Adenoid Cystic Carcinoma Research Foundation

ACCRF Researcher Spotlight - March 2009

Dr. Andy Futreal

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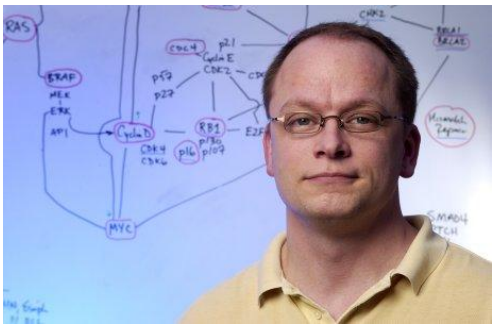

My research interests are in investigating the molecular genetics of human disease, most specifically focused on cancer. In addition to the main focus of work in the Cancer Genome Project on identification of somatic mutations in human cancer via large-scale genomic approaches, other interests include the application of molecular genetics to potential elucidation of therapeutic targets in cancer, the potential role of somatic genetics in patient stratification to conventional cancer therapies and the functional investigation of mutations identified in the Cancer Genome Project. In addition, I am interested in developing our platforms for investigating the genetic etiology of rare, essentially orphan, monogenic disorders.

The Cancer Genome Project has been running now for nine years. In this time we have pioneered the use of large-scale exon resequencing as an approach to identifying cancer genes in various tumor types. These efforts have begun to elucidate the complexity of cancer genomes at the sequence level and provided substantial evidence for their being a likely large number of relatively infrequently mutated genes which are contributing to cancer development. All of these efforts will hopefully identify those genes and pathways which can be investigated for potential therapeutic exploitation. We have more recently been working to exploit next generation sequencing technologies in investigation of cancer genomes. This work is giving us new insights into the type and number of alterations in solid tumours such as ACC. As well, this work is providing the framework for approaches that aim to re-sequence entire cancer genomes providing for a nearly complete assessment of the complexity, challenges and potential opportunities to go from cancer genetics to cancer treatment.

I have been pleased, along with my lead project researcher Phil Stephens, to contribute to the ACC Research Foundation's Research Agenda through our extensive work to identify Somatic Mutations active in ACC. Our initial findings have begun to validate that a small number of mutations are likely at play in ACC. In February of this year, I presented our current findings to many in the ACC research community via the quarterly ACCRF Research Call teleconference and we are actively sharing our input regarding possible mutation targets with the broader network of ACCRF-sponsored researchers.

My team and I look forward to continuing our work with ACCRF. We are currently discussing potential work to expand our resequencing coverage as well as a potential project to investigate Somatic Genomic Rearrangements at play in ACC. We are enthusiastic about how our efforts can accelerate translation of research findings to clinical treatments and believe the work sponsored by the ACCRF can have far reaching impact beyond ACC to other rare cancers.