miR-211 regulates ovarian cancer malignancy by targeting Cyclin D1 and CDK6.

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Epithelial ovarian cancer (EOC) accounts for the highest tumor-related mortality in women with gynecologic malignancy. Mature forms of miRNA silence gene expression by binding to the 3′ UTR of target mRNA and initiate translational repression or cleavage of cognate mRNA and play important roles in cancer development and progression. The microRNA miR-211 is localized on intron 6 of the Trpm1 gene at 15q13-q14, a locus that is frequently lost in neoplasms. Its function and loss-of-function have been described in normal and cancer cells and tissues. miR-211 is known to be dysregulated in ovarian cancer: however, its function and the downstream effect of its loss-of-function in ovarian cancer have not been described before.

We analyzed miR-211 expression in clinical samples of primary EOC tissues compared to normal epithelial ovarian tissues and in the EOC cell lines: OVCAR3, Caov3, OVCA429, SKOV3 and A2780 compared to human ovarian surface epithelial cells. We found that the expression of miR-211 is downregulated in EOC tissues and cell lines compared to normal epithelial ovarian tissue and human ovarian surface epithelial cells, respectively. From multiple bioinformatic tools, we found Cyclin D1 and CDK6 were predicted as targets of miR-211. A luciferase reporter system was developed to confirm miR-211 regulation of the predicted targets of Cyclin D1 and CDK6.

Our results demonstrate that Cyclin D1 and CDK6 were direct targets of miR-211 and miR-211 might play a pivotal role in EOC development . More investigation needs to be carried out in the future to identify the effect of miR-211 in EOC cells that regulate the process of malignancy.