Single cell analysis in cancer

Benjamin L. Emert, Eduardo Torre, and Arjun Raj

***Short Abstract* — Cancer treatment often involves the use of drug that kill most, but not all cancer cells. These remaining cells often contribute to therapy resistance, leading to relapse. We use quantitative experimental methods to reveal the ways in which single cells survive therapy. These mechanisms may be exploited to make new treatment regimens designed to prevent therapy resistance.**

***Keywords* — Single cell biology, cancer.**

Cancer is a disease that originates from single cells, and the treatment of cancer also is a problem of single cells: anti-cancer therapies can often kill the vast majority of tumor cells but a few rare cells remain and grow despite treatment. Often, it is thought that the underlying basis for the behavior of these rare cells is a genetic difference. However, we and others have shown that non-genetic differences may be a key driver of rare, drug resistant cells, yet the precise molecular nature of these differences often remains mysterious. We here describe the development of a cellular "time machine" that allows us to link the ultimate cellular fate to the initial cellular state on a single cell basis, thus revealing markers for pre-resistant cells in the population. Further, we use genetic screening technologies to elucidate the pathways that control the formation of these rare cells and discuss their therapeutic implications.