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## 174 LONGITUDINAL MULTIOMIC ANALYSIS ASSOCIATES T CELL DYNAMICS WITH CHEMOTHERAPY OUTCOME IN OVARIAN CANCER PATIENTS

[1,2]Rachel H Ng*, [1]Dan Yuan, [1]Rongyu Zhang, [1]Sarah Li, [1]Lauren Jatt, [1]Rick Edmark, [1]Inyoul Lee, [3]Charles Drescher, [1]James Heath, [1]Andrew T Magis, [1]Pamela Troisch. [1]*Institute for Systems Biology, Seattle, WA, USA*; [2]*University of Washington, Seattle, WA, USA*; [3]*Swedish Cancer Institute, Seattle, WA, USA*

**Background** In the US, ovarian cancer is a relatively rare but lethal cancer that causes the 5th most cancer deaths in women. Current standard of care involves surgery and chemotherapy. While there are attempts to introduce immunotherapy, clinical trials of immune checkpoint blockade showed limited effect thus far. There is a need to understand the cancer-intrinsic and patient-intrinsic factors that would affect patient outcome, especially factors related to immune engagement.

**Methods** We performed deep multiomic longitudinal analysis of 29 ovarian cancer patients before and after chemotherapy. We analyzed blood plasma proteomics and metabolomics, and profiled circulating T cells and tumor infiltrating lymphocytes (TIL) for single-cell whole transcriptome, surface proteins, and T cell receptor (TCR) sequences. Cancer cells from baseline tumor resection surgery were analyzed by bulk whole exome sequencing and RNA-seq for prediction of neoantigens.

**Results** Mean profile analysis of longitudinal plasma proteomics revealed statistically significant suppression of TCR signaling and T cell activation post-chemotherapy in patients with recurrence. This is accompanied by contraction of memory T cells and increased proportion of naïve T cells based on single cell analysis of circulating T cells. Analysis of tumor mutational burden and tracking of T cell clones across compartments revealed differences in immunogenicity that may contribute to development of long-term protection against cancer recurrence.

**Conclusions** Our characterization of patients' longitudinal response identified biomarkers and T cell dynamics predicting patient outcome. These findings guide future design of immunotherapies that would synergize with chemotherapy in ovarian cancer patients.

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