develops a dendritic cell vaccine

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 IFNγ 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.

REFERENCES


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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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 hematologic/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