International congress on transposable elements (ICTE 2024) in Saint Malo: breaking down transposon waves and their impact

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Mobile DNA

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International congress on transposable elements (ICTE 2024) in Saint Malo: breaking down transposon waves and their impact

Pascale Lesage[1*], Emilie Brasset[2], Gael Cristofari[3], Clément Gilbert[4], Didier Mazel[5], Rita Rebollo[6] and Clémentine Vitte[7]

Abstract

From April 20 to 23, 2024, three hundred ten researchers from around the world gathered in Saint-Malo, France, at the fourth International Congress on Transposable Elements (ICTE 2024), to present their most recent discoveries on transposable elements (TEs) and exchange ideas and methodologies. ICTE has been held every four years since 2008 (except in 2020, when it was exceptionally transformed into a seminar series due to the Covid-19 pandemic) and is organized by the French network on Mobile Genetic Elements (CNRS GDR 3546). This fourth edition offered two keynote presentations and four sessions presenting the latest findings and encouraging discussions on the following topics: (1) TEs, genome evolution and adaptation; (2) TEs in health and diseases; (3) TE control and epigenetics; (4) Transposition mechanisms and applications. The 2024 edition also included a half-day satellite workshop on new challenges in TE annotation, organized in collaboration with the TE Hub. The meeting gathered long-term TE enthusiasts, as well as newcomers to the field, with 77% of the participants attending ICTE for the first time.

Introduction

Transposable elements (TEs), also known as transposons or mobile DNA, are present throughout the tree of life. They play a major role in the biology of prokaryotes and eukaryotes, have implications in agriculture and medicine and are useful biotechnology tools. Given their fascinating ability to move within genomes, along with their structural and functional impact on host genomes, a wide range of research is dedicated to TEs, in a broad spectrum of organisms, exploring various biological processes and methodologies.

The goal of the fourth International Congress on Transposable Elements (ICTE 2024) was to provide a multidisciplinary forum through which scientists from various scientific areas could meet and benefit from each other's expertise. The themes covered diverse fields such as evolution, epigenetics, biochemistry, structural biology, ecology, genomics, bioinformatics, plant biology,

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microbiology, neurobiology, aging research, and oncology. In addition to fostering idea exchanges, this meeting also increased awareness of the power of new cutting-edge technologies in DNA and RNA sequencing, genetics, genomics, biochemistry, and bioinformatics. ICTE 2024 hosted two keynote speakers, 15 invited speakers, 22 selected speakers, and around 300 poster presenters.

Organizers

E. Brasset, G. Cristofari, C. Gilbert, P. Lesage, D. Mazel, R. Rebollo, C. Vitte.

French network on Mobile Genetic Elements (GDR3546): https://www.mobil-et.cnrs.fr/en/.

Keynote lectures

Richard Durbin (University of Cambridge, Cambridge, UK) presented a keynote lecture on the latest advances in decoding the genomes of species across the tree of life. He first explained how new long-read-based genome assemblies are complete and highly accurate, spanning repeats including TEs and centromeres, and are becoming increasingly available for virtually any species whose genome has been fully sequenced. This comprehensive overview of the structure and content of genomes enables a new perspective on TE-related evolution. He then showed that comparison of diploid sequence assemblies, using the newly developed Pantera tool, allows the identification of TE sequences based on their polymorphism, thus improving TE annotation. He highlighted that in many species, TE polymorphism dominates the landscape of genetic variation, likely making TEs major contributors to functional variation. He finally presented evidence for repeated evolutionary turnover in centromeric sequences between tandem satellite-repeat based sequences and "TE nest" sequences.

In her keynote talk, **Sandra Duharcourt** (Institut Jacques Monod, Université Paris Cité, Paris, France) presented a comprehensive overview of how epigenetic mechanisms can lead to a unique and extreme strategy to silence TEs by removing them at once from the soma in the ciliate *Paramecium*. The pathway involved in TE elimination shares similarities with the nuclear Piwi-interacting RNA (piRNA) pathway: germline-specific piRNAs guide histone modifications on TEs, yet with an evolutionary twist. Instead of using a conventional heterochromatin-targeting histone H3 lysine 9 (H3K9) methyltransferase like the G9A or SUV39 enzymes in animals, the small RNA machinery recruits the ciliate ortholog of the Polycomb Repressive Complex 2 (PRC2) that has a dual substrate specificity on lysine 27 and lysine 9 of histone H3. Once they are produced, Piwi-bound small RNAs are selectively degraded, leaving only those corresponding to TEs, which eventually triggers TE sequence elimination. Several factors, including *Paramecium* Gtsf1, were shown to physically interact with Piwi and to be required for the coordinated degradation of Piwi and its bound small RNAs.

Session 1. TEs, genome evolution and adaptation

This session was rich in exploring the negative and positive impacts of TEs on their hosts. **Tanay Ghosh** (Altos Labs-Cambridge Institute of Science, Cambridge, UK) illustrated that TEs can be beneficial to their hosts through their co-option to underlie key cellular functions. He showed that *RetroMyelin*, a retrotransposon RNA of retroviral origin present in all jawed vertebrates, is essential for the expression of myelin genes. Using rats as a model, *RetroMyelin* was shown to bind SOX10 transcription factor, this binding being essential for regulating the transcription of Mbp, a major protein constituent of myelin. It functions in rats, zebrafish, and frogs, highlighting a central role for retroviral endogenization in the emergence of vertebrate myelin. TE co-option also occurred recurrently in non-vertebrate organisms, as reported by **Irina Arkhipova** (Marine Biological Laboratory, Woods Hole, USA), who described *rvt* genes. These genes form a large group of domesticated Reverse-Transcriptase (RT)-derived enzymes with a broad cross-kingdom taxonomic distribution. They show strong transcriptional inducibility by a diverse range of environmental stresses. Found in eukaryotes and bacteria, they are likely of ancient origin, predating that of other RT-derived genes such as *TERT* and *Prp8*.

Another two talks highlighted how TEs can be essential to centromere function and evolution. First, **Rob Martienssen** (Howard Hughes Medical Institute, Cold Spring Harbor Laboratory, NY, USA) showed that *ATHILA* retrotransposon small RNAs can rescue the centromere 5 mis-segregation observed in mutants impaired in both DECREASE IN DNA METHYLATION1 (DDM1) and RNAi pathways. He proposed a model in which the insertion of *ATHILA* silences centromeric transcription, while simultaneously making centromere function dependent on retrotransposon small RNAs in the absence of DDM1. Interestingly, the human homolog of DDM1, HELLS, is also required for centromere function and underlies ICF syndrome (Immunodeficiency, Centromere function, and Facial abnormalities). Second, **Cécile Courret** (Université Paris-Saclay, Gif-sur-Yvette, France) discovered that centromeric sequences underwent dramatic reorganization in three *Drosophila* species, *D. simulans*, *D. sechellia and D. mauritiana*, involving recurrent shifts between retroelement and satellite DNA within less than 250,000 years. The results highlight the rapid turnover of centromeric sequences among the *melanogaster* clade, likely caused by recurrent genetic conflict.

Evidence is also emerging that, beyond old TEs, active ones could be beneficial to the host. First, **Cédric**

Feschotte (Cornell University, Ithaca, NY, USA) tested the provocative idea that transpositionally active TEs are required for embryonic development. Using zebrafish as a model, he showed that two related endogenous retrovirus families, Bhikhari-1 and Bhikhari-2, are both recently active and transcribed in the mesoderm and neural crest, respectively. Through knock-down and rescue experiments, he showed that the GAG protein encoded by Bhikhari-1 is required for mesoderm development, while the one encoded by Bhikhari-2 causes defects in neural crest development, both proteins having an intrinsic ability to modulate cell adhesion/migration in a cell-autonomous fashion. **Josefa Gonzalez** (Institute of Evolutionary Biology, CSIC, Barcelona, Spain) highlighted that specific TE copies of actively-transposing families may also contribute to the adaptation of insects. In *Drosophila*, polymorphic TEs pinpoint regions under selection overlooked by SNPs, and combined analysis of SNPs and TEs provides a more complete picture of the genetic basis of adaptation. In *D. montana*, a species adapted to harsh cold environments, nearly 511 new TE consensus sequences have been identified, and half of the cold-tolerant genes contain TE insertions that harbor conserved regulatory sequences. She also presented ongoing work on the role of TEs in the urban adaptation of *Anopheles* mosquitoes.

Several speakers also tackled the question of how TEs move between cells or species *via* horizontal transfer and the consequences of these transfers. While the envelope ORF typically provides infectious capacities to many retroviruses and retrotransposons, **Maya Voichek** (Institute of Molecular Biotechnology, Vienna, Austria) reported the discovery of a non-enveloped endogenous retrovirus able to transit between cells in the *Drosophila* ovary. Infectivity is likely conferred by a unique short protein encoded by the retroviral genome, which has structural features similar to known cell-cell fusogens, and is predicted to be widespread among LTR retrotransposons/retroviruses in insects. **Alejandro Burga** (Institute of Molecular Biotechnology, Vienna, Austria) further provided evidence that *Maverick* elements have acted as vectors of horizontal gene transfer in nematodes. Capture by *Mavericks* of a fusogen structurally similar to the glycoprotein B from Herpes simplex virus 1 allowed *Mavericks* to spread cargo genes horizontally among multiple nematode species. The results identify the first widespread vector of horizontal gene transfer in animals and highlight how the intertwined biology of viruses and TEs can impact gene flow between populations, shaping the evolution of the species that carry them. Finally, **Russell Corbett-Detig** (University of California, Santa Cruz, CA, USA) uncovered several cases where intron-generating TEs, referred to as 'introners', have been transmitted across eukaryote species through horizontal transfer. Introners were found in 693 species spanning nearly all represented eukaryotic lineages, have highly diverse transposition mechanisms, and gave rise to a large number of introns in multiple unrelated species.

Another key question addressed in this session is how and how fast hosts can evolve and counteract the activity of TEs and retroviruses. **Harmit Malik** (Fred Hutchinson Cancer Center, Seattle, WA, USA) asked how easily a major primate virus-restriction factor (TRIM5α) can evolve the capacity to restrict a set of new viruses, including HIV-1. Through deep mutation scanning, they found that most mutations generated in the 'v1' loop of TRIM5α weakly increased its antiviral capacity, and that the protein is mutationally resilient. In contrast to HIV-1, single missense mutations in the v1 loop of human TRIM5α were not able to restrict another primate lentivirus (SIVsab). While single missense mutations and combinations of such mutations are unlikely to generate a gain of restriction against this virus, human TRIM5α can acquire such capacity through small insertions in its v1 loop.

Session 2. TEs in health and disease

The session dedicated to TEs in health and disease opened with **Geoff J. Faulkner** (University of Queensland, Brisbane, Australia), who presented his work on Long Interspersed Nuclear Elements 1 (LINE-1 or L1) retrotransposition in mouse parvalbumin (PV) interneurons, both in vivo and in cultured neurons. Faulkner identified hypomethylated "escapee" L1s that drive endogenous L1 expression in this lineage, and also alter surrounding gene expression, thereby influencing neuron morphology. He introduced the idea that by studying somatic cells where L1s are active, we can unravel exapted L1 regulatory sequences. On TE regulation, **Vivien Horvath** (Lund University, Sweden) explained how SVAs are suppressed in neural progenitor cells through H3K9me3 and DNA methylation. This dual-layer repression, mediated by ZNF91, has implications for diseases like X-Linked Dystonia-Parkinsonism, where loss of DNA methylation exacerbates the condition.

At the post-transcriptional level, **Victoria Belancio** (Tulane School of Medicine, LA, USA) reported on the role of the nucleotide excision repair (NER) pathway in repressing germline and somatic L1 retrotransposition using NER-deficient mice as a model. **John Sedivy** (Brown University, Providence, RI, USA) discussed the reactivation of retrotransposons in aging human somatic tissues. This phenomenon, linked to epigenetic loss, contributes to a wide array of age-related diseases through genome instability and activation of innate immune responses in postmitotic cells.

Maria-Carla Saleh (Institut Pasteur, Paris, France) and **Ana Ariza-Cosano** (Genyo, University of Granada,

Spain) offered a different perspective, presenting beneficial roles of TEs. Saleh described the active participation of retrotransposons in insect antiviral immunity, through reverse transcription of viral RNA into viral DNA, which boosts antiviral immunity and is necessary for insect survival upon infection. Ariza-Cosano's research in zebrafish suggests that a small subset of endogenous retroviruses ERV1-3 copies have co-evolved with the host and integrated into the conserved Nodal signaling pathway, with their mRNA and/or encoded proteins playing a crucial role in somitogenesis.

Kathleen H. Burns (Dana-Farber Cancer Institute, Boston, MA, USA) and **Joshua T. Dubnau** (Stony Brook University, NY, USA) focused on the role of TEs in disease. Burns reviewed evidence nominating LINE-1 ORF1p as a cancer biomarker that can be detected in peripheral blood using ultrasensitive assays, and described LINE-1 ORF2p as a genome mutator, promoting chromosomal instability in cancers, while also creating dependencies of tumors on specific DNA repair pathways. Dubnau discussed the role of retrotransposons and endogenous retroviruses in neurodegenerative diseases, particularly those involving cytoplasmic aggregates of the TDP-43 protein, such as amyotrophic lateral sclerosis (ALS). He showed evidence of a feedback loop between TDP-43 aggregation and retrotransposon or endogenous retroviral element (ERV) expression, each capable of triggering the other, both in flies and human cells. He also suggested that ERVs contribute to the intercellular spread of this toxic cascade from glial cells to neurons.

Concluding the session, **Julia Fuchs** (Collège de France, Paris, France) presented a potential novel mechanism of TE-mediated cellular dysfunction, relevant to neurodegenerative diseases. Exploring ORF1p expression and subcellular localization in neurons, she demonstrated ORF1p interactions with nuclear proteins and its impact on nuclear envelope integrity.

Session 3. TE control and epigenetics

This session delved into the dynamic interplay between TEs and epigenetic control across various organisms, highlighting the evolutionary innovations that have emerged to balance the benefits and risks associated with these genomic elements.

The first two presentations highlighted the intricate regulatory mechanisms governing TE control in *Drosophila* germ cells. In these cells, the majority of piRNA populations that silence TE expression originate from dual-strand piRNA clusters, *via* an elaborate protein machinery centered on the heterochromatin protein 1 homolog, Rhino. Although Rhino is recruited to a subset of piRNA clusters via Kipferl, a zinc finger protein, **Abdou Akkouche** (Institute of Genetics, Reproduction and Development, Université Clermont Auvergne, France) described a Kipferl-independent mode of Rhino targeting, which depends on Enhancer of Zeste, the histone H3 lysine 27 methyltransferase, and the trimethylation of lysines 9 and 27 on histone H3 (H3K9me3 and H3K27me3), revealing a role for dual histone modifications in the specificity of protein binding to chromatin. **Maria Ninova** (University of California, Riverside, CA, USA) used diGly proteomics to identify SUMOylation sites in hundreds of proteins within the *Drosophila* ovary, with a notable enrichment of piRNA pathway proteins involved in TE control. Her research revealed that key effectors of piRNA-dependent TE silencing, such as Piwi, Spn-E, Mael, and Panx, undergo regulated SUMO modification. Interestingly, the SUMOylation of Spn-E and Mael is dependent on Piwi, whereas Panx SUMOylation is not. **Ronald Van Rij** (Radboud University Medical Center, Nijmegen, Netherlands) studied piRNA expression in somatic tissues across various arthropod species. He showed how the piRNA pathway is crucial in silencing LTR-retrotransposons in the soma of *Aedes albopictus*. His results highlight the importance of transcriptional silencing mechanisms in regulating TE activity and provide valuable insights into the molecular strategies that organisms use to control potentially harmful TE elements.

5-methylcytosine (5mC) is a DNA modification present in eukaryotes, primarily involved in TE silencing and gene regulation. **Deborah Bourc'his** (Institut Curie, Paris, France) reported a newly discovered restrictive pathway that specifically targets young endogenous retroviruses in mouse embryonic stem cells. This pathway involves the chromatin reader SPIN1 and its co-factor SPINDOC. The SPIN1-SPINDOC complex exerts its effects through the recruitment of chromatin remodelers and the stabilization of the DNA methylation machinery. These findings underscore the complexity and specificity of epigenetic mechanisms in maintaining genomic integrity. **Leandro Quadrana** (Université Paris Saclay, Gif-sur-Yvette, France) presented collaborative work with Taku Sasaki, where they identified and characterized diverse anti-silencing systems encoded by DNA TEs in plants. These systems contain coiled-coil dimerization domains and unrelated DNA-binding pockets and exhibit remarkable sequence specificity. They bind to specific DNA sequences within highly heterochromatic regions, inducing loss of DNA methylation and TE activation. These findings reveal the important role of anti-silencing factors in the ongoing evolutionary arms race between hosts and TEs.

In studying protists, **Alex de Mendoza** (Queen Mary University of London, UK) discovered that *Amoebidium*, one of the few unicellular eukaryotes closely related to animals that retains a full DNA methylation system,

contains hundreds of viral insertions in its genome, including endogenized giant viruses up to 200 kb long, which are silenced by DNA methylation. Experimental removal of DNA methylation leads to viral and TE transcriptional reactivation and suggests that this epigenetic mark allows large-scale mixing of host and viral genomes, highlighting the potential ancestral role of 5mC in regulating giant virus endogenizations. In insects, antiviral immunity is partly mediated by small RNAs. **Marie Fablet** (Laboratoire de Biométrie et Biologie Evolutive, Lyon, France) described how *Drosophila* C Virus (DCV) infection induces a release of TE control, which in turn participates in the reduction of viral replication. Her data illustrate the complex interactions between the host, TEs, and viral pathogens, with TEs contributing to the arms race against viral infections.

The work of **Sophie Lanciano** (Université Côte d'Azur, Nice, France) significantly advanced our understanding of the regulation of L1 expression at the individual copy level. She highlighted that L1 methylation does not necessarily reflect its expression level, challenging previous assumptions about the relationship between methylation and TE activity. **Christine Beck** (The Jackson Laboratory for Genomic Medicine and University of Connecticut Health Center, Farmington, CT, USA) identified thousands of polymorphic TE insertions and structural variants across 64 human haplotypes, revealing the significant impact of TEs on genomic architecture. Her work highlights the role of TEs in creating genetic diversity through retrotransposition and genomic rearrangements. This research underscores the importance of TEs in human genetic variation and their potential effects on health.

Session 4. Transposition mechanisms and applications

This last session highlighted the fascinating diversity of transposition mechanisms, enriching the toolbox of TE-derived genome engineering systems that can be used for medical or technological purposes. **Sam Sternberg** (Columbia University, New York, NY, USA) presented a novel example of molecular innovation between CRISPR-Cas immune systems and TEs, concerning the TE protein TnpB that, like Cas12 and Cas9, uses a guide RNA to target complementary, double-stranded DNA for cutting. TnpB has been domesticated multiple times during evolution, generating nuclease-dead, RNA-guided transcription factors, one of which was co-opted by bacteriophages and viruses to remodel the host flagella organelle. Conjugative TEs contribute to the emergence of multidrug-resistant pathogens, by driving horizontal gene transfer and the spread of antibiotic resistance genes across bacteria. **Orsolya Barabas** (University of Geneva, Switzerland) described how conjugative TEs mediate gene transfer and promote the spread of antibiotic resistance in bacteria, and presented high-resolution crystal and cryo-EM structures of protein-DNA assemblies involved in the conjugation of a widespread element from Gram-negative bacteria. These structures revealed how host and TE proteins coordinate the precise cutting, exchange, and rejoining of DNA strands in a controlled manner. Bacteriophages (phages) also facilitate horizontal transfer and contribute to the evolution and diversity of prokaryotes. **Jose Penades** (Imperial College London, UK) presented new and unpublished results demonstrating how a family of phage-inducible chromosomal islands hijacks different phage tails to extend their spread both intra- and inter-species. This new strategy promotes the widespread dissemination of these elements in nature. Integrons are bacterial genetic systems capable of storing and expressing genes embedded in cassettes, and are involved in bacterial adaptation to changing environments. **Baptiste Darracq** (Institut Pasteur, Paris, France) showed that the integron of *Vibrio cholerae* accumulates numerous cassettes conferring resistance to phages at a very low cost to the bacterial host. Activating the recombinatorial properties of integrons enables their expression and anti-phage activity.

The next three presentations focused on specific TE regulatory mechanisms in different biological contexts. **Mireille Bétermier** (Université Paris-Saclay, Gif-sur-Yvette, France) presented new and unpublished data showing that a condensin I complex helps the domesticated transposase PiggyMac to carry out programmed DNA elimination of TE DNA and related sequences from the germline genome during sexual reproduction in *Paramecium*. Condensin is known for its conserved role in chromosome compaction and segregation during mitosis and meiosis. These data highlight a non-canonical role for a eukaryotic condensin in a non-mitotic process. The presence of extrachromosomal circular DNA (eccDNA) is associated with TE activity. **Marie Mirouze** (Institut de Recherche pour le Développement, Perpignan, France) described how nanopore sequencing of eccDNA improves the characterization of these circular molecules and the identification of active TE families in different plant species. Using a hypomethylated mutant accumulating eccDNA in *Arabidopsis thaliana*, they could detect an impact of eccDNA on genome stability with tandem duplications notably at pathogen-responsive genes, suggesting that a high load of eccDNA may alter DNA repair pathways, triggering the accumulation of structural variants. **Severine Chambeyron** (Institute of Human Genetics, Montpellier, France) reported a genetic model where the temporary suppression of the piRNA pathway in *Drosophila* led to the activation of various TEs. Using long-read sequencing, they identified new integration sites for four endogenous retroviruses, each with distinct

epigenetic signatures of open chromatin and showed tissue-specificities in their expression. One of them, ZAM, has an extended period of expression that aligns with the open chromatin state of its preferred landing sites during late embryonic development. The significance of this niche partitioning in terms of potential competition between LTR retrotransposons within a genome is an open question.

The ORF2 protein (ORF2p) of L1 encodes reverse transcriptase (RT) and endonuclease (EN) activities and has been linked to cancer, autoimmunity, and aging. The two last talks in this session reported the first crystal and Cryo-EM structures of ORF2p, shedding light on the L1 transposition mechanism and enabling the design of retrotransposon proteins for gene therapy. **Martin Taylor** (Harvard Medical School, now at Brown University, Providence, RI, USA) presented high resolution structures of ORF2p Core (lacking EN and C-terminal domains) and low-resolution of full-length ORF2p, which combined with biochemical assays, reveal novel domains, conformational flexibility, and explain activities of nucleoside reverse transcriptase inhibitors. The data indicated that ORF2p is both highly efficient and processive, suggesting that host interference rather than enzyme dysfunction is a cause of abortive reverse transcription. **Akanksha Thawani** (University of California, Berkeley, CA, USA) showed a high-resolution cryo-EM structure of ORF2p reverse transcribing Alu SINE RNA native template to generate complementary DNA and presented biochemical reconstitutions of target-primed reverse transcription (TPRT) by ORF2p, where the enzyme independently nicks the target DNA to prime reverse transcription of template RNA. Strikingly, the target DNA architecture ideal for TPRT by ORF2p resembles the lagging strand in replication forks.

Flash talks and poster prizes

In addition to these thematic speaker sessions, two poster sessions took place, with over 300 posters, offering the opportunity for lively exchanges on TEs. Among them, several were introduced with flash talks by **Pierre Bourguet** (Gregor Mendel Institute of Molecular Plant Biology, Vienna, Austria), **Rocio Enriquez-Gasca** (The Francis Crick Institute, London, UK), **Florian Full** (University Medical Center, Freiburg, Germany), **Erin Kelleher** (University of Houston, TX, USA), **Brice Letcher** (Ecole Normale Supérieure de Lyon, France), **Miriam Merenciano** (Université Claude Bernard Lyon 1, France), **Charlotte Proudhon** (Université de Rennes, France), and **Manvendra Singh** (Max Planck Institute for Multidisciplinary Sciences, Göttingen, Germany).

Three posters received the best poster award following a vote involving all participants: '*GraffiTE: a Unified Framework to Analyze Transposable Element Insertion Polymorphisms using Genome-graphs*' presented by **Clément Goubert** (University of Arizona, Tucson, AZ, USA); *'How genes endure intronic transposable elements'* by **Victor Billon** (Université Côte d'Azur, Nice, France); and *'Deciphering the role(s) of PRC2-Ez*L1 *mediated histone H3 modifications in programmed DNA elimination in Paramecium'* by **Thomas Balan** (Institut Jacques Monod, Université Paris Cité, France).

TE Hub satellite workshop: new challenges in TE annotation

A half-day workshop with 75 participants was organized at the initiative of TE Hub to discuss the need for a unified benchmark for the evaluation of transposable element annotation methods. **Ting-Hsuan Chen** (Plant and Food Research, Lincoln, New Zealand), **Robert Hubley** (Institute for Systems Biology, Seattle, USA), **Hadi Quesneville** (Unité de recherche en génomique et bioinformatique, Versailles, France), and **Arian Smit** (Institute for Systems Biology, Seattle, USA), were invited to present their experience and approach to benchmarking TE annotation methods. From the discussion, emerged the creation of an expert group on benchmarking, moderated by **Clément Goubert** (University of Arizona, Tucson, AZ, USA) and **Johann Confais** (Unité de recherche en génomique et bioinformatique, Versailles, France). This group will meet regularly with a specific channel, #te-hub-benchmark on TransposonsWorldwide Slack, and report back to the general group. The expert group mission is to establish guidelines for the successful creation of a community-driven benchmark focusing on TE annotation, collect and standardize ground truth datasets from simulations or processed real data, create a software prototype and carry out evaluations. This strategy will then be applied to other analyses related to TE requiring the development of benchmarks. Workshops will be organized to assess progress and promote the benchmarks developed. A YouTube video of the session is available at https://www.youtube.com/watch?v=3qY06YxQpW0.

Conclusion

Overall, ICTE 2024 revealed new facets of TEs and their complex interactions with host genomes and was a great success. The 310 participants discovered the latest scientific advances related to TE in the magnificent setting of the city of Saint-Malo. The next ICTE is scheduled for April 2028. Until then, other international congresses dedicated to mobile DNA will take place, demonstrating the vitality of this scientific field. Already announced: Transposable Elements meeting (Cold Spring Harbor, USA, October 15–19, 2024); the Transposable Element workshop at the Plant and Animal Genome conference (PAG32, January 10–15, San Diego, USA), The Repetitive and Mobile Genome (Cold Spring Harbor Asia April

7–11, 2025), the FASEB conference (Porto, Portugal, July 20–24, 2025) and the EMBL conference (Heidelberg, Germany, November 4–7, 2025).

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EB, GC, CG, PL, DM, RR, CV organized the meeting and wrote the manuscript. PL coordinated the work and is the corresponding author.

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Data availability
No datasets were generated or analysed during the current study.

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
PL is Editor, GC and CG are Associate Editors, and EB, DM and CV are Editorial Board Members of Mobile DNA. GC has received honoraria for speaking engagements from Essilor Luxottica and is a compensated consultant for ONO Pharma UK.

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