A bioinformatic approach to neoantigen discovery in human oesophageal adenocarcinoma.

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Abstract

Oesophageal cancer is the sixth leading cause of cancer death worldwide, becoming the most common gastrointestinal tumor in the world. Surgical treatment only benefits patients with localize tumors and the procedure entails a 40% of incidence, making necessary the discovery of new treatment and early detection methods.

Studies over the past 12 years have established that all tumors contain between 2 to 8 drive tumorigenesis mutations. One of the result of these mutations are neoantigens, caused by damaged DNA and random errors, they generate antigens the immune system has not previously dealt with. The development of vaccines that help the immune system to recognize the neoantigens is one of the most promising strategies on cancer treatments.

In this study we have a unique dataset of 15 patients with Oesphageal Adenocarcinoma (OAC) composed by whole genome sequencing data, RNA sequencing and mass spectrometry analysis. This three different levels of information offer us the opportunity to explore and evaluate the tools for neoantigen discovery. Starting with the creation of custom pipelines for the analysis of next-generation sequencing data, our approach wants to follow and establish the best practice methods for neoantigen discovery in human cancer models.