of Philadelphia fusion chromosome, coding for BCR-ABL1 oncoprotein. The life-long treatment relies on using tyrosine kinase inhibitors (TKIs). In some cases, patients develop point mutations, leading to resistance to TKIs treatment, nearly in 2%. Allogeneic stem cell transplantation is the possible solution for these individuals in late stages of CML with success cure rate only approximately at 40%. Based on this funding new solutions for treating cancer with genetic etiology are considered. CRISPR/Cas system, composed of guide RNA, targeting endonuclease Cas9 to specific target genomic region has been used before to mediate breakage of Philadelphia chromosome at the site of oncogenic translocation, although at lower efficiency.

**Materials and Methods**

K562 cells, model for Philadelphia chromosome positive cells, were used. Constructs, expressing BCR-ABL1 targeting gRNA and Cas9, tethered via coiled-coil forming peptides to *E. coli* exonuclease EXOIII, were nucleofected into target cells. T7E1 assay to detect genome modifications was carried out. TUNEL assay, FACS analysis and bioluminescence measurement were used for cell death determination. SCID mice were used for a subcutaneous K562 cancer model.

**Results**

Our strategy was to couple Cas9 to the exonuclease to promote large deletion at the target site. Of the different exonucleases tested, the EXOIII exhibited the best performance in terms of deletion formation. To improve the rate of deletion genetic lesions, we connected Cas9 and EXOIII via coiled-coil forming peptides, bringing the two enzymes into close proximity (CRISPR-EXO). This resulted in an increased deletion formation compared to the standard CRISPR/Cas system. We performed a case study for the use of the CRISPR-EXO system as a potential anti-cancer therapeutic tool. In the case of our new system, we showed significant increase in cell death due to higher genome modification in BCR-ABL1 region. Later, these findings were confirmed also in an animal cancer model, where animals with tumors, electroporated with CRISPR-EXO system showed full survival and drastic reduction in tumor size.

**Conclusions**

CRISPR-EXO upgraded CRISPR system based on tethering Cas9 protein to exonuclease EXOIII by heterodimeric coiled-coil forming peptides, resulted in highly efficient editing of BCR-ABL1 fusion gene, leading to enhanced death of CML cancer cells.

**REFERENCES**

2. Lekometsev S, Aligianni S, Lapao A, Bürckstümmer T. Efficient generation and editing of BCR-ABL1 fusion gene, leading to enhanced death of CML cancer cells.

**Disclosure Information**

D. Lainšček: None. V. Forstnerič: None. Š. Malenšek: None. M. Skrbinek: None. M. Sever: None. R. Jerala: None.

**Background**

CCL22 is a macrophage-derived chemokine that exerts immunosuppressive functions by the recruitment of regulatory T cells (Treg) through the CCL22/CCR4 axis. It has been described to play a key role in the suppression of anti-cancer immunity in different cancer types including ovarian, breast, or pancreatic cancer and is thought to promote the suppression of anti-cancer immunity by Treg recruitment. Recently, we described that CCL22-specific T cells generated from cancer patients can kill CCL22-expressing tumor cells and directly influence the level of CCL22 in *in vitro*. In this study, we provide PoC data for a CCL22-targeting vaccine by assessing the immunotherapeutic efficacy of this approach in syngeneic mouse tumor models.

**Materials and Methods**

Peptide vaccines that induce expansion of CCL22-specific T cells were identified by measurement of vaccine-induced *ex vivo* response (IFNγ ELISpot) in BALB/c and C57BL/6 mice. The antitumor efficacy was evaluated in CT26, Pano2 and B16 syngeneic models. To investigate the vaccine’s mode of action, the tumor immune infiltration was analyzed through flow cytometry and qPCR.

**Results**

Vaccination with CCL22-specific peptide vaccines induced expansion of primarily CD8+*, CCL22-specific T cell responses (assessed by *ex vivo* IFNγ ELISpot). Treatment with CCL22 vaccines reduced tumor growth and increased survival in CT26, Pano2 and B16 tumor models. Assessment of gene expression in the tumors indicated that vaccination leads to a reduction of CCL22 expression in the tumor microenvironment (TME), as well as the expression of other immunosuppressive molecules such as IDO. Furthermore, vaccinated mice harbored an increased CD8+ T cell infiltration with a concomitant increase in M1/M2 ratio within the TME.

**Conclusions**

This study provides evidence that targeting CCL22 expressing cells by vaccination induces immune modulation in the TME, leading to augmentation of anti-tumor responses - thus provides a rationale for a novel immunotherapeutic approach in cancer.

**Disclosure Information**

I. Lecoq: A. Employment (full or part-time); Modest; IO Biotech. K.L. Kopp: A. Employment (full or part-time); Modest; IO Biotech. R. Christensen: A. Employment (full or part-time); Modest; IO Biotech. E. Martinenaite: A. Employment (full or part-time); Modest; IO Biotech. A.W. Pedersen: A. Employment (full or part-time); Modest; IO Biotech. M.H. Andersen: A. Employment (full or part-time); Modest; IO Biotech.

**P09.08**

**CLINICAL-GRADE MANUFACTURING OF ROR1 CAR T CELLS USING A NOVEL VIREUS-FREE PROTOCOL**


**Background**

Immunotherapy with T cells that were modified by gene-transfer to express a ROR1-specific chimeric antigen receptor (ROR1 CAR-T) has therapeutic potential in ROR1+ malignancies in hematology and oncology. The ROR1 tumor
antigen has a favorable expression profile with absence in vital normal human tissues. In this study, we sought to establish and validate clinical-grade manufacturing of ROR1 CAR-T to enable a Phase I/IIa clinical trial. In particular, we sought to integrate virus-free gene-transfer based on Sleeping Beauty transposition into this manufacturing protocol to permit scale-up and export to point-of-care manufacturing, and to reduce turn-around time, complexity and regulatory burden associated with conventional viral gene-transfer (biosafety level 2 to biosafety level 1).

**Materials and Methods** Buffy coats or leukaphereses were obtained from healthy donors to perform protocol optimization (n=7) and scale-up runs (n=1). CD4+ and CD8+ T cells were isolated separately by magnetic selection and stimulated with CD3/CD28 TransACT® reagent. T cells were transfected with mRNA encoding hyperactive Sleeping Beauty transposase (SB100X) and minicircle DNA (MC) encoding a pT2 transposon comprising the ROR1 CAR and an EGFRt marker gene using the MaxCyte GTx® electroporation platform. Following transfection, T cells were expanded for 10–13 days in G-REX® bioreactors and then harvested and formulated into the drug product at a 1:1 ratio of CAR-expressing CD4:CD8 T cells. The drug product underwent comprehensive phenotypic, functional and genomic analyses as part of product qualification.

**Results** The set of protocol optimization runs resulted in a highly robust process. On average, the stable gene-transfer rate at the end of the manufacturing process was 71% in CD4+ (n=5) and 54% in CD8+ T cells (n=7). The average yield of ROR1 CAR-T relative to the number of input T cells was 12.6-fold for CD4+ and 9.4-fold for CD8+ after 12–15 days of expansion, with an average viability of 84% for CD4+ and 82% of CD8+ T cells. The scale-up run was performed with a leukapheresis product from which 52.5 × 10^6 CD4+ and 109 × 10^6 CD8+ T cells were transfected. At the end of the manufacturing process (day 12), there were 844 × 10^6 CAR-expressing CD4+ (~16-fold expansion) and 857 × 10^6 CAR-expressing CD8+ T cells (8-fold expansion). In functional testing, ROR1 CAR-T showed specific recognition and potent elimination of ROR1+ target cells, as well as antigen-dependent cytokine production and productive proliferation in in vitro analyses. Experiments to determine the anti-tumor potency of the drug product in vivo and detailed genomic analyses are ongoing. Preliminary analyses suggest a favorable genomic insertion profile of the CAR transposon, and a transposon copy number that is well within the range acceptable for clinical use of the drug product.

**Conclusions** With this novel protocol, we aim to obtain clinical use of the drug product. The set of protocol optimization runs resulted in a highly robust process. On average, the stable gene-transfer rate at the end of the manufacturing process was 71% in CD4+ (n=5) and 54% in CD8+ T cells (n=7). The average yield of ROR1 CAR-T relative to the number of input T cells was 12.6-fold for CD4+ and 9.4-fold for CD8+ after 12–15 days of expansion, with an average viability of 84% for CD4+ and 82% of CD8+ T cells. The scale-up run was performed with a leukapheresis product from which 52.5 × 10^6 CD4+ and 109 × 10^6 CD8+ T cells were transfected. At the end of the manufacturing process (day 12), there were 844 × 10^6 CAR-expressing CD4+ (~16-fold expansion) and 857 × 10^6 CAR-expressing CD8+ T cells (8-fold expansion). In functional testing, ROR1 CAR-T showed specific recognition and potent elimination of ROR1+ target cells, as well as antigen-dependent cytokine production and productive proliferation in in vitro analyses. Experiments to determine the anti-tumor potency of the drug product in vivo and detailed genomic analyses are ongoing. Preliminary analyses suggest a favorable genomic insertion profile of the CAR transposon, and a transposon copy number that is well within the range acceptable for clinical use of the drug product.