

Academia Sinica Delegation Visit MINI-SYMPOSIUM

6-7 October 2014, CRG Barcelona

Agenda

Venue: PRBB, CMRB meeting room (863), 7th floor, north wing, facing the PRBB inner square

6th of October – Monday			
Time	Speaker	Title	Location
9:45 AM	Luis Serrano (CRG)	Opening Remarks	863
9:50 AM	Weng-Hsiung Li (AS)	<u>Keynote: Golden Opportunities in Plant and Agricultural Genomics</u>	863
10:45 AM		Coffee Break	Terrace, 5th floor
Session I (11:25 am – 1:55 pm)			
11:25 AM	Guillaume Filion (CRG)	Drosophila promoters interpret the chromatin context in diverse ways	863
11:50 AM	Trees-Juen Chuang (AS)	Investigation of trans-splicing, circular RNA, gene fusion, and in vitro artifact in transcriptome sequencing data	863
12:15 PM	Rory Johnson (CRG)	Long Noncoding RNAs and Ribosomes	863
12:40 PM	Hsin-Hung Yeh (AS)	Establishment of a high throughput system for analysis of transcription factors involved in plant defense in orchids and arabidopsis	863
1:05 PM	Arcadi Navarro (UPF)	tbd	863
1:30 PM	Fyodor Kondrashov (CRG)	Modeling epistasis in molecular evolution	863
Session II (3:25 – 5:00 pm)			
3:25 PM	John Wang (AS)	A supergene causes alternative colony organization in fire ants	863
3:50 PM	Jun-Yi Leu (AS)	Hsp90 controls phenotypic variation through regulating conserved protein network hubs	863
4:15 PM	Ben Lehner (CRG)	Why are individuals different?	863
4:40 PM	tbd (CRG)	tbd	863
4:55 PM		Coffee Break	Terrace, 5th floor



7th of October – Tuesday			
Time	Speaker	Title	Location
Session III (9 – 10:50 pm)			
9:00 AM	tbd (CRG)	tbd	863
9:15 AM	tbd (CNAG)	tbd	863
9:40 AM	Hsuan-Yu Chen (AS)	Whole Genome Sequencing Approach to Identify Rare Allele and Risk of Lung Adenocarcinoma- From Big Data to Individual	863
10:05 AM	Isheng Jason Tsai (AS)	Diversity of fungi and parasites in light of their genetics and pathogenicity	863
10:30 AM	Toni Gabaldón (CRG)	An evolutionary genomics perspective on the evolutionary emergence of virulence	863
10:55 AM	Coffee Break		Terrace, 5th floor
Session IV (11:35 am – 13:10 pm)			
11:35 AM	Cedric Notredame (CRG)	Bridging the gap between between Structure and Sequence based Phylogenetic Reconstructions.	863
12:00 PM	Jia-Ming Chang (IGH)	TCS: A New Multiple Sequence Alignment Reliability Measure to Estimate Alignment Accuracy and Improve Phylogenetic Tree Reconstruction	863
12:25 PM	David Torrens (BSC)	Supercomputing applied to biomedicine. From drug design to genome analysis.	863
12:50 PM	Roderic Guigo Serra (CRG)	Transcriptome variation across cell types, tissues, individuals and species	863

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Participants:

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