



The Society for Molecular Biology and Evolution  
**Satellite Meeting on De Novo Gene Birth**

Texas A&M University - College Station, TX  
November 6<sup>th</sup>-9<sup>th</sup>, 2023

**General Program  
&  
Contribute Talks**

# Monday November 6<sup>th</sup>

<i>Event/Talk</i>	<i>Start</i>	<i>End</i>	<i>Venue</i>
<b>Registration</b>	<b>8:00</b>	<b>8:50</b>	<b>Century I&amp;II</b>
<b>Opening remarks</b>	<b>8:50</b>	<b>9:00</b>	<b>Century I&amp;II</b>
<b>Session I – Chair: Vakirlis</b>			
<b>Diethard Tautz</b> <i>“Functional studies on de novo genes from mouse”</i>	<b>9:00</b>	<b>9:30</b>	<b>Century I&amp;II</b>
<b>Covadonga Vara</b> <i>“Investigating de novo gene formation in human populations”</i>	<b>9:30</b>	<b>9:50</b>	<b>Century I&amp;II</b>
<b>Shengqian Xia</b> <i>“Evolutionary novel genes with sexual conflict effect contribute to speciation”</i>	<b>9:50</b>	<b>10:10</b>	<b>Century I&amp;II</b>
<b>Nicolas Svetec</b> <i>“The birth and function of de novo genes in the Drosophila brain.”</i>	<b>10:10</b>	<b>10:30</b>	<b>Century I&amp;II</b>
<i>Coffee break</i>	<i>10:30</i>	<i>11:00</i>	<i>Century I&amp;II</i>
<b>Eve Wurtele</b> <i>“Compiling and compelling orphan genes”</i>	<b>11:00</b>	<b>11:30</b>	<b>Century I&amp;II</b>
<b>Claire Patiou</b> <i>“Unraveling the Origin, Evolution, and Role of de novo sORFs: A Case Study in the Arabidopsis Genus”</i>	<b>11:30</b>	<b>11:50</b>	<b>Century I&amp;II</b>
<b>Claudio Casola</b> <i>“Widespread signatures of reduced constraints against protein degradation in the 'dark proteome”</i>	<b>11:50</b>	<b>12:10</b>	<b>Century I&amp;II</b>
<b>Lunch break/Registration</b>	<i>12:10</i>	<i>1:10</i>	<i>Century I&amp;II</i>
<b>Session II – Chair: Casola</b>			
<b>Christian Rödelsperger</b> <i>“Evolutionary dynamics of novel genes in the shark-tooth nematode”</i>	<b>1:10</b>	<b>1:40</b>	<b>Century I&amp;II</b>
<b>Junhui Peng</b> <i>“The origin and structural evolution of de novo genes in Drosophila”</i>	<b>1:40</b>	<b>2:00</b>	<b>Century I&amp;II</b>
<b>Katherine Fleck</b> <i>“Novel gene evolution and 3D chromatin organization”</i>	<b>2:00</b>	<b>2:20</b>	<b>Century I&amp;II</b>
<i>Coffee break</i>	<i>2:20</i>	<i>2:50</i>	<i>Century I&amp;II</i>
<i>Free time</i>	<i>2:50</i>	<i>3:45</i>	
<b>PLENARY LECTURE:</b> <b>Erich Bornberg-Bauer</b> <i>“The Rise and Fall (or Assimilation) of De Novo Genes in a Cellular Context”</i>	<b>4:00</b>	<b>5:00</b>	<b>Century I&amp;II</b>
<b>Mixer</b>	<b>5:30</b>	<b>7:30</b>	<b>Hullaballoo</b>

## Tuesday November 7<sup>th</sup>

<i>Event/Talk</i>	<i>Start</i>	<i>End</i>	<i>Venue</i>
<b>Registration</b>	8:00	8:50	Century I&II
<b>Opening remarks</b>	8:50	9:00	Century I&II
<i>Session III – Chair: Zhao</i>			
<b>Victor Pai</b> <i>“Microproteins that Control Cell Fate”</i>	9:00	9:30	Century I&II
<b>Luuk Broeils</b> <i>“Evolutionarily young genes in pediatric cancer”</i>	9:30	9:50	Century I&II
<b>April Rich</b> <i>“Exploring transcriptional profiles of de novo ORFs using massively integrated coexpression analysis”</i>	9:50	10:10	Century I&II
<b>Idan Frumkin</b> <i>“Random Proteins provide Evolutionary Novelty by interacting with Diverse Cellular Pathways”</i>	10:10	10:30	Century I&II
<i>Coffee break</i>	10:30	11:00	Century I&II
<b>Gisela Storz</b> <i>“How do genes-within-genes evolve?”</i>	11:00	11:30	Century I&II
<b>Zachary Ardern</b> <i>“The non-canonical translome in bacteria and beyond”</i>	11:30	11:50	Century I&II
<b>Anne O’Donnell-Luria</b> <i>“The role of non-canonical open reading frames in Mendelian disease”</i>	11:50	12:10	Century I&II
<i>Lunch break/Registration</i>	12:10	1:10	Century I&II
<i>Session IV – Chair: Vakirlis</i>			
<b>Jorge Ruiz-Orea</b> <i>“Evolutionary origins, roles and developmental regulation of human small open reading frames”</i>	1:10	1:40	Century I&II
<b>Christos Papadopoulos</b> <i>“De novo gene intra-species diversity in Saccharomyces cerevisiae”</i>	1:40	2:00	Century I&II
<b>Emilios Tassios</b> <i>“A large-scale analysis of genetic novelty in budding yeast”</i>	2:00	2:20	Century I&II
<b>Kazuma Nakatani</b> <i>“NCYM, a human de novo evolved gene product, promotes tumorigenesis in a mouse cholangiocarcinoma organoid model”</i>	2:20	2:40	Century I&II
<b>Victor Luria</b> <i>“Novel genes enable protein structural innovation and function in the brain”</i>	2:40	3:00	Century I&II
<i>Coffee break</i>	3:00	3:30	Century I&II
<i>Free time</i>	3:30	4:30	Century I&II
<b>Poster session</b>	4:30	6:30	Hullaballoo & Reveille

## Wednesday November 8<sup>th</sup>

<i>Event/Talk</i>	<i>Start</i>	<i>End</i>	<i>Venue</i>
<b>Opening remarks</b>	<b>8:50</b>	<b>9:00</b>	<b>Venue</b>
<i>Session V – Chair: Luria</i>			
<b>Manyuan Long</b> <i>“Phenotypic Effects of De Novo Genes in Drosophila and Underling Evolutionary Forces”</i>	<b>9:00</b>	<b>9:30</b>	<b>Century I&amp;II</b>
<b>Josue Barrera-Redondo</b> <i>“Tracking down the evolution and functional integration of de novo emerged genes in the brown alga”</i>	<b>9:30</b>	<b>9:50</b>	<b>Century I&amp;II</b>
<b>Anna Grandchamp</b> <i>“Study of mutations underlying de novo gene emergence”</i>	<b>9:50</b>	<b>10:10</b>	<b>Century I&amp;II</b>
<b>Li Zhao</b> <i>“The dynamics and regulatory mechanisms of de novo gene expression”</i>	<b>10:10</b>	<b>10:30</b>	<b>Century I&amp;II</b>
<i>Coffee break</i>	<i>10:30</i>	<i>11:00</i>	<i>Century I&amp;II</i>
<b>David Begun</b> <i>“Investigating the population biology of de novo genes in Drosophila”</i>	<b>11:00</b>	<b>11:30</b>	<b>Century I&amp;II</b>
<b>Nikolaos Vakirlis</b> <i>“Ancestral Sequence Reconstruction as a tool to study de novo gene birth”</i>	<b>11:30</b>	<b>11:50</b>	<b>Century I&amp;II</b>
<b>Somya Mani</b> <i>“Population model characterizes genomic regions that are fertile for de novo gene birth”</i>	<b>11:50</b>	<b>12:10</b>	<b>Century I&amp;II</b>
<b>Luncheon</b>	<i>12:10</i>	<i>1:40</i>	<i>Century I&amp;II</i>
<i>Session V – Chair: Luria</i>			
<b>Christina Cheng</b> <i>“Repeat Sequences As Genetic Raw Material For New Genes Besides Antifreeze Proteins”</i>	<b>1:40</b>	<b>2:10</b>	<b>Century I&amp;II</b>
<i>Coffee break</i>	<i>2:10</i>	<i>2:40</i>	<i>Century I&amp;II</i>
<b>PLENARY LECTURE</b> <b>Anne-Ruxandra Carvunis</b> <i>“Systems Approaches to Decipher the Mechanisms of Evolutionary Innovation”</i>	<b>3:00</b>	<b>4:00</b>	<b>Century I&amp;II</b>
<b>Round-table Discussion</b> <b>Chairs: Luria/Vakirlis</b>	<b>4:30</b>	<b>5:30</b>	<b>Century I&amp;II</b>

## Thursday November 9<sup>th</sup>

<i>Event/Talk</i>	<i>Start</i>	<i>End</i>	<i>Venue</i>
Opening remarks	8:50	9:00	Century I&II
<i>Session VI – Chair: Luria</i>			
<b>Yusuke Suenaga</b> <i>“Targeting de novo gene NCYM for cancer therapy”</i>	9:00	9:30	Century I&II
<b>Hsieh Chen</b> <i>“Investigating De Novo Gene Birth in Populus”</i>	9:30	9:50	Century I&II
<b>Slava Tretyachenko</b> <i>“Mistranslation in protein function space exploration”</i>	9:50	10:10	Century I&II
Coffee break	10:10	10:40	Century I&II
<i>Session VII – Chair: Zhao</i>			
<b>Igor Fesenko</b> <i>“Large-scale analysis of the cryptic microproteome in prokaryotes”</i>	10:40	11:00	Century I&II
<b>Amir Karger</b> <i>“Improving gene age estimation”</i>	11:00	11:20	Century I&II
<b>Aaron Wacholder</b> <i>“A vast pool of short-lived de novo genes contribute to phenotype and fitness”</i>	11:20	11:40	Century I&II
Closing remarks and Awards	11:40	12:10	Century I&II

Lunch boxes will be available at 12:00 In Century I&II

**Invited Speakers**

**Contributing Speakers**



Network:  
**TAMU Hotel-CONFERENCE**

Password: **GigemTime2023**

## TITLES OF POSTERS

### 1 - Oyinoluwa O. Bola

Department of Biological Sciences; Sam Houston State University, Texas, USA

*Construction of Fish Species Composition Surveillance Database of Lake Raven, Huntsville Texas using Environmental DNA*

### 2 - Jianhai Chen

Department of Ecology and Evolution, The University of Chicago, Chicago, IL, USA

*Novel protein-complex driven by de novo genes*

### 3 - Jae Young Choi

Department of Ecology and Evolutionary Biology, University of Kansas

*Transposition of the telomerase RNA underlies the Monkeyflower (*Mimulus*) telomere sequence diversification*

### 4 - Lin Chou

Department of Computational and Systems Biology, School of Medicine, University of Pittsburgh, Pittsburgh, PA, USA

*Recent tandem repeat expansion of a human de novo ribo-seq ORF encoded in an oncogenic miRNA MY*

### 5 - D.M.K.C. Daundasekera

Department of Biology, Texas A&M University, College Station, TX, USA

*Identifying serpentine adaptation genes by tracing evolutionary-genomic history of *Streptanthus*, *Caulanthus* and their allied genera (*Brassicaceae*)*

### 6 - Luis Delaye

Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Unidad Irapuato, Irapuato, Gto., México

*The origin of a novel gene by overprinting in *E. coli*: an overview of its discovery 15 years later*

### 7 - Md. Hassan uz-Zaman

Department of Molecular Biosciences, University of Texas at Austin, Austin, TX 78712, USA

*Emergence and persistence of proto-genes in a long-term *Escherichia coli* evolution experiment*

### 8 - Yunzhe Jiang

Program in Computational Biology and Bioinformatics, Yale University, New Haven, CT, USA

*Identification of horizontal gene transfer in *Oryza sativa* pan-genome*

### 9 - Rishabh Kapoor

Department of Organismal and Evolutionary Biology, Harvard University, Cambridge, MA, USA

*Gene fusion and horizontal gene transfer*

### 10 - Ashit Kumar Dutta

East Tennessee State University, Johnson City, TN, USA

*T->C transitions disproportionately eliminate stop codons in *Drosophila* de novo ORFs*

**11 - Vinita Lamba**

Department of Biological Sciences, University of Arkansas, Fayetteville, AK, USA  
*Exploring New Gene Formation and their Adaptive Significance in Antarctic Notothenioids*

**12 - UnJin Lee**

Laboratory of Evolutionary Genetics and Genomics, The Rockefeller University, New York, NY, USA  
*Origination of a Testis-Specific lncRNA*

**13 - Matthew A. Marano**

Department of Ecology and Conservation Biology, Texas A&M University, College Station, TX, USA  
*The evolutionary origins of orphan genes*

**14 - Daniel Marten**

Broad Institute of MIT and Harvard, Cambridge, MA, USA  
*Analysis of large human genomic datasets shows expression and mutational constraint increase with gene evolutionary age*

**15 - Mayra Mendoza**

Department of Veterinary Integrative Biosciences, School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA  
*Assembly of repetitive sequences in long read-based chromosome-level Alpaca (*Vicugna pacos*) reference genome*

**16 - Seth O'Conner**

Department of Biology UNC Chapel Hill, Chapel Hill, NC, USA  
*Investigation of *Drosophila Melanogaster* Gene Conservation Throughout 101 Drosophilid Genomes*

**17 - Adekola Owoyemi**

Department of Ecology and Conservation Biology, Texas A&M University, College Station, TX, USA  
*Winning Against Unbalanced Datasets in a Machine Learning De Novo Genes Prediction Algorithm in Angiosperms*

**18 - Nathan Rives**

Department of Biological Sciences, University of Arkansas, Fayetteville, AK, USA  
*Evolutionary Origins and Mechanisms of Fish Antifreeze Protein in Unrelated Taxa: Insights into New Gene Birth*

**19 - Nozomu Saeki**

University of Pittsburgh, Pittsburgh, PA, USA  
*Investigating the impact of *de novo* genes on ion transport and homeostasis in *Saccharomyces cerevisiae**

**20 - Isabella Simon**

Department of Biological Sciences, Sam Houston State University, Huntsville, TX, USA  
*Characterization of *dennd5a/b* during early embryonic development of zebrafish*

**21 - Jeffrey Vedanayagam**

Developmental Biology Program, Sloan-Kettering Institute, New York, NY, USA

*Meiotic drive and suppression: de novo protamine copies and hairpin RNAs fuel intragenomic arms races in the male germline*

**22 - Vighnesh Ghatpande**

Department of Molecular Biosciences, University of Texas at Austin, Austin, TX, USA

*Non-canonical translation events in preimplantation mouse development*

**23 - --**

**24 - Yen-Wen Wang**

Yale School of Public Health, Yale University, New Haven, USA

*Origins of lineage-specific elements via gene duplication, relocation, and regional rearrangement in Neurospora crassa*

**25 - Chathuri Devmika Wickramasinghe**

Department of Biology, The University of Texas at Arlington, Arlington, TX, USA

*Recurrent co-domestication of PIF/Harbinger transposable element proteins in insects*

**26 - Sara Oppenheim**

American Museum of Natural History, New York, NY, USA

*What's in a name? Strain names are poor predictors of cannabinoid concentration in commercially available Cannabis products*



### **Oral presentations format**

The speakers will present their work without interruption for the allotted time (~15 minutes for 20-minute talks, ~25 minutes for 30-minute talks, 45-55 minutes for 1 hour plenary lectures). Speakers should allow at least 3-5 minutes for questions. Questions from the audience can be asked at the end of the talk, in the time provided for question and answers, and thus **not** during the talk. Since speakers must have the opportunity to present their work, disruptions during the talks will not be tolerated. Additionally, speakers are available for discussions during the whole meeting. We encourage free and open discussions. At the same time, we must maintain civility, and keep the meeting efficient and on time.

### **Policy on harassment, discrimination and liability**

The organizers will implement the SMBE code of conduct.

The meeting organizers are dedicated to providing a safe, hospitable, and productive environment for all attendees. Accordingly, all forms of discrimination and harassment are prohibited. Behavior that undermines the integrity of intellectual discourse is an impediment to scientific progress and will not be tolerated. Unacceptable treatment of others includes (but is not limited to) harassment, stalking, belittling, discrimination, bullying/intimidation, assault, trolling, and retaliation. Any misconduct on the basis of gender, gender identity, sexual orientation, age, disability, physical appearance, race, religion, national origin, ethnicity, or other descriptive category will not be tolerated. All meeting participants must treat others with respect and consideration. Disagreements about science are normal and healthy parts of meetings. Civil and constructive criticism of someone's work for a perceived methodological flaw or a misinterpretation of results is appropriate.

The code of conduct applies to all conference participants, including staff, volunteers, and attendees. If a participant engages in harassing or discriminatory behavior, the meeting organizers reserve the right to take action ranging from a simple warning to the offender to expulsion from the conference. Clear information will be available to participant, attendees, staff, and volunteers about how to report an incident to the meeting organizers. Confidentiality of the person reporting an incident will be maintained, unless legally compelled otherwise.

Violations of the code of conduct should be reported to any co-organizer in person or via email. The contact information of all co-organizers will be readily available to the meeting participants.

Any reported violation will be investigated by the organizing committee. Consequences can range from notification/warning to the offender to expulsion from current and/or future events or blocking social media accounts.

Registration for the meeting is considered an agreement to abide by the SMBE Meetings code of conduct, which will be posted on the registration website. The code of conduct or a link to it will be further advertised at the beginning of each day of the conference and present in the meeting booklet provided to each participant.

Liability. Neither SMBE nor the meeting organizers shall be responsible for any defamatory, offensive, or illegal conduct of Meeting participants, and shall not be held liable for personal injury, property damage, theft or damage of any kind suffered by the participants at or in connection with the SMBE Annual Meeting.

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