

Response prediction for cisplatin-based treatment regimens in non-small cell lung cancer using a protein-based assay

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Abstract

The majority of patients with non-small cell lung cancer (NSCLC) are treated with cisplatin-based chemotherapies in a one-size-fits-all approach. However, a significant number of patients do not benefit in terms of survival and, moreover, quality of life deteriorates due to side effects of this treatment.

Pinpointing NSCLC cancer patients who are more likely to derive clinical benefit from cisplatin-based chemotherapies using molecular markers, will improve clinical outcome and reduce both toxicity and health care costs.

Underlying the disparate responses of different tumors is their distinct genetic and protein molecular make-up, culminating in different states of cellular signalling pathways that direct responses to therapeutic intervention. A protein-based test provides a downstream read-out of the cell signalling state as it encompasses the functional outcome of genetic, epigenetic, and translational events. Therefore, a protein test is likely to be of high relevance for response prediction and can be implemented in the routine clinical setting.

The overall **aim** of this proposal is to develop a protein-based test for cisplatin response prediction in NSCLC patients. The combined previous *in vitro* and to be generated clinical proteomics datasets and follow-up in independent patient cohorts will allow us to develop a protein profile-guided response prediction tool using the most promising biomarkers.