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Meetings



Epigenetics 2009

The Epigenetics 2009 Australian Scientific Conference was held last week from 1-4th December in Melbourne, Australia. Local organisers Jeff Craig, Richard Saffery, Alex Dobrovic and Sam El-Osta together with ASN events did a fantastic job for the 260 registrants and 15 trade exhibitors. Delegates were exposed to four days of stimulating talks and were fortunate to hear about the latest research in epigenetics from many of the leading Australian epigenetic scientists, talented students and post-docs, as well as some amazing overseas guests.

Melbourne put on some sensational weather so that when one could finally drag oneself away from the scientific posters, Melbourne's rich culture could be thoroughly enjoyed. A short ride on an iconic tram delivered delegates to nearby St Kilda for some sea breeze or to Chapel Street for some boutique window shopping. Others chose to just stroll around the lake at beautiful Albert Park in the sun.

The conference kicked off with a thought provoking lecture from [Prof Moshe Szyf](#) from McGill University, Canada whose research explores the concept that epigenetic states are influenced by the social environment as well as the physical environment. Interestingly, it seems that socioeconomic position may be associated with methylation patterns and that wealthy people can be segregated according to patterns of promoter methylation. Furthermore, environmental influences both social and chemical are implicated in the dynamic and responsive nature of the methylome and that ultimately these things determine how you respond to the environment.

The lecture by Prof Moshe Szyf was followed by various sessions covering a plethora of all things epigenetic including epigenetics and cancer, non coding RNAs, imprinting, plant epigenetics, epigenetics and development and epigenetics and the environment.

Tuesday 1st December

Prof Jingde Zhu from Shanghai Cancer Institute, China kicked off the first epigenetics and cancer session with a discussion on the importance of the study of DNA methylation at both a genome-wide scale as well as in the clinical setting. This talk also brought to our attention the potential use of non-plasma bodily fluids for the detection of methylation-specific biomarkers in cancers such as urine in bladder cancer.

Congratulations to the following award winners:

Young Investigators

- Nicolas Wong, Murdoch Children's Research Institute
- Cheryl Li, Victor Chang Cardiac Research Institute

Poster Awards

- Romain Barres, University of New South Wales
- Rebecca Hinshelwood, Garvan Institute of Medical Research
- Kevin Knower, Prince Henry's
- Jason Lee, Seoul National University
- Ming Luo, CSIRO
- Phillippa Taberlay, USC/NCCC (USA)
- Kristina Warton, Garvan Institute of Medical Research



Photograph provided by Brian Gloss

Prof Sue Clark followed with a great talk detailing the use of integrated *in vivo* gene expression profiles from clinical samples and epigenome tiling arrays to map DNA methylation and histone modifications. Despite an explosion in the past ten years in epigenetic-associated cancer research, key questions still remain regarding what triggers the epigenetic changes that are commonly seen in cancer. Sue discussed further the recently described phenomenon of long range epigenetic silencing (LRES) and that in cancer, deregulation of the epigenome can occur in domains that span multiple genes, by replacement and reinforcement of either repressive or active histone marks. LRES seems to occur more commonly than originally thought, and the specific triggers and marks that predispose specific domains to such modifications is still the subject of ongoing research.

Dr Zdenko Herceg from the International Agency for Research on Cancer, France concluded this session with a thought provoking talk outlining the potential link between cancer associated epigenetic changes and environmental risk factors. Specifically, he discussed the nicotinic acetylcholine receptor gene cluster that reside at a lung cancer susceptibility locus - raising the question that perhaps this could be also associated with a susceptibility to addictions. These CpG island - associated genes have an enigmatic role in non-neuronal tissue and some interesting data was presented using calcium influx assays, shRNA and 5-AZA-dC which placed the receptors functionally within the PI3-K cascade, with some crosstalk to an apoptosis pathway involving caspase3.

The afternoon session was dedicated to epigenetics and the environment and started with **Prof Sir Peter Gluckman** from the University of Auckland whose insight into developmental plasticity was fascinating. The fact that the environmental conditions in the foetal period and in infancy affect disease susceptibility in life is well accepted however Prof Gluckman described the difference between immediate adaptive response and predicted adaptive response, with elegant examples the whole audience could relate to. Firstly, as an example of an immediate adaptive response, it was interesting to note that if you were a tadpole born into an evaporating pond, you would be likely to undergo metamorphosis early in order to survive. However, the flip side is that this short-term survival mechanism comes at a long-term cost as smaller body size is an evolutionary disadvantage. Secondly, the Pennsylvania Meadow Vole was used as an example of predictive adaptive response, as the coat will change depending on its birth time being summer or spring - in order for its survival in the following winter. Also, data was presented on the change in methylation patterns in a cohort of children born in the UK in 1990-1991. MeDIP was used to identify potential genes with greater than 10% variation at birth compared with samples taken at 9 years of age. It was determined that as the methylation of specific genes such as RYRA increased at specific CpG sites, the fat mass at 9 years of age also increased. The implications of this work are that the epigenetic state at birth can predict the later phenotypic outcome, independent of birth weight and poses interesting questions relating to human disease, particularly type II diabetes.

Dr Jean Finnegan from CSIRO, Plant Industry was the first to introduce Arabidopsis to the Epigenetics 2009 conference with her talk on epigenetic mechanisms that help plants weather the winter. Dr Finnegan was also featured in the Nov/Dec issue of The Australian Life Scientist Magazine. In cold-climates, flowering is promoted by a process called vernalization, or prolonged exposure to low temperatures. Several genes have been identified in this process, but Dr Finnegan's lab have identified another gene which is regulated by polycomb proteins called VIN3. This work demonstrated that VIN3 can be transiently expressed in these plants which suggests that polycomb regulation can mediate not only long term gene repression but also could facilitate dynamic responses to the changing environment.

The welcome function organised for Tuesday evening allowed for mingling and tour of the trade displays - providing a number of opportunities to win great prizes while appreciating the new and exciting products on offer!

Wednesday 2nd December

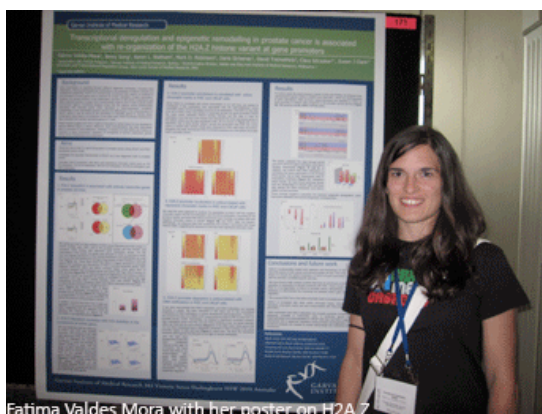
Prof Art Petronis from the University of Toronto, Canada started bright and early with an 8:30am talk covering the epigenetics of major psychiatric disease in mono and dizygotic twins in family, twin and adoption studies. Interestingly Schizophrenia is 70% heritable yet only 1% is explained by genetic mutation. The



Rebecca Hinshelwood with her poster award



Melbourne sights - Brunswick street Fitzroy



Fatima Valdes Mora with her poster on H2A.Z



challenge is to tease out the epigenetic mechanisms involved in these complex diseases.

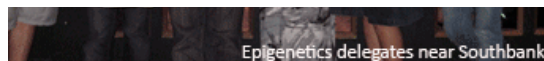
Dr Cath Suter from the Victor Chang Cardiac Research Institute in Sydney followed with an extension to her previously published work on the Agouti mouse and the finding that the phenotype can be affected by not only the mother, but also the environmental pressures imposed on the grandmother. Watch this space for exciting results to follow on the short and long term affect of prolonged methyl-supplementation, and to see for how many generations such heritable epigenetic changes can be carried.

Prof Peter Jones from USC/Norris Comprehensive Cancer Center, USA presented the nucleosome - the epicentre of the epigenome. In cancer, nucleosome positioning has become the focus of extensive research and it was interesting to note that treatment with DNA demethylating drugs also leads to nucleosome eviction, an observation that adds a further dimension to the regulation of expression and has implications in the clinical setting when considering epigenetic therapy.

Dr Scott Poethig from the University of Pennsylvania, USA continued with the plant theme and brought to our attention the phenomenon of vegetative phase change and the fact that these phases are most obvious in our indigenous plant species such as eucalypts. The transition from juvenile to adult is accompanied by a dramatic change in leaf shape. The mechanisms involved in this transition have not been well described but here we heard about several miRNA which have recently been identified to play a critical role.

Dr Suyinn Chong from the lab of Prof Emma Whitelaw (who was also interviewed for the Nov/Dec issue of The Australian Life Scientist Magazine) elegantly presented her work on Dnmt3L^{-/-} mice and described the paternal effect on the Y-chromosome stability and the fact that Dnmt3L^{-/+} sires have less male pups, despite there being a normal proportion of implanted males. This suggested a gradual loss of the Y chromosome during development.

The first poster session concluded the fact-filled Wednesday, after which the thoroughly questioned poster presenters dispersed to discover the various offerings of the Melbourne evening.



Do you have photos, stories or highlights from the recent Epigenetics conference in Melbourne? [Email](#) 📧

Thursday 3rd December

Five hand-picked young investigators set the scene for an exciting Thursday with **Cheryl Li** and **Nick Wong** winning awards for their presentations on epigenetic programming in response to maternal nutrition and the DNA methylation signature of paediatric B-cell precursor ALL respectively.

Prof Wendy Bickmore from MRC Human Genetics Unit, UK enticed the audience imagination by describing that wrapping the DNA twice around a histone, condenses the DNA seven fold, however in order to cram 2m of DNA into each tiny nucleus, 100 fold compaction is required. Clearly there are other mechanisms involved in higher chromatin structure and Prof Bickmore went on to show some fascinating fluorescent immunofluorescence (FISH) images demonstrating that the mean square inter-probe separation could be linearly related to genome separation.

Prof David Tremthick from John Curtin School of Medical Research in Canberra continued the theme of chromatin structure. Little is known about the structure of chromatin beyond the 30nm fibre formation and Prof Tremthick's work is focussed on histone variants that add an additional layer of complexity to the epigenetic code. Specifically he used an example of H2A, which contains an acidic patch within the molecule. This acidic patch is critical for the formation of the 30nm fibres and even very subtle changes to this patch can have profound effects on chromatin formation.

Dr Thomas Down from Gurdon Institute, UK addressed a topic relevant to all of us, with high throughput technologies and genome-wide analyses becoming more utilised. He described a novel method for analysing Me-DIP data in language the non-bioinformaticians in the room could understand. Batman - as the method has been named is a Bayesian Deconvolution method and Dr Down has used this to generate a comprehensive methylation profile for a mammalian genome.

Dr Mukesh Verma from National Cancer Institute and National Institutes of

Health, USA changed tack in the last session of the day to cover potential funding opportunities available to Australian epigeneticists. See

<http://epi.grants.cancer.gov> and www.grants.gov

The second poster session on Thursday evening was followed by the conference dinner at the Sebel, Albert Park State Ballroom. A special mention went to Assoc. Prof Sam El-Osta and Prof Sue Clark who had the highest number of abstracts submitted (11 and 9 respectively). The remainder of the awards were presented for talks and poster presentations to very deserving recipients (top right). The dinner provided a great opportunity to finish scientific conversations started during the poster session whilst enjoying a variety of culinary delights from the buffet. Dancing of course concluded the evening.

Friday 4rd December

Prof John Mattick from the University of Queensland presented to a weary yet eager audience on Friday morning in the popular session dedicated to non-coding RNAs. Prof Mattick reminded us of the importance of non-coding RNAs by explaining that amazingly, the earthworm and sponge have roughly the same number of protein coding genes as humans, however 98.8% of the human genome is non protein coding. Also, 70% of mouse genes have antisense transcripts. A link was also made to Prof Peter Jones' talk on nucleosome positioning as the work in Prof Matticks group has identified a new class of tiny RNAs (18nt) that are associated with transcription start sites. These sequences are located adjacent to the first nucleosome and may be transcribed as a consequence of PolII back tracking and hence may play a role in nucleosome positioning.

Prof Marilyn Renfree from the University of Melbourne demonstrated her amazing knowledge of our native marsupial fauna and their unique and complex reproductive strategies. Part of the session on imprinting, Prof Renfree presented her work which addressed the question of the origin and control of genomic imprinting. Apart from the very cute images shown of the various marsupial species, the talk itself and the results presented on body weight and level of precociousness from a cross-fostering experiment were fascinating.

In summary the Australian Epigenetics Conference 2009 brought together experts with a huge variety of epigenetic-related research interests. The Friday sessions were concluded with the Annual General Meeting of the Australian Epialliance. Representatives from each state got together to discuss plans, concerns and ideals for the Epialliance. Specific action items and plans included compiling a resource of general methods, developing the website and documenting state and special interest group meetings. The next Australian Epigenetics Conference will be held in the lovely Adelaide - South Australia so stay tuned!