A MULTI-MODAL ANALYSIS APPROACH LEVERAGING MULTIPLEXED SPATIAL PHENOTYPING AND MULTI-OМICS ANALYSIS TO BETTER UNDERSTAND THE PROGNOSTIC VALUE OF TERTIARY LYMPHOID STRUCTURES IN NSCLC

Julie Berthe*, 1Sriram Sridhar, 1Felix Segerer, 1Marco Testori, 1Megha Saraiya, 1Lorezen Bagnoni, 1Harald Hessel, 1Alma Andoni, 1Andreas Spitzmüller, 1Mari Heininen-Brown, 1Jorge Blando, 1Felicia Ng, 1Emma Jones, 1Sophie Willis, 1Michael Surace, 2Rieneke van de Ven, 2Tanja de Graaf, 1Helen Angell. 1AstraZeneca, Cambridge, UK; 2Cancer Center Amsterdam, Amsterdam, Netherlands

Background Tertiary Lymphoid Structures (TLS) are highly organized ectopic lymphoid structures found in inflamed or tumor tissues, acting as sites of lymphoid recruitment and immune activation. A high TLS density within the tumor is commonly associated with an increased prognostic effect of TILs and with an improved disease free survival and overall survival for patients. However, the existence of conflicting studies suggest that multiple TLS features should be taken into account when assessing their prognostic value, such as their location, cellular composition, maturation stage and spatial organisation, as those may affect their functionalities.

Methods With the aim of gaining insights into TLS biology and evaluating the prognostic role of TLS in Non-Small Cell Lung Carcinoma according to their multiple features, we developed a TLS multiplex immunofluorescent (mIF) panel that includes T cells (CD3, CD8), B cells (CD20), Follicular Dendritic cells (CD21, CD23) and mature dendritic cells (DC-LAMP) markers. We deployed this panel across a cohort of primary tumors from NSCLC patients (n=408) and established a mIF image analysis workstream to assess the status and spatial location of each cell within the tissue. A H&E staining of the same tissue section was performed to evaluate mIF spatial data in relation to the tumor context. Additional multi-omics assessments were conducted across the same cohort including; whole exome sequencing, NanoString transcriptomics, and immunohistochemistry (e.g. PD-L1, FOXP3, NKp46, LKB1, CTLA4). We have leveraged clinical metadata, including demographics (e.g. age, sex, smoking status) and clinical risk factors (e.g. stage, grade, Standard of Care treatment) with clinical follow up (e.g. OS, PFS) for prevalence analysis, novel biomarker identification, and survival association.

Results Assessment of the prevalence of each cell phenotype within the tumor tissue and TLS, the cell-cell interactions, the distance between each cell type, and the distance of non-TLS immune cells to the closest TLS will be described, demonstrating the different types of lymphoid aggregates and TLS and their functional status. An integrative analysis combining spatial biology data with multi-omics and clinical data will be presented evaluating the prognostic value of TLS composition, maturation status and spatial organization, in correlation with additional biomarkers and clinical characteristics.

Conclusions This exploratory study using cutting-edge technologies enables us to better understand how TLS orchestrate an organised anti-tumour response, defining TLS spatial biomarker signatures, TLS gene signatures, and TLS features associated with patient outcomes to evaluate in the clinic.

REFERENCES