Docket #: S22-056

Combinatorial cellular programming

Stanford researchers developed a technology that efficiently identifies combinations of genetic interventions with lasting, effective therapeutic functions by constructing genetic perturbation libraries containing the desired combination of phenotypes extracted from each cell.

Cell therapies utilize engineered cells to achieve specific effects in a patient's body. However, those desired therapeutic phenotypes are usually regulated by multiple genes in the human body, and current technologies, which act on a single genetic pathway, cannot program such polygenic behaviors into cells. To get around this issue, we need to identify combinations of genetic and pharmacological interventions that achieve the desired polygenic therapeutic function. However, identifying the desired combination of genes and programming cells with these complex phenotypes at scale is intractable and requires a scalable platform for engineering cells with complex phenotypes.

Stanford researchers, therefore, developed a novel technology that provides a data-driven solution to the combinatorial scaling problem of polygenic phenotypes. The technology leverages recent advances in machine learning, modern genome editing, and high-throughput single-cell phenotyping to construct genetic perturbation libraries for which different phenotype combinations can be extracted from each cell. Therefore, new polygenic cell therapies can be designed through an efficient, data-directed exploration of high-dimensional combinatorial perturbations.

Stage of Development

- Proof of concept

Applications

- Engineering specific, well-controlled cell therapies, including polygenically programmed chimeric antigen receptor T and NK (CAR-T/NK) cells and

engineered T helper cell subtypes.

Advantages

- It is the only approach capable of systematically screening cells for phenotypes that require synergistic perturbation of more than five genes.
- This approach enables phenotypic screening of trillions of combinatorial perturbations, revealing complex phenotypes that are unobservable through any monogenic screening approach.

Patents

- Published Application: WO2023177819

Innovators

- Sandy Klemm
- Samuel Kim
- Jacob Blum
- William Greenleaf

Licensing Contact

Cheryl Cathey

Senior Licensing and Strategic Alliance Manager

Email