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**Serum proteome profiling of colorectal cancer using SWATH-MS analysis**

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**ABSTRACT**

Colorectal cancer (CRC) is one of the most common cancers worldwide. CRC is associated with high lethality and is among the leading causes of cancer-related deaths globally. There is an urgent need to identify reliable and sensitive biomarkers to facilitate clinical management of CRC patients and to improve disease outcome. This study aimed to discover cancer-associated protein changes in the serum as biomarkers for CRC via proteomic analysis. For this purpose, we first evaluated the performance of two affinity columns for depletion of the top two and top twelve abundant proteins from the human serum samples for proteomic analysis. The depleted serum samples from CRC (n=15) and controls (n=15) were then analyzed using SWATH-MS (sequential window acquisition of all theoretical fragment ion spectra mass spectrometry) proteomic approach based on data-independent acquisition method. Depletion of the top twelve high abundant proteins was demonstrated to enhance the detection of less abundant proteins and led to an increase in protein sequence coverage. In our preliminary analysis, we found distinct protein profiles associated with the cancer and control groups and identified proteins with altered expression between the two groups. Interestingly, we discovered a number of glycoproteins such as alpha-1-acid glycoprotein 1, alpha-1-antitrypsin and haptoglobin with significant differential expression. Further studies are needed to confirm the biomarker candidates. Moreover, detailed analysis of the changes in the glycoprotein profiles should be undertaken to uncover clinically relevant biomarkers and to understand their roles in cancer biology. In conclusion, our study showed that SWATH-MS is a useful approach for cancer biomarker discovery and our findings suggested that glycoproteins constitute an important resource of potential disease biomarkers.