Ovarian cancer

Long non-coding RNAs (IncRNAs) have emerged as critical regulators of tumorigenesis, and yet their mechanistic roles remain challenging to characterize.

Lin et al., integrated functional proteomics with IncRNA-interactome profiling to characterize Urothelial Cancer Associated 1 (UCA1), a candidate driver of ovarian cancer development. Reverse phase protein array (RPPA) analysis indicates that UCA1 activates transcription coactivator YAP and its target genes. In vivo RNA antisense purification (iRAP) of UCA1 interacting proteins identified angiomotin (AMOT), a known YAP regulator, as a direct binding partner. Loss-of-function experiments show that AMOT mediates YAP activation by UCA1, as UCA1 enhances the AMOT-YAP interaction to promote YAP dephosphorylation and nuclear translocation. Together, we characterize UCA1 as a IncRNA regulator of Hippo-YAP signaling and highlight the UCA1-AMOT-YAP signaling axis in ovarian cancer development ¹⁾.

Outcome

For ovarian cancer patients, the Prognostic nutritional index is better at predicting 1-year death and 30-day readmission after discharge, and the Nutritional Risk Screening 2002 is superior for predicting 1-year recurrence ²⁾.

Brain metastases from ovarian cancer

see Brain metastases from ovarian cancer.

1)

Lin X, Spindler TJ, de Souza Fonseca MA, Corona RI, Seo JH, Dezem FS, Li L, Lee JM, Long HW, Sellers TA, Karlan BY, Noushmehr H, Freedman ML, Gayther SA, Lawrenson K. Super-Enhancer-Associated LncRNA UCA1 Interacts Directly with AMOT to Activate YAP Target Genes in Epithelial Ovarian Cancer. iScience. 2019 Jun 20;17:242-255. doi: 10.1016/j.isci.2019.06.025. [Epub ahead of print] PubMed PMID: 31307004.

2)

Xing L, Chen R, Qian J, Ren J, Deng X. A comparison of three preoperative nutritional assessment methods for predicting ovarian cancer patient prognosis: which is better? Support Care Cancer. 2022 Mar 9. doi: 10.1007/s00520-022-06941-7. Epub ahead of print. PMID: 35260921.

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