

TRIM31: A Protein With an Oncogenic Role in Esophageal Adenocarcinoma

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Background: Esophageal adenocarcinoma (EAC) is a major cancer in the United States with increasing incidence. It is an aggressive cancer involving columnar-type cells different from the normal esophageal (NE) squamous cells. This metaplasia often involves an intermediary morphology called Barrett's esophagus (BE), which occurs from repeated acid exposure of the esophagus from gastroesophageal reflux disease (GERD). GERD leading to BE is a common pre-occurrence in EAC patients, but the mechanism remains obscure. To explore the mechanism and its components, we compared gene expression in BE and EAC cells with normal cells and discovered the overexpression of TRIM31 in the pathogenic cells. Although previous studies have shown oncogenic potential of TRIM31 in some cancers, its role in EAC is yet to be understood.

Methods: RNA sequencing and transcriptomic profiling were performed on human NE, BE, and EAC epithelial tissue samples. TRIM31 expression in NE cell line (Het-1A) and EAC cell lines (OE19, Flo-1, OE33, SK-GT-2, and OACM5.1C) were identified by Western blot. The Het-1A cell line, after exposure to acidic pH and bile acid, was assessed for variable TRIM31 expression. Cell viability analysis of NE and EAC cell lines after exposure to acidic pH and bile acids was observed by WST-1 assay.

Results: RNA sequencing, transcriptomic profiling, and western blot revealed overexpression of TRIM31 in BE and EAC epithelium. Exposure of Het-1A cells to bile acids in acidic pH changed the cell morphology with enhanced expression of TRIM31. WST-1 revealed that EAC cells were more resistant to acidic pH and bile acid exposure.

Conclusions and potential impact: Our data suggests that increased TRIM31 expression correlates with esophageal epithelium resistance when exposed to bile acids and acidic pH. Consequently, TRIM31 may be a key player in the metaplasia of GERD-induced EAC development and may be an innovative therapeutic target and marker for EAC.