Transcriptomic profiling of cisplatin resistance signet ring gastric carcinoma cell line

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Abstract: (1) Background: Gastric cancer is the fourth most common cancer worldwide and is the second most common cancer related death. Although cisplatin-based chemotherapy is effectively used in treatment of gastric cancer, development of drug resistance is still increasing. Cisplatin resistance is multifactorial: failure in binding of drug to its targets; enhance DNA repair, or suppression of apoptosis that antagonize cisplatin cytotoxicity. So, in this study, next generation sequencing approach and bioinformatics were used to explore the difference in gene expression level between cisplatin resistance and sensitive gastric cancer cell line (2) Methods: Cisplatin resistance gastric cancer cell line KATO/DDP was derived from parental KATOIII signet ring cell gastric carcinoma by stepwise treated with cisplatin and RNA sequencing was performed in both cell line by illumine HWI-ST1276 platform with paired-end sequencing strategy. Bioinformatics analysis was used to identify the differential genes expression and candidate genes. (3) Results: In KATO/DDP cell line, 5966 genes were differentially expressed, of which 2571 genes were upregulated while 3395 were down regulated when compared to drug sensitive cell line KATOIII. Moreover, it showed 13 hub genes UGT1A1, UGT1A10, CYP1A1, CBR3, HSD17B2, AKR1C1, AKR1C3, CXCL8, CXCL11, CXCL13, NMUR2, ADCY7 and SSTR5 that play an important role in development of drug resistance. (4) Conclusions: This study indicated that 13 candidate genes were promoting the drug resistance by increasing the metabolism of the drug, modulating immune system, and enhancing epithelial to mesenchymal transition.

Keywords: Signet ring cell gastric carcinoma; Cisplatin resistance; RNA sequencing

Funding: This research was funded by Faculty of Medicine Research Fund, Chiang Mai University.

Acknowledgments: This research study was supported by Chiang Mai University, Faculty of Medicine Research Fund.

Conflicts of Interest: The authors declare no conflict of interest.