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P01.03 TARGETING DIACYLGLYCEROL KINASE ALPHA AND ZETA BY SELF DELIVERING RNAI TO OPTIMIZE TLYMPHOCYTES FOR ADOPTIVE THERAPY OF SOLID TUMORS

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Background Evidence indicates that diacylglycerol kinases (DGK) are promising targets for the optimization of T cell activity, for example in the setting of adoptive cell therapy (ACT). The tumor microenvironment (TME) of human renal cell carcinoma (RCC) is an immunosuppressive setting where T and NK cell functionality is blocked. DGK- α is a negative regulator of TCR signaling, functioning by metabolizing diacylglycerol to phosphatidic acid and thereby limiting the activation of MAPK/ERK1/2 signaling pathway. DGK- α is found increased in tumor-infiltrating lymphocytes (TIL) from RCC patients and also in adoptively transferred T cells after infiltrating into the TME.¹ We previously reported that inhibition of DGK- α restored functionality of unresponsive CD8 T cells and NK cells from RCC-TIL. Other studies demonstrated that knockdown or pharmacologic inhibition of DGK- α and DGK- ζ alone or together increased target cell killing and cytokine production, and protected T cells from inhibitory factors in the TME.² However, there are no inhibitors for DGK- ζ and available DGK- α inhibitors have undesired pharmacokinetic/pharmacodynamic properties and are highly toxic precluding their clinical application. Here, we present data using a novel RNA interference (RNAi) technology that can specifically target each DGK isoform.

Materials and Methods INTASYL™ compounds incorporate drug-like properties into RNAi, resulting not only in enhanced cellular uptake in the presence of serum but also eliminating the need for further transfection reagents. Toxicity of compounds applied alone or in combination was assessed by 7-AAD flow cytometry analysis and WST assay. Silencing of mRNA and protein was analyzed by RT-qPCR and SimpleWestern. Downstream signaling pathways and T cell function were analyzed to demonstrate pharmacological efficacy.

Results Two DGK- ζ compounds and one DGK- α compound were analyzed using Jurkat T cells and primary human TCR-transduced T cells. No effects were seen on cell viability for the compounds applied alone or in combination. On-target knockdown was achieved in Jurkat T cells evidenced by RT-qPCR and SimpleWestern. Silencing of mRNA and protein occurred quickly after 24h, peaked between 48h and 72h and lasted at least for 96h. Stimulation under DGK-targeting INTASYL treatment resulted in enhanced levels of phosphorylated ERK1/2 and enhanced secretion of IL-2.

Conclusions INTASYL™ self-delivering RNAi compounds represent a promising approach to target intracellular immune

checkpoints such as DGKs. The good toxicity profile allows for combined application of several compounds enabling targeting of multiple checkpoints, which likely is necessary to counteract the complex and heterogeneous inhibitory influences of the TME. The technology enables the anti-tumor activity of T and NK cells for immunotherapy, and can be used in ACT and direct therapeutic applications towards the TME.

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P01.04 LENTIVIRAL PROTEIN VPX DELIVERY SYSTEMS AS POTENTIAL WEAPONS TO IMPROVE CYTARABINE TREATMENT RESPONSE AGAINST ACUTE MYELOID LEUKEMIA

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Background Acute myeloid leukemia (AML) is an aggressive cancer of the blood, where malignant myeloid blasts accumulate in the bone marrow. One of the challenges of effective AML treatment is resistance to cytarabine (or ara-C), a standard AML chemotherapeutic drug used in front-line treatment today. In 2017, Schneider *et al.* reported the dNTPase sterile alpha motif and HD-domain-containing protein 1 (SAMHD1) to be a targetable biomarker for ara-C treatment response.¹ The intracellular triphosphorylated active form of ara-C, ara-CTP, was recognized as a substrate by SAMHD1 and is hydrolyzed back to ara-C. This led to a decrease in the amount of ara-CTP within the cells and consequently reduced cytotoxicity.¹ SAMHD1 can be targeted by the lentiviral accessory protein Vpx for proteasomal degradation by interacting with the proteasomal degradation complex and SAMHD1. This study aims to use Vpx to target SAMHD1 in AML cells to improve ara-C sensitivity.

Materials and Methods In order to manipulate SAMHD1 levels using Vpx, different Vpx delivery systems were developed. These are virus-like particles (VLPs) packaged with different homologs of Vpx from Simian Immunodeficiency Viruses (SIV) and HIV-2, and cell-penetrating peptides (CPPs) bound to either a 67 amino acid truncated SIVmac Vpx (67aaVpx) or to the WT full-length form. Two different CPPs were used in the synthesis: TAT and CPP44. The latter

was chosen, as significantly better uptake of the CPP was observed in AML cell lines and primary blasts compared to healthy PBMCs.²

Results Upon treating AML cell lines with the VLPs, we observed different SAMHD1-degradation capacities of the different Vpx homologs. SIVmac239 Vpx and HIV-2 7312a Vpx were most efficiently loaded into the VLPs, showed the highest SAMHD1-degradation and improved ara-C sensitivity up to 80-fold. In contrast, HIV-2 Rod9 Vpx did not show any SAMHD1 degradation or improvement in ara-C sensitivity despite its high packaging efficiency in the VLPs. As for the CPPs, CPP44 bound to 67aaVpx showed better uptake and SAMHD1 degradation compared to the TAT bound 67aaVpx in THP-1 cells, which is an AML cell line with high SAMHD1 expression levels. Upon co-treatment with ara-C, up to a 5-fold reduction in IC50 was observed when treated with CPP44-bound 67aaVpx. In order to increase the efficiency further, full-length Vpx-bound CPPs will be prepared, and trials using these CPPs are currently underway.

Conclusions

We demonstrate that inducing SAMHD1 degradation by Vpx delivered via VLPs or CPPs efficiently improved ara-C sensitivity in AML cell lines. Combining a Vpx delivery system with treatments containing ara-C might improve treatment outcomes in SAMHD1-high patients who are otherwise non-responsive.

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P01.05

DECIPHERING THE FUNCTION OF THE UBIQUITIN-PROTEASOME-SYSTEM IN REGULATING THE IMMUNE CHECKPOINT PROTEIN B7-H3 (CD276) IN NON-SMALL CELL LUNG CANCER

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Background Cancer cells use the expression of immune checkpoint proteins on their surface to evade immune responses. Targeting these checkpoints with antibodies has substantially advanced cancer therapy in the past years, especially the treatment of lung cancer. However, the prognosis of metastatic lung cancer patients still remains poor and lung cancer remains to be the leading cause of cancer death worldwide. Further therapeutic concepts are therefore urgently needed.

It has been shown that protein expression levels of the immune checkpoint protein PD-L1, a member of the B7 protein family, is regulated by the ubiquitin-proteasome system (UPS). Ubiquitin-ligases (E3-ligases) and deubiquitinating enzymes that regulate immune checkpoint levels on the cell surface are therefore considered promising potential drug targets. Inhibiting enzymes that increase immune checkpoint surface levels might increase the anti-cancer immune response.

Here, we investigate whether another B7 family member, immune checkpoint protein B7-H3, is regulated by the UPS in non-small cell lung cancer (NSCLC).

Materials and Methods B7-H3 expression in NSCLC cell lines and patient samples was evaluated using mRNASeq data from open databases. Immunoblotting and FACS were used to analyse total endogenous protein levels and surface expression of B7-H3 in different NSCLC lines under normal growth conditions and in response to various inhibitors (MG-132, Chloroquine (CQ) and Cycloheximide (CHX)). Immunoprecipitation of FLAG-tagged B7-H3 followed by a TUBE IP using ubiquitin-binding beads and in-vivo ubiquitylation assays based on co-overexpression of HA-tagged ubiquitin and/or HA-tagged K48/K63-linkages specific ubiquitin together with FLAG-tagged B7-H3 or FLAG-tagged B7-H3 K526R mutant in HEK-93T cells were performed to analyse ubiquitination on B7-H3. Mass spectrometry analysis of FLAG-purified B7-H3 was performed to identify possible interaction partners.

Results Database analysis revealed that B7-H3 expression is higher in lung cancer samples than in healthy lung tissue. We found that B7-H3 is highly expressed in different NSCLC lines on RNA and protein levels. Treatments with either proteasomal (MG-132) or lysosomal (CQ) degradation inhibitors alone showed only minor effects on B7-H3 protein abundance. However, CHX treatment of H1437 cells decreased B7-H3 over time and this decrease was recovered by adding MG-132 or CQ suggesting that both the lysosome as well as proteasome are involved in the degradation of B7-H3. In vivo ubiquitination and TUBE assay showed K48 and K63 B7-H3 ubiquitination. Mass spectrometry analysis of FLAG-tagged purified B7-H3 revealed E3-ligase Trim21, which has recently been identified as a ligase of PD-L1 in lung cancer lines, as a potential interaction partner. Further experiments are planned to validate the result and to identify other UPS-related enzymes involved in post-translational B7-H3 surface level regulation.

Conclusions Our experiments indicate that immune checkpoint B7-H3 levels are regulated by the ubiquitin-proteasome system in NSCLC lines. With further experiments, we aim to identify UPS-related enzymes that stabilize B7-H3 on the cell surface. Pharmacological inhibition of such enzymes might reduce the immune checkpoint's surface levels and increase anti-tumour immune responses.

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P01.06

OVERWEIGHT AND OBESITY AS BIOMARKERS FOR SURVIVAL OUTCOMES AND IMMUNE RELATED ADVERSE EVENTS UNDERGOING IMMUNOTHERAPY – A SYSTEMATIC REVIEW AND META-ANALYSIS

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Background The impact of overweight/obesity in cancer patients treated with immune checkpoint inhibitors (ICIs) is controversial. To further contribute to this debate, we