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CORRECTION

Correction to: Risk of relapse after anti-PD1 discontinuation in patients with Hodgkin lymphoma

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The authors regret that the abstract that appears in the original article is incorrect.

The correct abstract appears below.

Introduction

Patients with relapsed/refractory Hodgkin lymphoma (R/R HL) experience high response rates upon anti-PD1 therapy. In these patients, the optimal duration of treatment and the risk of relapse after anti-PD1 discontinuation are unknown.

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Methods

We retrospectively analyzed patients with R/R HL who responded to anti-PD1 monotherapy and discontinued the treatment either because of unacceptable toxicity or prolonged remission. A machine-learning algorithm based on 17 candidate variables was trained and validated to predict progression-free survival (PFS) landmarked at the time of discontinuation of anti-PD1 therapy.

Results

Forty patients from 14 centres were randomly assigned to training (n=25) and validation (n=15) sets. At the time of anti-PD1 discontinuation, patients had received treatment for a median duration of 11.2 (range, 0 – 33.5) months. Patients discontinued anti-PD1 treatment either because of prolonged remission (N=27, 67.5%) or unacceptable toxicity (N=13, 32.5%). Most patients were in CR (N=35, 87.5%) at the time of anti-PD1 discontinuation.

In the training set, the machine-learning algorithm identified that the most important variables to predict PFS were patients' age, time to best response, and presence or absence of CR. The performance observed in the training set was validated in the validation set.

Conclusion

In this pilot, proof of concept study using a machine-learning algorithm, we identified biomarkers capable of predicting the risk of relapse after anti-PD1 discontinuation (age, time to best response, quality of response). Once confirmed, these simple biomarkers will represent useful tools to guide the management of these patients.