Talk Abstract

2nd International Workshop on Protein Analysis of Tissues
Munich, Germany, February 17-18, 2011

PAXgene Tissue Reagents: A New Fixation Method for Morphology and Multi-modal Biomarker Analyses from One Sample

D. Grölz
QIAGEN GmbH, Hilden, Germany

Current tissue fixation methods used in traditional histology are of limited use for molecular analysis. Fixatives which contain formaldehyde cross-link bio-molecules and modify nucleic acids and proteins during fixation. Cross-links cannot be removed completely and the resulting chemical modifications lead to macromolecule fragmentation and can cause inhibition in sensitive downstream applications such as quantitative PCR or RT-PCR. To overcome this disadvantage, PAXgene Tissue, a new formalin-free fixation and stabilisation reagent system for simultaneous preservation of histomorphology and bio-molecules in paraffin-embedded tissue samples, was developed by PreAnalytiX in a high-throughput screening approach. This new reagent system was tested within the European FP7 project SPIDIA, a consortium consisting of 7 public research groups, 8 biotechnology companies and a standards organization, aimed to standardize and improve pre-analytical procedures for in vitro diagnostics.
Data generated within SPIDIA demonstrate preservation of morphology, proteins and nucleic acids in PAXgene Tissue-fixed and paraffin-embedded (PFPE) human tissue samples. Despite some differences, morphology and antigenicity of PFPE tissue are preserved equally or better in most tissue types compared to FFPE tissue and can be analysed by conventional histochemical or immunohistochemical staining. Bio-molecules purified from PFPE tissue are of high molecular weight and integrity. Non-degraded and immunoreactive proteins can be recovered from PFPE tissue suitable for Western blotting and Reverse Phase Protein Microarray, and sections of PFPE tissue can be used for in situ proteomic studies using MALDI imaging MS. DNA can be used for demanding applications like long-range and multiplex PCR. Expression profiles of RNA and non-coding small RNAs can be quantified with real time PCR arrays and show high concordance to the expression profiles from snap frozen samples, generated from the same tumor.