عنوان مقاله:

Linc-ROR and its spliced variants ۲ and ۴ are significantly up-regulated in esophageal squamous cell carcinoma

محل انتشار:

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تعداد صفحات اصل مقاله: 5

نویسندگان:

Reza Sahebi - *Department of Molecular Genetics, Faculty of Biological Sciences, Tarbiat Modares University, Tehran, Iran*

Mahshid Malakootian - *Cardiogenetic Research Center, Rajaie Cardiovascular Medical and Research Center, Iran University of Medical Sciences, Tehran, Iran*

Baharak Balalaee - *Department of Molecular Genetics, Faculty of Biological Sciences, Tarbiat Modares University, Tehran, Iran*

Alireza Shahryari - *Stem Cell Research Center, Golestan University of Medical Sciences, Gorgan, Iran*

Masoud Khoshnia - *Golestan Research Center of Gastroenterology and Hepatology, Golestan University of Medical Sciences, Gorgan, Iran*

Mohammad Reza Abbaszadegan - *Division of Human Genetics, Immunology Research Center, Avicenna Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran*

Abdolvahab Moradi - *Golestan Research Center of Gastroenterology and Hepatology, Golestan University of Medical Sciences, Gorgan, Iran*

Seyed Javad Mowla - *Department of Molecular Genetics, Faculty of Biological Sciences, Tarbiat Modares University, Tehran, Iran*

خلاصه مقاله:

Objective(s): Similar characteristics of molecular pathways between cellular reprogramming events and tumorigenesis have been accentuated in recent years. Reprogramming-related transcription factors, also known as Yamanaka factors (OCT۴, SOX۲, KLF۴, and c-MYC), are also well-known oncogenes promoting cancer initiation, progression, and cellular transformation into cancer stem cells. Long non-coding RNAs (lncRNAs) are a major class of RNA molecules with emerging roles in stem cell pluripotency, cellular reprogramming, cellular transformation, and tumorigenesis. The long intergenic non-coding RNA ROR (lincRNA-ROR, linc-ROR) acts as a regulator of cellular reprograming through sponging miR-۱۴۵ that normally negatively regulates the expression of the stemness factors NANOG, OCT۴, and SOX۲. Materials and Methods: Here, we employed a real-time PCR approach to determine the expression patterns of linc-ROR and its two novel spliced variants (variants ۲ and ۴) in esophageal squamous cell carcinoma (ESCC). Results: The quantitative real-time RT-PCR results revealed a significant up-regulation of linc-ROR (P=۰.۰۰۹۸) and its variants ۲ (P=۰.۰۲۵۰) and ۴ (P=۰.۰۰۰۲) in tumor samples of ESCC, compared to their matched

non-tumor tissues obtained from the margin of same tumors. Our data also demonstrated a significant up-regulation of variant ۴ in high-grade tumor samples, in comparison to the low-grade ones (P=۰.۰۴). Moreover, the ROC curve analysis demonstrated that the variant ۴ of ROR has a potential to discriminate between tumor and non-tumor samples (AUC=۰.۶۶, P<۰.۰۵). Conclusion: Our data suggest a significant up-regulation of linc-ROR and its variants ۲ .and ۴ in ESCC tissue samples

کلمات کلیدی:
Esophageal squamous - cell carcinoma, Linc-ROR, Non-coding RNA, Spliced variants