Project abstract

Background

Peripheral T-cell lymphomas are a heterogeneous group of rare lymphoid malignancies. With current treatment options, the majority of patients does not achieve remission or experience relapse after completion of therapy, generally with dismal outcome. (1,2) Mechanisms of progression and relapse remain elusive and predictive biomarkers do not exist, precluding clinical progress.

Hypothesis

We hypothesize that utilizing a unique collection of clinically annotated samples from our ViVi-biobank (Vienna viable Biobank) with the identification of tumor sub clones and their ant-cancer drug response will unravel pivotal mechanisms determining intra-tumor heterogeneity and clinical behavior of PTCL.

Aims

Aim 1: Identification of tumor sub clones and description of the evolutional process of sub clones in PTCL.

Aim 2: Discrimination of resistant and sensitive tumor cells after anti-cancer drug perturbation.

Aim 3: Selection of a treatment combination targeting all identified tumor sub clones.

Methods

This study will be based on biopsy samples of patients in relapse or refractory state diagnosed with PTCL, NOS or TFH. Single cell RNA-Sequencing, Whole Genome Sequencing and flow based drug screening will be correlated with clinical parameters, including progression and outcome.

Expected results & impact

This study will provide a comprehensive characterization of drug responses of different sub clones in lymphomas diagnosed with PTCL. The search for a combination treatment targeting all different sub clones is a potential key to overcome relapses in patients with PTCL.