

Implementation and refinement of high throughput functional genomic screening

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Acute myeloid leukemia (AML) is a cancer of blood cells. It is the most common leukemia in adults and accounts for about 20% of childhood leukemias. Standard therapy usually includes chemotherapies with severe side effects and cures less than half of patients with AML. So, new strategies to treat AML are urgently needed. We have performed large-scale experiments exploring most human genes (over 15,000) using biological and computational techniques. In doing so, we have generated lists of hundreds of targets, which if inhibited, appear to make AML cells more sensitive to anti-leukemia therapy.

We proposed to use a new, high-throughput method to validate these potential therapeutic targets and use this information to design better computational techniques to reduce our false positive rates for the study of other cancers.

With support from the GAC, we have implemented and refined this high-throughput methodology and continue to work on improving the computational algorithms to analyze the data. In doing so, we have identified a novel target that may be exploited to improve treatment for AML. We have recently submitted some of this work for publication. GAC supported work has also contributed to the development of several collaborative efforts aimed at other cancers including brain tumors, colorectal cancer, head and neck cancer, and melanoma. Moreover, we have submitted several grant applications based on these principles and methods, which have been reviewed favorably. In fact, GAC funded work has contributed to the receipt of over \$640,000 in research awards from 4 different organizations in less than 6 months. Larger, collaborative grant applications are in preparation.