FSBSI “IGPP”

BGRS/SB-2024

14th International Multiconference

Bioinformatics of Genome Regulation and Structure / Systems Biology

Competing Endogenous RNAs as Non-small Cell Lung Cancer Markers

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The study is supported by the FGFU-2022-0007 state assignment

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There is a hypothesis that miRNA binding sites (miRNA response elements, MRE) can be considered as “letters” of the “RNA language”, and transcripts can actively interact with each other, regulating appropriate expression levels.

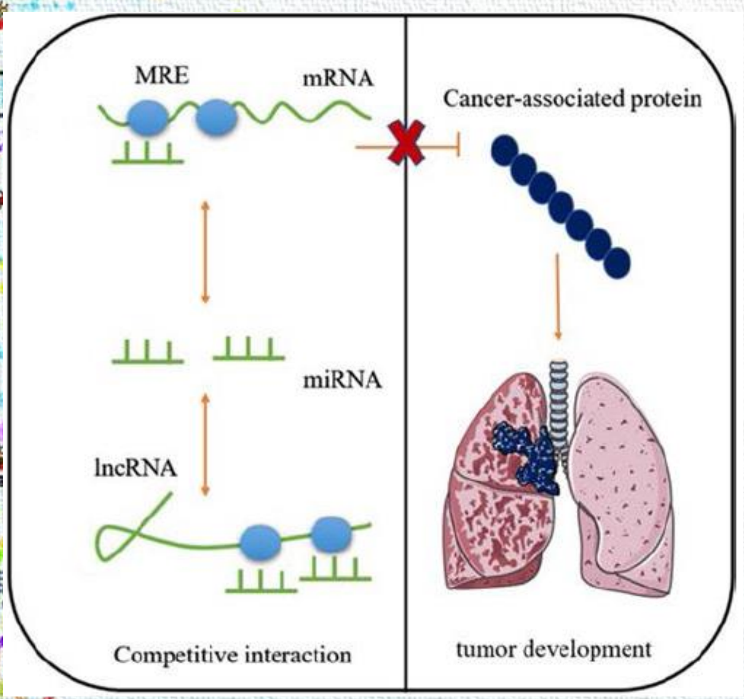


Figure. 1. ceRNA hypothesis. Overexpression of LncRNAs increases the cell concentration of a particular MRE, resulting in derepression of the miRNA target gene. It causes overexpression of lung cancer related genes, which in turn leads to tumor progression.

Methods and Algorithms

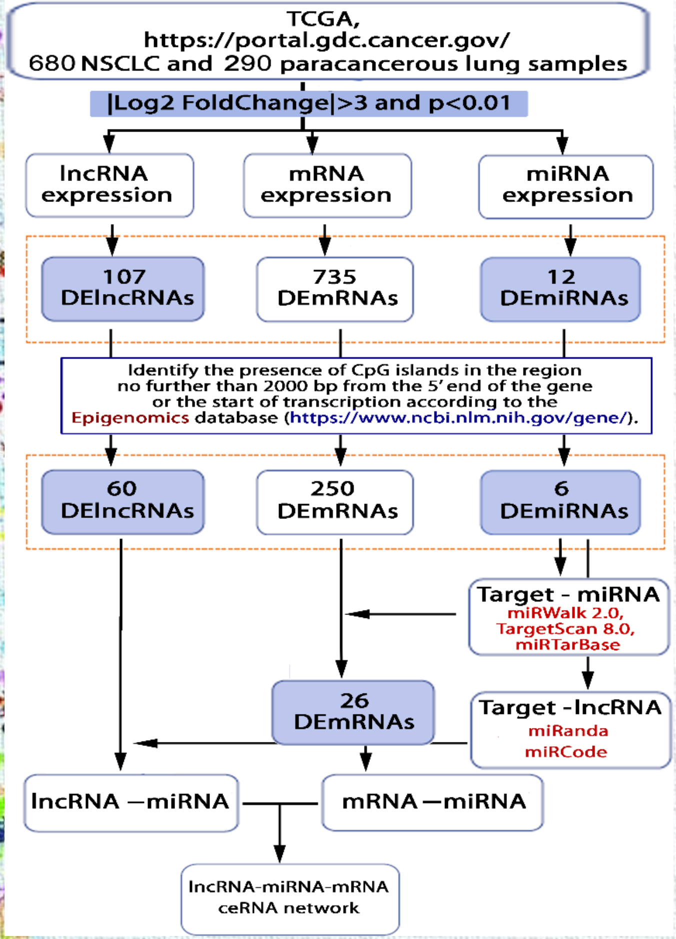


Figure 2: Main procedure followed when constructing the ceRNA network.

A total of 6 lncRNAs (ADAMTS9-AS2, HAND2-AS1, HOTAIRM1, MEG3, SNHG12, NCK1-AS1), 4 miRNAs (miR-124-3p, miR-203a-3p, miR-125b-5p, miR-129-5p) and 26 mRNAs were involved in the network of ceRNAs.

Results

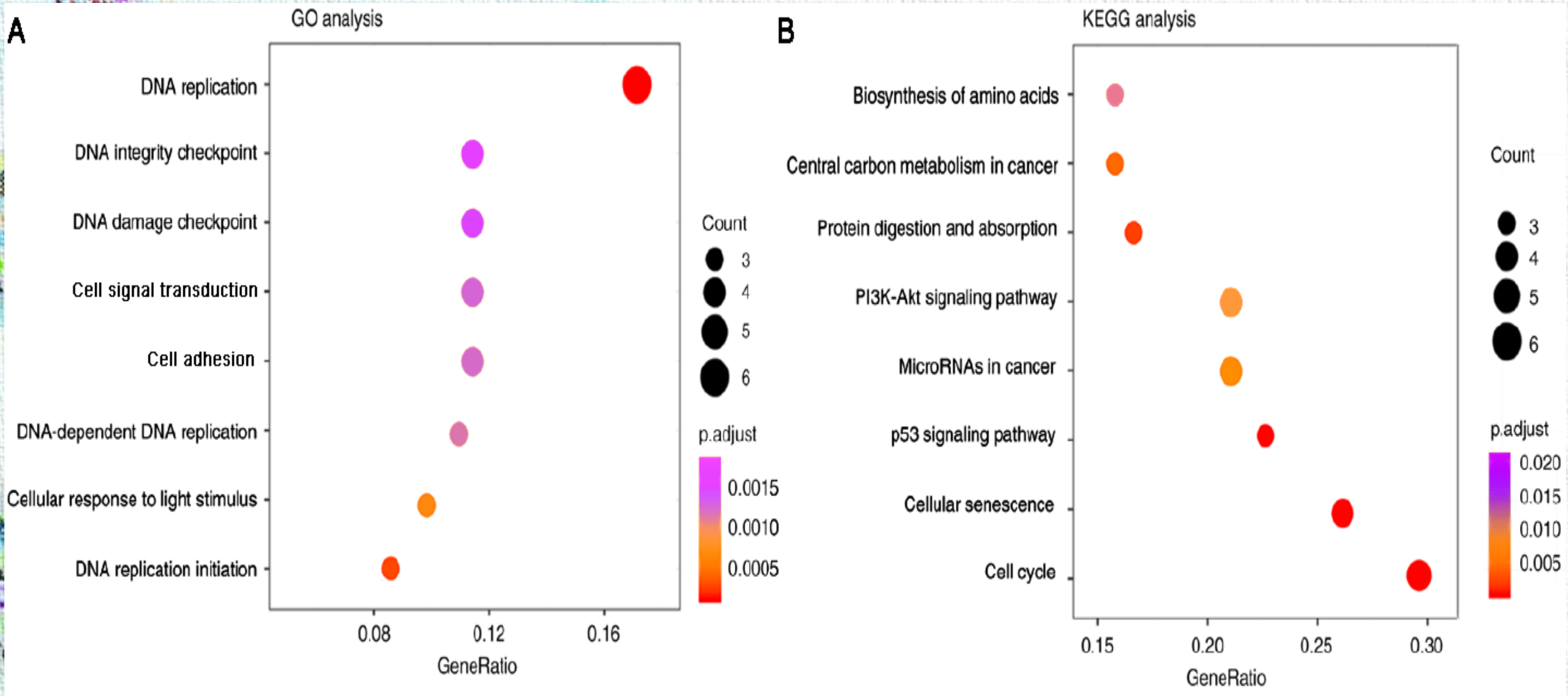


Figure 3. Potential functions of the differentially expressed lncRNAs analyzed by GO and KEGG analyses. (A) The GO analysis of biological processes, cellular components, molecular functions. (B) The KEGG analysis of potential pathways.

Results

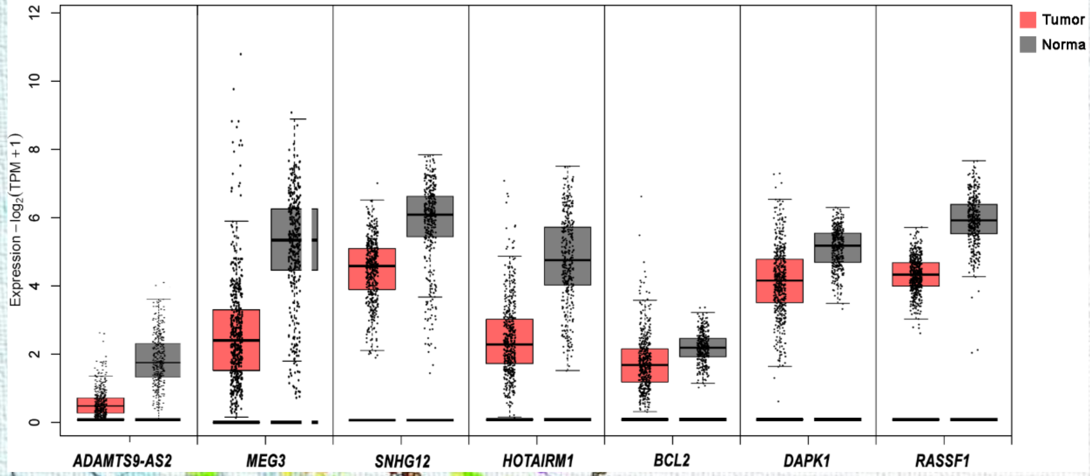
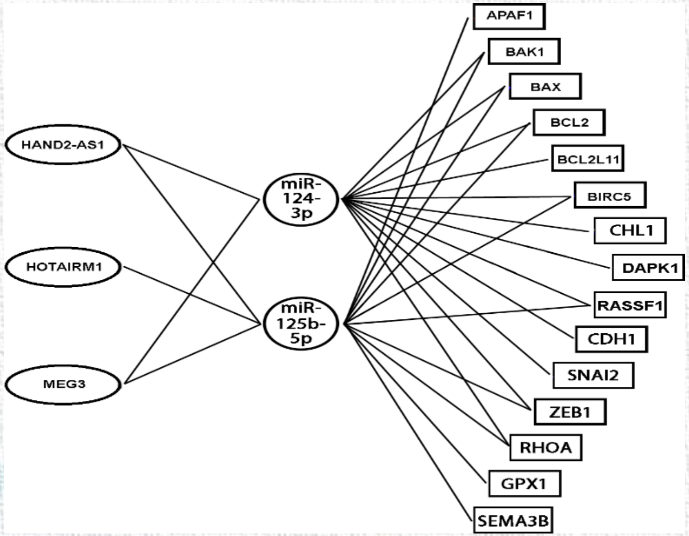


Figure. 4. Changes in the expression levels of lncRNA ADAMTS9-AS2, MEG3, SNHG12, HOTAIRM1 and mRNA BCL2, DAPK1, RASSF1 in non-small cell lung cancer; p<0.01. TPM – transcripts per million

Figure. 5. The ceRNA network in NSCLC. Ovals, circles, and rectangles represent lncRNA, miRNAs and mRNA, respectively.



Conclusion. This study allows us to more deeply evaluate the roles of each element of the endogenous RNA network in patients with NSCLC, and some of the genes in this network may be used as new potential therapeutic targets.