ESMO Open
Cancer Horizons

Tumor evolution in non-small-cell lung cancer

Marina Parry

To cite: Parry M. Tumor evolution in non-small-cell lung cancer. *ESMO Open* 2018;**3**:e000436. doi:10.1136/esmoopen-2018-000436

Received 16 August 2018
Accepted 16 August 2018

BMJ Publishing Group, London, UK

Correspondence to
Marina Parry; marina.anne.parry@gmail.com

Click here to listen to the Podcast

In this podcast, Marina Parry, ESMO Open Digital Editor, speaks to Nicholas McGranahan, Junior Group Leader of the Cancer Genome Evolution Group at University College London's Cancer Institute about the role of bioinformatics in translating genomics research into the clinic and his most recent paper "Allele-Specific HLA Loss and Immune Escape in Lung Cancer Evolution", Cell, 2017 https://www.cell.com/cell/pdf/S0092-8674(17)31185-6.pdf

With the volume and complexity of genomic data available continuing to increase, people and tools who are able of making sense of it all are in high demand. After his PhD with Charlie Swanton working on cancer evolution and on the world leading TRACERx project, Nicky McGranahan has formed his own group whose aim is to further our understanding of how a tumour evolves over time. Using sequencing data, with a focus on multi-region sequencing, to reconstruct the tumour's phylogenetic history and ultimately predict what the key steps are in its development, as well as the direction in which it may go next and ultimately treat it accordingly in clinic.

The aim of the work described in his most recent paper on HLA loss of heterozygosity was to explore whether potential neoantigens may be rendered silent due to loss of antigen presentation machinery. They found that in 40% of patients, loss of HLA was observed, and they are currently exploring whether this holds true in other tumour types.

We also discuss the future of genomic medicine within our current healthcare system, as well as the directions the field is taking, borrowing from evolution to predict the course a tumour will take and ultimately use adaptive therapies to improve outcomes for patients, while considering the extensive heterogeneity which is often seen and the sampling bias coming from use of a single site or timepoint.

Competing interests None declared.

Patient consent Not required.

Provenance and peer review Not commissioned; internally peer reviewed.