Therapeutic Application of Agomirs and Antagomirs in Gastric Cancer Based on Transcriptomic Analysis, Phase 2

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Gastric adenocarcinoma is the fourth most common type of cancer in Brazil, often diagnosed at advanced stages, when the cure rate drops to 30%. MicroRNAs (miRNAs) are essential post-transcriptional regulators that inhibit mRNA translation and play a fundamental role in the initiation and progression of various cancers, including gastric cancer. This study aimed to evaluate the impact of miRNAs on the regulation of key molecular pathways involved in tumor progression, contributing to the development of novel therapeutic strategies for gastric adenocarcinoma. The methodology involved database analyses to compare gene expression in neoplastic and normal tissues, identifying relevant target genes in carcinogenic tissues. Analysis of miRNA expression profiles in gastric cancer revealed that hsa-miR-192, hsa-miR-215, hsa-miR-34a, hsa-miR-214, hsa-miR-221, hsa-miR-222, and hsa-miR-454 are downregulated, regulating the RB, P53, PTEN, CBX7, RB1, CNTN, and CYLD genes, respectively. In contrast, hsa-miR-143, hsa-miR-135b, hsa-miR-429, and hsa-miR-675 are overexpressed, modulating the MAP3K7, CLIP4, CMYC, BCL-2, and RUNX1 genes, respectively. Based on these interactions, agomirs were designed for downregulated miRNAs, and antagomirs for overexpressed miRNAs, targeting each specific miRNA. These findings enabled the classification of regulated genes into two groups: those requiring reduced expression and those needing increased expression to suppress tumor progression. This study reinforced the potential of agomirs and antagomirs as promising therapeutic approaches, paving the way for innovative strategies in combating this disease. Keywords: gastric cancer, miRNA, agomirs, antagomirs.

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