

Evaluation of the role of circulating long non-coding RNA H19 as a promising novel biomarker in plasma of patients with gastric cancer

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Background: Gastric cancer (GC) is ranked as one of the most common causes of cancer-related deaths worldwide, despite the improvement in management strategies of radical surgeries and novel chemotherapies. Long non-coding RNAs (LncRNAs) have been implicated to regulate a range of biological functions and the disruption of some of these functions, such as genomic imprinting and transcriptional regulation, plays a critical role in cancer development and metastatic events. One of the first LncRNA genes reported was the imprinted *H19* gene with loss of imprinting and subsequent strong gene expression in a variety of cancers. *H19* is one of the LncRNA that is related to the progression of many diseases including cancers. This work was carried out to study the level of the long non-coding RNA; *H19*, in plasma of patients with gastric cancer (GC) and to assess its significance in their clinical management.

Methods: A total of 62 participants were enrolled in the present study. The first group included 32 GC patients, while the second group was formed of 30 age and sex matched healthy volunteers serving as a control group. Plasma samples were used to assess *H19* gene expression using real time quantitative PCR technique.

Results: *H19* expression was up-regulated in GC patients with positive correlation to TNM cancer stages.

Conclusions: Up-regulation of *H19* is closely associated with gastric cancer and correlates well with tumor staging. Convenient, efficient quantification of *H19* in plasma using real time PCR technique implements its role as a potential non-invasive prognostic biomarker in gastric cancer, that predicts patient's outcome and most importantly as a novel target in gastric cancer treatment with better performance achieved on using both CEA and *H19* simultaneously.

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