16th Annual Meeting of the International Society for Stem Cell Research (ISSCR) 2018

A report by Lena Dorsheimer

This year I had the great opportunity to join one of the most prestigious and the world's largest stem cell-focused meeting in Melbourne, Australia, from the 20th to 23th of June. With the help of the German Stem Cell Network (GSCN), I could attend this meeting which is known to bring together senior scientists and trainees as well as researchers, scientists and industry. Invited speakers like Jennifer Doudna, Douglas A. Melton, Stanley R. Riddell and Connie Eaves are renowned and successful scientists in the field of stem cells. The quality of the talks and posters was outstanding and it was very impressing to see unpublished work of such an importance.

The main focus was surrounding the field of induced Pluripotent Stem Cells (iPSCs) and Organoids. Since I'm working on Hematopoietic Stem Cells (HSCs) I was very interested in the studies of other groups around the world also focusing on Hematopoiesis. On the other hand it was very helpful for my progress as a scientist to hear about the work in other stem cell-focused fields, the methods and techniques which are used in these research areas and how all these different topics (from plants to humans and all kind of stem cells) can be combined. Ben Scheres gave a talk about integrated control of stem cell activity in plants in which he showed how signal accumulation leads to the activation of a small suite of transcription factors that together maintain the multipotent state, and how a gradient of these transcription factors regulates the transitions from stem cell to differentiation state. Connie Eaves received the ISSCR Tobias Award Lecture and talked about a prospective analysis of human leukemogenesis and reviewed her work from the first steps to current results. A very important talk for me and the projects I'm currently working on was given by Leonard I. Zon with the title "The start of cancer – Stem cell changes, clonal expansion, and niche regulation". His group uses the Zebrafish to model early events such as the accumulation of mutations in specific genes (e.g. ASXL1, GATA2, DNMT3A/B and TET2) in their blood to study the beginning of leukemia. They model mutations in these genes, label each stem cell in a different color and watching for a color to become dominant in the blood. The results of these studies give important hints to understand the developments of diseases like Acute Myeloid Leukemia or Myelodysplastic Syndrome.

The daily poster sessions gave me the exceptional opportunity to network, to talk with other young scientists about their work and also to present my work about functional dominance of Clonal Hematopoiesis of indeterminate potential (CHIP)-HSCs in patients undergoing autologous stem cell transplantations. I received a lot of very helpful, important and positive feedback. I was very impressed by a poster presented by Mimi R. Borrelli from the lab of Irv Weissman with the title "A method to isolate and transplant mouse hematopoietic stem cells along with their niche allowing functional hematopoietic stem cell engraftment without myeloablation" indicated that isolating and transplanting HSC-Niches facilitates ex vivo HSC survival and non-myeloablative HSC engraftment and with this suggests a new paradigm for stem cell therapy of intact stem cell-niche units for ex-vivo culture/modification and site-specific transplantation.

At the Meet the Experts Luncheon with Connie Eaves I had also the chance to talk with her about the projects I'm working on. To talk with such a renowned scientist gave me a lot not only because of her experiences in Hematopoiesis but also because of the long time that she is now working as a scientist and her personal thoughts in respect of being successful and satisfied by your work. I also joined other events

like the Young Investigator Social Night, and the Meet up of the GSCN which both were a nice way to meet fascinating people.

All in all I had a lot of fun, learned a lot about the extensive field of stem cell research, met nice and impressive people and got great insights into the work of other groups. The international environment of the meeting was inspiring and interesting. I'm very happy that I had the chance for all these experiences by receiving the travel grant of the GSCN. With this I also want to thank the GSCN.

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Report of the ISSCR 2018 Annual Meeting in Melbourne, Australia, June 20th-23rd

by Roman Goetzke, Stem Cell Biology and Cellular Engineering, Helmholtz-Institute, Aachen

This year´s annual meeting of the ISSCR gathered more than 3000 attendees from all over the world to discuss current findings and questions in stem cell research. The conference was located in the Melbourne Convention and Exhibition Center harboring a large plenary room, several small meeting rooms and a large exhibition hall where the industry exhibition and poster sessions took place.

The conference was officially started off with short opening remarks by Victoria´s governor Linda Dessau and former ISSCR president Hans Clevers followed by a number of outstanding talks by ISSCR award winning researchers. Dr. Shuibing Chen was awarded outstanding young investigator for her contributions in iPSC drug screening methods, Dr. Connie J. Eaves received the ISSCR Tobias award for her research on CML and the blood-forming system, and finally, Dr. Michele De Luca and Graziella Pellegrini were given the ISSCR award for innovation for regeneration of the entire human epidermis by using transgenic stem cells. The plenary sessions comprised a huge variety of stem cell related topics including stem cell activity in plants, single cell analysis of pluripotent and hematopoietic stem cells, disease modelling using organoids and different animals, epigenome reconfiguration, and cancer related stem cells.
However, the most stunning plenary session, to me, was on stem cell based disease modelling. For instance, Dr. Steven A. Goldman presented his findings on the contribution of glial pathology in neurodegenerative diseases showing that hiPSC-derived glial progenitor cells that are transplanted into immune deficient mice can outcompete the murine counterpart and lead to better cognition. In between, Daniel Feller, founder of the non-profitable facility “Genetic Cures Australia (GCA)”, gave an inspiring talk on how his foundation supports medical research to find a genetic cure for inherited eye disease. His son Harry is affected by Usher syndrome type 1F causing deafness and early onset of lost vision. Harry´s hearing is already aided by the use of cochlear implants, his retina degeneration, however, is so far unstoppable. GCA therefore teamed up with key scientists at the Centre For Eye Research Australia (CERA) to find new genetic approaches to cure rare eye diseases. Finally, Dr. Michele De Luca demonstrated translational use of stem cells. Together with his colleague Dr. Graziella Pellegrini he replaced the epidermis of a young boy who suffers from a rare mutation in the

LAMB3 gene that caused loss of 80% of his body skin by transplanting autologous epidermal cultures transduced with a retroviral vector carrying the *LAMB3* cDNA.

Although slightly underrepresented, it was the studies for clinical stem cell therapy using iPSCs that struck me the most. In the “road to the clinic II” session Dr. Peter Coffey introduced the London Project which aimed to bring to the clinics a therapy for age-related macular degeneration. So far, two patients with sub-retinal bleeds received implants with patches of iPSC-derived retinal pigmented epithelial layer (RPE) which recovered eye sight. Dr. Barti Kabhil introduced a very similar approach to cure blinding eye disease. His team, in addition to RPE patches, adds iPSC-derived micro-vessels that are bioprinted opposite of the patch and which act similar to native choroidal vessels. Moreover, Dr. Dan S. Kaufman demonstrated the generation of iPSC-derived NK cells that have directed and potent activity against liquid and solid tumors. His team evaluated different combinations of NK cell-specific CARs to produce a highly effective, persistent, and targeted NK cell therapy.

After the lecture sessions, there was plenty of time and opportunity to get in contact with young investigators and researchers. The poster sessions were really fruitful to gain new inspiration and discuss protocols related to my own work. In addition, the junior investigator career panel offered to get in contact with a diverse panel of scientists who have created their own venture and who gave a close insight into the work as patent advocate, journal editor, or as senior director of a company offering cell therapy. In the evening, the junior investigator social night offered young scientists to meet for a beer at the Munich Brauhaus. Last but not least, the GSCN WunderBar evening event was a great chance to meet familiar and new faces in a relaxed atmosphere.

I would like to cordially thank the GSCN for giving me the chance to attend this great meeting.

Sincerely,
Roman Goetzke

GSCN Travel Award Report

Event: International Society for Stem Cell Research (ISSCR) Annual Meeting 2018
Date: June 20-23, 2018
Location: Melbourne, Australia
Recipient: Dr Nancy Mah, Charité - Universitätsmedizin Berlin

Background:

This year's ISSCR meeting returned to Australia more than 10 years after its last appearance in Cairns in 2007. As expected, the largest number of the 2150 attendees (source: attendee directory) came from Australia & New Zealand (472), followed by the US (447), Europe (273), Japan (242), South Korea (213) and China (184).

Highlights:

Focus Session: Tools for Basic and Applied Research
Prior to the start of the ISSCR, there was a morning of Focus Sessions. One of these was "Tools for Basic and Applied Research", organized by Stem Cell COREdinates (https://coredinates.org/), a consortium of human pluripotent stem cell (hPSC) core facilities across (mostly) Europe and the US. German members of COREdinates include Berlin, Göttingen, and Freiburg. The COREdinates network was founded to facilitate open communication between core facilities and to lay the ground work for "best practices" for working with PSC. To this end, there were speakers from core facilities, as well as other interested parties, such as the International Stem Cell Banking Initiative (ISCBI), the Global Alliance for iPS Therapies (GAiT), the International Stem Cell Forum (ISCF) and the Human Pluripotent Stem Cell Registry (hPSCreg). Overall, the following issues were frequently mentioned: 1) consent for PSC/PSC-derived line usage (research / commercial/ therapy); 2) confirming cell line identity (STR); 3) characterization of cell line genetic stability; 4) characterization of lines for cell type (ie. primed pluripotent, naive pluripotent); 5) CRISPR/Cas9 genome editing for isogenic lines and the assessing quality of editing. For my part, I presented an overview of hPSCreg: "an international database of ethically and scientifically qualified pluripotent stem cell lines".

ISSCR International Affairs Committee Luncheon:
The Committee invited the representatives of various stem cell organizations to a networking lunch meeting. Andrew Elefanty (Chair, ISSCR IA Committee) announced the Merit Award (top 5% of scored abstracts, independent of the travel award), in addition to the ISSCR Travel Awards (need-based). Nancy Witty (CEO, ISSCR) mentioned that there would be a new format for the next ISSCR in Los Angeles: there will be shorter talks to accommodate more speakers in the plenary sessions. Jeremy Sugarman (ISSCR Ethics Committee) presented a draft of the Universal Informed Consent Concept. The basic elements of the Standard Consent were: 1) Regulatory Information; 2) Benefits and Risks (explanation of risks, alternative treatment options, long-term risks). This document is in the development stage and is actively in feedback and review with the clinical translation committee. The future use of a standard consent template should discourage the use of unproven stem cell-based treatments.

Single cell RNA-sequencing as an Emerging Technology:

Single cell RNA-sequencing (scRNA-seq) is rapidly becoming widely used in all areas of life sciences. I was particularly interested in learning more about the scRNA-seq methods that researchers were using and how they went about analyzing the scRNA-seq data. More often than not, scRNA-seq results presented at oral presentations were boiled down to a single colourful tSNE plot, without details of the data analysis. The poster sessions were an excellent opportunity to talk to researchers first-hand about their experiences. I also presented a poster ("RNA-sequencing of Human Pluripotent Stem Cell-derived Kidney Cells"), in which we profiled single cells from kidney organoids and compared them to published single cell kidney datasets (mouse). In conversations with other poster presenters, I came across other groups who were experiencing difficulties in reproducing results of cells cultured in a proprietary (discontinued) media and its new alternative. This point appeared to be rather crucial for producing kidney organoids. There were also two talks featuring scRNA-seq data: 1) Jian Shu (Broad Institute) presented a computational analysis called "Reconstructing reprogramming landscapes by scRNA-seq", in which time series data was used to reconstruct trajectories from transcriptional snapshots. A novel TF (Obox6) was found to increase reprogramming efficiency. 2) Alexander Combes presented "HT scRNA-seq of developing mouse kidney and human kidney organoids reveals a roadmap for recreating the kidney". Some notable observations: so-called "specific" markers are actually expressed in multiple lineages. This is not surprising given the breadth and sensitivity of scRNA-seq. Also, the proximal/distal tubules from their human kidney organoids appeared to be missing key markers. These results point to the underlying complexity of "marker" expression: 1) what is a marker; 2) are markers conserved across species. An additional comparison of the human organoids to a recently published human fetal kidney scRNA-seq dataset showed that indeed, there were species-specific marker expression differences.