Scientific Program

Day 1

July 27, 2015

08:30-09:00 Registrations

Hall 1



09:00-09:25

Opening Ceremony

Keynote Forum

09:25 -09:30 Introduction

09:30-09:55 Glen M Borchert

University of South Alabama, USA

09:55-10:20 William McCombie

Cold Spring Harbor Laboratory, USA

Networking & Refreshment Break 10:20-10:35

Track 2: RNA Editing and RNA Interference:Interplay,

Track 3: Next Generation Sequencing (NGS) Technologies

Track 4: Disease Interrogation and Applications of RNA-Seq

Session Introduction

Session Chair: Momiao Xiong, University of Texas Health Science Centre, USA

Session Co-Chair: Yongming Sang, Kansas State University, USA

Title: Integrative image and RNA-Seq data analysis

10:35-10:55 Momiao Xiong, University of Texas Health Science Centre, USA

Title: Reduction of systematic bias in transcriptome data from human peripheral blood mononuclear cells for

10:55-11:15 transportation and biobanking

Atsushi Shimizu, Iwate Medical University, Japan

Title: Genome-wide transcriptomes integrate animal intra- and inter-organism processes and evoke the

11:15-11:35 ecoimmunological concept in animal health

Yongming Sang, Kansas State University, USA

Title: Identification by deep sequencing and profiling of conserved and novel hickory microRNAs involved in

11:35-11:55 the graft process

Bingsong Zheng, Zhejiang A & F University, P.R. China

Title: RNA Sequencing in degraded tumor RNA samples: Two natural enemies finally reconciled

Michael Bonin, IMGM Laboratories GmbH, Germany

12:15-12:35 Title: RNA Editing alters MicroRNA targeting in human breast cancer

Glen M Borchert, University of South Alabama, USA

12:35-12:55 Title: Genome-scale mapping promoter variation through exome sequencing

Sang Ming WANG, University of Nebraska Medical Center, USA

Group Photo

Lunch Break 13:00-13:45

13:45-14:30

Workshop on "RNA editing and Next Generation Sequencing" by Glen Borchert, University of South Albama, USA

Track 1: Transcriptome analysis and Gene Expression-An Overview

Track 5: Exploring the complexity of the Transcriptome

Track 6: Refining expression analysis

Session Introduction

Session Chair: Andrey S Krasilnikov, Penn State University, USA Session Co-Chair: Yan Li, The Fourth Military Medical University, China 14:30-14:50 Title: Transcripts to cleave transcripts: Structure and function of RNA-based Ribonucleases P and MRP

Andrey S. Krasilnikov, Penn State University, USA

Title: The mitochondrial transcription factor and the interaction on Cell Aging 14:50-15:10

Marcelo S. Ferro, University Sao Judas Tadeu, Brazil

Title: NDRG2, a new estrogen-targeted gene

15:10-15:30

Yan Li, The Fourth Military Medical University, China

Title: Expression analysis of candidate genes present in the QTL regions for both Iron and Zinc in the F7 RILs

15:30-15:50 of Madhukar x Swarna

Sai Vishnu Priya, Centre for Cellular & Molecular Biology, India

Networking & Refreshment Break 15:50-16:05

Track 8: Functional Impact of Non-Coding RNA (ncRNA)

Track 9: Cancer Genomics: Integrative And Computational Approaches

Track 12: Transcriptional Regulation and Transcriptional Attenuation

Session Introduction

Session Chair: Harry Jarrett, University of Texas San Antonio, USA Session Co-Chair: Ding-Gan Liu, Chinese Academy of Sciences, China

16:05-16:25 Title: T3 transcriptomics

Harry Jarrett, University of Texas, USA

16:25-16:45 Title: Independent 3'untranslated region RNA: A novel non-coding regulator RNA

Ding-Gan Liu, Chinese Academy of Sciences, China

Title: Transcription-based chronobiology of receptor tyrosine kinases: relevance to cancer progression 16:45-17:05

Yosef Yarden, Weizmann Institute of Science, Israel

Title: Parathyroid hormone regulates Nhe3 gene core promoter: EGR1 and Sp3 might regulate the RNA

17:05-17:25 polymerase II pause?

Nancy Amaral Reboucas, University of Sao Paulo, Brazil

Panel Discussion

July 28, 2015 Day 2

Hall 1

08:30-09:00 Registrations

Track 7: Epigenetics

Track 11: Clinical Applications and Related Disorders

Session Introduction

Session Chair: Max H Garzon, The University of Memphis, USA

Session Co-Chair: Yingwei Mao, Pennsylvania State University, USA

Title: A critical role of an exon junction complex (EJC) factor in regulation of embryonic neurodevelopment and

09:00-09:20 implications in neurodevelopmental disorders

Yingwei Mao, Pennsylvania State University, USA

Title: Transcription interference networks examined by Single Molecule Long Read Sequencing Technology 09:20-09:40

Zsolt Boldogkoi, University of Szeged, Hungary

Title: A comparative transcriptome provides candidate genes for determination the cause of males infertility 09:40-10:00

Krzysztof Wieczerzak, University of Rostock, Germany

Workshop on "Impact of variation in regulatory region on gene expression" 10:00-10:45 by San Ming Wang, University of Nebraska Medical Centre, USA

Networking & Refreshment Break 10:45-11:00

Track 14: Transcriptomics and Proteomics of Microorganisms

Session Introduction

Session Chair: Subha Bhassu, University of Malaya, Malaysia

Session Co-Chair: Ilana Kolodkin, Weizmann Institute of Science, Israel

11:00-11:20 Title: Quantitative analysis of the mitochondrial proteome and phosphoproteome in the yeast Saccharomyces cerevisiae Claire Lemaire, National Center for Scientific Research, France

Title: Maintaining motile cells inside the biofilm through cell-to-cell signaling, transcription regulation and evolution Ilana Kolodkin, Weizmann Institute of Science, Israel

Title: Transcriptomic and proteomic profiling of infectious hypodermal and hematopoietic necrosis virus 11:40-12:00 (IHHNV) in giant freshwater prawns

Subha Bhassu, University of Malaya, Malaysia

Title: Transcriptome analysis of nematode-trapping fungi during infection of plant- parasitic nematodes

Dharmendra Kumar, Narendra Deva University of Agriculture & Technology, India

12:20-12:40 Title: Characteristics of Pseudorabies virus transcripts analyzed by PacBio and Illumina sequencing techniques
Dora Tombacz, University of Szeged, Hungary

Lunch Break 12:40-13:25

13:25-14:10

Workshop on "On the way to disentangling the enigma of angiosperm egg activation" by Zsolt Ponyal, Kaposvar University, Hungary

Track 10: Expression Profiling

Track 13: Genomics, Proteomics and Bioinformatics

Session Introduction

Session Chair: Sang Ming WANG, University of Nebraska Medical Center, USA

Session Co-Chair: Punit Kaur, Morehouse School of Medicine, USA

14:10-14:30 Title: Genomic Positioning Systems for DNA and the Tree of Life

Max H Garzon, The University of Memphis, USA

Title: The long noncoding RNA MALAT1 promotes tumour-driven angiogenesis by up-regulating pro-angiogenic

14:30-14:50 gene expression

Tao Liu, University of New South Wales, Australia

Title: Studying the expression pattern of auxin-associated genes in Carya cathayensis (Hickory) during the

14:50-15:10 grafting process

Bingsong Zheng, Zhejiang A & F University, P. R. China

15:10-15:30 Title: Aggressive phenotype of triple-negative breast cancer stem cells (TNBC-CSC)

Punit Kaur, Morehouse School of Medicine, USA

15:30-15:50 Title: Locating Disease-associated Single Amino Acid Polymorphisms on Proteins

Baris E. Suzek, Mugla Sitki Kocman University, Turkey

15:50-16:10 Title: SLUG and SOX9 cooperatively regulate tumor initiating niche factors in breast cancer

Babak Behnam, Iran University of Medical Sciences, Iran

Networking & Refreshment Break 16:10-16:25

Young Researchers Forum

16:25-16:45 Title: Pathway analysis for female osteoporosis

Yu Zhou, Tulane University, USA

16:45-17:05 Title: Characterization of 5-methylcytosine patterns in Pseudorabies virus

Peter Olah, University of Szeged, Hungary

17:05-17:25 Title: De novo transcriptome assembly and identification of cold and freeze responsive genes in sea buckthorn

Saurabh Chaudhary, Guru Gobind Singh Indraprastha University, India

Panel Discussion

17:35-18:35 POSTER COMPETITION

Day 3 July 29, 2015

Hall 1

Track 15: Transcriptomics and Proteomics of Plants

Track 16: Transcriptome technologies market

Track 17: New Horizons to the Transcriptome

Session Introduction

Session Chair: Patrick Xuechun Zhao, Samuel Roberts Noble Foundation, USA

Session Co-Chair: Zsolt Ponya, Kaposvar University, Hungary

Title: The LegumeIP (2015 release) - a web-based comparative genomics and gene expression atlas platform

09:30-09:50 to study gene function and genome evolution in legumes

Patrick Xuechun Zhao, Samuel Roberts Noble Foundation, USA

09:50-10:10 Title: Comparative transcriptome analysis between mature pollen and stigma of Brassicaceae and Triticeae crop species

Vishwanath Sollapura, Agriculture and Agri-Food, Canada

Title: How gamete micromanipulation and cell engineering can contribute to establishing a time scale for performing

10:10-10:30 transcriptomics studies in wheat (Triticum aestivum L.) during fertilisation and proembryo formation

Zsolt Pónya, Kaposvár University, Hungary

Networking & Refreshment Break 10:30-10:45

10:45-11:05 Title: Transcriptome and small RNA gene expression changes in synthetic allohexaploids of Brassica Jianbo Wang, Wuhan University, China

Title: Molecular characterization of the unintended and unexpected effects of genetic engineering on the endogenous Solanum tuberosum genome

11:05-11:25

Lerato Bame Tsalaemang Matsaunyane, Agricultural Research Council-Vegetable and Ornamental Plant Institute,
South Africa

Title: Differential regulation of antioxidative gene expressions in response to salt stress in rice

Ozge Celik, Istanbul Kultur University, Turkey

11:45-12:05 Title: Isolation and fuctional characterization of cold stress inducible promoter CATO1 from Tomato

Monika Bansal, Lovely Professsional University, India

Panel Discussion	
	Lunch Break 12:15-13:00
	Closing Ceremony
Poster Presentations	
ICT-001	Title: Paving the way for transcriptomics analysis in the reproduction processes of hexaploid wheat (Triticum aestivum L.) A Aniko Dobosy, Kaposvar University, Hungary
ICT-002	Title: Genes that respond to H2O2 are also evoked under light in Arabidopsis Dianjing Guo, Chinese University of Hong Kong
ICT-003	Title: Investigation on glandular trichome transcriptome of Artemisia annua L Cao Yong, Harbin Institute of Technology, China
ICT-004	Title: Characteristics of Pseudorabies virus transcripts analyzed by PacBio and Illumina sequencing techniques Dora Tombacz, University of Szeged, Hungary
ICT-005	Title: Generation of a CTO gene mutant Pseudorabies virus Istvan Prazsak, University of Szeged, Hungry
ICT-006	The path to understanding salt tolerance in plants: Transcriptome assembly, profiling and analysis of the halophyte, Suaeda fruticosa Joann Diray-Arce, Brigham Young University, USA
ICT-007	Title: RNA binding antibodies as tools for probing transcriptomes Joseph A Piccirilli, The University of Chicago, USA
ICT-008	Title: Transcriptionally regulated gma-miR166a and its target GmPHB in two different soybean genotypes under various stresses Nang Myint Phyu Sin Htwe, Chinese Academy of Agricultural Sciences, China
ICT-009	Title: Identification of novel splicing form of Decapentaplegic (Dpp) gene in Bombyx mandarina Seung-Won Park, Catholic University of Daegu, South Korea
ICT-010	Title: Assessment and diagnostic relevance of novel serum biomarkers for early decision of ST-elevation myocardial infarction Suk Woo Nam, The Catholic University of Korea, Republic of Korea
ICT-011	Title: Transcriptome analysis of Arabidopsis light and brassinosteroid mutants Sunghwa Choe, Advanced Institutes of Convergence Technology, Korea
ICT-012	Title: A text-mining based comparison of RNAi screening assays to NIH chemical probes Tugba Onal-Suzek, Mugla University, Turkey
ICT-013	Title: Coupled processing of snoRNA 5' and 3' termini in Saccharomyces cerevisiae Zaneta Matuszek, University of Warsaw, Poland
ICT-014	Title: Analysis of long non coding transcripts in wild type and knock-out mutant Pseudorabies virus strains Zsolt Csabai, University of Szeged, Hungary
ICT-015	Title: Does sequence specificity of the 5'end of mRNA affect ribosome loading? Anjali Pai, University College Cork, Ireland

Bookmark your dates

2nd International Conference on

Transcriptomics

August 15-17, 2016 Portland, Oregon USA