

Methods Of Predicting Responses To Disease Treatments

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The Invention

UW-Madison researchers have developed a novel method for predicting optimal treatment responses in oncology patients based on DNA and RNA sequences in circulating tumor cells. They termed this new method TARGETS (TreAtment Response Generalized Elastic-neT Signatures). The researchers trained TARGETS drug response models using Elastic-Net regression using data from the publicly available Genomics of Drug Sensitivity in Cancer database. The final validation step involved independent clinical validation using the West Coast Prostate Cancer Dream Team (WCDT) data, and the researchers found that the TARGETS androgen receptor signaling inhibitors (ARSI) signature successfully predicted clinical treatment response in metastatic castration-resistant prostate cancer with a statistically significant interaction between the TARGETS score and PSA response. The inventors noted in the paper that to reduce noise in the training data, they included genes only identified in the COSMIC Cancer Gene Census database. They trained their algorithm to develop pharmacogenetic response signatures for all drugs included in the Genomics of Drug Sensitivity in Cancer database. They validated their system using data from the Cancer Cell Line Encyclopedia (CCLE), and on clinical samples from The Cancer Genome Atlas (TCGA) and Stand Up to Cancer/Prostate Cancer Foundation West Coast Prostate Cancer Dream Team. The inventors now have identified genetic patterns associated with positive responses to widely prescribed chemotherapeutic drugs as well as a system for looking for those patterns.

Tech Fields

• <u>Drug Discovery & Development : Precision medicine</u>

For current licensing status, please contact Rafael Diaz at rdiaz@warf.org or 608-960-9847