NSCLC, early stage

PROGNOSTIC IMPACT OF VEGFA IN RESECTABLE NON-SMALL-CELL LUNG CANCER

S. Calabuig Fariñas, E. Jantus-Lewintre, M. Usó, S. Gallach Garcia, R. Sirera Perez, A. Blasco, C. Camps
1 Molecular Oncology Laboratory, FHGU, Valencia, SPAIN
2 Universidad Politecnica, Valencia, SPAIN
3 Medical Oncology, Hospital General Universitario de Valencia, Valencia, SPAIN
4 Medicine, Universitat de València, Valencia, SPAIN

Aim: Angiogenesis is a main process which happens in tumors and that promotes its growth, invasive capacity and metastasis. Host genetic variability within VEGF pathway may affect angiogenic signaling and alter patient’s sensitivity to anti-angiogenic therapies and therefore the prognostic. The goal in the present study is to analyze the prognostic value of several SNPs in angiogenic genes and the relative expression of those genes, using a cohort of patients diagnosed with resectable non-small cell lung cancer.

Methods: This study included 127 resectable (I-IIIA) NSCLC patients. RNA and DNA extractions from tissues were performed using Trizol®. 20 ng of DNA were used for studies of SNPs allelic discrimination using TaqMan probe [VEGFA gene: +936C > T (rs3025039), -460T > C (rs833061) and -405C > G (rs2010963)]. Analysis of VEGFA expression was performed by RTqPCR using hydrolysis probes (TaqMan, Applied Biosystems); expression levels were normalized using GUSB as endogenous gene. All statistical analyses were considered significant at p< 0.05.

Results: Baseline characteristics of the patients were: 85% males, median age 65 years [26-82] and 85% were former or current smokers. The most common histological subtype was squamous (46.5%), followed by adenocarcinoma (41.7%). In survival analysis, patients with the CC genotype of SNP rs833061 showed a better prognosis in TTP (NR vs. 35.36 months, p = 0.026), PFS (NR vs. 31.50 months, p = 0.020) or OS (NR vs. 53.30 months, p = 0.026) compared with other genotypes (TC + TT). Patients with higher levels of expression of VEGFA have a worse outcome in TTP (NR vs. 23.67 months, p= 0.043) and OS (82.60 vs. 46.63 months, p= 0.071).

Conclusions: In conclusion, our results show that expression levels and polymorphisms in VEGFA have potential value as prognostic biomarkers in early-stage NSCLC. This work was supported in part, by a grant [RD12/0036/0025] from RTICC, and PI12-02838 from ISCIII.

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