Docket #: S18-348

Method to predict response to cancer immunotherapy

Researchers at Stanford have identified polymorphisms in SIRPalpha that can be used to predict responsiveness to immunotherapy. Cancer cells can evade elimination by the immune system by expressing the CD47 "don't eat me" signal. CD47 binds to SIRPalpha, an inhibitory receptor on macrophages, and blocks phagocytosis thereby allowing the cancer cells to survive. Agents that disrupt this binding restore phagocytosis (and elimination) of CD47-expressing cancer cells. Thus, these agents hold great promise for the treatment of several cancers. However, patient response to such immunotherapy is highly variable. There is a great need for methods to predict patient responsiveness to therapeutic blockade of CD47-SIRPalpha signaling. To help meet this need, the inventors have identified single nucleotide polymorphisms (SNPs) within the SIRP gene locus that affect SIRPalpha expression. The inventors leveraged this group of SNPs to develop a method of predicting which patients will respond to therapeutic blockage of CD47-SIRPalpha signaling. This technology has the potential to improve cancer treatment as it provides a method to predict patient responsiveness to CD47-SIRPalpha blockade-based therapies.

Stage of research
Development is ongoing. Initial studies show great promise.

Applications

- Prognostic for cancer immunotherapy responsiveness

Advantages

- Enables more informed selection of appropriate immunotherapy to treat cancer

- Stratifies patients for CD47 blocking immunotherapies
- Has potential to inform treatments for autoimmune disease, allergy and infectious disease.

Patents

- Published Application: WO2020068431

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