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Overexpression of MAGE-A1 in lung cancer: a novel biomarker for prognosis, and a possible target for immunotherapy

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Recently, broad advances have been made in diagnostic and therapeutic modalities against lung cancer. However, little improvement in patient outcome has been achieved, especially for advanced, recurrent, and metastatic lung cancers that have a significantly poor prognosis. We investigated melanoma-associated antigen A1 (MAGE-A1) expression in lung cancer tissues and its correlation with prognostic factors. In this cross-sectional study, samples from 101 patients with lung cancer [including 80 NSCLCs (frequency of NSCLC subtypes, SCC = 43, AC = 23, undifferentiated carcinoma = 9, and LCC = 5) and 21 SCLCs] were obtained between 2007 and 2014 and stained for MAGE-A1 by immunohistochemistry. Correlation with prognostic factors was assessed by t-test and χ^2 and Pearson tests. MAGE-1 IHC staining was positive in 56 (55.44%) patients with different degrees of staining; PN1 in 13 (12.9%), PN2 in 24 (23.8%), and PN3 in 20 (19.8%) patients. Eighty nonsmall cell and 21 small cell lung cancer specimens were stained for MAGE-A1. MAGE-A1 was detected more commonly in adenocarcinomas and was expressed more frequently in male ($P = 0.0001$) and patients >60 years ($P = 0.005$). MAGE-A1 expression was more frequent in the elderly, male patients, and those with advanced stage and adenocarcinoma subtypes of lung cancer. Further investigations are needed to assess MAGE-A1 expression as a potential cancer biomarker. This retrospective study had all of the limitations associated with this type of longitudinal cohort study. However, our study included a considerable number of patients, which was done for the first time in our region. Also, we assessed the expression of MAGE-A1 as the products of CT-X genes (instead of its presence, such as in studies that were conducted by PCR). This feature of our study provided preliminary information for future investigation in term of new immune checkpoint therapy drugs.

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