Exploitation of the 2D graphene oxide biomolecule corona in secretome-based cancer biomarker discovery

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Nanotechnology has emerged as a promising tool for cancer biomarker discovery. Nanoparticles (NPs) undergo rapid modification once they come into contact with the biological milieu to form a "biomolecule corona" due to their interfacial reactivity [1]. Analysis of the biomolecule corona by mass spectrometry-based proteomics has shown an enhanced discovery of previously unidentified low-abundant proteins and has attracted significant interest as a promising technology in cancer biomarker discovery [2].

Graphene oxide is a two-dimensional (2D) nanomaterial with a distinctively large surface area and high surface reactivity [3]. In this study, the biomolecule corona formed around graphene oxide nanosheets is exploited to provide an in-depth analysis of the secretome and identify unique proteomic signatures of different cancer cell lines.

The secretome of lung cancer (A549), glioblastoma (GL261 and U251) and cervical cancer (HeLa) cell lines was obtained by harvesting the conditioned media of the cultured cancer cells. The collected secretome was incubated with graphene oxide nanosheets to form the biomolecule corona. Using the 2-step NanoOmics purification protocol [4], the graphene oxide biomolecule corona was isolated via a combination of size exclusion chromatography and membrane ultrafiltration. Proteomic mass spectrometry analysis of the isolated biomolecule corona showed a significant increase in the number of identified proteins in the corona-processed secretome of all the cancer cell lines when compared to the unprocessed secretome samples. Significant enrichment of low-abundance secreted protein was observed due to the corona-processing. Ultimately, the graphene oxide corona-processing protocol enhanced the discovery of uniquely secreted proteins from different cancer cell lines.

In the future, we plan to utilize the graphene oxide biomolecule corona platform to correlate the cancer secretome proteomic fingerprints with proteomic analysis of plasma samples obtained from cancer patients, with the ultimate goal to identify highly-specific blood biomarkers for cancer early detection.

References

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