SCIENTIFIC PROGRAM

SESSION LECTURE

No. 21

Adaptive Evolution of Animals Room: 307A

Co-Chairs: Fumin Lei



Guojie Zhang



Day 2 October 28 th (Sunday) 13:30 – 17:00		
Time	Speaker	Title
13:30-14:00	Rasmus Nielsen University of California at Berkeley, USA	The genomic footprints of human physiological adaptation
14:00-14:30	Manyuan Long University of Chicago , USA	The second evolutionary force acting on new genes: Sexual selection and sexual conflict
14:30-15:00	Wen Wang Northwestern Polytechnical University, China	Genomes of Ruminantia animals provide insights into their phylogeny and evolution
15:00-15:30	Tea Break	
15:30-16:00	Bing Su Kunming Institute of Zoology, Chinese Academy of Sciences, China	Comparative Methylome Analyses Identify Epigenetic Regulatory Loci of Human Brain Evolution
16:00-16:30	David Nogués-Bravo Natural History Museum of Denmark	Climate change erodes genetic diversity in mammals
16:30-17:00	Guojie Zhang University of Copenhagen, Denmark	Genomic mechanisms underlying rapid radiation of birds
17:00-17:30	Fumin Lei Institute of Zoology, Chinese	What determines the high species

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Fumin Lei

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Dr. Fumin Lei is a professor of Institute of Zoology, Chinese Academy of Sciences. His research interests include avian evolution, systematics, biogeography, and molecular epidemiology of wildlife diseases (e.g. avian influenza). He is focusing on diversity and distribution, adaptive evolution of birds by phylogenomics, comparative genomics and other approaches. He is the president of China Ornithological Society and the vice-president of International Ornithologists' Union. Over 140 papers have been published in the international peer-reviewed SCI journals.



Rasmus Nielsen

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Rasmus Nielsen is Professor and Sackler Chair of Computational Biology at University of California at Berkeley. He is also a Professor at the University of Copenhagen at the Museum of Natural History. His work focuses of development and application of computational methods in genomics and evolutionary biology. He has worked extensively on elucidating genetic adaptation in humans and on understanding human migration patterns using genetic data.



Wen Wang

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Prof. Wen Wang has been studying evolutionary genomics of natural and domestic species, with focus on origin and evolution of genetic novelties in genomes. He is now leading the international Ruminant Genome Project and a strategic research program on complex traits of animals.



Bing Su

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Dr. Bing Su is a professor of Kunming Institute of Zoology, Chinese Academy of Sciences. His research focus on dissecting the genetic mechanism of human origin and evolution. He aims to understand how genetic divergence between humans and nonhuman primates leads to phenotypic and functional modifications, especially our sophisticated central nervous system and superior cognitive ability. He also studies genetic variations in human populations to reveal the role of natural selection in shaping up human genetic makeup.



Guojie Zhang

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Guojie Zhang is full Professor at Department of Biology in University of Copenhagen, Denmark. The major research interests in his group are on biodiversity genomics and genome evolution. Zhang tackles the biodiversity and evolutionary questions with large-scale comparative genomics and has revealed the molecular mechanisms underlying speciation and adaptation for a broad spectrum of animal taxa. His group is also trying to establish ants as model systems for eco-evodevo study of social behavior.



Manyuan Long

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The Edna K. Papazian Distinguished Service Professor of the department of Ecology and Evolution, University of Chicago, USA. The aims of his research are to understand how genes with novel functions originate, and also to identify the related pattern and evolutionary force.



David Nogués-Bravo

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David Nogués-Bravo is associate Professor in Historical Biogeography at the Center for Macroecology, Evolution and Climate (Natural History Museum of Denmark). His grand research objective is to unveil why species go extinct and identifying the underlying evolutionary, ecological and anthropogenic factors driven them, to reveal how ongoing and future global changes will impact the distribution and extinctions of species in the forthcoming decades. He answers these questions using biogeographical and macroecological approaches applied to large databases on the distribution of species and genes in vertebrates.