



Abstract 776 Figure 4

The percentage of circulating CD3+PD-1+ cells and CD3+CD4+TIGIT+ cells positively correlated with a better treatment response in the post-treatment setting. The percentage of CD3+, CD3+CD4+ and CD3+CD8+ cells expressing ICs in peripheral circulation and infiltrating OAC tissue in the post-neoadjuvant treatment setting was correlated with each other, patient demographics and clinical features of the tumour. Patient demographics and clinical features included gender (female=0, male=1), age, tumour type (OAC=0 and OGJ=1), neo-adjuvant treatment received (CROSS=0 and FLOT=1), treatment response (determined by radiographic features using PET/CT), tumour regression grade (TRG), clinical tumour stage and nodal involvement, pathological tumour stage and nodal involvement, body mass index (BMI kg/m²), peri-neural invasion, serosal invasion and lymph-vascular invasion. BMI and weight measurement was recorded post-treatment. Spearman correlation. Only significant data shown.

as a result of an induced-anti-tumour immune response following immunogenic chemotherapy/chemoradiotherapy treatment and may be a useful strategy for stratifying patients into chemotherapy/chemoradiotherapy responders or non-responders. A therapeutic rationale is also highlighted for combining ICIs with chemotherapy regimens in OAC patients to enhance anti-tumour T cell-mediated responses and potentially boost response rates to chemotherapy treatment.

Acknowledgements We would like to thank all the patients who kindly donated their samples to our research

Ethics Approval The work was performed in accordance with the Code of Ethics of the World Medical Association (Declaration of Helsinki) for experiments involving human samples.

Consent Patients provided informed consent for sample and data acquisition, and the study received full ethical approval from the St. James's Hospital/AMNCH Ethical Review Board.

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778 PRECLINICAL STUDY USING A GLUTAMATERGIC SIGNALING AND IMMUNE-CHECKPOINT INHIBITORS IN A SPONTANEOUS MELANOMA PRONE MOUSE MODEL

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Background Much progress has been made in understanding melanoma pathogenesis within the last few years through targeted therapies and immunotherapies. However, resistance to small molecule inhibitors remains an obstacle. Immunotherapies such as checkpoint inhibitors against PD-1/PD-L1 lead to durable responses but only in a subset of melanoma patients. Mouse models reflecting human cancers provide invaluable tools towards the translation of basic science discoveries to clinical therapies, but many of these in vivo studies are short-term and do not accurately mimic patient circumstances. Our lab has a melanoma-prone transgenic mouse model which is driven by ectopic expression of a normal neuronal receptor, metabotropic glutamate receptor 1 (GRM1). This mouse model recapitulates melanoma development and progression frequently associated with melanoma patients, where aberrant GRM1 expression is detected. We have shown that in >90% of late-stage melanoma patients, there is atypical GRM1 mediated signaling and expression.

Methods In this study, we are using these mice, TGS, to determine the long-term, 18-week, therapeutic consequences of troriluzole, a prodrug for riluzole, which is an inhibitor of glutamatergic signaling plus anti-PD-1, an immune-checkpoint inhibitor. Tumor burden is monitored every 6 weeks for 18 weeks using a small imaging system, IVIS and tumor burden is quantified using ImageJ software. Blood, lymphoid, and tumor samples were collected at several time points during the study for molecular, and immune analyses.

Results Preliminary results suggest a gender-biased treatment response and that the combination of troriluzole and anti-PD-1 is more efficacious than either agent alone. In males, a 43.9% reduction in tumor burden was observed while in females there was a 29.6% increase in tumor burden in the combination group compared to vehicle. In concordance, after the removal of the treatment modality, the male mice in the combinatorial group survived 42 days longer compared to vehicle controls with sustained tumor reduction by 68.3%. In female mice no significant advantage in survival or reduction in tumor burden was noted.

Conclusions N/A

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779 IMMUNE CHECKPOINT BLOCKADE IMPACTS THE SUPPRESSIVE PHENOTYPE AND FUNCTION OF REGULATORY T CELLS IN AN ENDOGENOUS MOUSE LYMPHOMA MODEL

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Background Antibodies against programmed cell death protein 1 (PD-1) and cytotoxic T-lymphocyte-associated protein 4 (CTLA-4) have become established part of anti-cancer therapy.

However, the mechanisms contributing to the therapeutic success have not been entirely uncovered by now. Here we focus on the impact of PD-1/CTLA-4-blocking antibodies on regulatory T cells (Tregs), which are known to be involved in tumor immune evasion in many cancer types.

Methods To evaluate how Tregs are affected by anti-PD-1/CTLA-4 therapy, we used a MYC-transgenic mouse model of spontaneously arising B-cell lymphoma, which can be effectively treated by immune checkpoint inhibition. Data were acquired by flow cytometry.

Results As earlier shown, Tregs were involved in immune escape of MYC tumors. The Treg to effector T cell (Teff) ratio was elevated within the CD4-positive cell compartment. Tumor-infiltrating Tregs were predominantly thymic Tregs, which recognized overexpressed tumor-derived self-peptides in an MHC class II-restricted manner and showed upregulated expression of activation markers, Foxp3, CD25 and IL-10. To examine whether these phenotypic alterations correlated with the immunosuppressive capability of Tregs, an in vitro suppression assay was established. In this setting, MYC Tregs turned out to suppress proliferation and IFN- γ release of Teff cells more effectively than wildtype Tregs. The suppression observed in vitro was mediated by cell contacts and IL-10. Further suppressive mechanisms are likely to play a role, such as competition for MHC-II ligands and a consumption of IL-2. To investigate if immune checkpoint blockade interferes with these Treg-dependent immunosuppressive pathways, MYC mice were treated with a combination of anti-PD-1 and anti-CTLA-4 antibodies. Tregs from treated MYC mice showed decreased expression of CD69, CD137, Foxp3, CD25 and IL-10 as compared to Tregs from untreated MYC mice. This correlated with a lower suppressive capacity of Tregs from treated animals in the in vitro suppression assay.

Conclusions Taken together, the data show that immune checkpoint blockade impairs the development of the suppressive phenotype of intratumoral Tregs. Thus, apart from the initially described Teff reactivation, other mechanisms are also relevant for unfolding the therapeutic effect of immune checkpoint inhibitors.

Ethics Approval All animal experiments were approved by Regierung von Oberbayern, approval number 55.2-1-54.

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QUANTITATIVE CELL-BASED BIOASSAYS TO ADVANCE IMMUNOTHERAPY PROGRAMS TARGETING IMMUNE CHECKPOINT RECEPTORS

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Background The human immune system is comprised of a complex network of immune checkpoint receptors that are promising new immunotherapy targets for the treatment of a variety of cancers and autoimmune disorders. The Nobel prize for Medicine in 2018 was awarded for seminal studies on the role of immune checkpoint targets in T cell activation and furthermore, combining different strategies to release the brakes on the immune system with the aim of eliminating tumor cells even more efficiently. Immunotherapies designed to block co-inhibitory receptors (e.g. PD-1, CTLA-4, TIGIT) are showing unprecedented efficacy in the treatment of cancer. However, not all patients and tumor types respond to this approach.

This has resulted in broadening of immunotherapy research programs to target additional co-inhibitory (e.g. LAG-3, TIM-3) and co-stimulatory (e.g. 4-1BB, GITR, OX40, ICOS) receptors individually and in combination.

A major challenge in the development of antibody-based biologics is access to quantitative and reproducible functional bioassays. Existing methods rely on primary cells and measurement of complex functional endpoints. These assays are cumbersome, highly variable and fail to yield data required for drug development in a quality-controlled environment.

Methods To address the need of access to a robust and reliable functional assay for immunotherapy drug development programs, we have developed a suite of cell-based functional bioassays to interrogate modulation of immune checkpoint receptors individually (e.g. PD-1, CTLA-4, LAG-3, TIM-3, GITR, 4-1BB, OX40, CD40) and in combination (e.g. PD-1 + CTLA-4, PD-1 + 4-1BB). These assays consist of stable cell lines that express luciferase reporters driven by response elements under the precise control of mechanistically relevant intracellular signals. Thus, the bioassays reflect mechanisms of action for the drug candidates designed for each immune checkpoint receptor and demonstrate high specificity, sensitivity and reproducibility. Here we describe the application of MoA-based immune checkpoint receptor bioassays as tools for biologics drug discovery, development, potency and stability studies.

Results We demonstrate that these bioassays measure response and inhibition with blocking drugs or potency changes from stressed samples.

Conclusions In summary, these reporter-based bioassays provide valuable tools for the development, stability testing, and potency determination in the manufacture of biologics that are targeted to immune checkpoint.

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VALIDATION OF THE COMBINATORIAL EFFECT OF BLINATUMOMAB AND NIVOLUMAB IN CANCER THERAPY

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Background Cancer immunotherapies, including immune checkpoint inhibitors, CAR-T, cancer vaccines and bispecific antibodies, have been brought to spot light in recent years as several therapeutic strategies targeting the immune system have produced exciting clinical results. Bispecific antibody typically play dual roles in blocking the immune checkpoint and redirecting/re-boosting the function of the immune effector cells. Blinatumomab belongs to CD3 bispecific T cell engager (CD3 BiTE), which was engineered to harbor two arms binding with CD3 and CD19 simultaneously and direct CD8+ T cells to specifically recognize CD19 positive lymphoma cells to execute cytotoxicity. Approval of Blinatumomab for patients with relapse/refractory B cell acute lymphoblastic leukemia (ALL) has driven remarkable increase in combination studies of Blinatumomab with other immunotherapies such as checkpoint inhibitors.

Methods In this study, we developed CD8+ T cytotoxic system targeting different B lymphoma cell line and fully validated the function of Blinatumomab in promoting target tumor cell lysis by primary CD8+ T cells (figure 1). In addition, we established a mixed lymphocyte and tumor system to