Docket #: S13-274

Cancer outcomes predicted by using genomic profiles

Stanford researches have formulated a robust database called PRECOG (Prediction of Clinical Outcomes from Genomics) that connects cancer genome expression and patient survival/outcomes in a more predictive and extensive collection than any other signature on the market. By integrating almost 18,000 patients with 39 types of cancer types (more than 26,000 tumors), inventors meticulously extrapolated genetic patterns and ultimately discovered key pathways of cell malignancy.

This resource allowed scientists to target prognostic genes such as KLRB1 (encoding CD161) which is involved in tumor associated leukocytes. A gene called FOXM1 was shown to have poor outcome in cancer patients. Additionally, CIBERSORT, a software identifying leukocyte cells was able to help find 22 significant leukocyte subsets related to cancer survival.

These meaningful correlations offer a distinct passageway to develop new resources and tools -- to accelerate the discovery of biomarkers, prognostic genes, leukocyte subsets, and novel therapeutic targets in a diverse population of cancer patients. This invention has solved the inconsistencies of other technologies by utilizing genomic profiles from public sources and by refining the clinical outcome and responses to treatment with superior precision and reproducibility. Understandably, these therapeutic targets may revolutionize cancer treatment in millions of patients worldwide.

Stage of Development:

Research is continuing with additional comprehensive datasets and tools to refine and leverage the underlying database. A web-based interface is being developed to continue examining the genomic profiles.

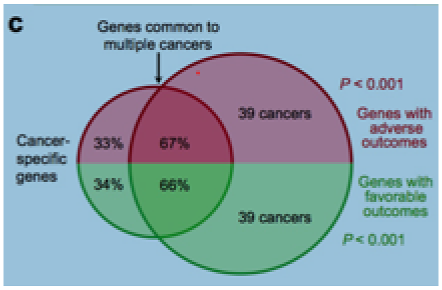

Figure C: Approximately 2/3 of prognostic genes (continuous Cox regression; P0.001) are prognostic in at least two cancers, while the remaining 1/3 are cancer-specific. Image credit -- inventor publication listed below

Applications

- **Broad reach** of patients: Identify prognostic and predictive signatures across many cancers
- Ascertain **survival outcome** in patients
- **Identify treatment and response to medicine(s)**

Advantages

- **Most extensive database** of annotated patient genomic profiles with survival outcomes and treatment responses
- **More robust and comparative power** across studies
- **Provides practical new resources and tools** to accelerate the discovery of biomarkers and novel therapeutic cancer targets
- **Increased cancer science research** – PRECOG and CIBERSORT combined makes an unprecedented first in line database

Publications

- Gentles, Andrew J, Aaron M Newman, Chih Long Liu, Scott V Bratman, Weiguo Feng, Dongkyoon Kim, Viswam S Nair, Yue Xu, Amanda Khuong, Chuong D Hoang, Maximilian Diehn, Robert B West, Sylvia K Plevritis, and Ash A Alizadeh. "The Prognostic Landscape of Genes and Infiltrating Immune Cells across Human Cancers." Nature Medicine Nat Med, 2015, 938-45.

- Krista Conger, Team links gene expression, immune system with cancer survival rates, Stanford Medicine News (published 20 July 2015).

Innovators

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