AWARDEE REPORT FORM

NAME	Dr. Frank Schubert
UNIVERSITY	University of Portsmouth
NAME OF AWARD	Symington Bequest

PURPOSE OF AWARD *conference attended (full name) with city and dates*

Spring Meeting of the British Society of Developmental Biology
University of Warwick
15-18 April 2018

REPORT: What were your anticipated benefits?

The Spring Meeting is the main conference of the BSDB. This year marked the 70th anniversary of the society, an occasion to bring together most of the scientists who have shaped UK developmental biology in the last decades. I expected an overview of current trends in the field, and an idea of future directions. With so many of the top scientists in the field assembled in Warwick, I also expected networking opportunities, exchange of ideas, and the chance to discuss possible collaborations.

COMMENTS: Describe your experience at the conference~~ / lab visit / course / seminar~~.

Starting (Eric Wieschaus) and ending (John Gurdon) the conference with Nobel Laureates set the scene for a spectacular line-up of speakers. Eric Wieschaus focused on the role of polarised cell tension, mediated by apical myosin accumulation, in mesoderm internalisation during gastrulation. The physical principles governing cell change and their role in morphogenetic processes were also the topic of Maria Leptin's talk that followed, and were a recurring theme throughout the conference for both animal and plant development.

The interplay of chromatin organisation, enhancers and transcription factors was a core element in two sessions on developmental gene regulatory networks and mechanisms of global gene regulation. Among the many highlights here were Edith Heard's unravelling how chromatin domains influence X chromosome inactivation and Petra Hajkova's explanation of the epigenetic reprogramming process in primordial germ cells. Michael Levine's talk demonstrated the power of the Drosophila model for live imaging of gene transcription, allowing to investigate how enhancer strength affects the frequency of transcription bursts. Eileen Furlong, also in Drosophila, applied high resolution imaging and Hi-C genomics to investigate how chromatin domains change during development, and how this influences enhancer-promoter interactions and gene expression.

While the established model organisms (mouse, chicken, zebrafish, *Xenopus*, *Drosophila*) were still dominant in the talks and posters, quite a number of presentations used new emerging models to answer specific questions. Elly Tanaka is using newts and axolotl to study the regeneration process, revealing that adult fibroblasts during regeneration can become multipotent. Jordi Solana uses planarians as another

regeneration model. Using single cell transcriptomics he is reconstructing the lineages of the main planarian cell types. Marianne Bronner investigates how the distinct head and trunk neural crest populations evolved by characterising the neural crest in the lamprey as sister group to the jawed vertebrates.
Always a highlight of the BSDB spring meetings are the talks of the Prize winners. This year's Beddington medallist, a prize awarded to the best PhD student, was Emilia Favuzzi, who presented her work on the regulation of cell-type specific synapse formation of GABAergic neurones in the mammalian cortex. The winner of the Cheryll Tickle medal, Christiana Ruhrberg, discussed the connection of vasculature and nervous system, and particularly the role of Neuropilin mediating both Semaphorin and VEGF signalling in the development of neurones and neural crest cells. The Waddington medal is always announced at the meeting. This year's winner was Richard Gardner who took us on a journey through early mouse development and the technique of blastocyst injection, a key method in stem cell research and developmental genetics.

REPORT: In relation to skills, what were the most important things you gained? *(does not apply to equipment grant)*

It was interesting to see how quickly new technologies are adopted in the field. Genome editing using CRISPR/Cas is now already well-established, even though this technique only emerged a few years ago. ATAC-Seq has made epigenetic analyses accessible for non-specialist laboratories, and was frequently mentioned in the presentations. Likewise, single cell profiling by transcriptome analysis seemed a remote possibility until very recently, and now featured in a large number of talks at the conference. This is particularly interesting from an anatomy perspective, since it gives more insight into the cellular composition of tissues, organs and whole embryos.

REPORT: How do you think you will put this learning experience into practice in the future?

Genome editing is rapidly expanding the toolbox for developmental biologists, and is certainly a technique that I will also apply in the chicken embryo model. Since the key role of the chromatin state in gene regulation and hence cell differentiation is becoming more and more evident, techniques like ATAC-Seq are certainly another direction that I will explore for our work.
More specifically, I got the opportunity to discuss a collaboration for one of our ongoing projects.

SIGNATURE		DATE	11 May 2018

If submitted electronically, a type-written name is acceptable in place of a hand-written signature

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