Blood biopsy profiles circulating tumour cells which hold clues to cancer treatment

Wenfa Ng

Unaffiliated researcher, Singapore, Email: ngwenfa771@hotmail.com

Abstract

Tumours shed cells over the course of its development and these cells migrate to the bloodstream after overcoming multiple barriers at the cellular and tissue level. Such cells are known as circulating tumour cells (CTCs). Thus, opportunities exist for using a simple blood draw to help isolate the circulating tumour cells that could inform cancer treatment. Specifically, circulating tumour cells could be isolated from the blood, concentrated and sent for DNA sequencing to identify the mutational signature of the cells. If circulating tumour cells are sequenced at the population rather than single cell level, the information obtained would inform the oncologist about the aggregate mutational pattern of a cancer in a patient. If circulating tumour cells are from a multitude of cancers in a patient whose disease has metastasized, the aggregate profile would remain useful in identifying the mutations present and possible drugs that could be used. On the other hand, if single cell DNA sequencing is used, circulating tumour cells could illuminate, through phylogenetic clustering, the cancer of origin in cases where multiple types of cancer are present in a patient with metastasized cancer. Such information would reveal the clonal origin of a cancer and the most aggressive tumour type amongst a mix of tumour types. Knowledge such as these could potentially revolutionize cancer treatment in identifying the most aggressive cancer to tackle where significant clinical benefit could be obtained. Thus, blood biopsy holds important utility as a tool for informing the cancer types present through DNA sequencing of isolated circulating tumour cells. Such information could emanate from single cell sequencing or pooled processing of a population of cells. Specifically, pooled population informs the aggregate mutational signature useful for chemotherapeutic drug selection, while single cell sequencing identifies particular mutational profile in each cancer type in a patient with metastasized cancer. But, a future beholds where single cell RNA-sequencing is applied to circulating tumour cells at the clinical level, which could potentially yield differential gene expression information that could identify active molecular targets in need of inactivation by chemotherapeutic drugs such as inhibitors.

Keywords: circulating tumour cells, DNA sequencing, RNA sequencing, single cell, population level, differential gene expression, mutational signature, molecular targets, metastasized cancer, chemotherapeutic drug,

Subject areas: biochemistry, genomics, cell biology, bioinformatics, biotechnology,

Conflicts of interest

The author declares no conflicts of interest.

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