Abstract

Retroviruses are viruses which are able to integrate to genome of host cell. Nonrandom integration of provirus near or inside some cellular genes may result in their deregulation, activation or silencing. This can later lead to cell transformation and tumor formation.

This thesis discusses identification of viral integration sites (VIS) and common integration sites (CIS) in tumors originating from different organs (mostly kidneys, lungs and liver) with using mostly avian retroviruses subgroup J, specifically first natural isolate HPRS-103 and laboratory made virus MAV-J, which was made by replacing gene envB by envJ. Infection was made in ovo using chicken breeds Brown Leghorn and White Leghorn and tumors were isolated from 8 to 28 weeks after infection. For molecular analyses was used inverse PCR method and sequencing.

From 74 molecularly analyzed tumors there was detected 373 VIS and 6 CIS with statistical significance over 2.10^{-2}. Gene with the highest number of hits was FRK (14 times), then TERT (5 times), CTDSPL (5 times), EGFR/ERBB1 (3 times), MYB (3 times) and MYC (3 times). Except 6 CIS there were other genes found, which had smaller statistical significance.

Keywords: retrovirus, insertional mutagenesis, subgroup J, oncogenesis, oncogenes, MAV-J, HPRS-103, proviral integration sites, tumors