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Aberrant Transcripts of FHIT, TSG101 and PTEN/MMAC1 Genes in Normal Peripheral Mononuclear Cells

Wang, Nancy M. ; Chang, J. G. ; Liu, T. C. ; Lin, S. F. ; Peng, C. T. ; Tsai, F. J. ; Tsai, C. H.

Abstract

Aberrant transcripts of FHIT and TSG101 using nested RT-PCR were reported in many human tumours. The role of these aberrant transcripts in tumourigenesis is not clear. We, therefore, analyzed the aberrant transcripts of FHIT, TSG101 and PTEN/MMAC1 in peripheral mononuclear cells of normal individuals using nested RT-PCR to explore the role of these genes in cancer development. The results showed that there are at least five types of aberrant transcripts: type I is the deletion at junction located in-between normal exon and intron; type II has deletion of some bases and subsequent insertion of several bases in the deletion area; type III accommodates splicing donor or acceptor site-like sequence; type IV has homologous sequences near the deleted junction; and type V comprises the homologous sequences at the deletion junction. A normal healthy person can have more than one aberrant transcripts of FHIT, TSG101 and PTEN/MMAC1 genes. The size and the number of the transcripts vary and the diversity is unconstrained. It is not depended on the time, condition of the reaction, or the isolation method. From these results, we suggested that the aberrant transcripts of FHIT, TSG101 and PTEN/MMAC1 genes may be the imperfect products of splicesome which occur one in every thousands, ten thousands or more. As a result, these data implied no direct association between the aberrant transcripts and tumourigenesis.