Application of genomics and proteomics technologies to early diagnosis of reproductive organ cancers

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Abstract

Advances in molecular biology over the past decade have helped enhance understanding of the complex interplay between genetic, transcriptional and translational alterations in human cancers. These molecular changes are the basis for an evolving field of high-throughput cancer screening techniques using microscopic amounts of patient-based materials. LASER capture microdissection allows pure populations of cells to be isolated from both the tumor and stroma in order to identify subtle differences in RNA and protein expression. Comparative analysis of these alterations between normal, pre-invasive, and invasive tissues, using powerful bioinformatic programs, has allowed us to identify novel tumor markers, profile complex protein pathways, and develop new molecular-based therapies. Continued refinement of such high-throughput micro-technologies will enable us to rapidly query patient specimens to identify novel methods for early diagnosis, treatment, and follow-up of a wide array of human cancers.

There has also been an explosion in the development of new tools to analyze proteomic data of blood cells and other bodily fluids and materials in recent years. Analysis of a proteome would enhance the possibility of identifying protein signatures for cancer. Surface enhanced LASER desorption and ionization with time of flight diagnosis (SELDI-TOF) spectral analysis is linked with a high-order analytical bioinformatic approach to define optimal discriminatory signature proteomic patterns. This technology is now being widely used in laboratories around the world for biomarker discovery in the early stages of cancer in general and breast cancer and cancers involving the reproductive organs such as ovary, prostate, cervix and endometrium in particular.

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