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MicroRNA network analysis identifies key microRNAs and genes associated with precancerous lesions of gastric cancer

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ABSTRACT. To identify potential targets for the early treatment and prevention of gastric cancer, microRNA (miRNA) expression profiles of precancerous lesions of gastric cancer were investigated. The miRNA microarray dataset GSE24839 was downloaded from Gene Expression Omnibus (GEO) and included 10 *Helicobacter pylori*-related gastritis samples and 10 gastric intestinal metaplasia samples. Differentially expressed miRNAs (DEMs) were screened using the Student *t*-test; $P < 0.05$ was considered to be statistically significant. Co-expression networks of total miRNAs and DEMs were constructed based on the Pearson correlation coefficient for the two diseases. Target genes of the DEMs were retrieved using miRecords and pathway-enrichment analysis was performed using a hypergeometric test. A total of 20 DEMs were obtained for *H. pylori*-related gastritis and gastric intestinal metaplasia samples, including 12 up-regulated and 8 down-regulated miRNAs. The identified DEMs appear to play key roles in gastric cancer, as the average degree of the DEM sub-network was higher than that of the

total miRNA co-expression network. Furthermore, target genes for 6 DEMs (hsa-miR-106b, hsa-miR-193a-3p, hsa-miR-204, hsa-miR-30e, hsa-miR-519d, and hsa-miR-524-5p) are in Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways, including signal transduction, cell growth and death, and transport and catabolism. Among the target genes, 5 (RAB22A, SOX4, IKZF2, PLAG1, and BTBD7) were of interest because they can be simultaneously regulated by several DEMs. These findings suggest that these genes may be targets for modulating gastric cancer progression.

Key words: MicroRNAs; Gastric cancer; Differential expression; Network analysis

