

Academia Sinica scientists visiting ENS de Lyon (July 2-July 3)

Yi-Shuian Huang, Deputy Director, Institute of Biomedical Sciences, Academia Sinica



Yi-Shuian Huang focuses on **molecular neuroscience, RNA biology, and translational control**. Her research investigates how RNA modifications regulate gene expression during development and neurological function. In particular, her work examines cap 2'-O-methylation, a conserved modification found on higher eukaryotic messenger RNAs. Recent studies from her laboratory have revealed that cap methyltransferase 2 (CMTR2), beyond its established role in distinguishing cellular RNAs from foreign genetic material, plays a critical role in regulating gene expression programs during cerebellar development. Her findings demonstrate that CMTR2 controls the integrated stress response required for proper Purkinje cell maturation, highlighting an unexpected connection between RNA modification and neurodevelopment. By combining molecular, genetic, and cellular approaches, her research uncovers fundamental mechanisms that govern neuronal development, synaptic function, and memory. Overall, her work bridges RNA biology and neuroscience to explain how post-transcriptional regulation shapes brain development and function.

Chen-Hui Chen, Institute of Cellular and Organismic Biology, Academia Sinica



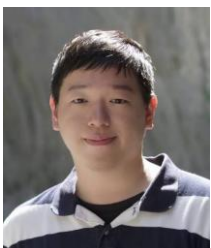
Chen-Hui Chen studies **regeneration, developmental biology, and tissue dynamics** using zebrafish as a vertebrate model system. His laboratory develops innovative multicolor cell-barcoding technologies, large-scale live imaging platforms, and quantitative computational approaches to monitor individual cells throughout living organisms. By tracking the behavior of every cell across tissues and over extended periods, his research reveals how collective cellular actions drive development, regeneration, and tissue repair. Recent work has uncovered previously unseen patterns of coordination among skin and muscle cells that only become apparent through whole-organism imaging. His group combines advanced microscopy, genetics, and image analysis to understand how cellular decisions are regulated across multiple spatial and temporal scales. Ultimately, his research seeks to uncover the principles governing collective cell behavior and tissue organization, providing insights relevant to developmental biology, regenerative medicine, and disease.

Sheng-Feng Shen, Institute of Ecology and Evolutionary Biology, Academia Sinica



Sheng-Feng Shen is an **evolutionary biologist whose research explores how organisms adapt and diversify across changing environments**. His work increasingly applies artificial intelligence and machine learning to address fundamental questions in evolution and biodiversity. By using deep learning to analyze large-scale biological datasets, including images of insects and genomic information, his research reveals hidden patterns that are difficult to detect through traditional approaches. Recent studies demonstrate how AI can reconstruct ancestral traits, predict ecological characteristics from images, and identify biological features that drive evolutionary diversification. Using moths and butterflies as model systems, his work shows how traits linked to essential functions such as flight remain evolutionarily constrained while other characteristics, including coloration and patterning, diversify extensively. More broadly, his research highlights how AI is transforming biological discovery by converting complex visual and genomic data into new insights about the evolution, ecology, and diversity of life.

Hung-Hsin Chen, Institute of Biomedical Sciences, Academia Sinica



Hung-Hsin Chen focuses on **human genetics, genetic epidemiology, and precision medicine**. His research leverages large-scale biobank resources and multi-omics datasets to uncover the genetic basis of complex diseases and traits. A major component of his work is the Taiwan Precision Medicine Initiative (TPMI), which has generated genomic and clinical data from more than 500,000 Taiwanese individuals, creating one of the largest genetic resources for non-European populations. Using genome-wide genomic analyses, his team has identified population-specific genetic architecture and causal genes underlying cardiometabolic diseases, autoimmune disorders, cancers, and infectious diseases. These discoveries have enabled the development of polygenic risk score models with strong predictive performance across multiple disease categories, validated in independent cohorts including the

Taiwan Biobank, UK Biobank, and All of Us Project. Overall, his work aims to advance precision medicine by improving disease prediction and understanding how genetic variation contributes to health outcomes in East Asian populations.

Yi-Jyun Luo, Biodiversity Research Center, Academia Sinica



Yi-Jyun Luo studies **evolutionary genomics and the origins of biological diversity, with a focus on marine invertebrates and early animal evolution**. His research integrates chromosome-scale genome sequencing, comparative genomics, single-cell transcriptomics, and evolutionary developmental biology to understand how new traits and cell types emerge. By examining large-scale genomic structural changes such as chromosome rearrangements and fusions, his work provides new insights into animal evolutionary relationships and the timing of key innovations. Recent studies of corals and related cnidarians have demonstrated how genome architecture can resolve longstanding evolutionary questions while linking the emergence of novel cell types to the evolution of coral skeleton formation. His laboratory combines genomic and cellular approaches to connect changes in genome organization with the development of new biological functions. Overall, his work advances our understanding of how genome evolution drives the origin of animal diversity and evolutionary novelty.