

Bankhead-Coley Cancer Research Program

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Shared Instrument Grant
(1-year project)*

Project Title: Illumina Beadstation: High-Throughput Genotyping and Gene Expression Shared Instrumentation

Project Summary: This grant proposed the purchase of the Illumina BeadStation 500GX as part of the Cancer Center Molecular Genetics Core Facility to provide access to a high-throughput technology for whole genome scan and expression profiling to enhance cancer researchers in four multidisciplinary research programs within the Sylvester Comprehensive Cancer Center at the University of Miami (UM) Miller School of Medicine—Biobehavioral Oncology and Cancer Control, Hormone-Regulated Cancers, Tumor Immunology, and Viral Oncology. These research programs not only address important aspects of the cancer challenge, they reflect UM/Sylvester's strengths and priorities as a research institution. Serving more than five million people as the only academic medical center in South Florida, the UM Miller School of Medicine has earned international acclaim for research, clinical care, and biomedical innovations. The school ranks in the top third among U.S. medical schools in terms of research funding awarded. UM/Sylvester serves as the hub for cancer-related research, diagnosis, and as a treatment center that handles more than 1,400 inpatient admissions annually, performs 3,000 surgical procedures, and treats 3,000 new cancer patients. Most human traits, such as predisposition to cancer or drug response, are not caused by a single gene or even a single variation in the genome, but rather are associated with many genes across the whole human genome. Many association studies have been carried out using the candidate gene approach. Although they have been successful in discovering several risk-associated genes, they may miss out on critical regions of the genome. Therefore, it is important to be able to identify many of the genetic variations across the genome that may contribute to cancer risk. Recently, whole-genome scan has been successfully used to identify a number of human diseases, including cancer. Genetic variations are suitable for automated high-throughput detection methods, and we now have the potential of using this approach to carry out association studies for human cancers. A number of genes with involvement in cancer susceptibility or treatment outcome could be identified in a single large experiment. The whole genome association studies are more powerful for identifying the multiple genetic variants that are expected to increase cancer risk in the general population. Therefore, the current research emphasis has been placed on "personalized medicine" with the utilization of inherited genetic factors and expression profiling to predict cancer risk, treatment response, targets for prevention, and clinical outcomes, including recurrence, in cancer patients. For example, gene-expression profiles have already provided a useful tool to refine the prediction of a patient's risk of cancer recurrence and, in principle, to impact decisions regarding the use of chemotherapy in cancer patients. At the present time, there is a gene expression core facility at UM to support researchers at the medical school. With the advancement of the high-throughput technology, such as the Illumina's BeadArray technology, it will become feasible for performing whole genome scan and targeted genetic variations studies (Project 1), gene expression profiling (Projects 2, 4, 5, and 6), and changes in tumor tissues (Project 3) in a larger number of samples with adequate

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statistical power. The BeadArray technology has become one of the most popular platforms and has been used in several large-scale genetic studies. In summary, the proposed Illumina system will provide the critical high-throughput advanced technology to move the specific cancer-related research projects identified in this grant forward rapidly and will contribute to the entire cancer research and training activities at the UM/Sylvester and to the field of targeted cancer prevention and treatment.