

Conference Report

Evolution in a Changing World—Meeting Report of SMBE 2026, Copenhagen Denmark, June 28–July 2, 2026

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There is a hint of tautology in the title “evolution in a changing world” which is meant to convey how molecular evolutionists who met at the annual meeting of the SMBE in Copenhagen in late June 2026 are coping with “climate change” in the broadest sense. On the one hand, the climate for basic science, at least in the US, is changing. On the other hand, the meeting had a much more translational tone than in the past, reflecting increased emphasis on the study of how organisms are adapting in real time, as well as the implications of molecular evolutionary studies for human health.

The five plenary sessions reflect these two themes. They were excellently chosen (and presented) to convey recent trends. Current SMBE President Juliette de Meaux (University of Cologne, Germany) led off with an overview of her efforts to document genome evolution in urban populations of *Arabidopsis*. Her presentation was complemented in the final plenary given by Moisés Expósito-Alonso (University of California at Berkeley, USA) who described the results to date of a global transplant-and-evolve initiative wherein hundreds of accessions of the cress have been grown at dozens of sites to document genotype-by-environment effects on short-term adaptation. Both talks raise important concerns about declining genetic diversity and resilience, while also showing a way forward for highly collaborative consortium-driven evolutionary biology.

Emma Teeling (University College Dublin, Ireland) gave an inspiring address about bat phylogeny, updating her consortium’s two-decade-and-counting efforts to eventually sequence the whole genomes of a thousand species of bats. The rationale is simple: understanding mechanisms of aging and resistance to coronavirus morbidity, both of which she argues are a consequence ultimately of metabolic and other physiological adaptations necessary for mammalian flight. Also on a more biomedical note, Nandita Garud (University of California at Los Angeles, USA) presented her recent studies providing evidence of genomic selection in human microbiomes utilizing novel strategies to quantify linkage disequilibrium and homozygosity in complex populations of diverse microbial strains. Proving that passionate curiosity is alive and well in the research community, Mehmet Somel (Middle East Technical University, Ankara, Türkiye) gave an inspiring talk in the domain of molecular anthropology showing how analysis of multi-generation ancient DNA samples from burial sites leads to new insights into human cultural practices and kinship patterns.

The overarching themes of this conference were carried forward in the 44 parallel sessions held over the four days of the meeting. Suffice it to say that the breadth of molecular evolution on display was tremendous. That said, there were fewer evo-devo presentations than several years ago, and phylogenetics topics are more likely to be addressed at the Evolution meeting - gone are the days of spirited arguments among cladists and phyleticists at SMOE. In their place, many presentations examined applications of artificial intelligence (including a session that was so over-subscribed that the fire marshals threatened to intervene!) and novel genomic technologies, including single cell and spatial RNA sequencing in the service of comparative biology. A lovely example of this was the presentation by Margarida Cardoso Moreira (Francis Crick Institute, London, England) on how the emergence of a new cell type has been coopted on five separate occasions to drive novel patterns of placentation in Poeciliid fish. Combining whole genome sequencing, multi-omic scRNAseq and snATACseq, and contemporary fluorescent imaging, she was able to elucidate how regulatory gene networks have evolved to support transitions from egg-laying to live-bearing life history strategies.

One standout symposium focused on deep time human genomics. Organized by Leo Speidel (RIKEN, Tokyo, Japan) and Hiroki Oota (University of Tokyo, Japan), it highlighted how advances in ancient DNA and population genetic methods are expanding our ability to reconstruct human evolutionary history. Several presentations unveiled important new datasets, including a high-coverage Neanderthal genome from Goyet Cave in Belgium (Mateja Hajdinjak, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany). Other talks presented evidence for previously unrecognized "ghost" introgression into southern African Khoisan populations (Martin Kuhlwilm, University of Vienna, Austria) and demonstrated that populations across Asia and Oceania experienced multiple, distinct episodes of Denisovan introgression (Moisés Coll Marcià, Institut de Biologia Evolutiva, Barcelona, Spain). Methodological advances were equally prominent, with inverse coalescence rates identifying multiple deep admixture events, including back-migration from Eurasia into Africa (Hrushikesh Loya, University of Oxford, England). Another presentation examined how stabilizing and directional selection can reduce the predictive accuracy of polygenic scores when applied to ancient genomes (Diego Ortega-Del Vecchyo, National Autonomous University of Mexico, Mexico City). The key idea here is that selection can cause large-effect alleles to be lost over time. However, one lingering question is how strong selection on a trait needs to be before it substantially affects the accuracy of ancient polygenic scores.

Many talks and posters focused on the nexus of ecology and evolution. Cataloguing rates of change in genetic diversity is an urgent need, as are efforts to understand empirically how different classes of organism are coping with anthropogenically-induced change. Climate change, urbanization, habitat fragmentation, forced migration, and hybridization are all impacting life on earth across the Kingdoms. Still missing, unfortunately, is more explicit incorporation of quantitative genetics into molecular biology and evolution: changes in heritability are surely as important as changes in genetic diversity. Perhaps this is an area where human population geneticists and genomicists can lead the way.

Each symposium at this year's conference incorporated a substantial number of five-minute oral presentations. This format broadened participation by giving many more researchers, particularly early-career scientists, the opportunity to present their work in an oral session rather than a poster. At the same time, the compressed schedule necessarily emphasized breadth over depth, leaving less time for speakers to dive deeply into methodology or have an extended discussion with the audience. Although the format successfully showcased the diversity of research being conducted across molecular biology and evolution, future meetings may benefit from balancing these brief presentations with a greater number of 15-minute talks. Going forward, SMBE will alternate between a global meeting and extended regional meetings, with next year's global conference being held from June 20-24, 2027, in Québec City, Canada. This increased focus on regional meetings is intended to reduce environmental impact and lower travel costs, while promoting regional collaboration.

Declarations

Ethics Statement

Not applicable.

Consent for Publication

Not applicable.

Availability of Data and Material

Not applicable.

Competing Interests

Greg Gibson and Joseph Lachance are members of the Editorial Board of the journal *Human Population Genetics and Genomics*. The authors were not involved in the journal's review of or decisions related to this manuscript. The author has declared that no other competing interests exist.

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