Expression analysis of angiogenesis-related genes in Bulgarian patients with early-stage non-small cell lung cancer

Svetlana Nikolova Metodieva¹, Dragomira Nikolaeva Nikolova¹, Radostina Vlaeva Cherneva¹, Ivanka Istalianova Dimova¹, Danail Borisov Petrov², and Draga Ivanova Toncheva¹

¹Department of Medical Genetics, Medical University, Sofia; ²Department of Thoracic Surgery, University Hospital for Pulmonary Diseases “St Sofia”, Sofia, Bulgaria

ABSTRACT

Aims and background. Angiogenesis is a key process in the early stages of tumor development. In this study we aimed to evaluate the expression of a panel of angiogenesis-related genes in a group of Bulgarian patients with early-stage non-small cell lung cancer (NSCLC).

Methods and study design. We analyzed the expression of 84 genes associated with the angiogenic process in 12 NSCLCs of two histological subtypes: 7 adenocarcinomas and 5 squamous cell carcinomas. Eight peripheral nontumorous tissues were used as controls. We performed real-time PCR on pathway-specific gene arrays (SABiosciences).

Results. Our pilot study identified upregulated genes in early-stage NSCLC including growth factors (TGFA and EFNA3), the adhesion molecule THBS2, cytokines and chemokines (MDK, CXCL9, CXCL10), and the serine protease PLAU. Several genes showed downregulation including one growth factor (FIGF), the receptors for growth factors TEK and S1PR1 as well as adhesion molecules (COL4A3 and CDH5), the cytokine IL6, the matrix protein LEP and the transcription factor NOTCH4. The study demonstrated deregulated genes specific for the two histological subtypes including the transcription factor HAND2, which was overexpressed in squamous cell carcinomas but not adenocarcinomas.

Conclusions. Despite the limited number of patients, our results demonstrated the potential of angiogenesis-related genes as biomarkers in the early stages of NSCLC development. Free full text available at www.tumorionline.it

Key words: angiogenesis, expression, squamous cell carcinoma, adenocarcinoma.

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Correspondence to: Svetlana Nikolova Metodieva, Department of Medical Genetics, Medical University, 2 Zdrave Str, 1431 Sofia, Bulgaria. Tel +359-2-9520357; fax +359-2-9520357; e-mail svetlana.metodieva@yahoo.com

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