prevents the vaccine from being immunosuppressive itself. In our studies, we demonstrate that VLVs are able to induce strong, broad, and long-lasting ERV Env specific CD8+ T cell by flow cytometry and antibody responses by ELISA in mice. Furthermore, the modified vaccine is of special interest to future research as it proved to significantly delay mouse tumor growth in a therapeutic setup. Nevertheless, we now need to address the principal host related developmental uncertainties in translating our achievements into the clinical setting. This goal can be accomplished by raising human T cells capable of targeting human cancers *ex vivo*. Furthermore, to support the translation of our work, we tested the ability to rise adaptive responses upon vaccination in non-human primates (NHP) which endogenously express ERVs similar to humans (in collaboration with IPB University, Indonesia). Fellowship granted by Innovation Fund Denmark.

Disclosure Information J. Daradoumis: A. Employment (full or part-time); Significant; InProTher Aps. B. Research Grant (principal investigator, collaborator or consultant and pending grants as well as grants already received); Significant; Innovation Fund Denmark. P.J. Holst: A. Employment (full or part-time); Significant; InProTher Aps. E. Ownership Interest (stock, stock options, patent or other intellectual property); Significant; InProTher. K.N. Nielsen: A. Employment (full or part-time); Significant; InProTher Aps.

P04.09

DEVELOPMENT OF A DENDRITIC CELL VACCINE AGAINST HEPATOCELLULAR CARCINOMA USING VSV-NDV

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10.1136/jitc-2020-ITOC7.77

Background Activated Dendritic cells (DC) are the immune system's allrounder: they initiate innate and adaptive immune responses; they induce instant immune reactions as well as immunologic memory. Therefore, there is growing interest in using them as a potential anticancer vaccine.¹ Here we use the beneficial immune-stimulatory properties of the novel oncolytic hybrid virus VSV-NDV to create a DC vaccine against hepatocellular carcinoma.²

In our therapeutic approach, a sample of the patient's tumor cells is lysed *in vitro* with VSV-NDV (=oncolysate). The patient's DCs are then co-cultured *in vitro* with the oncolysate in order to activate them and load them with tumor antigens. In the end, the stimulated DCs are injected into the patient, where they can lead to a personalized and broad anti-tumor immune response.

Materials and Methods To investigate the potential of the approach in a cell culture system, human monocyte-derived dendritic cells were generated from PBMCs of healthy donors and incubated with VSV-NDV-lysed HepG2 hepatoma cells. Afterwards their state of activation was investigated via flow cytometry and cytokine measurement, whereas their functionality was assessed in co-culture with T-cells. In a murine system, dendritic cells were generated

from bone marrow stem cells, incubated with a VSV-NDV-lysed murine HCC clone and investigated as in the human system.

Results Flow cytometry of oncolysate-stimulated DCs showed a significant upregulation of the activation markers CD86, MHC-I, MHC-II and PD-L1 ($p < 0.05$). Moreover, these stimulated DCs released increased amounts of cytokines. Upon co-culture of the DCs with T-cells, an elevated secretion of IFN γ by the T-cells, as well as an upregulation of T-cell activation markers could be shown, demonstrating the functional potential of the oncolysate-stimulated DCs. These results apply to both the human and the murine system.

Conclusions Our *in vitro* data demonstrates that the oncolysate-stimulated human and murine DCs are not only activated, but furthermore have a high functional potential. Further *in vitro*-experiments will be necessary to translate the process to patient-derived samples, whereas murine *in vivo*-experiments will give further insights into the effect of the therapeutic approach.

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Disclosure Information J. Gold: None. L. Hanesch: None. T. Krabbe: None. C. Lozano-Simon: None. G. Hänel: None. M. Rothe: None. A. Klopp: None. S. Göttert: None. S. Heidegger: None. U. Protzer: None. M. Subklewe: None. J. Altomonte: None.

P05 Precision Medicine Meets Immunotherapy (Immuno-Monitoring)

P05.01

COMPARATIVE ANALYSIS OF RNA VERSUS DNA AS INPUT MATERIAL FOR IGH REPERTOIRE SEQUENCING PANELS FOR IMMUNO-ONCOLOGY APPLICATIONS AND RARE CLONE DETECTION

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10.1136/jitc-2020-ITOC7.78

Background Recent progress in tumor immunotherapies have shown the importance of next generation sequencing (NGS) T cell repertoire profiling to characterize T cell immune response to treatment. Understanding the role of the B cell repertoire upon stimulation of the immune system by checkpoint blockade is paramount for immunotherapeutic approaches in treatment of B cell malignancies, as well as understanding B cell function within traditional I/O strategies. The ability to detect low frequency B cell clones enables numerous hematology/oncology research applications, including identification of potential biomarkers and minimal residual disease (MRD) research. Historically, efforts to track the frequency of malignant B cells by IGH chain sequencing have utilized DNA input given potential challenges in accurately quantifying