



Genomics and Translational Medicine in Myeloma

July 12-13, 2024 • Barcelona, Spain

Friday, July 12

12:00-12:05	WELCOME	
12:05-12:15	MEETING PURPOSE AND GOALS	
12:15-14:30	THERAPEUTICS TO TARGET IN HIGH RISK MYELOMA CO-CHAIRS: <i>Leif Bergsagel</i>	
12:15-12:30	Role of CAR T Cells	TBC
12:30-12:45	Role of Bispecifics	Niels van de Donk
12:45-13:00	Role of Newer Agents in Development	Saad Usmani
13:00-13:15	Genomic Characterization in Subgroup Analysis	TBC
13:15-14:30	Discussion	Session faculty + Keith Stewart
14:30-14:45	BREAK	
14:45-16:30	FUTURE OF (11;14) CO-CHAIRS: <i>Philippe Moreau and Shaji Kumar</i>	
14:45-15:00	Diversity of t(11;14) breakpoints	Jill Corre
15:00-15:15	Secondary alterations in t(11;14) patients	Mark Bustoros
15:15-15:30	Role of high risk genomic events in Multiple Myeloma Patients Treated with Venetoclax	TBC
15:30-15:45	Integrated epigenetic and transcriptional single-cell analysis of t(11;14) multiple myeloma and its BCL2 dependency	Paola Neri
15:45-16:00	t(11;14) plasma cell disorders	Raphael Szalat
16:00-16:30	Discussion	Session faculty + Kwee Yong

16:30-18:00	BIOMARKER DRIVEN THERAPY	
	CO-CHAIRS: <i>Kenneth Anderson and Marivi Mateos</i>	
16:30-16:45	Venetoclax in t(11;14) patients and others	Nizar Bahlis
16:45-17:00	Personalized therapy for t(4;14) MM	Gareth Morgan
17:00-17:15	Immuno therapy target profiling	TBC
17:15-17:30	Approaching Ultra High risk Multi-Hit Tumors for optimum treatment strategies	Martin Kaiser
17:30-18:00	Discussion	

18:00-18:15 **RECAP**

Saturday, July 13

8:00-8:15 **INTRODUCTION AND WELCOME**

8:15-10:00	NOVEL SEQUENCING PLATFORMS	
	CO-CHAIRS: <i>Faith Davies and Jesus San Miguel</i>	
8:15-8:30	Long read sequencing platforms in MM	Jonathan Keats
8:30-8:45	CAS13/Perturb seq	Eugenio Morelli
8:45-9:00	Proteomics	Marc Raab
9:00-9:15	Optical sequencing	Adam Sperling
9:15-9:30	Profiling CTC and cfDNA	TBC
9:30-10:00	Discussion	Session faculty + Eileen Boyle

10:00-10:30 **BREAK**

10:30-12:15	SINGLE CELL GENOMICS	
	CO-CHAIRS: <i>Herve Avet-Loiseau and Marta Chesi</i>	
10:30-10:45	Spatial genomics of MM cells	Niels Weinhold
10:45-11:00	Microenvironment signatures?	Irene Ghobrial
11:00-11:15	Spatial sequencing to resolve MM and microenvironment interactions	TBC
11:15-11:30	Dissecting high risk cells using single cell sequencing	Brian Walker
11:30-11:45	Detecting and profiling MRD+ cells with single cell omics	Bruno Paiva
11:45-12:15	Discussion	Session faculty + Suzanne Trudel

12:15-13:00 **LUNCH**

13:30-15:15

CLONAL EVOLUTION

CO-CHAIRS: *Nikhil Munshi and Felipe Prosper*

13:30-13:45	Clonal evolution of precursor conditions to NDMM	Francesco Maura
13:45-14:00	Single cell CNA - DNA	Mehmet Samur
14:15-14:30	How many clones are there at diagnosis?	Katja Weisel
14:30-14:45	Clonal evolution beyond myeloma	Steven Treon
14:45-15:15	Discussion	Session faculty + Anjan Thakurta

15:15-15:30

BREAK

15:30-17:30

REDEFINING EPIGENOMIC MYELOMA

CO-CHAIRS: *Norma Gutierrez and Sundar Jagannath*

15:30-15:45	MM methylation	Lawrence Boise
15:45-16:00	Acquired resistance to a GPRC5D-directed T-cell engager in multiple myeloma is mediated by genetic or epigenetic target inactivation	TBC
16:00-16:15	Stroma and Cell signaling	TBC
16:15-16:30	Epigenomic diversity at single cell resolution	TBC
16:30-16:45	Single Nuclei Multiomics Analysis of Transcriptional and Chromatin Accessibility of Tumor Cells Uncovers Molecular Signatures and Regulatory Elements of Malignant Clonal Evolution in Multiple Myeloma	Fenghuang Zhan
16:45-17:30	Discussion	

17:30

CONCLUSIONS AND CLOSING