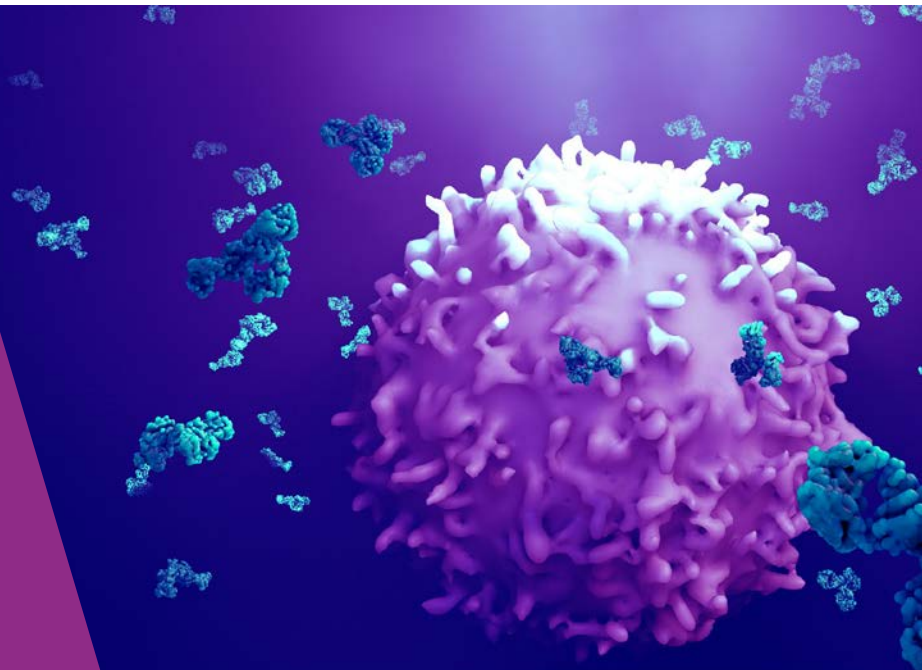




IMMUNE SAFETY AVATAR

Nonclinical mimicking of the immune system effects of immunomodulatory therapies



Deliverable 2.4

CPI immune safety assessment research roadmap

DELIVERABLE REPORT

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Abstract

Checkpoint inhibitors frequently trigger immune-mediated adverse events in patients. Similar to many other organs, liver toxicity is induced by aberrantly activated immune cells but likely less influenced by microbiota or other environmental factors. We discuss currently available in-vitro systems for their suitability to capture mechanisms of in-vivo drug effects. We conclude that an in-vitro workup of checkpoint inhibitor-induced hepatotoxicity is not advised in the consortium due to mechanistic complexity and insufficient translation of antigen specificity of T cells in experimental systems. We propose to refine hypotheses by patient-based workup, and potentially revisit in-vitro systems if this is successful.

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1. Results

Background

Checkpoint inhibitors (CPI) have revolutionized the treatment options for cancer and are now indicated for various malignancies, e.g., metastatic melanoma or non-small cell lung cancer (NSCLC) (Lewis et al., 2020; Anderson et al., 2019). CPI induce an anti-tumor response by inhibiting immune checkpoints such as the cytotoxic T-lymphocyte antigen-4 (CTLA-4) or the programmed death-1/-ligand-1 (PD-1/PD-L1) pathway. These pathways are physiologically responsible for the downregulation of T-cell responses and hence protect the body from a possible damaging immune response. However, some tumors are able to hijack and exploit these checkpoints and consequently evade the immune response. By reactivating the immune system, checkpoint inhibitors restore a potentially efficacious anti-tumor immunity in a wide range of cancer types (Ramos-Casals et al., 2020).

In 2011, the Food and Drug administration (FDA) approved the first CIP, ipilimumab, for the treatment of metastatic or unresectable melanoma (Almutari et al., 2020). Ipilimumab is an inhibitor of a negative regulator of the anti-tumor T-cell response called **CTLA-4** (Tarhini et al., 2010). T-cell activation requires multiple stimulatory signals to turn into an effective response. The first step to achieve specificity of the T-cell activation is ensured by the binding of the T-cell receptor (TCR) with the antigen-presenting major histocompatibility complex (MHC) presenting an antigen recognized by the TCR. Additional co-stimulatory signals are obtained via the binding of CD28 molecules, located on the T-cell, with B7-1 or B7-2 molecules that are located on the antigen-presenting cells (APC). If sufficient, these two concomitant signals result in T-cell proliferation, increased survival and differentiation. Conversely, co-inhibitory signals such as CTLA-4 intervene at the priming stage of the naïve T-cell activation to delete potential autoreactive T-cells. CTLA-4 is a homolog of the CD28 with a higher affinity to the B7 molecules. Unlike the CD28/B7 binding, the CTLA-4/B7 binding does not result in a co-stimulatory response but rather in an inhibitory signal. In addition to this inhibitory signal, the competitive binding of CTLA-4 and CD28 may lead to a decreased CD28/B7 co-stimulatory signal. Thus, by adding an anti-CTLA-4 antibody, the inhibitory signal can be interrupted. However, the exact mode of action of anti-CTLA-4 antibodies in promotion of cancer immunity remains unclear. It has been proposed that blocking the CTLA-4 acts on the immune priming phase in the lymph node by aiding the activation and proliferation of effector T-cells and/or reducing the immune suppression mediated by Tregs. Thus, through the inhibition of CTLA-4 by ipilimumab an effective anti-tumor immune response occurs (Buchbinder et al., 2016).

Other approved CPI inhibit either the programmed death receptor 1 (**PD-1**) such as nivolumab and pembrolizumab or they inhibit the programmed-death ligand-1 (**PD-L1**) such as **atezolizumab**, durvalumab and avelumab (Akinleye et al., 2019, Alexander et al., 2016). These inhibitors act through a similar mechanism of action by modulating the immune cell-tumor cell interaction. PD-1 is expressed on activated T-cells located primarily in the peripheral tissue. The need to control the degree of inflammation wherever antigens are expressed and to secure normal tissue from damage has led to the emergence of the PD-1/PD-L1 pathway (Buchbinder et al., 2016, Alsaab et al., 2017). When an antigen presented by the MHC is recognized by a T-cell, inflammatory cytokines are produced and initiate the inflammatory process. As a consequence, these cytokines lead to the PD-L1 expression in the affected tissue and thus cause the activation of the PD-1 pathway in T-cells resulting in immune tolerance. However, tumor cells can exploit this protective PD-1 signaling pathway by overexpressing PD-L1 along the MHC on different types of cancer, e.g. melanoma or lung carcinoma, to evade the generation of an anti-tumor immune response. Through this inhibition, the T-cell suppression is lifted and the antitumor immunity restored. (Akinleye et al., 2019, Alsaab et al., 2017).

The main differences between the CTLA-4 and the PD-1/PD-L1 pathways are the timing of downregulation and the anatomic location of the immune inhibition. CTLA-4 operates during the priming phase of the T-cells (in the lymph node) while PD-1 functions during the effector phase in peripheral tissue. CTLA-4 expression is mostly restricted to T-cells, but PD-1 on the other hand is more broadly expressed, i.e. PD-1 can be found on activated T-cells, B-cells and myeloid cells (Alsaab et al., 2017, Zitvogel et al., 2012).

Despite the advantages of CPI, not every individual treated with CPI is responsive to them. In patients treated for solid tumors only between 15-30% of the patients respond to the treatment whereas patients treated for melanoma have a slightly higher response rate between 45-60%. However, this leaves a significant proportion of patients unresponsive to CIP treatment (Das et al., 2019). Furthermore, unique inflammatory unwanted effects termed **immune-related adverse events** (irAEs) may occur and pose a major challenge to CIP treatments (Ramos-Casals et al., 2020; Das et al., 2019). The mechanisms underlying the occurrence of these irAEs have not been completely elucidated yet (Das et al., 2019) and the biological triggers of irAEs may differ between the different types of CIP (Ramos-Casals et al., 2020) - exemplified by reports that CTLA-4 inhibitors cause irAEs in a dose-dependent manner while PD-1/PD-L1 inhibitors cause toxicities independently of dosages (Ramos-Casals et al., 2020). Data on patient subpopulations and animal models suggest a localized activation and expansion of tissue-resident adaptive cells, which are without therapy held in check by tissue-resident checkpoint expression (e.g. PD-L1 on macrophages; Damo et al, 2021). Other concepts propose a CPI-induced exacerbation of the immune response against latent infections with endemic viruses like CMV (Hutchinson et al., 2021). Irrespective of the trigger, the mechanism of irAEs might be tied to CPI's mode of action in immunological homeostasis, rendering an untangling of safety and efficacy challenging. Genetic factors of Th17 cell polarization, previously linked to psoriasis and vitiligo, can indeed be linked to overall survival after PD-L1 blockade - while concurrently, a cohort with mild skin irAE also shows increased overall survival (Khan et al., 2020). With phenotypic similarities between irAE and idiopathic skin diseases, it is intriguing to speculate that a genetically or environmentally driven adaptive immunity pattern is beneficial in anti-tumor immunity, but may induce irAE when dysbalanced or in unwanted tissues. This concept is also supported by multiple other mechanistic hypotheses of efficacy and safety in CPI therapy (Ramos-Casals et al., 2020).

Unlike for autoreactive T cells, the contributions of B cells and autoantibodies are less clarified. Still, anti-drug antibodies (ADA) are frequently observed in CPI-treated patients, and it is yet unclear whether the immune-stimulating MoA contributes to increased B cell activation, e.g. by Tfh activation. As some irAE are considered a complex interplay of therapeutics and immune-complex forming ADA, further mechanistic exploration promises to support patient prioritization or irAE mitigation. Furthermore, cytokine release might contribute to the occurrence of irAEs (13). Interestingly, ipilimumab is associated with different types of irAEs compared to PD-1/PD-L1 inhibitors, as it is linked to higher rates of gastrointestinal toxicities, pruritus and rash whereas PD-1/PD-L1 inhibitors are associated with higher rates of pneumonitis and hepatotoxicity (14). However irAEs are not considered to be organ-specific, although some organ systems are affected more frequently such as the liver, gastrointestinal tract and lung (13, 15) sometimes leading to severe consequences for the patients.

Given the potential severity of hepatotoxicity for patients, the consortium laid a first focus on modeling hepatic immune related adverse events with the help of in vitro tools. Other organ toxicities share underlying mechanisms, but may be significantly more complex due to influences of non-host, environmental factors (esp. Microbiome, nutritional cues, physical challenges).

In-vitro Models of hepatic irAE and non-ir AE

The liver is an important organ to consider during early drug development and often the subject of many off-target-related investigations. As the liver is responsible for the metabolism and detoxification of intrinsic and extrinsic molecules, including drugs, almost all compounds pass the liver. This can lead to undesired drug-induced liver injuries (DILI) and made in-vitro liver toxicity testing a mainstay of small molecule drug development.

For the assessment and investigation of DILI findings in vitro, different cell sources and cultivation methods have been described, all featuring benefits and drawbacks. **Hepatic cell lines** are generated from tumor tissue or by genetic engineering and are, due to their availability and high proliferation capacity, widely used cell sources in research. Although these cell lines are suitable tools in certain research fields, their phenotype and functionality differ substantially from the in vivo situation (Rodríguez-Antona et al., 2002; Sison-Young et al., 2015). Another promising approach includes the use of stem-cell derived hepatic cells, differentiated from either adult, embryonic, or **iPS**-derived stem cells (Snykers et al., 2011; Wills and Rajagopalan, 2019). Here, a lot of progress has been made over the last decades, although the differentiation into fully functional and mature hepatic cells is still not fully understood and the focus of many research groups (Hu et al., 2018; Kouï et al., 2017; Takayama et al., 2012; Wang et al., 2016).

So far, **primary hepatocytes** are considered the gold standard in DILI research, as they, compared to the cell sources described above, most closely resemble the in vivo situation upon isolation. The cultivation of these primary cells in suspension or traditional 2D culture settings, however, leads to rapid dedifferentiation, loss of viability, phenotype and liver-specific functions, which renders their use in more complex, and prolonged DILI investigations difficult (Elaut et al., 2006; Rowe et al., 2013)

Therefore, new and better ways to cultivate primary liver cells have been established, which help to avoid the dedifferentiation of hepatocytes, thereby stabilizing the viability and functionality over a prolonged period of time (Lauschke et al., 2016). Primary hepatocytes can be cultivated in a **sandwich** configuration between two layers of extracellular matrix (ECM), which consists of collagen or Matrigel. This configuration better mimics the microenvironment in the liver, which promotes the stability of the cellular phenotype over a prolonged period of time, improves hepatocyte polarization, and leads to the formation of functional bile canaliculi (Knobeloch et al., 2012; Schyschka et al., 2013). However, in a sandwich configuration, the dedifferentiation of the cells is substantially retarded, but not completely prevented (Rowe et al., 2013), and collagen and Matrigel, both rodent-derived materials, raise concerns due to batch-to-batch variability, immunogenicity and technical challenges during handling (Serban and Prestwich, 2008).

A step towards more complex liver systems has been introduced by **micro-patterning** of primary hepatocytes. Here, hepatocytes are cultured as “islands”, surrounded by fibroblasts, which reflects the physiological microenvironment in the liver (Khetani and Bhatia, 2008; Ukairo et al., 2013). This culture-system maintains its liver-specific functionality for up to 6 weeks and has been successfully used to predict the DILI potential of known drugs (Khetani et al., 2013), including slow-metabolizing compounds (Chan et al., 2013). However, the system’s throughput is rather low and liver specific (adaptive) immune cells are missing in this system.

The inclusion of the liver-adaptive immune system, comprising Kupffer cells (KCs), Stellate cells (SCs), and Liver Sinusoidal Endothelial cells (LSECs), has been identified as a critical component towards a more physiological relevant liver model as the inclusion of these cells (1) can additionally help to prolong the viability and functionality of primary hepatocytes (Dash et al., 2009) and (2) is necessary to address immune-related liver effects (Hasmall et al., 2000), thereby providing a liver in vitro tool which covers the broad range of DILI mechanisms.

Primary hepatocyte **spheroids** have emerged as a promising 3D tissue model, as they self-assemble by adhering to each other, so that no artificial scaffold is needed. Spheroid cultures require ~20x fewer cells compared to 2D cultures and can be produced at low costs and high throughput, even in an automated way. Several studies have demonstrated liver-specific functions and long-term viability of primary liver spheroids over multiple weeks, while they maintained transcriptomic and proteomic signatures similar to those observed in vivo (Bell et al., 2017, 2016; Messner et al., 2018; Ohkura et al., 2014; Vorrink et al., 2017). Spheroids have been used to assess the hepatotoxicity of drugs in experiments that require long-term exposure, metabolic activation, or the accumulation of bile acid or reactive oxygen species. The toxicity was measured at concentrations similar to relevant serum levels, which indicates that spheroids are a physiologically relevant system to assess and investigate DILI effects of compounds in early drug development (Hendriks et al., 2016; Messner et al., 2013; Tostões et al., 2012). Considering the composition of those spheroids and their architecture, liver spheroids do not reflect the in vivo morphology, as cells (particularly the NPCs) are randomly distributed throughout the spheroids.

Different advanced liver models including microfluidics – so called organ-on-chip - have been established in the last decades, which helped to gain important information about DILI and related mechanisms. The **CNBio** model (Domansky et al., 2010) features a mechanical (polystyrene) scaffold, where both, hepatocytes and NPCs can grow in a three-dimensional (3D) surrounding, while constantly applied flow of cell culture medium through the system generates physiological shear stress and an oxygen gradient. Both are important features which can hardly be provided in a 2D cell culture setting (Powers et al., 2002). The CNBio system can be maintained for up to 1 month, it has been used for metastatic cancer studies and to investigate the metabolism of hydrocortisone in an inflamed liver (Sarkar et al., 2015; Wheeler et al., 2014).

Microfluidic, multi-compartmental in-vitro systems can be used to mimic in-vivo tissue architecture (e.g. in commercial Emulate liver chips). Consortium members have previously used such systems in the past for tissue-immune interactions. They are complex to set up, and mononuclear immune cell recruitment from the “vascular” channel requires many modifications that introduce artefacts. We would advise against exploring these for hepatitis.

Despite the unquestionable success of these mentioned liver models in drug toxicity testing, irAE in cancer immunotherapy pose a challenge of biologic complexity. Unlike with most small molecules, CPI-induced liver toxicity (and almost all other organ damages) depend on a dysbalanced immune activation, especially of cytotoxic CD8 T-cells (see above). As these T cells are specific for antigen presentation in an MHC context, in-vitro models may face non-resolvable issues of antigen specificity and allogenicity, if tissues and cells from different donors are combined in vitro. T cell may be aberrantly activated by physiologic HLA-peptide presentation (Shlomchik, 2007). Using an autologous cell system, HLA-matching or benchmarking of donors will likely be necessary for any in-vitro workup, but questions on the existing pool of antigen-specific T cells will remain close to impossible to address.

Importantly, this mechanistic background separates checkpoint inhibitors from targeted therapies like BiTEs or CAR-T cells. For the latter, an activation in-vitro may be comparable to in-vivo, which makes them valuable tools for the preclinical safety assessment. They are already established to some degree, and used in regulatory processes by consortium members and other pharmaceutical companies.

Aside from the mere activation of the immune system, the recruitment of immune cells to the actual organ is tightly regulated in vivo by inflammatory and homeostatic lymphocyte homing mechanisms (Butcher & Picker 1996). The recapitulation of immune cell migration into tissues is a challenge faced by the entire field of in-vitro models, and likely requires diligent separation into individual mechanistic steps

if this biology is relevant for CPI-induced toxicity (e.g. via the chemokine-dependent recruitment of T cells into the intestine after activation of resident memory T cells; Luoma et al., 2020).

2. Conclusion

This complexity in setup and raw tissue sourcing, in conjunction with the only superficial mechanistic description of CPI-induced toxicity (Adam et al., 2021; Affolter et al., 2019, Malnick et al., 2021) lead us to conclude that an experimental workup of hepatotoxicity is not feasible in the consortium. We rather propose to focus on a different angle of workup, e.g. starting with the deep phenotypical or transcriptional characterization of patient tissue with observed side effects. Upcoming technologies (spatial transcriptomics, multiplex IHC) are available in some of the consortium members' labs, and should be assessed for their suitability to generate mechanistic hypotheses. If this is successful, a second step can be to emulate these specifically in in-vitro systems.

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