Preventive Medicine & Public Health

July 16-17, 2018
London, UK

ASSOCIATIONS OF LONG NON-CODING RNAS AND LEUKEMIA: A META-ANALYSIS

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Accumulating evidences support that the expression and function of long non-coding RNAs (lncRNAs) associated with blood cancers development and progression. Here, we evaluate the aberrant expression of lncRNAs in the prediction of leukemia risk by a meta-analysis of the 16 published studies involving 697 healthy controls and 781 individuals with leukemia. The combined analysis showed that lncRNAs was associated with the increased risk of leukemia (OR= 89.83, 95% CI: 29.50-273.55 P<0.00001). Quantitative analysis of single lncRNA showed that low expression of lncRNAs-H19 (OR= 112.9, 95% CI : 24.08−529.39), the overexpression of DLEU1(OR= 74.41, 95% CI: 1.08-5104.09), DLEU2 (OR=76.14, 95% CI:1.53−3782.4), LUNAR1(OR=291.65,95% CI:15.66−5433.21), P15AS (OR=87.25, 95% CI:7.72−986.52) and HULC (OR=201.97, 95% CI: 24.96−1634.33) were associated with the increased risk of leukemia. Moreover, the abnormal expression of LUNAR1, p15AS, HULC were related to acute leukemia, while DLEU2 and H19 abnormally expressed were related to chronic leukemia patients. In addition, MLL-r acute leukemia related to 7 lncRNAs (OR= 14.97, 95% CI: 5.37-41.75). These results identified strong associations between lncRNAs abnormal expression and leukemia. Some lncRNAs may be novel diagnostic markers for leukemia.

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