A New Method for Simultaneous Processing and Analysis of Prostate Core Biopsies

Introduction and Objective: Patterned biopsies play a major role in the early detection of prostate cancer. Maintaining site-specific information regarding individual biopsy cores is of critical importance. While individual processing is prohibitively expensive, current methods of parallel processing (tissue microarrays, color coding, multi-compartment cassettes, etc.) are either not accurate, cumbersome, or both. Our objective was to achieve an inexpensive and precise method for parallel processing of prostate core biopsies which generates high yields and minimal losses.
Materials and Methods: A multiplex grooved matrix was constructed from a protein gel (HistoBest Biopsy Chip™) and used for aligning the specimens by the urologist who collected the biopsies from 30 patients suspected of prostate cancer. Up to 12 biopsy cores per patient (gauge 18) were collected with an ultrasound-guided biopsy gun in a single matrix. Hematoxylin-eosin staining was performed at minimum four levels, 50 micrometers apart. For every level, four additional sections were saved for special stains. Outcome measurements and statistical analysis: aggregate length of cores on slides, sample distribution statistics.
Results: The biopsies did not show curling during processing, remained properly oriented, and maintained intact tissue relationships even when the cores were fragmented. The aggregate length of the cores on slides was 130.6 ± 24.7 mm (min: 79 mm, max: 170 mm). Sectioning was greatly facilitated by the matrix employed and at least 50% of the bioptic material was saved in the paraffin block. Reporting of the histopathological findings was made in a quantitative fashion, and spatial representations of the neoplastic tissue were recorded.
Conclusions: The multiplex method of harvesting, processing and reporting of prostate biopsies is an easily applicable, cost-effective method, provides tumour location information and creates consistent duplicate arrays for analysis and research purposes. Unlike other methods, it can be used efficiently for parallel quantitative analysis of various biopsy samples.