CORRECTION Publisher Correction: Early memory differentiation and cell death resistance in T cells predicts melanoma response to sequential anti-CTLA4 and anti-PD1 immunotherapy

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Genes & Immunity (2022) 23:260; https://doi.org/10.1038/s41435-022-00189-1

Correction to: Genes & Immunity https://doi.org/10.1038/s41435-021-00138-4, published online 02 June 2021

Abstract

Immune checkpoint blockers (ICBs)-based immunotherapy has revolutionised oncology. However, the benefits of ICBs are limited to only a subset of patients. Herein, the biomarkers-driven application of ICBs promises to increase their efficacy. Such biomarkers include lymphocytic IFNγ-signalling and/or cytolytic activity (granzymes and perforin-1) footprints, whose levels in pretreatment tumours can predict favourable patient survival following ICB-treatment. However, it is not clear whether such biomarkers have the same value in predicting survival of patients receiving first-line anti-CTLA4 ICB-therapy, and subsequently anti-PD1 ICBtherapy (i.e., sequential ICB-immunotherapy regimen). To address this, we applied highly integrated systems/computational immunology approaches to existing melanoma bulk-tumour transcriptomic and single-cell (sc)RNAseq data originating from immunooncology clinical studies applying ICB-treatment. Interestingly, we observed that CD8+/CD4+T cell-associated IFN γ -signalling or cytolytic activity signatures fail to predict tumour response in patients treated with anti-CTLA4 ICB-therapy as a first-line and anti-PD1 ICB-therapy in the second-line setting. On the contrary, signatures associated with early memory CD8+/CD4+T cells (integrating TCF1-driven stem-like transcriptional programme), capable of resisting cell death/apoptosis, better predicted objective response rates to ICB-immunotherapy, and favourable survival in the setting of sequential ICB-immunotherapy. These observations suggest that sequencing of ICB-therapy might have a specific impact on the T cell-repertoire and may influence the predictive value of tumoural immune biomarkers.

This article is part of the Special Issue "Immunology of cell death in cancer & infection", Guest Editor: Professor Abhishek D. Garg, Katholieke Universiteit Leuven, Belgium. It was unintentionally published in issue 22-2 (2021).

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