartments, which associate amongst each other. HiC also showed that B domains display a higher density of pairwise contacts as compared with A domains, which might suffice to account for apparent compactness of heterochromatin. Noteworthy, A/B partitioning is universally found in all Eukaryotes, including in the highly divergent yeast *Saccharomyces cerevisiae*, suggesting conservation of basic molecular mechanisms for genome organization in spite of key chromatin players being clearly not conserved.

50% of chromatin domains along chromosome arms in the human genome can be found either in the A or B compartment according to cell type, which correspond to domains specifying one differentiation state or another and A/B partitioning is therefore a signature for a given differentiation state. Conversely, approximately 20% of chromatin domains are "always A" and the same for B domains.

Strikingly, gene density was found to be higher in "alwaysA" domains, whereas "alwaysB" domains, also known as lamin-associated domains (LADs) contain virtually no genes and are essentially made up of repeat sequences.

We decided to dig deeper into this analysis, and to ask whether some repeat sequences (RepSeq) might be more enriched than others in the B compartment.

We defined a set of 45 RepSeqs whose presence and density strongly correlate with the "B character", as defined by the Eigen vector value derived from HiC analysis. Although enriched in B domains, these 45 RepSeqs can also be found in A-domains. Strikingly however, within this list, HERV elements partition essentially into the B compartment, whereas LINE elements are found in both or more in the A-compartment, in particular in H3K9me9 islands within euchromatin. Furthermore, when all types of HERVs are taken into account there is a clear enrichment in the B compartment whereas LINEs are more equally distributed between A and B.

---

\*Speaker

Based on fundamental mechanisms underlying heterochromatin function as early defined using genetics in the yeast *S.cerevisiae*, we will discuss two mechanisms by which HERVs and LINEs on the one hand and simple repeats that also correlate with the B character on the other hand, may promote heterochromatin assembly and maintenance. Namely, these sequences may act : (1- as protosilencer ; (2- as enhancer of nucleosome positioning. We will illustrate how such concepts helps to understand genome remodeling during the cancer process and more precisely why repeat sequences are found transcribed in cancer whereas they are mostly silent otherwise (3, 4).

**Keywords:** genome organization, human genome, A & B compartment, HERVs, LINEs, *S.cerevisiae*, protosilencer, cancer

---

# Role of transposable elements in the control of sexual genes in teleost fish

Corentin Dechaud<sup>\*1</sup>, Manfred Schartl<sup>2</sup>, Jean-Nicolas Volff<sup>1</sup>, and Magali Naville<sup>1</sup>

<sup>1</sup>Institut de Génomique Fonctionnelle de Lyon (IGFL) – École Normale Supérieure - Lyon, Institut National de la Recherche Agronomique : UA1288, Université Claude Bernard Lyon 1, Centre National de la Recherche Scientifique : UMR5242 – Ecole Normale Supérieure de Lyon 46 allée d'Italie 69364 Lyon CEDEX07, France

<sup>2</sup>Physiologische Chemie, Biozentrum, Universität Würzburg, Würzburg, Germany – Lehrstuhl für Physiologische Chemie Am Hubland 97074 Würzburg, Germany

## Abstract

Teleost fishes show a high level of diversity affecting almost all facets of their biology. Their genome also contain many more families of transposable elements (TEs) than other vertebrates do [Chalopin & al. 2015]. In this project, we investigate the impact of TEs in fish diversification by focusing on sexual development, which appears hypervariable in this clade [Volff & al 2007 , Parichy & Spiewak 2015]. Preliminary results were obtained from the transcriptome analysis of four medaka species male and female gonads. In *Oryzias latipes*, sexual differentiation is under the control of the master gene *Dmy*, transcription of which is controlled by *Izanagi*, a TE inserted in its promoter region [Herpin & al. 2010]. The integrative analysis of gonads transcriptome data along with TE annotations allows to systematically detect such candidate cases of TE-regulated-genes. We identified a transposable element (~6000 copies in *O. latipes* genome) that is found in 34 UTRs of male-biased genes and that carries a binding site for a transcription factor involved in sex development. The systematic identification of such TE-derived regulatory sequences will allow a better assessment of the role of TEs in the lability of the pathway.

**Keywords:** Gene regulation, sex, transposable element, gene regulatory networks

---

<sup>\*</sup>Speaker

---

# Distribution and evolution of Tc1-mariner superfamily in plants

Maryem Bouallègue<sup>\*†1</sup>, Wafa Ben Lazhar-Ajrout<sup>1</sup>, Maha Mezghani-Khemakhem<sup>1</sup>, Nathalie Casse<sup>2</sup>, Aurore Caruso<sup>2</sup>, Benoît Chénais<sup>2</sup>, Mohamed Makni<sup>1</sup>, and Pierre Capy<sup>3</sup>

<sup>1</sup>Université de Tunis El Manar, Faculté des Sciences de Tunis, Laboratoire Biochimie et Biotechnologie, (LR01ES05) – 2092, Tunis, Tunisia

<sup>2</sup>Mer, Molécules, Santé (Le Mans) (EA2160) – Le Mans Université – Le Mans Université, Avenue O. Messiaen, 72085 Le Mans Cedex 09, France, France

<sup>3</sup>Laboratoire Evolution, Génomes, Comportement, Ecologie (EGCE) – CNRS, Université Paris-Sud, IRD, Université Paris-Saclay, – 1 avenue de la Terrasse, 91198 Gif-sur-Yvette Cedex,, France

## Abstract

Genomes contain diverse repetitive sequences of transposable elements (TEs), contributing to their plasticity, adaptability and evolution. In a context of host stress, such sequences may accelerate adaptation to TE environment challenges. While, TEs are usually vertically transmitted, they can be horizontally transferred from one species to another. In eukaryotes, transposons are frequently described in species belonging to the same phylum and little is known about their distribution among the main evolutionary lineages and about their potential transfer across different phylum like animals and plants. In this work, presence of members of the *Tc1-mariner* superfamily (*Class II* element) generally described in unikont species (animals, fungi and Entamoeba), has been investigated in several plant genomes. From homology searches, 391 sequences distributed in 37 plant genomes, including moss, algae and angiosperms, are identified. They were subdivided into six clusters based on their catalytic site (*Tc1* DD34E, *rosa* DD41D, *mariner* DD34D, *maT* DD37D, and two new clusters *i.e.* *Tc1* DD35E and DD35D). While most sequences are truncated or with internal deletions, 125 complete elements are characterized, including 31 potentially active copies found in six genomes (moss and angiosperms). Phylogenetic and evolutionary analyzes, including these elements and those of unikonts, have shown several cases of high similarities.

**Keywords:** Tc1, mariner, Transposable Elements, Plants, Evolution, Horizontal transfers

---

<sup>\*</sup>Speaker

<sup>†</sup>Corresponding author: maryem.bouallegue@gmail.com

---

# Exploratory analysis of transposable element expression in mouse early embryo

Federico Ansaloni<sup>\*†1</sup>, Stefano Gustincich<sup>2</sup>, and Remo Sanges<sup>‡1</sup>

<sup>1</sup>Scuola Internazionale Superiore di Studi Avanzati / International School for Advanced Studies (SISSA / ISAS) – via Bonomea, 265 - 34136 Trieste - Italy, Italy

<sup>2</sup>Istituto Italiano di Tecnologia (IIT) – Via Morego, 30 - Genova, Italy

## Abstract

After fertilization, sperm and oocyte haploid genomes must be unified to create the genome of the zygote. The newly formed zygotic cell must then be reprogrammed into a totipotent state and therefore its genome undergoes chromatin remodeling. During the first phases of this epigenetic reprogramming the zygotic genome remains transcriptionally silent and the embryo development is driven by maternally inherited transcript and proteins. The transcriptional zygotic genome activation (ZGA) is nevertheless required for the complete development of the embryo and, in the mouse, it is thought to occur at 2cell stage. Transposable elements (TEs) have been described to be actively transcribed during the embryo reprogramming phases. TEs are repetitive and mobile elements that make up 40-45% of human and mouse genomes and usually are overall repressed by several cellular mechanisms. TE transcriptional activity during early embryo development is necessary for proper embryo development and appears to be fundamental in processes such as gene regulation, chromatin remodeling, pluripotency maintenance and immune response priming. Here, we present an exploratory analysis of TE expression in a mouse early embryo single-cell RNA-seq (sc-RNAseq) public dataset. The dataset is composed by 259 single-cell samples representing 10 embryonic stages (zygote, early-2cell, mid-2cell, late-2cell, 4cell, 8cell, 16cell, early-blastocyst, mid-blastocyst and late-blastocyst). To measure TE expression in each single cell avoiding the quantification of TE fragments that may have been co-opted as portion of coding/long noncoding transcripts, we developed a python-based bioinformatic pipeline. Operatively, the pipeline first creates a reference fasta file merging transposome and transcriptome together, then maps the RNA-seq reads against the reference file using STAR. Using samtools, the best-scored alignments are identified. Then, reads mapping with best alignment score exclusively on TEs are selected. Finally, through bedtools coverage, TE expression is quantified counting the TE-specific reads mapped on the transposome. Our results suggest that, in the dataset here analysed, between 45 and 90% of the TE-best mapping reads map with best alignment score also on coding/long noncoding transcripts. These ambiguous reads, that we call TE-not-specific reads, cannot be uniquely assigned nor to TE consensus sequences neither to annotated transcripts and, if taken into account, may lead to an over-estimation of TE expression levels between 2 and 10-fold. The magnitude of this effect depends on the embryonic stage: before ZGA (zygote and early-2cell stages) the potential over-estimation is relatively small (~2-fold), then it hugely increases when ZGA

---

<sup>\*</sup>Speaker

<sup>†</sup>Corresponding author: fansalon@sissa.it

<sup>‡</sup>Corresponding author: remo.sanges@gmail.com

occurs ( $\sim 10$ -fold) and gradually decreases reaching a plateau at early-blastocyst ( $\sim 2.5$ -fold). This may suggest, as already reported, that chimeric TE-gene transcripts are particularly expressed in mouse embryonic cells after ZGA. We next proceed to the analysis of all the mouse-specific annotated TEs considering only TE-specific reads. Our results evidenced a small amount of TE mRNAs in transcriptionally inactive embryo stages (zygote and early-2cell), suggesting that TE mRNAs are part of the maternally inherited transcripts. As soon as ZGA occurs, the amount of TE mRNAs increases  $\sim 6$ -fold, remaining constant until the 16cell stage and slightly decreasing at early-blastocyst. Inspecting the expression levels of the different TE classes we could observe specific behaviours for each class. Our analysis allowed us to appreciate the developmental expression dynamics of different TE classes during mouse early development at an unprecedented resolution.

**Keywords:** Transposable elements, transposon, RNAseq, single cell, early embryo, embryogenesis, bioinformatics pipeline

---

# Living with a million-year long infection

George Kassiotis

The Francis Crick Institute, London, UK

## **Abstract**

Despite eliciting host immunity, several viruses establish chronic, often life-long infection in humans that can affect immune function. The ultimate form of parasitism and evasion of host immunity is for the virus genome to enter the germ line of the host. Retroviruses have invaded the host germ line on the grandest scale, and this is evident in the extraordinary abundance of endogenous retroelements in the genome of all vertebrate species that have been studied. Recent studies suggests that such viral endogenisation events continue to shape host immunity over long evolutionary times and through diverse mechanisms, including triggering host innate and adaptive immune responses or regulating immune gene expression or function. Although recent integrations may be more detrimental to host immunity, evidence will be presented that integrations acquired millions of years ago were positively selected and continue to shape host immunity in humans.

---

# Insertion sequence massive expansion, gene expression and pseudogenization: insights into the transcriptome of the rice weevil's primary endosymbiont *Sodalis pierantonius*

Mariana Ferrarini<sup>\*1,2</sup>, Nicolas Parisot<sup>1</sup>, Carole Vincent-Monégat<sup>1</sup>, Rita Rebollo<sup>1</sup>, Marie-France Sagot<sup>2</sup>, and Abdelaziz Heddi<sup>1</sup>

<sup>1</sup>Biologie Fonctionnelle, Insectes et Interactions (BF2I) – Institut National de la Recherche Agronomique : UMR0203, Institut National des Sciences Appliquées de Lyon – INSA Bat. L. Pasteur 20 avenue Albert Einstein 69621 Villeurbanne cedex, France

<sup>2</sup>Laboratoire de Biométrie et Biologie Evolutive - UMR 5558 (LBBE) – Université Claude Bernard Lyon 1, Institut National de Recherche en Informatique et en Automatique, VetAgro Sup, Centre National de la Recherche Scientifique : UMR5558 – 43 Bld du 11 Novembre 1918 69622 VILLEURBANNE CEDEX, France

## Abstract

Mutualistic associations between obligate intracellular bacteria and insects have been extensively studied particularly with regards to the evolutionary consequences for their genome structure (Toft & Andersson, 2010). Usually, these bacteria harbor extremely small genomes (~0.5 Mb), derived from degenerative processes that may involve insertion sequences (IS) massive expansion and subsequent loss, accompanied by gene inactivation and decay early following endosymbiosis establishment (Siguier *et al.*, 2014, Gil *et al.*, 2010).

Here, we studied the complete transcriptome of *Candidatus Sodalis pierantonius*, the primary endosymbiont of the rice weevil *Sitophilus oryzae*. *Ca. S. pierantonius* is similar to facultative secondary endosymbionts in terms of the age of the association (~28 000 years) and the genome size (~4.6 Mb) (Oakeson *et al.*, 2014).

The genome of *Ca. S. pierantonius* is rich in IS elements (819 copies, 500 full-length) and we hypothesize that such copies may impact the expression and possibly the degeneration of neighbor genes. Hence, we have analyzed the pattern of expression of all IS copies belonging to six families. Interestingly, a minor family ISNCY/ISPlu15, with only two complete copies in total, had the highest expression among all families. We further assessed the expression of genes within 1kb upstream and downstream of IS elements in order to define the enrichment of biological functions around them. Finally, we have performed a genome-wide analysis to identify whether each gene is under negative or positive selection.

This work provides insightful evidence of a highly dynamic genome undergoing rapid degeneration in the nascent stages of symbiosis.

---

\*Speaker



C. Toft & S.G.E. Andersson (2010) Evolutionary microbial genomics: insights into bacterial host adaptation. *Nature Reviews Genetics*, 11: 465–475.

P. Siguier, E. Gournay, M. Chandler (2014) Bacterial insertion sequences: their genomic impact and diversity. *FEMS Microbiology Reviews*, 38(5):865-891.

Gil et al IS

R. Gil, E. Belda, M.J. Gosalbes, L. Delaunay, A. Vallier, C. Vincent-Monégat, A. Heddi, F.J. Silva, A. Moya, A. Latorre. (2008) Massive presence of insertion sequences in the genome of SOPE, the primary endosymbiont of the rice weevil *Sitophilus oryzae*. *International Microbiology* 11(1):41-8.

K.F. Oakeson, R. Gil, A.L. Clayton, D.M. Dunn, A.C. von Niederhausern, C. Hamil, ..., C. Dale (2014) Genome degeneration and adaptation in a nascent stage of symbiosis. *Genome Biology and Evolution*, 6(1): 76–93.

**Keywords:** Endosymbiosis, Transcriptomic Assembly, Insertion Sequences, Pseudogenes, Degenerative Genome Evolution

---

# Characterizing the host range of SXT ICEs, vectors of antibiotic resistance genes in aquatic environments, by the innovative approach of epicPCR

Véronica Roman<sup>1</sup>, Christophe Merlin<sup>1</sup>, Jesse Vääntinen<sup>2</sup>, Marko Virta<sup>2</sup>, and Xavier Bellanger<sup>\*†1</sup>

<sup>1</sup>Laboratoire de Chimie Physique et Microbiologie pour les Matériaux et l'Environnement (LCPME) – Centre National de la Recherche Scientifique : UMR7564, Université de Lorraine – Université de Lorraine, 405 rue de Vandœuvre, 54600 Villers-les-Nancy, France

<sup>2</sup>Department of Food and Environmental Sciences – University of Helsinki, Helsinki, Finland

## Abstract

SXT is an integrative and conjugative element (ICE) belonging to a family of closely related genomic islands that can horizontally self-transfer between bacteria by conjugation and that are particularly involved in the dissemination of antibiotic resistance genes in pathogens of the genus *Vibrio* and close genera. The spread of ICEs from the SXT family is related to the consumption of certain antibiotics that may have a selective role favoring bacteria carrying SXT elements, but also stimulate the transfer of SXT ICEs when they generate genotoxic stress within the cytoplasm cell. The objective of this work is to study the spread of SXT ICEs in aquatic environments impacted by anthropogenic pressure by (i) studying their abundance in different ecosystems, and (ii) characterizing the bacterial host range of these elements considering the pollution levels and characteristics of the studied environments. The abundance of SXT ICEs was determined by quantitative PCR using a new set of primers specifically designed for this study. Analysis of several aquatic ecosystems shows that SXT ICEs form a family of relatively abundant elements, with 10<sup>5</sup>copies / 16S rDNA in wastewater treatment plant effluents, and more generally 10<sup>4</sup>to 10<sup>6</sup>copies / 16S rDNA in other environments (rivers, ponds, fish ponds). The host range of SXT ICEs was characterized by epicPCR[1](Emulsion, Paired Isolation and Concatenation PCR), an innovative technique of single-cell genomics. Briefly, around 20 millions of bacteria from an environmental sample are isolated in polyacrylamide beads before a fusion PCR is performed for binding a DNA fragment of the phylogenetic marker (16S rDNA) carried by each bacterium with a DNA fragment specific to SXT ICEs only when one of them is present in the embedded cell. The amplicons resulting from the fusion PCR are then sequenced by NGS in order to identify the bacterial taxons hosting SXT ICEs. Contrary to what was up to now reported in literature data obtained from isolation and characterization of bacteria, we demonstrated using epicPCR that the host range of SXT ICEs is not restricted to few bacteria belonging to the *Vibrio* or *Proteus* genera. Indeed, SXT ICEs were also found in Proteobacteria specific to the environments studied such as *Nitrospira* spp. These results also show that the acquisition of antibiotic resistance genes in pathogens of the *Vibrio* genus could follow a very complex dissemination pathway involving environmental bacteria as intermediary hosts of SXT ICEs.

---

\*Speaker

†Corresponding author: xavier.bellanger@univ-lorraine.fr

**Keywords:** Antibiotic resistance genes, Mobile genetic elements, Single cell genomics, Bacterial host range, Aquatic environments

---

# Transposable element domestication in Vertebrates: Functional and evolutionary study of a gene family derived from Harbinger transposons

Ema Etchegaray<sup>\*1</sup>, Magali Naville , Zofia Haftek-Terreau , and Jean Nicolas Volff

<sup>1</sup>Institut de Génomique Fonctionnelle de Lyon (IGFL) – CNRS 5280, Université Lyon 1, ENS Lyon –  
32-34 avenue Tony Garnier, 69007 LYON, France

## Abstract

New gene formation is one of the major sources of evolutionary innovations for organisms. These events can arise *de novo*, by gene duplication, or by transposable element (TEs) molecular domestication (Kaessmann 2010), which makes TEs crucial actors of evolutionary innovations. The global impact of TE molecular domestication on early Vertebrate evolution is probably still underestimated. The cases of *rag1* and *rag2*, at the basis of the adaptive immune system, and the *syncytins*, involved in placental development, have already highlighted the role TEs can have on gene formation. Further investigating this aspect, we have identified an entire family of genes deriving from the Myb-like protein of *Harbinger* DNA transposons. Preliminary results suggest the formation of five genes from independent *Harbinger* transposon molecular domestication in Jawed Vertebrates (around 500 Mya). We also identified one gene arising from the duplication of a *Harbinger*-deriving gene in sarcopterygians (around 400 Mya), and one retropseudogene in simians (around 60 Mya), transcribed and interestingly positioned in a cluster of 40 non-coding RNA genes. The genes present a major expression in zebrafish brain or testes. Furthermore, two genes of this family show a significant expression in the human brain, particularly during fetal development. The functional and evolutionary analysis of this gene family originating from recurrent and concomitant molecular domestication of *Harbinger* transposons will give more insight into the impact of TE molecular domestication on early Vertebrate evolution.

**Keywords:** Harbinger transposons, TE molecular domestication, Vertebrate evolution, Zebrafish

---

<sup>\*</sup>Speaker

---

# Hominoid-specific regulatory sequences and their controllers shape human genome regulation

Julien Pontis\*<sup>1,2</sup>

<sup>1</sup>Julien Pontis – EPFL, Switzerland

<sup>2</sup>Didier Trono – EPFL, Switzerland

## Abstract

Transposable elements (TEs) are key to the evolutionary turnover of regulatory sequences. How they can play such an essential role in spite of their genotoxic potential is unknown. Here, we propose that Krüppel-Associated Box (KRAB)-containing zinc finger proteins (KZFPs) control the timely and pleiotropic engagement of TE-derived *cis*-regulators of transcription. We first observed that evolutionary recent TEs of the SVA, HERVK and HERVH subgroups are major contributors to chromatin opening during human embryonic genome activation and act as Krüppel-Like Factors (KLFs)-stimulated enhancers in naïve human embryonic stem cells. We then found that KZFPs of corresponding evolutionary ages are simultaneously induced and repress the transcriptional activity of these TEs. We finally determined that the same KZFP-controlled TE-based enhancers later serve as developmental and tissue-specific regulators of gene expression. Thus, by taming the transcriptional impact of TEs during early embryogenesis, KZFPs allow for their genome-wide incorporation into transcriptional networks, thereby contributing to the species-specificity of human genome regulation.

**Keywords:** Human, Enhancer, Stem cells, KRAB, Zinc Finger, Krüppel, like Factor

---

\*Speaker

---

# Tc1/mariner phylogeny and the unexplored world of pogo elements

Mathilde Dupeyron<sup>\*1</sup>, Toby Baril<sup>1</sup>, Kumar Sing<sup>1</sup>, Chris Bass<sup>1</sup>, and Alexander Hayward<sup>1</sup>

<sup>1</sup>University of Exeter – University of Exeter, Centre for Ecology and Conservation - Biosciences, College of Life and Environmental Sciences, Penryn Campus, Treliever Road, Penryn TR10 9FE Cornwall, United Kingdom

## Abstract

*Tc1/mariner* transposons are widespread DNA transposable elements (TEs), which have been extensively studied since their discovery in the 1980s. Following recent developments in genome sequencing and the availability of many new eukaryotic genomes, *Tc1/mariner* TEs have been detected in many new taxa across all major branches of the eukaryotic tree of life. Consequently, the host range of *Tc1/mariner* elements is considered to be one of the most diverse known for any TE group.

The *Tc1/mariner* superfamily is well known among DNA TEs, due to the membership of several famous elements to the group. *Sleeping Beauty* is a well-known *Tc1/mariner* element that was reconstructed by reverse engineering from several defective elements found in multiple salmon genomes. *Sleeping Beauty* is widely used as a robust and stable genetic tool for gene transfer, along with several other well-characterized *Tc1/mariner* TEs (e.g. Himar1, Frog Prince, Hsmar1). Meanwhile, the *Centromere protein B* gene (*CENP-B*) is an important gene for host physiology that is involved in centromere chromatin assembly in mammals, and originates from a domesticated *pogo*-like *Tc1/mariner* transposase sequence.

A variety of studies have focused on the structure, diversity and evolution of *Tc1/mariner* elements, but these typically focus on just one, or a small number of host lineages. Consequently, much remains to be learned about the evolution of the *Tc1/mariner* group. To date, seven major groupings are recognised for *Tc1/mariner* TEs in eukaryote genomes, based on the number of amino acids between the second and third aspartic acid (or glutamic acid) of the transposase DDD/E domain. Considering the substantial recent increase in available eukaryotic genome sequences and the diversity of new groups of *Tc1/mariner* elements identified in several Metazoan species (e.g. Pacific oyster, American mink, coffee berry borer), we aimed to investigate the diversity and evolutionary relationships between lineages in these groups by searching available eukaryote genome sequences.

We mined the non-redundant and nucleotide databases on NCBI using BLASTp and tBLASTn searches, using reference transposase references from each major *Tc1/mariner* group, to reconstruct evolutionary relationships in the group. The resulting phylogeny shows that each described major group is highly supported and *pogo* is a much larger and more diverse *Tc1/mariner* group than previously appreciated.

The identification of a large diversity of *pogo*-like elements in arthropods suggests that much work remains to improve understanding of the diversity and evolution of DNA TEs in eukaryotes.

---

<sup>\*</sup>Speaker

**Keywords:** DNA transposons, Tc1/mariner, transposase, pogo, phylogenetic analysis, evolution

---

# The role of Piwi pathway genes and histone modification in transposable element misregulation of *Drosophila* hybrids

Maria Pilar Garcia Guerreiro<sup>\*†1</sup>, Victor Gamez-Visairas , Valeria Romero-Soriano , Joan Marti-Carreras , Marie Fablet , and Cristina Vieira

<sup>1</sup>Universitat Autònoma de Barcelona (UAB) – Departament de Genètica i Microbiologia Facultat de Biociències 08193 Bellaterra (Barcelona), Spain

## Abstract

Transposable element (TE) proliferation in hybrids between *D. buzzatii* and *D. koepferae* species has been reported in previous studies and has been associated with a deregulation of TE expression. The causes of TE bursts in *Drosophila* interspecific hybrids are still a controversial issue where different factors such as differences between maternal piRNA pools and genetic divergence between the two parental piRNA pathways come into play. Indeed, piRNA pathway genes are known to carry adaptive evolution marks leading to cross-species incompatibilities.

To elucidate the molecular basis of TE deregulation in interspecific *D. buzzatii-D. koepferae* hybrids, we focused our study in the piRNA pathway genes and histone modification. We found that gene structure is, in general, maintained in both species and that four genes are under strong positive selection. Moreover, some of them displayed higher expression values in hybrids than both parental species while others had RNA levels similar to the parental species with the highest expression. The study of Histone methylation marks revealed variations in chromatin states between hybrids and parental species affecting some genes.

The overall results revealed an extraordinarily complex mechanism of TE deregulation in hybrids where the increase of transcription rates in some piRNA genes can be a primary response to hybrid stress. We hypothesize that gene deregulation together with protein incompatibility, because of these genes' rapid evolution, could be related to the TE silencing failure in cross-species hybrids observed in our previous studies.

**Keywords:** *Drosophila*, interspecific hybrids, Transposable elements, misregulation, piRNA genes

---

<sup>\*</sup>Speaker

<sup>†</sup>Corresponding author: mariapilar.garcia.guerreiro@uab.es



---

# The role of natural transposable element insertions in stress response

Josefa Gonzalez

Instituto de Biologia Evolutiva (CSIC-UPF), Barcelona, Spain

## Abstract

Transposable elements are ubiquitous, abundant, and active components of genomes. Most of the mutations caused by transposable elements are most likely deleterious or neutral. However, transposable elements have also been shown to induce adaptive mutations. Our lab focuses on elucidating the role of those TEs involved in adaptation. While most studies so far have analyzed reference TE insertions, we are currently generating new reference genomes that will allow us to investigate insertions beyond those present in a single North American strain. To detect, annotate, and analyze TE insertions, we are using the REPET package. As a proof of concept, we have re-annotated the reference genome, and have identified 2.7x more TEs than previously annotated. The combined analysis of the 13 new reference genomes revealed additional TE copies from 26 families that were not previously identified in *Drosophila melanogaster*, and several unknown, putatively new, families. We are currently investigating the potential role of these insertions in three ecologically relevant traits: insecticide resistance, tolerance to heavy metals, and desiccation tolerance. Indeed, an initial analysis has shown that TEs are likely to contribute a significant fraction of stress-related transcription factor binding sites in *D. melanogaster* and humans.

---

# Transposable element distribution along high-quality chromosome-level assembly reveals recent rose genome history

Jérémy Just, Olivier Raymond, Léa François, Marion Verdenaud, Mohammed Bendahmane.

On the behalf of the Rose Genome Sequencing Consortium<sup>1</sup>

Laboratoire Reproduction et Développement des Plantes, Univ. Lyon, ENS de Lyon, UCB Lyon 1, CNRS, INRA, Lyon, France

## Abstract

Roses are among the most commonly cultivated ornamental plants worldwide since antiquity, and have high cultural and economic importance for the ornamental plant market and in the perfume industry. The genus *Rosa* contains approximately 200 species, more than half of which are polyploid. Owing to natural self-incompatibility and artificial interspecific hybridisations, all roses have highly heterozygous genomes that are challenging to assemble despite their relatively small size (560 Mb). During the past years, we generated a number of biotechnology and molecular tools that allowed discovering the molecular mechanisms controlling flower formation and scent biosynthesis<sup>2-6</sup>. However, to date, attempts to assemble rose genomes with short reads have led to highly fragmented assemblies composed of thousands of scaffolds. To overcome these bottlenecks and obtain a reference genome, we produced a homozygous genome from *Rosa chinensis*, known to have extensively participated in breeding and the creation of modern roses, through an original *in vitro* culture protocol<sup>7</sup>, and we sequenced this homozygous genome with long-read sequencing technology.

We used PacBio Single Molecule Real-Time sequencing at a depth of coverage of 80× and an original meta-assembly approach to obtain a very high-quality genome assembly<sup>1</sup>. The final assembly was composed of 82 contigs for an N50 of 24 Mb. Using a genetic map and Hi-C chromosomal-contact-map data, we successfully built the seven pseudomolecules of *R. chinensis*, containing 97.7% of the assembly. This sequencing strategy also gave access to the full repeated sequence complement of the genome.

An analysis of transposable element distribution along the chromosomes, and a comparison with resequencing data of 14 major genotypes that contributed to rose domestication, allowed us to accurately reconstruct recent rose genome history, highlighting the mosaic origin of the genome of modern rose hybrids, that combine European species traits and Chinese species traits<sup>1</sup>. These resources provide a solid foundation for understanding the mechanisms governing rose traits and their diversity and will accelerate improvement in roses, *Rosaceae* and ornamentals. For example, a recent TE insertion has already been found to be linked to a trait selected during domestication.<sup>8</sup>

1. Raymond et al. (2018). *Nature Genetics* **50**:772–777. DOI: 10.1038/s41588-018-0110-3.

2. Bendahmane et al. (2013). *J Exp Bot* **64**(4):847–857.

3. Dubois et al. (2012). *BMC Genomics* **13**:638.

4. Dubois et al. (2011). *PLoS ONE* **6**:e28455.

5. Dubois et al. (2010). *PLoS ONE* **5**:e9288.

6. Magnard et al. (2015). *Science* **349**:81–83.

7. Vergne et al. (2018). *Protocol Exchange*. DOI: 10.1038/protex.2018.067.

8. François et al. (2018). *Scientific Reports* **8**:12912. DOI: 10.1038/s41598-018-30918-4.

---

# Genomic impact of TEs in *Oryza*

Olivier Panaud

Laboratoire Génome et Développement des Plantes, UMR CNRS/UPVD 5096, Université de Perpignan  
Via Domitia, 52 Avenue Paul Alduy., 66860 Perpignan Cedex, France

Institut Universitaire de France, 1 rue Descartes, 75231 Paris Cedex 05, France

## Abstract

Rice is the staple food crop for more than half of the world's population. Many factors are now jeopardizing a sustainable production of this cereal, among which, population size increase, environmental changes and reduction of arable land caused by cities expansion. As a consequence, rice has been the focus of intense research over the last decades, which lead to the development of large genomic resources such as several high quality genome assemblies for cultivated rice and several of its wild relatives, genome sequences for 3,000 rice varieties and transcriptomic data for many developmental stages and various physiological stresses. Therefore, the genus *Oryza* (to which cultivated rice belongs) is now one of the best models to study genome evolution using full scale genomic analyses. We took advantage of these resources to address the question of the impact of transposable elements (TEs) on the structure and evolution of this plant genome. Here, we show that TEs contribute to genomic turn-over at a rate which is much higher than in animal kingdom. We then looked at the transpositional landscape of cultivated Asian rice, taking advantage of the availability of the 3,000 genomes dataset. This resource provides the opportunity to study the impact of TEs at the species level. We show that retrotransposons (the major TE type in plants) are very active in this crop and contribute to genome diversification in agro. Our results suggest that one could tentatively search for TE insertion polymorphisms that may have been adaptive in the recent history of rice cultivation.

---

# Transposable elements found in conserved noncoding elements of *Drosophila* genome

Tristan Berr<sup>1</sup>, Aurélie Peticca<sup>1</sup>, and Annabelle Haudry<sup>\*1</sup>

<sup>1</sup>Laboratoire de Biométrie et Biologie Evolutive (LBBE) – CNRS : UMR5558, Université de Lyon,  
Université Lyon 1 – F-69622 Villeurbanne, France, France

## Abstract

Identification of regulatory regions within genomes is a key challenge for understanding the influence of functional traits on species evolution. Conserved Noncoding Elements (CNEs, *i.e.* untranslated sequences highly similar across divergent species) were early identified as candidate regulatory regions in metazoans, plants, and fungi. CNEs have been repeatedly discriminated from mutational cold-spots, but only few studies have assessed their functional relevance at a genome-wide scale. In the present study, we used a whole-genome alignment of 27 insect species to build a coherent mapping of CNEs in the genome of *Drosophila melanogaster*. We then exploited polymorphism data from 48 European populations of *D. melanogaster* to estimate levels of nucleotide diversity and adaptive evolution in CNEs. We show here that about 35% of *D. melanogaster* autosomes fall into conserved noncoding regions that exhibit reduced genetic diversity and undergo purifying selection. In addition, we report six insertions of transposable elements in the genome of *D. melanogaster* showing high levels of conservation across *Drosophila* species, which represent potential relics of ancient TE domestication events.

**Keywords:** conserved non coding elements, *Drosophila*, selection

---

<sup>\*</sup>Speaker

---

# Investigating the effects of genomic transposable element proliferation on diversification rates of Corydoradinae catfishes.

Ellen Bell<sup>\*†1</sup>, Chris Butler<sup>1</sup>, Levi Yant<sup>2</sup>, Tracey Chapman<sup>1</sup>, and Martin Taylor<sup>1</sup>

<sup>1</sup>University of East Anglia [Norwich] (UEA) – Norwich Research Park, Norwich, NR4 7TJ, UK, United Kingdom

<sup>2</sup>University of Nottingham, UK (UON) – University of Nottingham University Park Nottingham NG7 2RD, United Kingdom

## Abstract

Transposable element (TE) activity is a potentially potent source of novel mutations which in turn may lead to increased rates of diversification and speciation. The role of TEs has historically been largely viewed as deleterious, though this view is being challenged by a number of recent studies. Despite this, there remain large gaps in our understanding of the evolutionary dynamics and implications of TE proliferation. The Corydoradinae are a species rich subfamily of Neotropical catfishes composed of over 170 described species. They have a highly convoluted evolutionary history, and are currently subdivided into nine genetic lineages which have undergone as many as two whole genome duplication events within the last 70MY. RAD sequencing has also revealed that genomic TE abundance is highly variable among these different lineages. Some TE families, such as TC1-Pogo have increased in abundance from < 1% to ~70% of the genome across the lineages. As such the Corydoradinae present a novel system for further investigation of the effects of genome wide TE proliferation on mutation and diversification rates and may allow us to shed further light on the role of TEs in evolutionary contexts.

**Keywords:** Genome, Corydoradinae, Diversification, Whole genome duplication

---

<sup>\*</sup>Speaker

<sup>†</sup>Corresponding author: ellen.bell@uea.ac.uk

---

# The siRNA and piRNA pathways interplay and modulate transposable element transcription upon viral infection in *Drosophila*

Marlène Roy<sup>1,2</sup>, Barbara Viginier<sup>2</sup>, Frederick Arnaud<sup>2</sup>, Maxime Ratinier<sup>2</sup> and **Marie Fablet**<sup>1</sup>

<sup>1</sup> Laboratoire de Biométrie et Biologie Evolutive (LBBE), UMR CNRS 5558, Université Lyon 1, Université de Lyon – 43 boulevard du 11 novembre 1918, 69622 Villeurbanne Cedex, France

<sup>2</sup> Infections Virales et Pathologie Comparée (IVPC), UMR 754 – Université Lyon 1 – 50 avenue Tony Garnier 69366 Lyon Cedex 7, France

## Abstract

All genomes contain genomic parasites called transposable elements (TEs), some of which resemble viruses. TEs are controlled by small RNAs of the piRNA class, and viruses are fought against by small RNAs of the siRNA class. Considering these similarities in structure and control pathways between TEs and viruses, reciprocal impacts of TE control and antiviral immunity are suspected. Indeed, in a *Drosophila* system, upon viral infection, TE transcript amounts are modulated, as well as their controlling small RNAs. Altogether, these data demonstrate an impact of viral infection on TE control, likely mediated by RNAi pathway in *Drosophila*. In addition, the effect is virus-specific. Whether viral infections also affect somatic or germline transposition rates still need to be demonstrated, which would indicate a strong evolutionary impact.

---

# Transcriptional abundance and diversity of transposable elements within a species rich group of armoured catfish (Corydoradinae).

Christopher Butler<sup>\*1</sup>, Ellen Bell<sup>1</sup>, Tracey Chapman<sup>1</sup>, and Martin Taylor<sup>1</sup>

<sup>1</sup>University of East Anglia [Norwich] (UEA) – Norwich Research Park, Norwich, NR4 7TJ, UK, United Kingdom

## Abstract

Transposable element (TE) proliferation is increasingly viewed as a potential contributor to speciation events. However, despite numerous studies investigating the landscape of genomic TEs, there is a current paucity of knowledge related to how genomic TE content may differ at a transcriptional level. Here, we highlight findings on the abundance and diversity of TEs within the transcriptome of several species of Corydoradinae; a sub-family of Neotropical catfishes, which have radiated into over 170 described species across the last ~70 million years. We found that expressed TE abundance was an order of magnitude lower than known Corydoradinae genomic content, suggestive of efficient pre-transcriptional silencing. We also established the presence of at least one significant increase in transcriptional TE abundance across the Corydoradinae phylogeny. Finally, we provide an account of the interplay between TE age and transcriptome abundance. These findings provide a better understanding of the processes that shape active TE landscapes and will allow for future inferences to be made regarding the effect of TE expansion on the adaptive radiation of the Corydoradinae.

**Keywords:** Transcriptome, Corydoradinae, Phylogenetics, Speciation

---

<sup>\*</sup>Speaker

---

# High frequency horizontal transfer in Jockey families (Order LINE) in Drosophilids

Izabella Tambones\*<sup>1</sup>, Annabelle Haudry\*<sup>2</sup>, Maryanna Simao\*<sup>3</sup>, and Claudia Carareto\*<sup>4</sup>

<sup>1</sup>The Brazilian Center for Research in Energy and Materials (CNPEM) – 10000, Giuseppe Máximo Solfaro, - Polo II de Alta Tecnologia, Campinas - São Paulo State, 13083-970, Brazil, Brazil

<sup>2</sup>Université Claude Bernard Lyon 1 (UCBL1) – Univ Lyon, Université Claude Bernard Lyon 1, CNRS UMR 5558, LBBE, F-69100, Villeurbanne, France – 43 Boulevard du 11 Novembre 1918, 69100 Villeurbanne, France, France

<sup>3</sup>São Paulo State University (UNESP), Institute of Biosciences, Humanities and Exact Sciences, São José do Rio Preto (UNESP/IBILCE) – 2265, Cristóvão Colombo Street, São José do Rio Preto - São Paulo State, 15054-000, Brazil, Brazil

<sup>4</sup>São Paulo State University (UNESP), Institute of Biosciences, Humanities and Exact Sciences (UNESP/IBILCE) – 2265, Cristóvão Colombo Street, Jardim Nazareth, São José do Rio Preto, São Paulo State, 15054-000, Brazil, Brazil

## Abstract

The use of large-scale genomic analyses has resulted in an improvement of transposable elements (TEs) sampling and in significant increase in the number of HTT (horizontal transfer of transposable elements) reports. Given the scarcity of HTT records of *Jockey* elements (LINE order) in Drosophilids (only one case), we aimed to broaden our understanding of the rate of HTT in this clade. We used 109 *Jockey* sequences deposited in the Repbase and 118 sequences sampled from 29 genomes belonging to species of three subgenera of *Drosophila* and one of the *Zaprionus* genus. We describe 11 potential HTT events involving eight Jockey families evidencing the flow of genetic material favored by the spatio-temporal sharing of these species present in Asia or Africa. The addition of 11 HTT events of Jockey elements contribute to increase the rare records of HTT of specific families of LINE elements. More importantly, we identified the species involved in these exchanges and formulated hypotheses about the spatio-temporal relationships between species that made these exchanges possible. We show that the use of both criteria, phylogenetic to classify TE families and biogeographical information of the species involved in the transfers, are essential for a robust inference of HTT.

**Keywords:** *Drosophila*, *Zaprionus*, Horizontal Transfer, VHICA

---

\*Speaker



---

# The epigenetic and evolutionary importance of palindromic motifs in the regulatory region of LTR retrotransposons

Elias Primetis\*<sup>1</sup> and Alexandros Bousios<sup>1</sup>

<sup>1</sup>University of Sussex, School of Life Sciences (UoS) – Brighton BN1 9RH, United Kingdom

## Abstract

Sirevirus LTR retrotransposons harbour an intriguing genome structure and are highly abundant in plants. Of particular interest are the repeated palindromic motifs (RPMs) located in the regulatory region of their LTRs. Research in maize has shown that the RPMs are hotspots of siRNA targeting, prone to form secondary structures, and loci of rapid evolution. Sireviruses are targeted by siRNAs as a decreasing function of age, but old elements remain highly targeted, partially by siRNAs that cross-map to young elements. Based on these data, it is likely that RPMs form the hotspot of an evolutionary arms-race between Sireviruses and host defences. Decoding the sequence and positional diversity of RPMs across Sirevirus families and hosts is the first step towards investigating this conjecture. By developing appropriate computational tools, we found at least nine different versions of RPMs. They all maintain a GC-rich symmetrical core, and are 10-13nt in length depending on the number of additional nucleotides in the central part of the motif. Sirevirus LTRs contain on average eight RPMs clustered in four discrete loci, but are gradually lost as a function of age. These data will allow the sensitive examination of the epigenetic and evolutionary interactions between host defences and Sireviruses.

**Keywords:** LTR retrotransposons, Plants, Epigenetics, Evolution

---

\*Speaker

---

# Transposable element dynamics and regulation in a major crop pest: *Sitophilus oryzae*

Caroline Blanc<sup>\*1</sup>, Théo Chancy<sup>1</sup>, Agnès Vallier<sup>1</sup>, Séverine Balmand<sup>1</sup>, Clément Goubert<sup>2</sup>, Mariana Galvao Ferrarini<sup>1</sup>, Elisa Dell'aglio<sup>1</sup>, Nicolas Parisot<sup>1</sup>, Abdelaziz Heddi<sup>1</sup>, Cristina Vieira<sup>2</sup>, and Rita Rebollo<sup>†1</sup>

<sup>1</sup>Biologie Fonctionnelle, Insectes et Interactions (BF2i) – Institut national de la recherche agronomique (INRA), Institut National des Sciences Appliquées (INSA) - Lyon – Bat. L. Pasteur 20 avenue Albert Einstein 69621 Villeurbanne cedex, France

<sup>2</sup>Laboratoire de Biométrie et Biologie Evolutive - UMR 5558 (LBBE) – Université Claude Bernard Lyon 1, Institut National de Recherche en Informatique et en Automatique, VetAgro Sup, Centre National de la Recherche Scientifique – 43 Bld du 11 Novembre 1918 69622 VILLEURBANNE CEDEX, France

## Abstract

*Sitophilus* spp. cereal weevils are crop pests causing an estimated worldwide loss of hundreds of millions of dollars. These insects thrive on a nutritionally poor and unbalanced diet, and highly rely on intracellular symbiotic bacteria (endosymbionts) that supply them with components lacking in their habitats. Endosymbiont metabolic complementation improves insect biological traits and increases its adaptive and invasive abilities, posing an important agronomical challenge. **While many studies target the host-endosymbiont interaction, there is a clear lack of knowledge on the host genome evolution and dynamics.** Nearly all genomes possess transposable elements (TEs), DNA sequences capable of moving throughout the genome potentially causing harmful mutations. Preliminary sequencing of *Sitophilus oryzae*'s genome (an oligophagous grain feeder coleopteran) revealed that more than 50% of its genome is composed of repeated sequences, making *Sitophilus* one of the most repeat-rich insect genomes. In addition, TE transcripts represent up to 10% of *S. oryzae*'s transcriptome, suggesting such elements are still active. Our main objective is to understand how *S. oryzae*'s genome copes with a massive proportion of transposons, and at identifying the molecular partners implicated in the host-transposon interaction.

**Keywords:** transposable element, crop pest, weevil, small RNAs

---

<sup>\*</sup>Speaker

<sup>†</sup>Corresponding author: rita.rebollo@insa-lyon.fr

---

# Optimizing the de novo annotation of transposable elements in large, TE-rich genomes

Maud Fagny<sup>\*1</sup>, Véronique Jamilloux<sup>2</sup>, Johann Joets<sup>1</sup>, and Clémentine Vitte<sup>\*†1</sup>

<sup>1</sup>Génétique Quantitative et Evolution - Le Moulon (Génétique Végétale) (GQE-Le Moulon) – Institut National de la Recherche Agronomique : UMR0320, Université Paris-Sud - Paris 11, AgroParisTech, Centre National de la Recherche Scientifique : UMR8120 – UMR de Génétique Quantitative et Evolution - Le Moulon, Ferme du Moulon F-91190 GIF SUR YVETTE, France

<sup>2</sup>Unité de Recherche Génomique Info (URGI) – Institut National de la Recherche Agronomique : UR1164 – INRA, Centre de recherche de Versailles, bat.18 Route de Saint Cyr 78000 Versailles, France

## Abstract

Transposable elements (TEs) are major constituents of plant genomes and contribute to their dynamics and evolution. The extent to which they contribute to local adaptation nevertheless remains to be fully elucidated. To better characterize the potential role of TEs in maize local adaptation, we aim at characterizing TE polymorphisms in a set of 7 maize inbred lines of contrasted origins. We have *de novo* assembled the genome sequences of these maize lines, and are now focusing on TE annotation and polymorphism discovery. Several softwares and pipelines are available to *de novo* annotate TEs in genomes. They rely on (i) approaches that use characteristic structural features of TE super-families to detect complete copies and/or (ii) approaches that use the repetitiveness of TE copies across the genome. These approaches are often completed by the detection of coding domains to classify of TEs into families. Existing softwares have proven useful for TE annotation of small genomes of a few hundreds of megabases, but remain challenging to apply on larger genomes, mainly due to the amount of genomic data to analyze and to the structural complexity of these genomes.

With a ~2.1 Gb genome, 85% of which is occupied by TE sequences that are often nested within one another, maize is a typical average diploid angiosperm genome. Improving tools for maize TE genome annotation will therefore leverage TE annotation for a large amount of plant species. After reviewing existing approaches to *de novo* annotate TEs, we will discuss their advantages and limits to annotate TEs in the maize genome. We will then suggest ways to improve *de novo* TE annotations in such a genome.

**Keywords:** transposable elements, de novo annotation, maize

---

<sup>\*</sup>Speaker

<sup>†</sup>Corresponding author: clementine.vitte@inra.fr

---

# Comparative Analysis of Transposable Element Dynamics and Gene Association Preference in Aphids

Tobias Baril<sup>\*1</sup>, Alex Hayward<sup>†1</sup>, Mathilde Dupeyron<sup>1</sup>, Chris Bass<sup>2</sup>, and Kumar Saurabh Singh<sup>2</sup>

<sup>1</sup>Centre for Ecology and Conservation, University of Exeter (CEC) – Penryn Campus, Penryn Cornwall TR10 9FE, United Kingdom

<sup>2</sup>Science and Engineering Research Support Facility, University of Exeter (SERSF) – Penryn Campus, Penryn, Cornwall, TR10 9FE, United Kingdom

## Abstract

Transposable elements (TEs) have been exapted for a diverse range of host evolutionary processes including placental development in mammals [1,2], adaptive immunity in vertebrates [3], camouflage in the peppered moth [4] and insecticide resistance in the fruit fly [5]. Whilst individual insertions are known to be fundamentally important in each of these examples, we currently lack an understanding of the extent to which the total quotient of TEs present in a host genome contribute to host evolution.

Aphids are a global economically-important crop pest that attack over 400 host plant species. Routine insecticide use has led to the emergence of insecticide-resistant aphid populations across the globe, including in *Myzus persicae nicotianae*, the tobacco-feeding peach potato aphid. TEs have been implicated in insecticide resistance previously in *Drosophila melanogaster*, and preliminary analysis of the *M. persicae nicotianae* genome reveals TE insertions in regions surrounding key genes associated with detoxification pathways in this nicotine tolerant lineage.

Given recently available genome sequencing data for a number of aphid species, we perform a comparative analysis of TE content and localisation relative to genetic features across available aphid genomes. Combined with functional genome annotations and information on aphid life-history, we investigate the features of TEs that expose them to exaptation to provide host benefits and facilitate genomic evolution. In particular, we focus on genes involved in xenobiotic resistance, given the high levels of selection acting on these, and their importance for host fitness and applied pest management.

## References:

1. Lynch, V. J., Leclerc, R. D., May, G. & Wagner, G. P. Transposon-mediated rewiring of gene regulatory networks contributed to the evolution of pregnancy in mammals. *Nat. Genet.* **43**, 1154–1159 (2011).

---

<sup>\*</sup>Speaker

<sup>†</sup>Corresponding author: alex.hayward@exeter.ac.uk

2. Emera, D. & Wagner, G. P. Transposable element recruitments in the mammalian placenta: Impacts and mechanisms. *Brief. Funct. Genomics* **11**, 267–276 (2012).
3. Kapitonov, V. V. & Koonin, E. V. Evolution of the RAG1-RAG2 locus: Both proteins came from the same transposon. *Biol. Direct* **10**, 1–8 (2015).
4. van't Hof, A. E. *et al.* The industrial melanism mutation in British peppered moths is a transposable element. *Nature* **534**, 102–105 (2016).
5. Ffrench-Constant, R. H., Daborn, P. J. & Le Goff, G. The genetics and genomics of insecticide resistance. *Trends Genet.* **20**, 163–170 (2004).

**Keywords:** Insects, Resistance, Evolution, Domestication

---

# Assessing the potential roles of DNA methylation in the excision of Internal Eliminated Sequences in the ciliate *Paramecium tetraurelia*

Suzanne Marques<sup>\*1</sup> and Eric Meyer<sup>2</sup>

<sup>1</sup>IBENS (IBENS) – Institut de Biologie de l'École normale supérieure (IBENS), Département de Biologie, Ecole Normale Supérieure, CNRS, Inserm, PSL Research University, F-75005 Paris, France.,

Université Paris-Sorbonne - Paris IV, CNRS : UMR8197 – 46 rue d'Ulm 75005 Paris, France

<sup>2</sup>IBENS – Institut de Biologie de l'École normale supérieure (IBENS), Département de Biologie, Ecole Normale Supérieure, CNRS, Inserm, PSL Research University, F-75005 Paris, France., CNRS :

UMR8197 – 46 rue d'Ulm 75005 Paris, France

## Abstract

Silencing Transposable Elements (TEs) is vital for eukaryotes, but how genome invaders (non-self) are distinguished from cellular genes (self) is ill-understood. This PhD project focuses on a large set of TE insertions of different ages in the *P. tetraurelia* genome. As in all ciliates, epigenetic silencing of multi-copy TEs triggers their deletion during development of a functional somatic macronucleus (MAC) from the silent germline micronucleus (MIC). In addition, ~45,000 short, single-copy Internal Eliminated Sequences (IESs) are precisely excised to reconstitute cellular genes. IESs are decaying remnants of ancient TE insertions, and the weak consensus at their ends does not contain sufficient information to specify the IES excision pattern genome-wide. Specific recruitment of the Pgm endonuclease to IESs depends in part on an original small RNA-based immune system: during MIC meiosis, genome-wide scnRNAs mediate a MIC-MAC subtraction which identifies MIC-specific sequences as non-self, allowing sexual progeny to reproduce their excision. However, recent studies indicate that the scnRNA pathway, though essential for deletion of TEs and the youngest IESs, is dispensable for excision of older IESs, implying that other recognition mechanisms remain to be discovered. The project aims at testing the hypothesis that DNA methylation is involved and includes two main objectives: (1) to determine whether stably maintained patterns of methylation in the germline genome may contribute to the recognition and excision of scnRNA-independent IESs, and (2) to determine whether scnRNA-dependent rearrangements themselves may require the targeting of transient DNA modifications during development.

**Keywords:** epigenetic, paramecium, ancient transposable element

---

<sup>\*</sup>Speaker

---

# The evolutionary depth of Sireviruses transposable elements in plants

Julie Dazeniere\*<sup>1</sup> and Alexandros Bousios<sup>2</sup>

<sup>1</sup>University of Sussex, School of Life Sciences (UoS) – University of Sussex, Falmer Campus, Brighton, BN1 9RH, United Kingdom

<sup>2</sup>University of Sussex, School of Life Sciences (UoS) – Brighton BN1 9RH, United Kingdom

## Abstract

Transposable elements (TEs) represent a large portion of plant genomes. Several TEs have been thoroughly investigated within specific hosts or among closely related species, but large-scale evolutionary analyses of TEs across the plant tree of life are currently under-represented. Given that numerous plant species are now fully sequenced, the opportunity arises for such studies to take place. Sireviruses are a TE genus exclusive to plants, with a genome structure unlike any other TE group investigated so far. Using MASiVE, a purpose-built algorithm to sensitively identify full-length Sireviruses, we scanned the genomes of 148 plants ranging from Bryophyta to Angiosperms, identifying 205,261 elements. Sireviruses are present in both Gymnosperms and Angiosperms, suggesting they appeared at least ~385 million years ago (Mya) when these two plant lineages split. Their amplification success ranges across hosts from a few copies in rice to 20% of the maize genome. Sireviruses mostly underwent activity bursts in recent evolutionary times (< 1Mya), even though they were active earlier in some species (e.g. ~6.5Mya in *Prunus*). Finally, Sireviruses could help us understand the evolution of their host: we showed that *Gnetum montanum*, a gnetophyte whose position in relation to seed plants is controversial because of its genomic features, may in fact be more closely related to Angiosperms. Overall, Sireviruses represent a critical component of plant genomes that deserve further investigation.

**Keywords:** plants, transposable elements, Sireviruses, evolution, phylogeny

---

\*Speaker

---

# Misexpression of genes and transposable elements in *Drosophila arizonae* and *D. mojavensis* hybrids

Cecilia Artico Banho\* , Claudia Carareto<sup>1</sup>, and Cristina Vieira<sup>2</sup>

<sup>1</sup>São Paulo State University (UNESP), Institute of Biosciences, Humanities and Exact Sciences (UNESP/IBILCE) – 2265, Cristóvão Colombo Street, Jardim Nazareth, São José do Rio Preto, São Paulo State, 15054-000, Brazil, Brazil

<sup>2</sup>Laboratoire de Biométrie et Biologie Evolutive UMR 5558 – Université Claude Bernard - Lyon I, CNRS : UMR5558, Université de Lyon, Université Lyon 1 – 43 Bld du 11 Novembre 1918 69622 VILLEURBANNE CEDEX, France

## Abstract

Interspecific hybridization is a stress condition, which can cause several consequences on the hybrid genomes. In *Drosophila* species with high divergence time, this process can lead to sterility and/or inviability by misregulation of genes and TEs. However, the consequences in recently diverged species it is not clear. *Drosophila mojavensis* and *D. arizonae* are an useful biological model for speciation studies, once they present recent divergence time (~1,5 m.y) and overlapping habitats, constituting allopatric and sympatric populations. They also can produce hybrids in laboratory, which present different phenotypes regarding cross direction and the source of maternal population. In order to analyze the impact of hybridization on the post-zygotic reproductive isolation, we have sequenced the transcriptomes from ovaries and testes of *D. arizonae*, *D. m. wrigleyi* and their reciprocal hybrids. Gene and TE expression analyses have shown that the most of genes and TEs present conservative expression levels related to parental lines. We have found that 84.6% and 87.6% of the genes are conservative in ovaries of HA (*D. m. wrigleyi* females x *D. arizonae* males) and HB (reciprocal cross) respectively. In testes we have seen 69.7% and 66% of conservative genes in HA and HB, respectively. For TEs we have found more conservative sequences in hybrid ovaries (HA=74.5% and HB=76.1%) than in testes (HA=55.8% and HB=55.3%). Among the differentially expressed genes and TEs, we have found 26 overexpressed genes in HA and HB ovaries, and 26 and 18 underexpressed genes in HA and HB, respectively. However, when we look at the testes, it was verified 61 and 114 overexpressed genes in HA and HB, while we have found 150 and 380 genes underexpressed in HA and HB, respectively. For TEs we have verified a similar pattern, once we have more misregulated TEs in female than male germline. In HA testes are 19 overexpressed and 2 underexpressed TEs, while 14 overexpressed and 12 underexpressed TEs are present in HB testes. On the other hand, in HA ovaries are 7 overexpressed and 4 underexpressed TEs, and in HB ovaries just 6 overexpressed TEs were found. This results show more instability in testes than in ovaries, which is in accordance with the phenotypic data, since it was reported that F1 hybrid males are sterile while females are fertile. When we looked at the misregulated genes in testes (mainly underexpressed genes), we have found, performing gene ontology analyses, that most of the down-regulated genes are related to the spermatid formation, cytoskeleton and microtubule organization, meiosis

---

\*Speaker



and establishment of mitotic spindle localization, which are essential functions for reproduction. Regarding the TEs overexpressed in hybrid testes, we have verified that most of them are LTR elements (47.3% in HA and 64.2% in HB). This TE overexpression in hybrid testes could be influencing somehow in the gene expression, since LTR retrotransposons in and around genes can play a role in

**Keywords:** repleta group, hybridization, reproductive isolation

---

# Transposable Elements as agents of adaptation in the invasive species *Drosophila suzukii* ?

Vincent Mérel<sup>\*1</sup>, Marie Fablet<sup>1</sup>, Matthieu Boulesteix<sup>1</sup>, Arnaud Estoup<sup>2</sup>, Patricia Gibert<sup>1</sup>, and Cristina Vieira<sup>1</sup>

<sup>1</sup>Laboratoire de Biométrie et Biologie Evolutive UMR 5558 – Université Claude Bernard - Lyon I, CNRS : UMR5558, Université de Lyon, Université Lyon 1 – 43 Bld du 11 Novembre 1918 69622 VILLEURBANNE CEDEX, France

<sup>2</sup>Centre de Biologie pour la Gestion des Populations (UMR CBGP) – Centre de Coopération Internationale en Recherche Agronomique pour le Développement : UMR55, Centre international d'études supérieures en sciences agronomiques : UMR1062, Institut national de la recherche agronomique [Montpellier] : UMR1062, Université de Montpellier : UMR1062, Institut de Recherche pour le Développement : UMR1062, Institut national d'études supérieures agronomiques de Montpellier – 755 avenue du Campus Agropolis, 34988 Montferrier sur Lez, France

## Abstract

Over the past few years we have witnessed an increase in the occurrence of biological invasions, which are often considered as having a negative impact on both the economy and environment. The understanding of population dynamics during an invasion and the associated molecular processes is then essential to elaborate efficient managing strategies. Considering their ability to generate mutations and modify gene expression, especially in case of environmental changes, transposable elements (TEs) could play an important role in the adaptation of invasive populations to their new environment. The crop pest *Drosophila suzukii* is a perfect model to address this question. Indeed, this species native from Asia and currently invading Europe and America provides a unique opportunity to study an ongoing invasion. Furthermore its fully sequenced genome and phylogenetic proximity to *D. melanogaster* facilitate genomic analyses. Using genomic sequencing data from 22 populations worldwide and bioinformatics programs we studied TE insertions frequencies regarding invasive and native areas of *D. suzukii*. We used these TE insertions frequencies to discriminate insertions potentially evolving under positive selection. We further examine the gene vicinity to determine the potential impact of the candidate TE insertions.

**Keywords:** Transposable Elements, adaptation, invasion

---

<sup>\*</sup>Speaker

---

# How to deal with environmental changes: molecular characterisation of mechanisms on invasive species model

Pierre Marin<sup>\*†1</sup>

<sup>1</sup>Laboratoire de Biométrie et Biologie Evolutive (LBBE) – Université Claude Bernard Lyon 1, Institut National de Recherche en Informatique et en Automatique, Centre National de la Recherche Scientifique – 43 Bld du 11 Novembre 1918 69622 VILLEURBANNE CEDEX, France

## Abstract

Evolution by natural selection of genetic variants is often assumed to be a long time scale adaptive mechanisms. However, an increasing number of examples highlight rapid adaptation within a short time, that can be relevant in the context of global changes. The underlying genetic or non genetic mechanisms involved in these rapid adaptations are still poorly understood and require further investigations. Transposable elements (TEs), often considered as non relevant part of the genome, can also play a role in rapid adaptation. Their insertion next to genes can confers a selective advantage as shown in several cases (i.e. *Drosophila* oxidative stress resistance).

Invasive species, which by definition encounter new/different environments are good models to mimic rapid adaptation. *Drosophila suzukii* is a recent invasive species, native from Asia, which concomitantly invaded U.S.A and Europe in 2008.

We asked the question if populations from *D. suzukii* present canalized response and/or local adaptation to changes in the environment, such as cold and oxidative stress. A first step was to characterise phenotypic responses of these populations from Japan, U.S.A. and Europe, then to evaluate the changes in the transcriptome between populations and environmental conditions. We found hundreds of genes differentially expressed (DE), with an important genotype:environment effect (GxE). We also looked to characterize TEs potential in the contrasted phenotypic responses by their impact on DE genes and their activity during stress.

**Keywords:** transposable elements, invasive species, environmental changes, stress, molecular mechanisms

---

<sup>\*</sup>Speaker

<sup>†</sup>Corresponding author: pierre.marin@univ-lyon1.fr