Biomarkers may help predict progression of Barrett's esophagus to esophageal adenocarcinoma

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A series of microRNA expression signatures that may help to define progression of the precancerous condition Barrett's esophagus into esophageal adenocarcinoma was reported recently in *Cancer Prevention Research*, a journal of the American Association for Cancer Research.

"Once a rare cancer representing only 5 percent of all esophageal cancers in the United States, esophageal adenocarcinoma is the cancer with the fastest-rising incidence—six-fold increase in the past three decades—and currently comprises more than 80 percent of all new esophageal cancer cases in this country," said Xifeng Wu, M.D., chair of the Department of Epidemiology, Division of Cancer Prevention and Population Sciences at The University of Texas MD Anderson Cancer Center, in Houston. "To reduce the mortality of esophageal adenocarcinoma, the best hope in the near term is to detect it at its early stage, or even better, to prevent the progression of esophageal adenocarcinoma from its premalignant lesion, which is called Barrett's esophagus."

Wu and colleagues evaluated microRNAs, which are a class of small ribonucleic acids in cells capable of regulating a large number of genes. Research has shown that aberrant expression of microRNAs is involved in cancer development.

The researchers compared hundreds of microRNAs in normal

esophageal epithelia and in Barrett's esophagus and esophageal adenocarcinoma tissues of different histological grades with distinct progression risks. They identified a number of differentially expressed microRNAs at each histological stage.

"The expression of microRNAs in Barrett's esophagus and esophageal adenocarcinoma tissues was remarkably similar, indicating that the microRNA aberrations were very early events in the development of Barrett's esophagus," Wu said. "These aberrations in microRNA expression may drive other late events that ultimately lead to carcinoma formation."

The researchers also identified a small number of microRNAs that were significantly different between Barrett's esophagus and esophageal adenocarcinoma. Specifically, downregulation of the microRNA miR-375 and upregulation of five microRNAs of the miR-17-92 and homologue family seemed to differentiate Barrett's esophagus and esophageal adenocarcinoma.

"Therefore, those patients with Barrett's esophagus with low levels of miR-375 and/or high levels of the other five microRNAs we found to be upregulated in esophageal adenocarcinoma are at increased risk for malignant progression and should be under intensive surveillance, screening and treatment of their Barrett's esophagus," Wu said.

"Defining the protein-coding genes targeted by the differentially expressed microRNAs we identified may provide significant biological insights into the development of esophageal adenocarcinoma," she added. "Moreover, these genes may themselves become promising biomarkers to predict Barrett's esophagus progression as well as potential preventive and therapeutic targets."