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PCR/SSCP Analyses of Epidermal Growth Factor Receptor (EGFR) Mutations in Malignant Mesothelioma

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Abstract

Introduction:
The tyrosine kinase inhibitor gefitinib, which targets the epidermal growth factor receptor (EGFR), has been approved as a single-drug therapy for non-small-cell lung cancer (NSCLC) in Japan. However, objective tumor responses were observed in only 10-19 percent of patients. Recently, Lynch et al. reported that mutations in exons 19 and 21 of the EGFR gene correlate with the clinical responsiveness to gefitinib in NSCLC patients, and it is suggested that these mutations may be predictors of the responsiveness to gefitinib. As most malignant mesothelioma (MM) tumors express EGFR, as shown by immunohistochemistry, it is thought that MM may also have a response to gefitinib, however, the usefulness of gefitinib for the treatment of MM has not been determined clinically until now. As the EGFR gene mutations may also predict the responsiveness to gefitinib in MM patients, we analyzed the presence of EGFR mutations in MM tumor tissues by the PCR/Single Strand Conformation Polymorphism (SSCP).

Methods:
DNA was extracted from MM tumor tissues using the standard methods. Exons 19 and 21 of the EGFR gene were amplified by PCR and the PCR products were analyzed by SSCP for the presence of mutational bands. DNA extracted from the tissue of 14 lung adenocarcinoma tumors was also examined in the same way.

Results:
Eleven MM tissues were examined. All were from males with a mean age of 69 years (range; 43 to 87 years). The histology was 3 epithelial, 5 mixed, and 3 sarcomatous. While four of the fourteen lung adenocarcinoma cases demonstrated EGFR mutations (two cases each of exons 19 and 21), no mutations were detected in any of the 11 MM samples.

Conclusion:
The presence of EGFR mutations in 28% of the lung adenocarcinoma samples confirms the usefulness of PCR/SSCP analyses as a screening test. Although the present study could not demonstrate EGFR mutations in the MM samples, more MM cases should be examined to obtain definitive conclusions, as there may be differences in the mutational status between the histological subtypes of MM tumor tissues.