Career situation of first and presenting author: Student for a master or a PhD.

Introduction Long non-coding RNAs (lncRNAs) have drawn increasing attention because of the pivotal roles which they play in various types of autoimmune diseases, including rheumatoid arthritis (RA). LncRNA HOTAIR is a crucial lncRNA function as an oncogene in multiple cancers. Fibroblast-like synoviocytes (FLSs), a prominent component of hyperplastic synovial pannus tissue, are critical to synovial aggression and joint destruction in RA. However, the functions of lncRNA and the potential mechanisms remain to be further elucidated in FLSs of RA patients.

Objectives Our present study aimed to investigate the expression and roles of lncRNA HOTAIR in RA-FLSs and explore its possible mechanism.

Methods FLSs were cultured from synovial tissues of joint. LncRNA and microRNA expression profiles in FLSs were screened by microarrays, and then we validated the results by Real-time Quantitative polymerase chain reaction (qRT-PCR). Small interfering RNA (siRNA) was then used to knock down the expression of HOTAIR in order to determine its role in RA FLSs. Cell viability was evaluated using the CCK-8 assay and flow cytometry. Cell invasion was analyzed by transwell chamber methodology. Bioinformatics analysis were performed to predict the possible competitive endogenous RNA (ceRNA) mechanisms via miRanda, PITA, RNAhybrid, as well as KEGG and Gene Ontology (GO) analysis.

Results Both microarray analysis and qRT-PCR showed the expressions of lncRNA HOTAIR were up-regulated in RA FLSs compared with healthy controls (HCs). Transfection of HOTAIR-siRNA significantly decreased the expression of lncRNA HOTAIR in RA FLSs. HOTAIR knockdown largely inhibited cell proliferation and invasion of RA FLSs. Furthermore, the bioinformatics analysis predicted that some of microRNAs and mRNAs may be the downstream molecules of lncRNA HOTAIR. Considering the microRNA expression profiles detected by microarrays and the results from qRT-PCR, we designated miR-138 and miR-17–5 p as potential ceRNAs which lncRNA HOTAIR could directly bind to. In addition, the expressions of miR-138 and miR-17–5 p were markedly downregulated in RA FLSs, whereas the knockdown of lncRNA HOTAIR upregulated the expressions compared with the negative control group (NC-siRNA).

Conclusions Our study illuminated that elevated lncRNA HOTAIR expression promoted the proliferation and invasion of RA FLSs. Meanwhile, it may function as a novel microRNAs sponging agent and regulate RA FLSs pathological behaviors via miR-138 or miR-17–5 p associated ceRNA network. In summary, the regulation of lncRNA HOTAIR may be a promising therapeutic strategy for RA in the future.

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Disclosure of Interest None declared