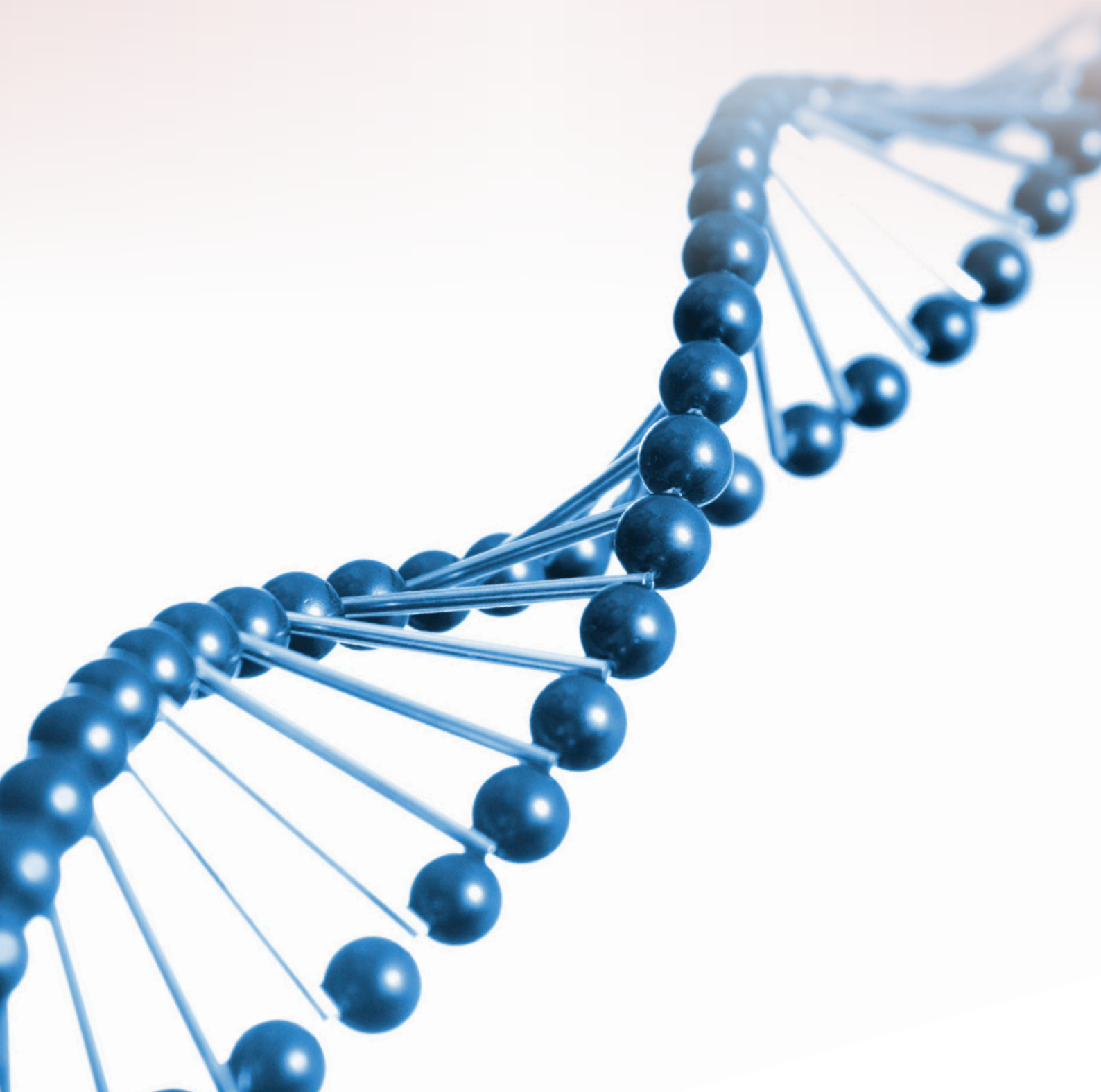
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2nd International Conference on

Transcriptomics

September 12-14, 2016 Philadelphia, USA

Scientific Program



08:30-09:30 Registrations

Independence A

conferenceseries.com 09:30-10:00

Opening Ceremony

Keynote Forum

10:00-10:05 **Introduction**

10:05-11:10 **Title: The centers of premeltons signal the beginning and ends of genes**
Henry M Sobell, University of Rochester, USA

Group Photo

Networking and Refreshment Break 11:10-11:30 @ Foyer

11:30-12:30 **Title: Microbiome functions identified by the metatranscriptome**
David L Perkins, University of Illinois at Chicago, USA

Track 1: Transcriptome Analysis and Gene Expression
Track 2: Cancer Transcriptome
Track 3: Transcriptomics and Proteomics in Plants

Session Chair: Henry M Sobell, University of Rochester, USA
Session Co-Chair: Andrew Grimson, Cornell University, USA

Session Introduction

12:30-13:00 **Title: Mining transcriptome data to identify consequential microRNAs and their targets**
Andrew Grimson, Cornell University, USA

13:00-13:30 **Title: Association of radiation-induced genes with non-cancer chronic diseases in Mayak workers occupationally exposed to prolonged radiation**
Michael Abend, Bundeswehr Institute of Radiobology, Germany

Lunch Break 13:30-14:30 @ Benjamin's Restaurant

14:30-15:00 **Title: YY1 controls long range DNA interactions of Ig heavy chain locus during class-switch recombination**
Arindam Basu, Penn State University, USA

15:00-15:30 **Title: The application of transcriptome sequencing: New insights into the understanding of sex-steroid hormone synthesis in echinoderms**
Alqaisi K M, University of Otago, New Zealand and Zarqa University, Jordan

15:30-16:00 **Title: Transcriptomics: Genes and ontogenes in Drosophila**
Nina B Fedorova, Institute of Cytology and Genetics, Russia

Networking and Refreshment Break 16:00-16:15 @ Foyer

16:15-16:45 **Title: RNA-seq analysis reveals significant transcriptome changes in the fine flounder *(Paralichthys adspersus)* and the red cusk-eel *(Genypterus chilensis)* under stress**
Juan Antonio Valdés, Universidad Andrés Bello, Chile

16:45-17:15 **Title: Breast cancer transcriptome: From triple negative breast cancer to HER2-overexpressing isogenic TNBC cells**
Rakesh Kumar, George Washington University, USA

17:15-17:45 **Title: Regulatory network analysis reveals miR-146b-5p within BCR-ABL1–positive microvesicles promotes leukemic transformation of hematopoietic cells**
An Yuan Guo, Huazhong University of Science and Technology, China

17:45-18:15 **Title: Drought stress-mediated transcriptome profile reveals NCED as a key player modulating drought tolerance in different cultivars of *P. davidiana* (Korean Aspen)**
Byung Wook Yun, Kyungpook National University, South Korea

Panel Discussion

Day 2 September 13, 2016

Independence A

Keynote Forum

09:00-09:05	**Introduction**
09:05-10:05	**Title: Mixed linear model approaches of association mapping for complex traits based on omics variants** **Jun Zhu**, Zhejiang University, China
10:05-11:05	**Title: MicroRNA expression profile in breast cancer** **Lyudmila Gulyaeva**, Russia Novosibirsk State University, Russia

Networking and Refreshment Break 11:05-11:25 @ Foyer

Track 4: Epigenetics
Track 5: Transcriptional Regulation & Attenuation
Track 6: Expression Profiling

Session Chair: Michael Abend, Bundeswehr Institute of Radiobology, Germany

Session Introduction

11:25-11:55	**Title: KDM5: More than just a histone demethylase** **Julie Secombe**, Einstein College of Medicine, USA
11:55-12:25	**Title: The transcriptomic studies on rice *(Oryza sativa)* developing embryo and endosperm** **Jianbo Wang**, Wuhan University, China

Workshop on

12:25-13:25	**Title: Regulation of gene expression by xenobiotics and microRNA** **Lyudmila Gulyaeva**, Russia Novosibirsk State University, Russia

Lunch Break 13:25-14:25 @ Benjamin's Restaurant

Young Researchers Forum

Session Chair: Lyudmila Gulyaeva, Russia Novosibirsk State University, Russia

Session Introduction

14:25:15:05	**Title: Application of transcriptomics on study of biological effects of magnetic field exposure** **Yongyan Sun**, Chinese Academy of Sciences, P.R China
15:05:15:35	**Title: Exploring underground networks: The transcriptional control of plant root development** **Erin E Sparks**, Duke University, USA
15:35:16:05	**Title: Inflammatory response in the pathogenesis of acute mountain sickness revealed by transcriptome analysis** **Bao Liu**, Third Military Medical University, China

Networking and Refreshment Break 16:05-16:30 @ Foyer

Poster Presentations @ 16:30-17:15

TRANS-001	**Title: Analysis of parent-of-origin allelic expression in Korean cattle (Hanwoo)** **Dajeong Lim**, National Institute of Animal Science, Republic of Korea
TRANS-002	**Title: Unique features of internal melanin pigmentation in Oyge black chicken** **Han Ha Chai**, National Institute of Animal Science, Republic of Korea
TRANS-003	**Title: *De novo* transcriptome assembly and the identification of gene-associated single-nucleotide polymorphism in ginseng roots** **Ick Hyun Jo**, National Institute of Horticultural and Herbal Science, Eumseong, South Korea
TRANS-004	**Title: The dysregulated telomere binding proteins are correlated with aberrant expression of splicing factors and RNA splicing profiles in Myeloproliferative neoplasm (MPN)** **Dawei Xu** , Karolinska Institutet, Sweden
TRANS-005	**Title: Identifying differentially expressed genes and their network under heat stress in muscle tissue of white pekin duck** **Jong Eun Park**, National Institute of Animal Science, Republic of Korea
TRANS-006	**Title: Application of transcriptomics on study of biological effects of magnetic field exposure** **Yongyan Sun**, Chinese Academy of Sciences, PR China

Panel Discussion

Award ceremony

Day 3 September 14, 2016

Networking & Lunch