

Methods for Selection of Cancer Patients and Predicting Efficacy of Combination Therapy

Ref. No. E-013-2012

Keywords: Therapeutic, cancer, myeloma, melanoma, lung, breast, histone deacetylase, HDAC, rapamycin, mTOR

Summary:

The [Lung Cancer Biomarkers Group](#) of the National Cancer Institute (NCI) seeks parties interested in collaborative research to further co-develop methods for selecting cancer patients for combination therapy.

Technology:

Available for co-development is a novel gene signature of thirty-seven drug-responsive genes that links changes in gene expression to the clinically desirable outcome of improved overall survival. Expression of these genes has been linked to prognosis in several cancers, including, but not limited to: multiple myeloma, melanoma, and lung and breast cancers. Patients identified by this signature would be predicted to benefit from combined HDAC inhibitor/mTOR inhibitor therapy.

Potential Commercial Applications:

- Development of a clinical diagnostic test to identify cancer patients who would benefit most from mTOR and HDAC combination therapy.
- Use as a surrogate biomarker related to drug response.
- Development of therapeutics targeting several cancers, including multiple myeloma.

Competitive Advantages:

- Implements a smaller gene set compared to current diagnostic gene signatures.
- Provides a basis for the development of a diagnostic for patient stratification or a response measurement related to the combined use of mTOR and HDAC inhibitors for cancer treatment.

Development Stage: Pre-clinical, *in vitro* and *in vivo* animal data available.

Patent Status: U.S. Provisional Application No. 61/558,402 filed 10 Nov 2011

Contact: Please submit an information request form at <http://techtransfer.cancer.gov> or contact:

John D. Hewes, Ph.D.
(301) 435-3121
hewesj@mail.nih.gov.

Last updated: 06/28/2012

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