EP012/#719 GENOME-WIDE CELL-FREE DNA ANALYSIS ALGORITHMS FOR EARLY DETECTION AND PREDICTION OF PROGNOSIS OF OVARIAN CANCER

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Introduction The purpose of the present study was to develop artificial intelligent (AI) algorithms for analyzing genome-wide cell-free DNA (cfDNA) for early detection and prediction of prognosis of epithelial ovarian cancer.
Methods Whole blood samples from epithelial ovarian cancer patients (n=120) stored in a biobank were used to develop AI algorithms for genome-wide analysis of cfDNA. Convolutional neural network (CNN) and multilayer perception (MLP) deep learning methods were used for algorithm development. Another batch of whole blood samples from the patients who were newly-diagnosed with ovarian tumor (both benign and malignant) were prospectively collected and run through the developed algorithms. Sensitivity and specificity of the developed algorithms in differentiating malignant tumors from benign tumors were explored.
Results A total of 219 whole blood samples from the patients who were newly-diagnosed with ovarian tumor were run through the algorithms and the probability scores of malignancy were calculated. The probability scores calculated by the analysis of DNA fragmentation size, patterns of sequence of end motif, regional mutation types and their density were found to be significantly higher in cancer patients than those with benign tumors. Furthermore, these scores became increasingly higher as the extent of disease assessed by the FIGO staging system increased. This machine-learning model incorporating genome-wide cfDNA analysis had sensitivities of detection at 92% at 98% specificity, with an overall area under the curve value of 0.99.
Conclusion/Implications The use of AI algorithms for analyzing cfDNA yielded high diagnostic accuracy for epithelial ovarian cancer demonstrating the potential value of precision oncology based on whole-genome analysis.

EP013/#1522 OU MC DECRESCENDO PHENOMENON AS A COMPONENT OF PHYSICAL ACTIVITY FOR CANCER PREVENTION

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Introduction The causal relationship between physical activity and anti-cancer effect are not proved by the current studies. Ou MC decrescendo phenomenon treatment (OuDPt) as a component of physical activity, shows an anti-cancer effect.
Methods We review the anti-cancer effects of the Ou decrescendo phenomenon treatment (OuDPt) in the context of physical activity and human body anatomical axes (HBAAs).
Results OuDPt showed to induce apoptosis and regression of uterine endometrial cancer, suppression of ovarian and pancreatic cancer growth, regression of early suspicious pancreatic cancer, enhancement of chemotherapy effect of pancreatic cancer and stop of cancer-related bleeding.
Conclusion/Implications However, such anti-cancer effect by OuDPt shows insufficient efficacy for advanced cancer in long term treatment. Nonetheless, the anti-cancer effect by OuDPt may be availed for cancer prevention. Further study is warranted. Reference: 1. Ou MC et al. Cancer Symposium: Hallmarks of Cancer. Seattle, WA, USA, 2019, P1.11. 2. Ou MC et al. 2nd JCA-AACR precision cancer medicine international conference. Kyoto, Japan, 2023, 5–4. 3. Ou MC et al. APJCP, 2023;24(8) (in press).

EP014/#682 EFFECT OF DECITABINE COMBINED WITH BELOTECAN ON T-CELL MEDIATED IMMUNITY IN OVARIAN CANCER

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Introduction We evaluated the effect of decitabine on T-cell mediated immunity in ovarian cancer cell lines when combined with topoisomerase I inhibitors
Methods We selected five human (ES2, OV90, SKOV3, TOV21G, TOV112D) and one mouse ovarian cancer lines (ID8). After we selected belotecan after comparison of the cytotoxic effect with topotecan, we determined the concentration of decitabine not showing the additive cytotoxic effect when combined with belotecan. We administered decitabine of 0.25 mg/kg six times every two days, followed by belotecan of 0.17 mg/kg five times daily eight weeks after we inoculated ID8 cells in the subcutaneous layer of C57BL/6, and then evaluated T-cell immunity in the spleen and tumor cells with expressions of PD-1 and CTLA4.
Results The cytotoxic effect of belotecan was superior to that of topotecan in the six cell lines, and mRNA expressions of PD-L1, TNF, IL6 and TFGβ were increased in ES2, SKOV3, TOV21G and TOV112D cell lines. Moreover, the low concentration of decitabine did not show the additive cytotoxic effect when combined with belotecan, whereas decitabine increased apoptosis by belotecan synergically in the five human ovarian cancer cell lines. Even though PD-1 and CTLA4 were not increased in the allograft C57BL/6 mouse by ID8, CD3+CD8+T cells were increased after administration of belotecan and decitabine in the spleen and tumor cells.
Conclusion/Implications Even though decitabine dose not increase expressions of PD-1 and CTLA4 as targets of immune checkpoint inhibitors, it may increase CD3+CD8+T cells in the spleen and ovarian cancer cells when combined with belotecan.