Possibility of detecting cancer using liquid chromatography mass spectrometry profiling of cancer signature metabolome in blood

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Abstract

Cancer cells exhibit myriad characteristics that differentiate them from normal cells; for example, cell surface markers, morphology, cellular metabolism, gene expression, and migratory tendency. Amongst the characteristics, cancer cell metabolism is the least appreciated but is increasingly recognized as a critical hallmark of cancer both from the treatment and diagnostic point of view. Specifically, studies have shown that cancer cells exhibit different metabolism from normal cells, which suggests that profiling the metabolome of cancer cells could inform both cancer diagnostic and treatment. However, few diagnostic tools in development are based on profiling cancer metabolism for either screening or diagnostic applications. This situation is further exacerbated by the fact that cancer remains difficult to detect using blood biopsy even though circulating tumour cells in blood have been isolated and concentrated. Hence, it would be a significant advance for cancer screening and diagnosis if different types of cancer could be differentiated by their unique metabolome signature in blood samples. Screening conducted using blood samples offers advantages of simplicity, ease of use and accessibility compared to tissue biopsy currently used in identifying the type and stage of cancer. To this end, possibility exists in detecting early stage cancer through profiling unique cancer metabolome present in blood. Specifically, different types of cancer might exhibit differentiated metabolic profile where an ensemble of metabolites are secreted extracellularly into the blood. Profiling such secreted metabolites using liquid chromatography mass spectrometry (LC-MS) might provide clues to the type of cancer and its clinical stage. The approach, however, could potentially suffer from high background noise as the secreted metabolites might be from normal cells exhibiting differential responses to changes in nutritional or environmental conditions. Hence, systematic analysis of the secreted metabolome of different cancer cells would help correlate unique metabolome signatures in blood plasma with different cancer types, and thus, provide the basis for a diagnostic tool able to discriminate between normal physiological metabolism and that of specific types of cancer. Further, modern pattern recognition algorithms should provide analytical help in discriminating between adnormal metabolism arising from metabolic disease and those due to cancer. Results obtained from profiling cancer secreted metabolome could be further augmented with confirmatory tests such as antibody-based enzyme linked immunosorbent assay (ELISA). Collectively, blood provides the most accessible medium for cancer detection and use of LC-MS augmented with pattern recognition algorithms might provide a platform for profiling secreted cancer metabolome unique to individual cancer types; thereby, enabling early screening of cancer.

Conflicts of interest

The author declares no conflicts of interest.

Funding