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Identification of Multidimensional Molecular Data Through Biomarkers

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DESCRIPTION

Due to a lack of diagnostic biomarkers for early stage disease and molecular targets for therapy, gastric cancer remains highly lethal. Plasma membrane proteins, which include cluster of differentiation proteins and receptor tyrosine kinases, are a biomarker reservoir. Recognizing that studying plasma membrane proteins individually misses out on complex interactions, we systematically examined the membrane proteomes and transcriptomes of six gastric cancer cell lines. Our findings revealed abnormally high levels of protein expression in proteins whose functions accurately reflect the clinical phenotype of gastric cancer, and we prioritised critical RTKs and CD proteins in gastric cancer. Flow cytometry and immunostaining of clinical gastric cancer tissues confirmed the expression of selected surface proteins. A cohort of gastric cancer tissues showed up-regulation of at least one of four proteins, namely MET, EPHA2, FGFR2, and CD104/ITGB4. In this study, all intestinal type gastric cancer tumours overexpressed at least one of three proteins: MET, FGFR2, and EPHA2. This study presents the first quantitative global landscape of the surface proteome of gastric cancer cells, as well as a list of potential gastric cancer biomarkers. Because of multidimensional alterations at the molecular, cellular, tissue, and organ levels, elucidating the mechanisms of complex diseases such as cardiovascular disease (CVD) remains a significant challenge. Data from multiple omics types genomics, epigenomics, transcriptomics, metabolomics, proteomics, and microbiomics from both humans and model organisms have become available to better understand CVD and offer insights into the underlying mechanisms and potential therapeutic strategies. Individual omics data types, however, capture only a subset of molecular mechanisms. To address this issue, numerous efforts have been made to develop integrative genomics methods that can use multidimensional information from various data types to derive comprehensive molecular insights. We summarise recent methodological advances in multidimensional omics integration, demonstrate their applications in cardiovascular research, and identify challenges and future directions in this emerging field. Cardiovascular disease is a widespread complex disease characterised by multiple risk factors, pathological changes in various cell types, tissues, and organs, and multidimensional molecular perturbations. CVDs such as coronary artery disease, myocardial infarction, and stroke are among the leading causes of death worldwide, necessitating a better understanding of the aetiology. We are witnessing an explosion of biomedical data as a result of the rapid advancements of omics technology, which has the potential to improve our understanding of the molecular underpinnings of clinical phenotypes. Bioinformatics methodologies and tools for analysing individual data types, as recently reviewed by us and others, are accompanying the growing data volume. However, it is becoming increasingly clear that focusing on a specific type of data only provides limited insights into the mechanistic black box that connects molecular traits and disease phenotypes. This is because biological processes do not operate through a single type of molecular data but rather manifest collectively as molecular cascades and interactions across omics domains to influence CVD aetiology. Only through the comprehensive integration of multidimensional omics data can a holistic view of pathogenic mechanisms be effectively captured. This article focuses primarily on multidimensional integrative methods for CVD. We begin with an overview of basic data types and multidimensional data integration principles, and then summarise methodologies and tools, as well as representative CVD applications. Finally, we summarise the field's remaining challenges and suggest future research directions for improving the effectiveness of multidimensional data integration.

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CONFLICT OF INTEREST

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