論 文 要 旨

RNA sequencing-based microRNA expression signature in esophageal squamous cell carcinoma: oncogenic targets by antitumor miR-143-5p and miR-143-3p regulation

（RNA シークエンスによる
食道扁平上皮癌・マイクロ RNA 発現プロファイルの作成：
癌抑制型 ***miR-143-5p*** と ***miR-143-3p*** が制御する
癌促進型遺伝子の影響）

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【Abstract

Aberrantly expressed microRNAs (miRNAs) disrupt intracellular RNA networks and contribute to malignant transformation of cancer cells. Utilizing the latest RNA sequencing technology, we newly created the miRNA expression signature of esophageal squamous cell carcinoma (ESCC). A total of 47 miRNAs were downregulated in ESCC tissues, and these miRNAs were candidates for antitumor miRNAs in ESCC cells. Analysis of the signature revealed that several passenger strands of miRNAs were significantly downregulated in ESCC, e.g., miR-28-3p, miR-30a-3p, miR-30c-3p, miR-133a-3p, miR-139-3p, miR-143-5p, and miR-145-3p. Recent studies indicate that some passenger strands of miRNAs closely involved in cancer pathogenesis. In this study, we focused on both strands of pre-miR-143, and investigated their antitumor roles and target oncogenes in ESCC. Ectopic expression of miR-143-5p and miR-143-3p significantly attenuated malignant phenotypes (e.g., proliferation, migration, and invasive abilities) in ESCC cell lines. We revealed that six genes (HN1, HMGA2, NETO2, STMN1, TCF3, and MET) were putative targets of miR-143-5p regulation, and one gene (KRT80) was a putative target of miR-143-3p regulation in ESCC cells. Our ESCC miRNA signature and analysis strategy provided important insights into the molecular pathogenesis of ESCC.