Prof. John Pettifor


Summary:
Background: To our knowledge, no studies have reported on the long-term variability of vitamin D status in adolescents.
Objective: To determine whether tracking of vitamin D status occurs in healthy adolescents, we assessed the variability of 25-hydroxyvitamin D [25(OH)D] every 2 y over a 10-y period in a longitudinal cohort of adolescents living in Johannesburg, South Africa (latitude 26°S).
Design: Healthy adolescents who had blood samples available on ≥3 occasions between 11 and 20 y of age were included in the study. Of the cohort of 504 children, 99 met the criteria. The mean 25(OH) D concentration at each time point was measured, and the individual 25(OH) D z scores based on year 11 values were used as the reference. All 25(OH) D concentrations for a subject were measured in a single assay.
Results: No significant correlation was found between 25(OH) D in the earlier and later years of adolescence, although significant correlations were found between year 11 and year 13 (r = 0.71, P < 0.0001) and between years 15, 17, and 20 (r ≥ 0.65, P < 0.0001). The percentage of adolescents whose 25(OH)D concentration changed by >20 nmol/L from year 11 was calculated for all age groups: 12% of the cohort had a change of >20 nmol/L at 13 y of age compared with 46% at 20 y of age. Just more than one-half (53%) of the cohort changed their category of vitamin D status between the ages of 11 and 20 y, and one-third of adolescents changed from being replete to insufficient over the same period.
Conclusions: The data suggest that the measurement of 25(OH) D at a single time point does not reflect the long-term vitamin D status of an adolescent. These findings may cast doubt on the veracity of those studies that suggest an association of vitamin D status with various disease states in which vitamin D status was only measured once.
The family members Batf, Batf2 and Batf3 belong to a class of transcription factors containing basic leucine zipper domains that regulate various immunological functions and control the development and differentiation of immune cells. Functional studies by others demonstrated a predominant role for Batf in controlling Th2 cell functions and lineage development of T-lymphocytes as well as a critical role of Batf, Batf2 and Batf3 in CD8α⁺ dendritic cell development. Moreover, Batf family member expression was measured in a vast collection of mouse and human cell types by cap analysis gene expression (CAGE), a recent developed sequencing technology, showing reasonable expression spectrum in immune cells consistent with previously published expression profiles. Batf and Batf3 were highly expressed in lymphocytes and the earlier moderately expressed in myeloid lineages. Batf2 was predominantly expressed in monocytes/macrophages. Functional studies in mice demonstrated that Batf2 has a central role in macrophage activation by regulating inflammatory responses during lipopolysaccharides stimulation and mycobacterial infection. Hence, Batf2 could be used as a biomarker and a potential host directed drug target in tuberculosis. Moreover, Batf2 act as a tumor suppressor gene and augmenting Batf2 in malignant cells might be an encouraging therapeutic treatment against cancer.
Prof. Robert P Millar

Article:

DOI: 10.1159/000441115.
Impact Factor: 4.373

Summary:
This special issue arises from symposia on GnRH and reproduction presented at the International Congress of Neuroendocrinology in Sydney, August 2014. The symposia and this special issue of Neuroendocrinology bring together a series of new aspects of GnRH research encompassing fundamental studies on the regulation of the GnRH neuron at a molecular and electrophysiological level, through studies on pulsatile gene expression in GnRH-promoter-luciferase transgenic mice, impacts of novel guidance proteins (semaphorins) on GnRH neuron migration, animal models of metabolic, immunological, bacterial and steroidogenic reproductive neuroendocrine programming, to clinical studies on the use of kisspeptin ligands to stimulate or inhibit the reproductive system.
Article:
Impact Factor: 3.993

Summary:
We show that the interpretation of molecular epidemiological data for extensively drug-resistant tuberculosis (XDR-TB) is dependent on the number of different markers used to define transmission. Using spoligotyping, IS6110 DNA fingerprinting, and DNA sequence data, we show that XDR-TB in South Africa (2006 to 2008) was predominantly driven by the acquisition of second-line drug resistance.
Prof Alan Christoffels

Article:

Impact Factor: 3.986

Summary:

Background: Transcription initiation regulation is mediated by sequence-specific interactions between DNA-binding proteins (transcription factors) and cis-elements, where BRE, TATA, INR, DPE and MTE motifs constitute canonical core motifs for basal transcription initiation of genes. Accurate identification of transcription start site (TSS) and their corresponding promoter regions is critical for delineation of these motifs. To this end, the genome scale analysis of core promoter architecture in insects has been confined to Drosophila. The recently sequenced Tsetse fly genome provides a unique opportunity to analyze transcription initiation regulation machinery in blood-feeding insects.

Results: A computational method for identification of TSS in newly sequenced Tsetse fly genome was evaluated, using TSS seq tags sampled from two developmental stages namely; larvae and pupae. There were 3134 tag clusters among which 45.4 % (1424) of the tag clusters mapped to first coding exons or their proximal predicted 5'UTR regions and 1.0 % (31) tag clusters mapping to transposons, within a threshold of 100 tags per cluster. These 1393 non transposon-derived core promoters had propensity for AT nucleotides. The -1/+1 and 1/+1 positions in D. melanogaster, and G. m. morsitans had propensity for CA and AA dinucleotides respectively. The 1393 tag clusters comprised narrow promoters (5 %), broad with peak promoters (23 %) and broad without peak promoters (72 %). Two-way motif co-occurrence analysis showed that the MTE-DPE pair is over-represented in broad core promoters. The frequently occurring triplet motifs in all promoter classes are the INR-MTE-DPE, TATA-MTE-DPE and TATA-INR-DPE. Promoters without the TATA motif had higher frequency of the MTE and INR motifs than those observed in Drosophila, where the DPE motif occur more frequently in promoters without TATA motif. Gene ontology terms associated with developmental processes were overrepresented in the narrow and broad with peak promoters.

Conclusions: The study has identified different motif combinations associated with broad promoters in a blood-feeding insect. In the case of TATA-less core promoters, G.m. morsitans uses the MTE to compensate for the lack of a TATA motif. The increasing availability of TSS seq data allows for revision of existing gene annotation datasets with the potential of identifying new transcriptional units.
1. **INTRAMURAL RESEARCH UNITS**

**Alcohol, Tobacco and Other Drug**

   **Impact Factor:** 1.632

**Biomedical Research and Innovation Platform**

1. **Espach Y, Huisamen B.** Myocardial functioning and response to ischemia/reperfusion injury following manipulation of the atm protein kinase. Journal of Molecular and Cellular Cardiology. 2015 Sept; 86 (Suppl): 43.
   **Impact Factor:** 4.655

**Biostatistics**

   **Impact Factor:** 3.347

**Centre for Tuberculosis**

   **Impact Factor:** 2.638

   **Impact Factor:** 5.997

   **Impact Factor:** 3.993

**Environment and Health**

1. **Wright CY, Wilkes M, du Plessis JL, Reeder AI, Albers PN.** In multiple situational light settings, visual observation for skin colour assessment is comparable with colorimeter measurement. Skin Research and Technology. 2015 Sep 08. DOI: 10.1111/srt.12261.
   **Impact Factor:** 1.309
Health Systems


Impact Factor: 2.264


Impact Factor: None


Impact Factor: 2.264

MRC Office of Cancer


Impact Factor: None

Non-Communicable Disease


Impact Factor: 2.264


Impact Factor: 3.270

  DOI: 10.1177/0379572115597588.
  Impact Factor: 1.148

  DOI: 10.1017/S0007114515003402.
  Impact Factor: 3.453

  DOI: 10.1371/journal.pone.0139210.
  Impact Factor: 3.234

  DOI: 10.1089/omi.2015.0124.
  Impact Factor: 2.362

**South African Cochrane Centre**

  DOI: 10.1093/ije/dvy142
  Impact Factor: 9.176


**Violence, Injury and Peace**

2. **EXTRAMURAL RESEARCH UNITS**

**Anxiety and Stress Disorders**


2. Dimatelis JJ, Vermeulen IM, Bugarith K, **Stein DJ**, Russell VA. Female rats are resistant to developing the depressive phenotype induced by maternal separation stress. Metabolic Brain Disease. 2015 Sep 7. DOI: 10.1007/s11011-015-9723-8. **Impact Factor: 2.638**


**Bioinformatics Capacity Development**


**Child and Adolescent Lung Health**


Developmental Pathways for Health

Drug Discovery and Development

Health Policy

Health Services to Systems

Herbal Drugs
**Hypertension and Cardiovascular Disease**


**Immunology of Infectious Disease**


**Inter-University Cape Heart**


**Maternal and Infant Health Care Strategies**

Receptor Biology
   DOI: 10.1159/000441115.  
   **Impact Factor:** 4.373

   DOI: 10.7196.sajbl.8408.  
   **Impact Factor:** None

Respiratory and Meningeal Pathogens
   DOI: 10.1093/ofid/ofv139.  
   **Impact Factor:** None

Rural Public Health and Health Transition
   DOI: 10.1371/journal.pone.0137352.  
   **Impact Factor:** 3.234
3. **GRANT FUNDED RESEARCH**

**Strategic Research Initiatives**

   DOI: 10.1016/j.ebiom.2015.09.025.
   **Impact factor:** None

   DOI: 10.7448/IAS.18.1.20240.
   **Impact Factor:** 5.090

**SHIP – Research**

   DOI: 10.1155/2015/534808.
   **Impact Factor:** 1.880

4. **CLOSED RESEARCH UNITS**

**Clinical and Biomedical Tuberculosis**

   DOI: 10.1371/journal.pmed.1001880.
   **Impact Factor:** 14.429
5. RESEARCH UNITS WITH NO QUALIFYING PUBLICATIONS

INTRAMURAL
- Burden of Disease
- Gender and Health
- HIV Prevention
- MRC Office of AIDS
- MRC Office of Malaria
- MRC Office of Tuberculosis

EXTRAMURAL
- Antiviral Gene Therapy
- Cancer Epidemiology
- Common Epithelial Cancer Research Centre
- Diarrhoeal Pathogens
- Gynaecological Cancer
- HIV/TB Pathogenesis and Treatment
- Human Genetics
- Medical Imaging
- Microbial Water Quality Monitoring
- Molecular Mycobacteriology
- Prospective Gastrointestinal Cancer
- Stem Cell Research and Therapy
## MRC LIST OF NEW CONTRACTS FOR SEPTEMBER 2015

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<th>MRC Unit</th>
<th>Funder</th>
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<td>Health Systems</td>
<td>University of Cape Town (UCT)</td>
<td>National Institutes of Health (NIH)</td>
<td>Using information to Align Services and line and retain men in HIV cascade.</td>
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<td>To develop interventions, specific to African context, which are focused on saving the</td>
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