Cleveland Clinic Innovations

PRODUCT

Multigene assay for prediction of therapeutic response to cisplatin

INDICATION

Solid tumors and hematologic malignancies treated with cisplatin

VALUE PROPOSITION

- Prediction of cisplatin chemotherapy benefit
- Minimization of both cisplatin overtreatment and undertreatment without compromising survival rate

DEVELOPMENT STAGE

Completed clinical pilot of CisSig to predict therapeutic response to cisplatin in muscle-invasive bladder cancer patients

INTELLECTUAL PROPERTY

US Pub. No.
US 2022/0235421 A1

RELATED PUBLICATIONS

Jessica A. Scarborough, et al. Exploiting convergent phenotypes to derive a pan-cancer cisplatin response gene expression signature. NPJ Precis Oncol. 2023;7(1):38

CONTACT INFORMATION

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Gene Expression Signature for Cisplatin Therapeutic Response

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UNMET NEED

Only about 7% of cancer patients benefit from targeted therapy based on patients' gene mutational status causing the disease. Even among the cancer patients who do benefit from gene mutation-targeted therapies, the costs of these drugs are high, and the responses are typically not durable, as cancer evolves eventually becoming resistant to the drug. Without an actionable gene mutation, cancer patients receive conventional chemotherapy. Cisplatin, while highly toxic, is one of the most heavily utilized chemotherapeutic agents for hematologic malignancies and solid tumors. However, treatment with cisplatin is associated with drug resistance and severe adverse side effects. There is a need to predict cancer patients' response to conventional chemotherapy agents without relying on changes in gene mutational status.

SOLUTION

Cleveland Clinic investigators have developed a gene expression signature extraction method informed by convergent phenotypes and based on identification of shared transcriptomic markers of drug response phenotype in cancers that appear genotypically disparate. By harnessing the power of a large dataset, investigators have identified cisplatin response signature, CisSig, and derived a score to determine how well an individual cancer patient would respond to cisplatin chemotherapy. Higher expression of identified gene signature is correlated with increased sensitivity to the drug, thereby demonstrating direct relationship between gene expression and drug response. Using this method, gene expression signatures can be extracted for hundreds of chemotherapeutic agents and combined to predict response to drug combinations commonly provided in clinical practice which may lead to a significant expansion of precision medicine in oncology.