To investigate the relationship between development of laryngeal cancer and the presence of polymorphisms of the MnSOD Val16Ala, CAT-262 C < T and GPx1 Pro198Leu genes in a smoking population.

PATIENTS AND METHODS:

Single nucleotide polymorphisms were determined in DNA from the peripheral blood erythrocytes of 48 heavy smokers (25 patients with laryngeal cancer and 23 cancer-free controls), using polymerase chain reaction.

RESULTS:

There were no significant differences in age, smoking duration or smoking intensity, comparing the two groups. The homozygous AA genotype of MnSOD Val16Ala was significantly more prevalent in the cancer group than the control group (92 vs 13 per cent, respectively), while the heterozygous AV genotype of MnSOD Val16Ala was more prevalent in the control group than the cancer group (87 vs 8 per cent, respectively) (p < 0.001). There were no significant differences between the cancer and control groups regarding GPx1 Pro198Leu or CAT-262 C < T polymorphisms.

CONCLUSION:

Polymorphism of the MnSOD Val16Ala gene may contribute to susceptibility to laryngeal cancer among smokers.

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