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Letter to the Editor

LncRNA colon cancer-associated transcript 1 (CCAT1) in ovarian cancer

Dear Editor,

We read the study published by Lai et al[1] with great interest. The complex nature of neoplastic transformation has an enormous impact at various moments of the cancer diagnostics and therapy protocols. Sophisticated individualized therapeutic approaches, supported by an increasing use of tumor-specific molecular tests, are now available[2,3].

In particular, more details are necessary among molecular differences of primary lesion and its metastases, because these are frequently responsible for the failure of systemic therapy[4-6]. In this contest, the study published by Lai and Cheng represent an interesting approach in order to study the molecular mechanism of metastasis and proliferation in ovarian cancer (OC).

In OC, more than in other types of tumors, morphologic diagnosis is no more sufficient to obtain a qualified therapeutic decision; therefore, the use of new molecular markers is mandatory to improve the clinical management of this type of cancer[7]. The authors of this study, for the first time, observed that the LncRNA colon cancer-associated transcript 1 (CCAT1) promotes OC proliferation and metastasis.

CCAT1 gene producing a long no coding RNA and it is resulted upregulated in different cancer cell types. In cancer progression process this RNA could be involved long range chromosomal interactions and as a molecular sponge for microRNAs. The gene is located at chromosome 8 and resulted than 200 bp transcript, and contains at least 2 exons and lacks proteins coding regions Figure 1.

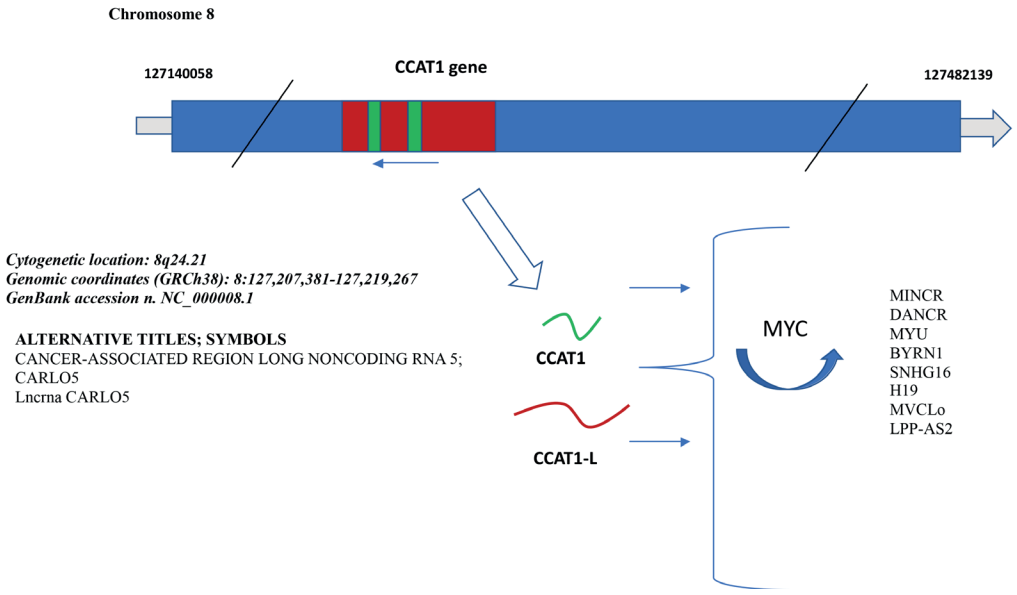

Figure 1. CCAT1 gene expression networks in oncogenic transformation, several miRNAs are involved but the interaction with the proto-oncogene MYC is one of the most frequently deregulated in cancer.

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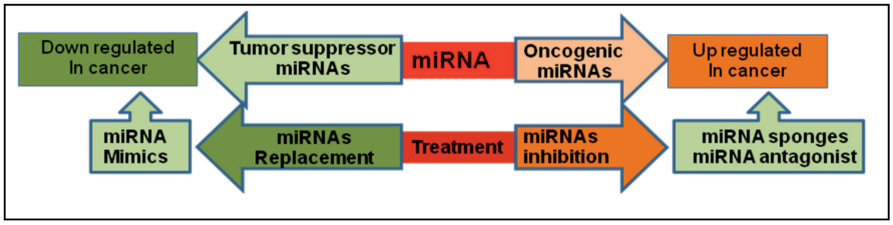

Figure 2. Schematic representation of several miRNA-based therapeutic strategies. (Adapted with modifications from Ref. 15).

For these reasons, they suggest that this long non-coding RNA over expression may be considered as a good novel prognostic biomarker, closely related to survival time, tumor size and lymph node metastasis. The LncRNA was recently studied in different kinds of cancer as molecular marker. Even if this RNA does not code any proteins, seems that his expression could regulate cancer processes at both genetic and epigenetic level, providing new targets for cancer treatment[8].

It is also important to briefly describe the molecular methods used in this study: a simple's systems like the quantitative Real-time polymerase chain reaction (qRT-PCR) and a more sophisticated analysis like the MicroRNA sponges. The expression of LncRNA CCAT1 in OC tissue and cell lines was determined using the fast, sensible and not expensive qRT-PCR method. This molecular system, frequently used to perform most of the diagnostic molecular test commercial available, represents the best standardizable system able to determine in all laboratories viral, genetic and epigenetic factors[9-11]. Therefore, this method could be easily routinely used not only in different cohorts of OC patients but could be also applied in other types of cancers[12].

The more sophisticated microRNA (miRNA) "sponge" method is a microRNA inhibitors system introduced few years ago as the best experimental approach to study the function of miRNA in cell lines and transgenic organisms[13,14]. This transgenic approach, an alternative to genetic knockouts or antisense oligonucleotide inhibitors, has proven to be an useful tool to probe miRNA functions in a variety of experimental systems.

Interestingly, seems that LncRNA CCAT1 could sponge miRNA in different cancers and, the authors of this study shown that this long non-coding RNA is able to inhibit in OC cells the miR-1290.

It is well-known that miRNAs could play a crucial role in cancer development, progression, and metastasis and that miR-1290 act as a tumor suppressor gene in gynecologic tumor. Therefore, the results of this study suggest that in OC cells LncRNA CCAT1 miR-1290 inhibition could promote proliferation and metastasis and, for this reason, might be considered as a potential target for OC treatment in future. This new therapeutic strategy, summarized in Figure 2, it was recently described for breast cancer[15,16].

Conflict of interest

The authors declare no conflicts of interest.

Footnotes/links

- GEneCards: http://www.genecards.org/cgi-bin/carddisp.pl?gene=CCAT1
- OMIM: https://www.omim.org/entry/617705
- Gene Script: https://www.genscript.com/gene/homo-sapiens/100507056/ccat1.html
- WeizmannInstitute: https://genecards.weizmann.ac.il/v3/cgi-bin/carddisp.pl?gene=CCAT1

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