Секция «Генетика»

LncRNAs, oxidative stress, and COVID-19. A bioinformatics analysis of potential prognostic biomarkers

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Background:

Coronavirus infection (COVID-19) is a highly contagious disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). There are about 774 million confirmed cases and more than 7 million deaths of COVID-19 globally, according to WHO (As of 28 January 2023).

Since the onset of the pandemic, databases have been flooded with research articles and reviews dedicated to better understand the pathogenesis of SARS-CoV-2. One of the most common subjects of interest was the variance of disease severity among individuals. Oxidative stress has been frequently considered as a key factor in the COVID-19 severe outcome. Therefore, its regulatory factors can be taken into account as potential prognostic biomarkers of the infection.

In this study, we performed a bioinformatics analysis to search for candidate long non-coding RNAs, which regulate the genetic expression of antioxidant enzymes, and could have a role in COVID-19 pathogenesis.

Materials and Methods:

LncRNA2Target v3.0 database (http://bio-annotation.cn/lncrna2target/index.jsp) was used to investigate the regulatory long non-coding RNAs of the genes of antioxidant enzymes: Superoxide dismutase (*SOD1*, *SOD2*), Catalase (*CAT*), Glutathione S-transferase P (*GSTP1*), and Glutathione peroxidase 4 (*GPX4*). LncRNADisease v3.0 database (http://www.rnanut.net/lncrnadisease/index.php/home) was used to determine which of the detected lncRNAs showed an evidence of association with COVID-19.

Results:

Changes in expression for *SOD1* were observed in studies involving the knockdown of lncRNAs such as RAD51-AS1, LOC440173, DANCR, TINCR, ANRIL, LINC00565, AK096729 and AC007128.1, as well as overexpression of lncRNAs NRAV and hTR. For *SOD2*, in addition to the above mentioned, changes of expression were observed with the knockdown of TUG1, DA125942, CAT2, CAT3, CAT5, CAT6, CAT8, CAT15, SLNCR1, HOXC-AS3, AF339830, LOC646329, DDGC and overexpression of NBAT1, IRENA, SPRY4-IT1, and LINC00473. For *CAT* the changes were observed in the knockdown of TUG1, lincFOXF1, lincMTX2, lincTNS1, lincZFP161, DA125942, lnrCXCR4, RAD51-AS1, NRCP, TINCR, HOXC-AS3, AF339830, IIRX, AK096729, LOC646329, MIR31HG, AC007128.1 and overexpression of NRAV, MIR503HG, IRENA and LINC00473. For *GSTP1*: the knockdown of lincFOXF1, lincTNS1, HIPSTR, LOC440173, DANCR, CASC15, ANRIL, ALAL-1, HOXC-AS3, AK096729, LOC646329, DDGC and the overexpression of NRAV, NBAT1, MIR503HG, SPRY4-IT1, ZNF593-AS. For *GPX4*: the knockdown of lincFOXF1, DEANR1, TINCR, ANRIL, AK096729, MIR31HG, AC007128.1, DIGIT and the overexpression of MIR503HG and ZNF593-AS.

According to LncRNADisease database, among the lncRNAs mentioned above, NRAV, RAD51-AS1, TUG1, NRCP, and CASC15 were reported to be associated with COVID-19. However, none of them showed a strong evidence of association.

Conclusion:

The performed analysis predicted the lncRNAs involved in the regulation of antioxidant enzymes genetic expression. In addition, we found that 5 of those lncRNAs could be linked to COVID-19. Our findings suggest NRAV, RAD51-AS1, TUG1, NRCP, and CASC15 as perspective targets for further research in order to confirm their role in COVID-19 infection, and therefore, to consider them as potential promising biomarkers.

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