International Lecture Series
Disease Biology and Molecular Medicine

ALL WELCOME!

Prof. Adam Mead

Associate Professor of Haematology
Weatherall Institute of Molecular Medicine, University of Oxford
John Radcliffe Hospital, Headington, Oxford
adam.mead@imm.ox.ac.uk

12 June 2017
18:00 h

Historischer Saal
Stadtmuseum Halle

Christian-Wolff-Haus
Große Märkerstr. 10
(ca. 100 m from
market square)

"Application of single cell genomics to unravel heterogeneity in normal and malignant haematopoiesis"

Adam Mead, MRCP FRCPath, is currently an associate professor in haematology at Oxford University, and a consultant physician in the Nuffield Division of Clinical Laboratory Sciences (NDCLS). Prof. Mead trained in medicine at Oxford, and then in haematology at St Bartholomew's Hospital and University College London. His 2007 PhD focused on the biology of myeloid leukaemias. His specialist interest is clinical and basic research into myeloid disorders. He runs a research group at the Weatherall Institute of Molecular Medicine (WIMM) in Oxford.

The major focus of Prof. Mead's current research programme is on the identification and genetic modelling of leukaemic and pre-leukaemic stem cells in myeloid malignancies. The aim is to identify the cellular and molecular biology of these key populations of cells which are capable of propagating disease relapse in patients and to understand how these cells might be more effectively targeted and eradicated. In order to achieve this, he aims to understand the normal cellular origin of leukaemic stem cells, and to thereby identify the perturbed molecular pathways, which result in the generation of preleukaemic clones, and eventually malignant transformation. There are 3 related approaches in this regard: 1. The development of genetically engineered leukaemia models to study the impact of specific mutation(s) on the establishment, evolution and propagation of leukaemic stem cells. 2. The study of leukaemia stem cells in patients with myeloid malignancies throughout their disease course, in order to understand the impact of novel targeted therapies and also to understand the cellular origins of clonal evolution, resistance to therapy and transformation to more aggressive forms of disease. These studies necessitate state of the art single-cell whole-transcriptome analysis of single blood cancer stem cells, a technique which has been established by his group. 3. To understand the clinical and biological consequences of germline genetic abnormalities in humans, which predispose to the development of myeloid malignancies later in life.

<u>Selected papers</u>

Mesa et al. 2017, **Lancet Haematol** 4, e225. Drissen et al. 2016, **Nat Immunol** 17, 666. Quek et al. 2016, **J Exp Med** 213, 1513. Psaila et al. 2016, **Genome Biol** 17, 83. Wills & Mead 2015, **Hum Mol Genet** 24, R74. Woll et al. 2014, **Cancer Cell** 25, 794. Grover et al. 2014, **J Exp Med** 211, 181. Böiers et al. 2013, **Cell Stem Cell** 13, 535. Sanjuan-Pla et al. 2013, **Nature** 502, 232. Mead et al. 2013, **Oncotarget** 4, 814. Mead et al. 2013, **Cell Rep** 3, 1766. Mead et al. 2013, **Blood** 121, 4156. Roy et al. 2012, **Proc Natl Acad Sci USA** 109, 17579.

Medizinische Fakultät
Martin-Luther-Universität Halle-Wittenberg

Contact: stephan.feller@uk-halle.de