Mapping of CpG island methylation and its prognostic relevance in lung cancer

Abstract

Aberrant methylation of 5' gene promoter regions is a frequent mechanism to inactivate cancer-related genes and plays an important role in the pathogenesis of lung cancer. This tumor type is the most common cause of death from cancer worldwide. In this project we plan to investigate the methylation pattern of CpG islands by combining immunoprecipitation of methylated DNA (MeDIP) with microarray analysis in the whole genome of patients with non-small cell lung cancer (NSCLC). The results will be compared with data from both disease-free and overall survival of the patients. Aims of this project are 1. to identify genes so far unknown to be inactivated by methylation, 2. to identifiy genes whose methylation status is of prognostic relevance for NSCLC patients and 3. to develop a test for determining the methylation status of prognostic relevant genes in an easy and fast way.

Keywords:
Lung cancer, methylation, microarray, prognosis

Principal Investigator: Sabine Zöchbauer-Müller
Institution: Medical University of Vienna

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Further links about the involved persons and regarding the project you can find at
https://archiv.wwtf.at/programmes/life_sciences/LS07-019