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Diagnostic implications of altered miRNA profiles in esophageal cancer

Rinu Sharma

Guru Gobind Singh Indraprastha University, India

The asymptomatic nature of esophageal cancer (EC) at early stages of the disease results in late clinical presentation leads to poor prognosis and limited success of therapeutic modalities. Despite advancement in diagnostic and therapeutic strategies, the five year survival rate of the disease still remains less than 20%. This is primarily due to lack of sensitive and specific markers for early diagnosis and monitoring response to therapy for this disease. Hence, there is a pressing need for establishment of novel non-invasive or minimally-invasive biomarkers for esophageal cancer. Growing evidence suggests importance of alteration in microRNA (miRNA) expression in development and progression of cancer. Moreover, presence of miRNAs in various body fluids such as serum, plasma, saliva and urine has opened a new era of disease research. Our group is interested in deciphering the clinical and functional significance of miRNAs in esophageal cancer. We have evaluated the expression of a panel of miRNAs in tissues as well as sera of esophageal cancer patients. The analysis revealed significant dysregulation of these miRNAs in EC tissues as compared to matched distant nonmalignant tissues. Receiver operated curves generated for these miRNAs in serum significantly distinguished EC patients from normal controls with a high sensitivity. The present paper will discuss the individual as well as collective diagnostic potential of these miRNAs and their targets in EC.

Biography

Rinu Sharma has obtained her Master's degree in Biotechnology and PhD in Biochemistry from All India Institute of Medical Sciences. She is a Faculty in School of Biotechnology, Guru Gobind Singh Indraprastha University, India. She has published more than 20 papers in reputed international journals; some of which are the first reports. Her current areas of interest are identification of non-invasive blood based biomarkers for early diagnosis of esophageal cancer and functional analysis of significantly altered genes using gene silencing and proteomic approaches.

rinusharma@gmail.com

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