

Genomics, Epigenetics and Gene Regulation Symposium

PROGRAMME

14th September 2017, University of Essex, Colchester

MORNING SESSIONS

Time	Event
8:30 – 8:50	Registration and coffee
8:50 – 9:00	Welcome (Antonio Marco)
	Session 1: Epigenetics I (chair – Radu Zabet)
9:00 – 9:15	Cecilia Lövkvist (JIC) <i>DNA methylation depends on local topology of CpGs and is maintained through collaboration between CpGs</i>
9:15 – 9:30	Myles Garstang (Essex) <i>High-throughput approaches for decoding enhancer activity in mammalian cell lines</i>
9:30 – 9:45	Kiran Batta (Manchester) <i>Microenvironmental and epigenetic mechanisms underlying the development and maintenance of haematopoietic stem and progenitor cells</i>
9:45 – 10:00	Leo Schalkwyk (Essex) <i>Histone acetylome-wide association study of Alzheimer's disease</i>
10:00 – 10:25	Invited speaker: Alessia Buscaino (University of Kent) <i>Genetic and epigenetic regulation of genome stability in the human fungal pathogen <i>Candida albicans</i></i>
10:25 – 10:50	Coffee break and posters
10:50 – 11:30	Keynote: Anne Ferguson-Smith (University of Cambridge) <i>Variable silencing of the repeat genome – implications for non-genetic inheritance</i>
	Session 2: Epigenetics II (chair – Pradeepa Madapura)
11:30 – 11:45	Myrto Kostadima (EBI) <i>Ensembl at the heart of gene expression regulation studies</i>
11:45 – 12:00	Shlomit Edri (Cambridge) <i>Establishment of an Embryonic Stem Cell tissue culture model for mammalian Neuro-Mesodermal Progenitors</i>
12:00 – 12:15	Graeme Thorn (Essex) <i>Microdomain formation in chromatin</i>
12:15 – 13:40	Lunch and posters

SPONSORS



<http://genomics.essex.ac.uk>

AFTERNOON SESSIONS

<i>Time</i>	<i>Event</i>
	Session 3: RNA (chair – Jordi Paps)
13:40 – 14:05	Invited speaker: Tamas Dalmay (University of East Anglia) <i>Searching for genes involved in microRNA turnover in Arabidopsis</i>
14:05 – 14:20	Lovorka Stojic (CRUK Cambridge) <i>Control of cell division by long noncoding RNAs</i>
14:20 – 14:35	Daphne Ezer (TSL Cambridge) <i>Deciphering the origins of gene expression bursts at dawn, using computer-aided experimental design.</i>
14:35 – 14:50	Antonio Marco (Essex) <i>Selection against microRNA target sites</i>
14:50 – 15:05	Wellcome Open Research presentation. Vicky Hellon
15:05 – 15:30	Coffee break and posters
	Session 3: Transcription Regulation (chair – Antonio Marco)
15:30 – 15:55	Invited speaker: Boris Lenhard (Imperial College London) <i>TADs are ancient features that coincide with Metazoan clusters of extreme noncoding conservation</i>
15:55 – 16:10	Chris Toseland (Kent) <i>Nuclear myosin and adaptor proteins as regulators of gene expression</i>
16:10 – 16:25	Radu Zabet (Essex) <i>Quantitative models of gene regulation: transcription factors binding to the genome</i>
16:25 – 16:40	Clara Novo (Babraham) <i>Super-enhancer interactome rewriting during pluripotency transition</i>
16:40 – 16:55	Jordi Paps (Essex) <i>The evolution of transcription factors and the Animal Kingdom</i>
16:55 – 17:00	Closing Remarks

POSTERS

<i>Author</i>	<i>Title</i>
Andrayas A (Essex)	<i>Considering the impact of smoking on the epigenome</i>
Clarkson C (Essex)	<i>Heterochromatin spreading during embryonic stem cell differentiation</i>
dos Santos A(Kent)	<i>NDP52 – A Putative Transcription Regulator</i>
Eleftheriou M (Nottingham)	<i>Specific features of the DNA methylome of paediatric and adult brain tumours</i>
Fabian C (Babraham)	<i>The role of polycomb-group proteins in human pancreatic cell differentiation</i>
Gorrie-Stone T (Essex)	<i>The bigmelon package: DNA methylation analyses in high dimensions</i>
Hari-Gupta Y (Kent)	<i>Role of Myosin VI in regulating hormone-dependent gene expression</i>
Jessop P (Nottingham)	<i>Studying the biological functions of the TET and TDG proteins during zebrafish embryonic development</i>
Larose Cadieux E (Crick)	<i>Integrating copy number analysis and tumour DNA methylation profiling</i>
Lewis L (Nottingham)	<i>Dynamics of 5-carboxylcytosine during hepatic differentiation: potential general role for active demethylation by DNA repair in lineage specification</i>
Martin P (Essex)	<i>ChIPAnalyser: Transcription factor binding prediction in R</i>
McKenna F (Essex)	<i>Deciphering the function of HOTTIP lncRNA in regulation of HOX genes and cancer development</i>
Ramsawhook A (Nottingham)	<i>Investigating the role of developmental epigenetic mechanisms in the origins of brain tumours</i>
Shafiei N (Essex)	<i>Nucleosome repositioning in cancer</i>
Siverns S (Coventry)	<i>Regulation of Hu genes in Neuroblastoma</i>
Trieu T (UEA)	<i>Functional analysis of Y RNA-derived sRNAs in the human breast cancer cells</i>