Uncovering Stochastic and Drug-Induced Phenotypic Transitions in Small Cell Lung Cancer

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ABSTRACT

Small cell lung cancer (SCLC) is an aggressive tumor type that relapses at high rates and metastasizes early. Despite these poor outcomes, the standard of care for SCLC has not changed in decades, because the mechanisms of acquired resistance are not well understood. Within the past decade, the role of intratumoral heterogeneity in tumor aggressiveness has become more apparent, as cooperation between subtypes of SCLC can potentiate metastasis [Calbo, 2011] and treatment evasion [Jahchan, 2016]. The discovery of multiple SCLC phenotypes necessitates further analysis to map the phenotypic space of SCLC. Consensus clustering and weighted gene co-expression network analysis (WGCNA) reveal 4 clusters, including a novel neuroendocrine variant (NEv2) distinguished by gene modules and drug response, and a transcriptional factor network is able to explain these four steady states. Analysis of human and mouse tumors suggests that SCLC phenotype is plastic, both stochastically and in response to drug. We use RNA velocity of single cell RNA-seq data to understand and quantify movement through the phenotypic landscape, and well as make predictions of perturbations that may induce those transitions. Characterization of the transitions between core SCLC phenotypes and predictions of perturbation strategies may suggest new methods of personalized treatment.

CLUSTERING CELL LINES BY GENE EXPRESSION REVEALS 4 BROAD SCLC SUBTYPES

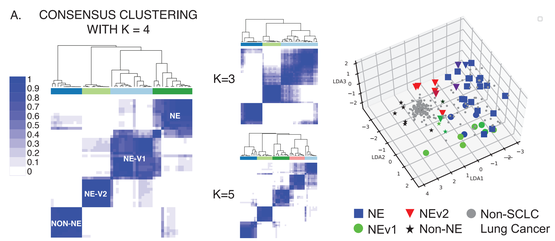


Figure 1 Consensus clustering of 50 CCLE SCLC cell lines reveals 4 transcriptional subtypes of SCLC (left), including 3 neuroendocrine subtypes (NE, NEv1, NEv2) and one non-neuroendocrine subtype (non-NE). The non-NE subtype is most similar to non-SCLC lung cancer cell lines by gene expression (right). Both NEv1 and NEv2 are similar to the canonical NE subtype, but differ greatly from each other.

SCLC SUBTYPES ARE DISTINGUISHED BY GENE EXPRESSION AND DRUG RESPONSE

Analysis of cell lines to 526 drugs and investigational agents shows NEv2 is least sensitive to over half of drugs tested. Specifically NEv2 shows increased resistance to AURK inhibitors.

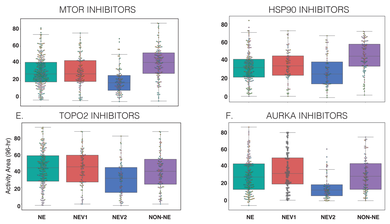


Figure 2 Comparison of drug responses across subtypes for Aurora kinase inhibitors, HSP90 inhibitors, topoisomerase inhibitors and mTOR inhibitors.

IN SILICO SIMULATION OF GENE REGULATORY NETWORK RECAPITULATES FOUR SUBTYPES

Genetic mutations are unable to distinguish between phenotypic subpopulations of SCLC completely; thus, we investigate a transcription factor (TF) network to explain the stability of multiple subtypes. Using TFs from each significant module and the literature, we simulated a network with quasi-Bayesian Boolean rules calibrated to cell line data. This led to 10 attractors that match our four expected phenotypes.

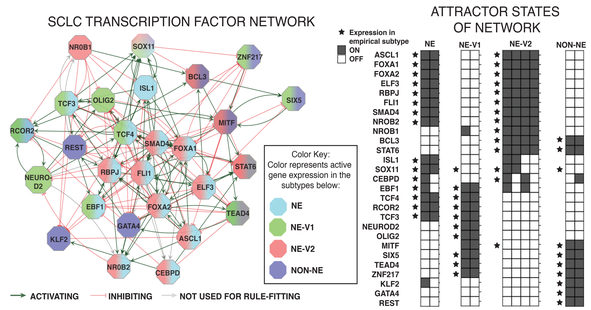


Figure 3 (Left) Gene regulatory network including TFs relevant to SCLC phenotypic heterogeneity. (Right) Simulations of the network are able to recapitulate the expected subtypes. Attractors are defined probabilistically as those states that are more probable than any neighboring state.

IN SILICO PERTURBATIONS SUGGEST STRATEGIES FOR REPROGRAMMING SCLC CELLS TOWARD SENSITIVITY

Boolean perturbations (TF held at 0 or 1) allow us to test the outcome of silencing (0) or activating (1) a specific gene. These perturbations suggest experimental strategies for destabilizing a subtype, or "pushing" a cell away from that attractor state. When applied to resistant cell types, such as NEv2 cells, reprogramming may provide a successful strategy for SCLC treatment.

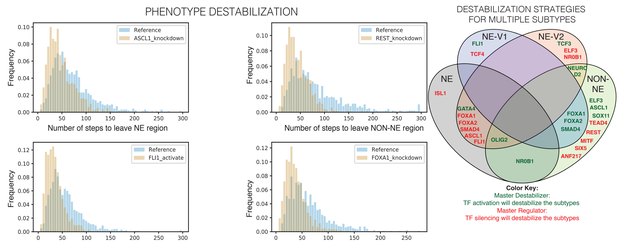


Figure 4 (Left) Examples of destabilization strategies for each subtype. Perturbation allows the simulation to leave a specified state's 4-TF neighborhood faster than a random walk, so a smaller number of steps is required, shifting the distribution of walk lengths to the left. (Right) Destabilization strategies for multiple subtypes. Four-circle Venn diagram shows which perturbations will destabilize (>20% average change in walk length) at least one subtype.

SUBTYPES ARE REPRESENTED ACROSS HUMAN AND MOUSE TUMORS

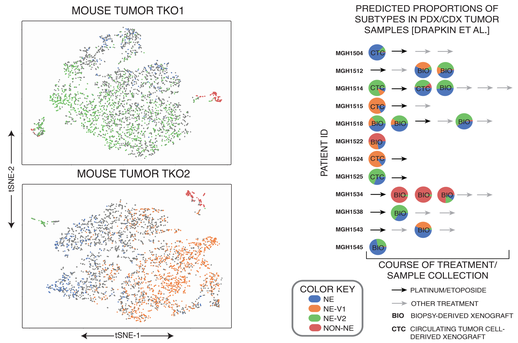


Figure 5 Using a nearest neighbor analysis, scRNA-seq data from two independent mouse tumors shows correlations with human cell line subtypes. CIBERSORT (Newman, 2015) was used to detect proportions of subtypes in human tumors before and after treatment (Drapkin, 2018).

HOW PLASTIC ARE SCLC SUBTYPES?

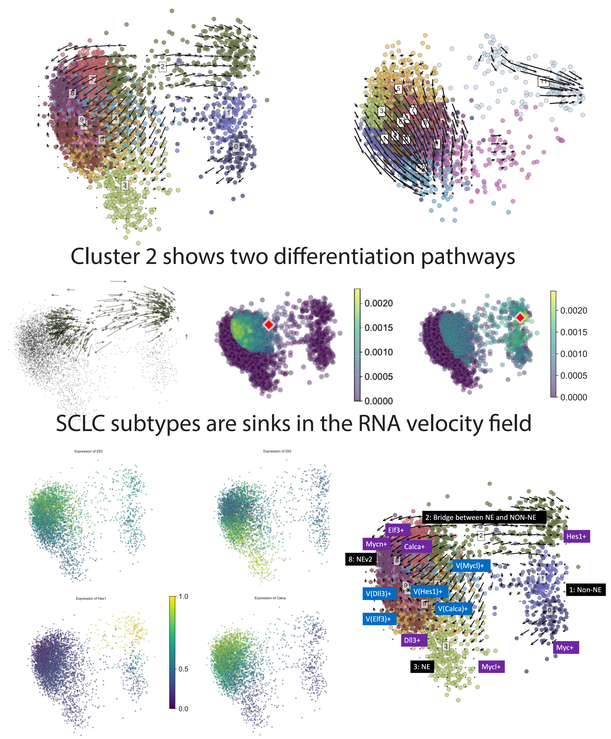


Figure 6 (Top) RNA velocity [La Manno, 2018] gradient field for scRNA-seq of two triple knockout (TP53, RB1, P130) mouse SCLC tumors. (Middle) Cluster 2 shows a consistent split into two paths through phenospace. (Bottom) Expression of various markers for SCLC subtypes overlaid on TK01. RNA velocity shows movement towards subtype "sinks," including a "bridge" between NE and non-NE.

PATH OF LEAST ACTION THROUGH PHENOTYPIC LANDSCAPE SUGGESTS REPROGRAMMING STRATEGIES

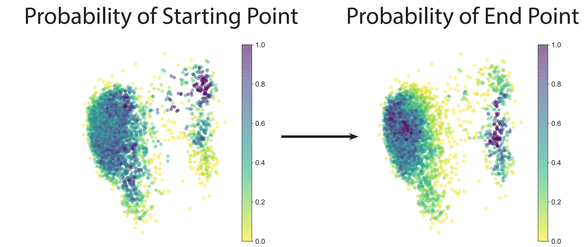
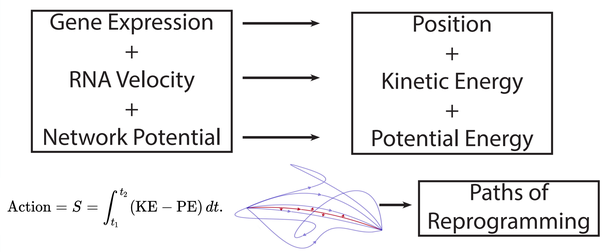


Figure 7 Distribution of starting point and ending point probabilities for a random walk through the landscape (random diffusion + velocity drift).



CONCLUSIONS AND FUTURE DIRECTIONS

- Consensus clustering identified four phenotypic clusters defined by WGCNA gene modules, with differential drug sensitivity and gene expression patterns.
- Stable states in a quasi-Boolean GRN recapitulate empirical results, and perturbations of these states suggest strategies for reprogramming. siRNA screens to text these predictions and their effects on drug response are underway.
- RNA velocity analysis suggests relatively plastic phenotypic states, and master TF expression dynamics show movement within the phenotypic landscape.
- Pseudo-temporal single cell data along an RNA velocity trajectory will be used to constrain the GRN model and define movement through the SCLC phenotypic landscape. States with low RNA velocity (sinks) should be represented as attractors of this network.

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