Cancer is based on dynamic changes of the genome that ultimately translate into an altered proteome, optimized for uncontrolled cell growth and division. In addition, many pathways, initially causing cancer further promote the propagation of altered genetic information, accelerating the adaption of cancer cells to new environments. This dynamic process becomes even more complex if taking into account the dynamic state of the cellular proteome that is regulated by protein synthesis and degradation, posttranslational modifications, protein localization, and the interaction of proteins with other proteins as well as with different classes of biomolecules. While the “cancer genome” can now be easily accessed due to advances in DNA sequencing technology, the information contained in the “cancer proteome” has remained largely untapped due to technical challenges in quantifying the large amount of proteins expressed in mammalian cells. Yet, the proteome holds an enormous potential to improve our understanding of the basic principles underlying cancer to revolutionize early diagnosis of the disease and to improve patient care. Up to date, virtually all targeted therapeutics in cancer treatment are targeting proteins. Understanding how these drugs alter the proteome has the potential to help us refine our approaches to drug design.

Despite the potentials of studying the proteome in order to improve our understanding of cancer, the proteome-contained information is substantially underused in cancer research. This is based on technical limitations of the proteomics technology, which for a long time did not match the capabilities of genetics tools already widely used in studying cancer. However, the past few years brought enormous improvements in all aspects of proteomics but especially in mass spectrometry, the main tool used in studying the proteome.
The Tandem Mass Tag MS3 (TMT-MS3) method allows the accurate quantification of up to ten proteome samples in a single experiment.

The level of high comprehensiveness in proteomics, which allows us to quantify almost all proteins and their post-translational modifications in a single experiment, was a first step in increasing the technology’s competitiveness in comparison to genomics tools. A second and more recent improvement was the enhancement of the technology’s throughput, which now enables us to quantify up to 10 different samples in one experiment. In addition to applying these new methodologies to samples from primary tumor and cell culture models, my lab is continuing to work on improving both aspects by developing methods that will allow a more efficient monitoring of levels of post-translational modifications and also by increasing the throughput of proteomics through enhancing its multiplexing capacity. Both directions are aimed at improving proteomics as a tool in basic research and also pushing the technology’s capacity to enable its use in a clinical environment.

We are applying existing and new methods in two specific areas. By establishing quantitative maps of protein concentration and site specific protein phosphorylation levels from an extensive number of cancer cell lines and primary tumors, we are searching for proteome biomarkers in order to direct targeted therapies for individual patients. We are focusing these studies on lung cancer and are working in collaboration with the laboratory of Cyril Benes to study cellular mechanisms that enable cancer cells to develop resistance against treatment by targeted therapeutics. We are working with cell line models to monitor changes in protein and phosphorylation levels while evoking resistance against the treatment with targeted therapeutics.

Selected Publications:


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