Hybrid BSC RS/Life Session: Somatic mutation in normal tissues

Objectives

Abstract: "Somatic mutations underpin cancer development and have been speculated to contribute to ageing and a range of diseases. Over the past decade, the ability to sequence cancer genomes has transformed our understanding of the genetics and evolution of a wide range of cancers. However, owing to technical limitations, much less is known about the earliest steps of cancer and how cells in our tissues accumulate mutations during normal ageing. In this talk, I will summarise our work over the past few years to unravel the extent of somatic mutation and clonal selection in normal tissues. I will also discuss how recent technological developments are opening new frontiers in this nascent and exciting field."

Short bio: My research focuses on understanding somatic mutation in normal tissues and disease. In 2015, we published the first comprehensive description of somatic mutation and selection in a healthy solid tissue, revealing that human skin is a patchwork of thousands of competing clones carrying cancer-driver mutations (Martincorena et al., Science, 2015). In subsequent studies, we described this phenomenon in normal oesophagus (Martincorena et al., Science, 2018) and bladder (Lawson et al., Science, 2020). We have also contributed to the study of selection and driver discovery in cancer genomes and normal tissues (Martincorena et al, Cell, 2017). Our current research involves the development of methods for the detection of somatic mutations at single molecule resolution (Abascal et al., Nature, 2021), studies exploring the impact of somatic mutations in diseases unrelated to cancer and forays into somatic mutation in other species

(Cagan, Baez-Ortega, et al., Nature, 2022).

Speakers

Speaker: Íñigo Martincorena, group leader at the Sanger Institute investigating somatic mutation in normal tissues, cancer and ageing
Host: Marta Melé, Transcriptomics and Functional Genomics Lab Group Leader

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