

‘Linking phenotypic differences between species to differences in their genomes’

Prof. Michael Hiller

Senckenberg Research Institute, Frankfurt Germany



Date: Dec 9th (Tue) 2025

Time: 10:30 am – 11:30 am

Venue: Taniguchi Memorial Hall

Chairs: Daron Standley (Professor, Biken)

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***This seminar is a credit seminar for the Graduate School of Medicine**

In the first part of the talk, Michael will present TOGA (Tool to infer Orthologs from Genome Alignments) version 2.0, the completely reimplemented successor to the original method that simultaneously annotates coding genes and infers orthologs. TOGA 2.0 provides several new features, among them deep learning-based splice site predictions, which enable the method to cope with exon boundary shifts and evolutionary exon-intron structure changes.

In the second and third parts, Michael will illustrate how TOGA can help illuminate changes in genes that are linked to adaptive traits in mammals and birds. Using a comprehensive screen for positive selection across 115 mammals, he found that immune gene adaptations are most prevalent in bat, providing genomic evidence that bats possess special immune system adaptations. Using a screen for gene losses in birds, he then found that the FBP2 gene is specifically lost in hummingbirds, a nectarivorous lineage comprising the only birds capable of sustained hovering flight. Molecular dating and functional experiments suggest that FBP2 loss likely contributed to muscle adaptations required for hovering flight.

Selected Publication:

1. Morales et al. Bat genome illuminate adaptations to viral tolerance and disease resistance, 2025, **Nature**
2. Kirilenko et al. Integrating gene annotation with orthology inference at scale, 2023, **Science**
3. Osipova et al. Loss of a gluconeogenic muscle enzyme contributed adaptive metabolic traits, 2023, **Science**