RNA Sequencing Reveals Novel Targets in Nano Curcumin Treated HT-29 Colorectal Cancer Cells

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Abstract

Introduction: Colorectal cancer is considered as an aggressive tumor with high mortality in the world. It has been shown that Gemini Nano-Curcumin (Gemini-Cur) affects viability of colorectal cancer cells. Nevertheless, the cellular and molecular mechanisms underlying its toxicity are debatable. Here, we planned to untangle the potential novel targets for nanocurcumin on p53-mutant HT-29 cancer cells by employing RNA sequencing.

Methods: HT-29 cell were incubated with appropriate doses of Gemini-Cur for 24 h. Total RNA was sequenced and DESeq2 tool was employed to find differentially expressed genes (DEGs). The enrichR tool was employed to do Gene Ontology (GO). Then, PPI network was constructed for 1200 DEGs using STRING, visualized by Cytoacape and analyzed with MCODE.

Results: About 1309 genes (Padj <0.05) in treated cells were obtained including 479 upregulated with P-value <0.05 & log2 FC >1) as well as 63 downregulated genes with P-value <0.05 and log2 FC < -1). 542 up and downregulated genes were mapped to 67 Reactome pathways. Our data illustrated that Nanocurcumin modulates predominantly cellular stress- and transporter-related genes. Using MCODE, Three modules were significantly identified (scores ≥ 1 and nodes ≥1).

Conclusion: Our data reveal that nanocurcumin might affects colorectal cancer cells through modulating different pathways predominantly cell stress- and transporter-related genes.

Keywords

Gemini Curcumin, HT-29 Cells, Colorectal Cancer, Gene Ontology, Differentially Expressed Genes (DEG), RNA Sequencing.