Reinhard Buettner, J Clin Exp Pathol 2017, 7:4(Suppl)
DOI: 10.4172/2161-0681-C1-036

13th EUROPEAN PATHOLOGY CONGRESS

August 02-03, 2017 Milan, Italy

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Experiences from the Network of Genomic Medicine (NGM)

Traditionally, tumors are classified by histopathological criteria, i.e., based on their specific morphological appearances. Consequently, current therapeutic decisions in oncology are strongly influenced by histology rather than underlying molecular or genomic aberrations. The increase of information on molecular changes however, enabled by the Human Genome Project and the International Cancer Genome Consortium as well as the manifold advances in molecular biology and high-throughput sequencing techniques, inaugurated the integration of genomic information into disease classification. We have therefore introduced multiplex deep sequencing of informative gene sets into routine histopathological diagnostics and molecular pathology. This comprehensive approach integrating morphological and molecular information is currently changing cancer diagnostics in five categories: (1) Somatic genomic or epigenomic alterations acquired during cancerogenesis may be used for disease classification as we show this approach adding important information to conventional morphological classifications. (2) A significant portion of solid tumors depend on oncogenic driver lesions, which provide molecular targets for prediction of effective and selective therapies. (3) Genomic alterations in signal transduction cascades and gene expression pattern may be used as prognostic parameters predicting the need and extent of adjuvant therapy. (4) In the case of multiple syn- or metachronous tumors, genomic profiling assists allocation of metastases from tumors with unknown primary (CUP) and correct staging as multiple small primary tumors and systemic metastases are reliable being discriminated. (5) Finally, mutational profiling of tumor circulating tumor DNA may facilitate monitoring the response of tumors to therapy and development of secondary resistance.

Taken together, comprehensive molecular tumor pathology and oncology paves the way for a new rational and the basis of personalized genomic medicine. This requires state-of-the art tumor diagnostics and therapies in an interdisciplinary approach. Therefore, we will eview current technology and applications of NGS for molecular and predictive cancer diagnostics.

Biography

Reinhard Büttner is Professor and Chairman of The Institute of Pathology at University Hospital Cologne, Köln, Germany, and the Co-Founder and Chief Scientific Officer of TARGOS Molecular Diagnostics. He completed his medical degree at the University of Mainz, Mainz, Germany, in 1985, before starting a residency at Rheinisch-Westfalische Technische Hochschule RWTH Aachen, Aachen, Germany. In 1987, he began post-doctoral work at the Gene Centre Munich and MD Anderson Cancer Centre, Houston, TX, USA (1987-1990). Returning to Germany in 1991, he took up a residency at the University of Regensburg, before becoming Professor and Chairman for Pathology at RWTH Aachen (1999-2001). After which, he worked as a Professor and Chairman of Pathology at the University of Bonn (2001-2011), before being appointed to his current position as Professor and Chairman of Pathology at the University of Cologne in 2011.

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