Abstract of Presentation

Identification of cancer biomarker and tissue microarrays in the era of proteomics

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Abstract :

Genetic and proteomic information is accumulating at a rapid pace from the new genomic and proteomic technologies and approaches. Only a fraction of these can ever be analyzed at the tissue level in large scale clinical materials. In a cDNA microarray (DNA chip) experiment, one can determine the expression level of 50'000 genes in a single experiment. These new technologies have revealed hundreds of new and potentially important cancer genes that would be important to analyze in a large series of clinical specimens. A similar development is expected due to the rapid development of proteomic technologies because these technologies will identify large numbers of novel proteins, relevant for cancer initiation and development. Despite these tremendous advances, it remains very difficult to distinguish relevant protein expression alterations ("major players") from secondary downstream changes ("bystanders"). The relevance of many of these proteins underlying tumor progression remains poorly understood because such studies require analysis of hundreds of tumors to provide statistically meaningful results. In this presentation, we illustrate how much translation of proteomic information to clinical applications, such as diagnostic tests, can be most appropriately carried out with high through-put tissue microarray approaches. As many as 1'000 cylindrical tissue biopsy specimens from individual tumors can be arrayed in a single tissue microarray block. We describe the parallel in situ detection of DNA, RNA and protein targets in tissue microarrays. This method drastically facilitates comprehensive profiling of cancer specimens, with minimal tissue requirements. We present examples, how the Zurich tissue microarray platform is used for biomarker discovery parallel to proteomic analysis.