

Conference report of the 66th annual meeting of the American Society of Hematology (ASH), 7th – 10th December 2024, San Diego, CA, USA

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The 66th annual meeting of the American Society of Hematology (ASH) featured the latest findings in clinical and experimental hematology.

Each year, a special highlight of the ASH annual meeting is the E. Donall Thomas Lecture, this time awarded to Sean Morrison. He recapitulated his decades-long characterization of regulators of hematopoietic stem cell (HSC) maintenance asking the question which cells in the perivascular niche are crucial for hematopoiesis. Morrison presented his discovery of HSC dependency on Lepr⁺ mesenchymal stromal cells. He and his team now uncovered that the latter secrete NGF to increase nerve fiber density after bone marrow injury. As they found that nerves regenerated the bone marrow by activating $\beta 2$ and $\beta 3$ adrenergic receptor signaling in Lepr⁺ cells, Morrison aimed to investigate the influence of $\beta 2/\beta 3$ blockade on bone marrow regeneration. His work indeed demonstrated that Carvedilol treatment phenocopied nerve loss after bone marrow transplantation, and he found worse overall survival of transplanted patients receiving $\beta 2/\beta 3$ blocking drugs.

Apart from many plenary sessions, the single cell multi omics session fascinated me a lot. John Dick described in detail how inflammation activates HSCs and that single cell multi omics techniques identified a second HSC cluster, representing the inflammation memory HSC pool. Apart from that, Allon Klein provided insights into novel tools for single cell multi omics: Micro-capsules designed to separate liquid phases. This opens up new avenues in droplet-based single cell sequencing as reagents can be washed in and out while nucleic acids are retained inside the droplets. In addition, Klein presented a single cell RNA sequencing atlas of variation. He and his team found that differentiated cells have the highest transcriptional variability whereas HSC are the most conserved cell types.

In the HSC sessions, Infencia Xavier Raj presented non-canonical functions of the DNA methyl transferase DNMT3A. She found that telomerase activity increases in HSCs upon DNMT3A knockout leading to telomere erosion and clonal expansion. Angelica Varesi shared her discovery of ATP2B1 as a novel human long-term HSC marker and Pamela Wenzel talked about the induction of embryonic hematopoiesis via shear-stress of the blood flow in the embryonic aorta. Another fascinating talk was given by Hui Wang who established ultra low input Ribo-seq to study translational heterogeneity in mouse HSCs. He and his team explored that the SNORD113 cluster sustains HSC reconstitution potential via regulation of rRNA modification and processing.

Finally, I had the wonderful opportunity to present my abstract “Hematopoietic differentiation from single codon perspective” in the HSC session. I shared our finding that hematopoietic cells can be distinguished based on their transfer RNA (tRNA) expression profile. Establishment of low input tRNA-sequencing in conjunction with matched mRNA-sequencing and quantitative proteomics enabled to study proteomic consequences of imbalances between tRNA demand and supply along the hematopoietic hierarchy. The subsequent discussion with several experts in the field provided a lot of valuable feedback stimulating ideas for new experiments and opened up new collaborations.

I am very grateful and excited that the GSCN travel award supported my participation in the ASH annual meeting 2024 in San Diego. It was a great experience to gain scientific and personal exchange with other conference attendants, and to receive so much feedback on my current project. Thank you GSCN!