A Systematic Investigation of the Malignant Functions and Diagnostic Potential of the Cancer Secretome

The collection of proteins secreted from a cell—the secretome—is of particular interest in cancer pathophysiology due to its diagnostic potential and role in tumorigenesis. However, cancer secretome studies are often limited to one tissue or cancer type or focus on biomarker prediction without exploring the associated functions. We therefore conducted a pan-cancer analysis of secretome gene expression changes to identify candidate diagnostic biomarkers and to investigate the underlying biological function of these changes. Using transcriptomic data spanning 32 cancer types and 30 healthy tissues, we quantified the relative diagnostic potential of secretome proteins for each cancer. Furthermore, we offer a potential mechanism by which cancer cells relieve secretory pathway stress by decreasing the expression of tissue-specific genes, thereby facilitating the secretion of proteins promoting invasion and proliferation. These results provide a more systematic understanding of the cancer secretome, facilitating its use in diagnostics and its targeting for therapeutic development.

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