Role of long non-coding RNAs in the formation of oncogenic chromosomal rearrangements associated with thyroid cancer

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Various types of cancer are characterized by certain chromosomal rearrangements, these mutations play a vital role in the oncogenesis often leading to the formation of fusion genes. However, the molecular mechanisms of oncogenic translocations have not yet been established. There is a hypothesis that this process is mediated by specific RNAs that have homology regions with two chromosomes areas near the junction site. Recently, an example of an RNA-mediated specific genomic rearrangement in mammalian cells has been described, with enhanced expression of *AZI1* mRNA in prostate cancer cells acting as an "initiator" RNA to induce oncogenic *TMPRSS2–ERG* gene fusion. Based on this hypothesis and approach, we assumed that lncRNAs may have similar roles in various osncogenic chromosomal rearrangements. We have developed an in silico method for searching for candidate lncRNAs that can potentially trigger the formation of chromosomal mutations, and compiled a database of candidates that can drive the following translocations in thyroid cells: *PAX8/PPARγ, CCDC6/RET, NCOA4/RET*. According to our preliminary data, expression of some of the candidate RNAs causes significant effects on the frequency of the corresponding oncogenic translocations. This work is supported by grant 19-74-10083 from Russian Science Foundation.

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