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Author(s)	IMANISI, Tetuya
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QUANTITATION OF *C-MYC* EXPRESSION IN
URETHAN-INDUCED MOUSE LUNG TUMORS BY
COMPETITIVE PCR ANALYSIS

Tetuya IMANISI

*Department of Radiation Biology,
Faculty of Veterinary Medicine,
Hokkaido University, Sapporo 060, Japan*

In A/He strain mice, the carcinogen urethan induces lung adenomas and adenocarcinomas. As one of the epidermal-growth factor-related proto-oncogenes, transcriptional activation of *c-myc* was investigated. At the 5th month after urethan-injection, tumors were too small to isolate RNAs sufficient for filter hybridization-analysis. Therefore we used the RT-competitive polymerase chain reaction method with nested primers. As a competitor we prepared RNA that was completely homologous with a part of *c-myc* gene exon 2 except for an internal 89 bp-insert. In 9 of the remaining 18 tumors, higher levels of expression of the *c-myc* gene were found in the tumor tissues. The amounts of *c-myc* RNAs were 129.9 to 4626.2 pg per μg mRNA, compared with 5.2–23.5 pg per μg mRNA in normal lung tissues. In 5 tumors, levels of expression were slightly higher than those of normal tissues. No significant difference was observed between the other 4 tumors and normal tissues. In spite of the histologic similarity, differentiated transcriptional activity of the *c-myc* gene in tumor tissue suggested diversity in the progression of the each urethan-induced adenoma or adenocarcinoma.