

Letter to the Editor

Long noncoding RNA GIHCG is a potential diagnostic and prognostic biomarker and therapeutic target for renal cell carcinoma

Dear Editor,

We think that the paper by He et al¹, published on European Review for Medical and Pharmacological Sciences and titled "Long noncoding RNA GIHCG is a potential diagnostic and prognostic biomarker and therapeutic target for renal cell carcinoma", is another important proof that circulating cell-free nucleic acids could serve as interesting non-invasive biomarkers for early diagnosis of several cancers. This is also the way forward to better personalize each therapy.

Renal cell carcinoma (RCC) is the most common subtype of kidney cancer. Approximately 90% of these tumors are classified as RCC and up to 80% as "clear cell" RCC. Most patients (> 75%) are diagnosed when the disease is already advanced or metastatic, mRCC, hence no more curable²⁻⁴. Recurrent and/or mRCC is associated with a poor 5-years survival, roughly 10%; however, in the last decade, a series of novel agents have been introduced in clinical practice and the outcomes are slowly improving^{5,6}.

In particular, this article focuses attention on the expression level of GIHCG in the serum of RCC patients. This serum level is significantly unregulated in RCC patients compared with that in healthy controls. Therefore, the authors analyzed the clinical values of GIHCG in RCC. Long noncoding RNA is a kind of RNA molecule with a length transcript of more than 200 nt, which has the function to regulate the gene expression at epigenetic level but does not have the protein-encoding capacity⁷⁻⁹. More and more reports have demonstrated that lncRNAs play an important role in the development of a variety of carcinomas with a crucial role in cell proliferation, differentiation, apoptosis, and in all pathological processes. However, despite the high number of lncRNAs identified, to date, little is known about their role in cancer for vast majority of them; unlikely, only a small fraction of them have been characterized.

The paper explored the correlation between GIHCG expression level and clinicopathological traits in 46 RCC patients with a result that GIHCG is markedly increased in RCC tissues with advanced TNM stages. Furthermore, GIHCG expression is also significantly increased in RCC tissues with Fuhrman III and IV grades compared with that in Fuhrman I and II grades. The positive correlation between increased GIHCG expression and advanced TNM stages is confirmed by Pearson χ^2 -tests. The confirmation of the association between GIHCG upregulated and an aggressive clinic-pathological traits and poor prognosis is given by Kaplan-Meier survival analysis. A crucial point of this study is the loss-of-function assays that show that deletion of GIHCG significantly represses cell proliferation and migration of RCC cells, highlighting the oncogenic roles of GIHCG.

Other reports have put in evidence the importance of lncRNAs for some clinical applications also in other cancer type. Nowadays, the role of lncRNAs as non-invasive biomarkers is beyond doubt. Surely the identification of all the dysregulated lncRNAs in RCC patient's serum on large-scale would help clinical choice especially in a period in which, given the many drugs registered, it becomes necessary to be able to predict, with good approximation, what is the best treatment for each patient^{10,11}.

Conflict of interest

The authors declare no conflicts of interest.

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