

INVITED SPEAKER PRESENTATION

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Personalized oncogenomics

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The comprehensive genetic characterisation of human tumours promises to contribute a profound understanding of the changes that contribute to and drive the oncogenic process. In one study, we have been able to determine the oncogenic mechanisms driving a rare adenocarcinoma of the tongue and provide clinically useful information to aid in its treatment, through the determination that the cancer was driven primarily by activation of the RET pathway. The administration of RET targeting kinase inhibitors, sunitinib and sorafenib, provided tumour stabilisation for several months, after which time therapeutic resistant tumours arose. This provided us with the opportunity to identify the genetic changes associated with drug resistance allowing the observation that resistance is correlated with an apparent up-regulation of the parallel proliferative AKT pathway.

However, the complete and comprehensive analysis of a genome using this technology is still nascent and many of the software tools required to achieve this are still in development. In the analysis of tumour normal pairs, it is not clear that current levels of sampling are sufficient to identify somatic changes accurately without further validation. Likewise, the level of false negatives that confound our analyses is unclear. Such considerations will be important if this technology is to be adopted in the routine provision of personalized medicine.

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