Review of the European Hematology Association 2025 Congress in Milan

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I had the great privilege of attending the EHA 2025 congress in Milan this June, this was my second opportunity to attend an international conference and present my research since beginning my doctoral studies. The congress this year has been invaluable to my development as an early career researcher and continues to reinforce my desire to contribute to important basic and translational research within haematology and the multiple myeloma field.

I was fortunate to present my project exploring how ageing pushes macrophages in the bone marrow to an M2-like phenotype and drives myeloma proliferation by loss of tumour associated phagocytosis as a poster on the Friday session. I always find this to be an excellent opportunity to defend the research I have performed, and to take constructive feedback on rationale, methodology and future studies. I had many positive discussions with experts within the myeloma and macrophage fields, often with aspects of the project aligning with methodology and findings they have observed. This was also my first opportunity to present scRNA-seq data, showcasing the bioinformatics work I have developed so far but also helped to identify areas of the analysis I can improve going forwards. Furthermore, I enjoyed going round to different posters and discussing with fellow researchers, including projects on glycolysis-driven immune evasion in AML and increasing tumour density associations with bone marrow stromal cell remodelling in MM patients. Another poster exploring the role of the gut microbiome in myeloma using in vivo models was intriguing and inspired positive discussions.

I found Prof Evangelos Terpos' update on the results of the phase 3 PERSEUS trial particularly uplifting, with an estimated 118 month improved PFS for daratumumab with VRd vs VRd alone in transplant ineligible newly diagnosed myeloma patients. Additionally, hearing about the novel JNJ-5322 trispecific therapy targeting CD3, BCMA and GPRC5D in myeloma highlighted an intriguing approach to improve selectively to myeloma and safeguard from antigen escape. I also enjoyed learning how WGS is being used to develop an MM-like score which may help to define risk of progression from MGUS and SMM to MM, together with scRNA seq analysis identifying immune evasion and cell adhesion dysfunction being prominent already in the MGUS state. This reinforced the clinical need to develop therapies that prevent the transformation of MGUS to MM. Another talk by Prof Markus Manz in the 'Ageing and Inflammation' session highlighted the importance of the gut microbiome in haematopoiesis and inflammation. I enjoyed hearing how microbial-associated molecular patterns (MAMPS) drive elevated IL-1 levels in the bone marrow, in turn triggering ageing-associated neutrophil, platelet and HSC increase - a phenotype that was absent in germ-free mice and in IL-1R KO mice. I hope to apply the new ideas I have initiated from EHA 2025 to my existing projects on immune modulation in ageing and obesity models of MM.

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