RESEARCH

Hodgkin lymphoma: the role of EBV plasma viral load testing in an HIV‑endemic setting

J. Opie[1](http://orcid.org/0000-0002-1408-2604) · Z. Mohamed[2](http://orcid.org/0000-0003-4730-4231) · D. Chetty³ · J. Bailey⁴ [·](http://orcid.org/0000-0001-7181-3015) K. Brown4 · E. Verburgh4 · D. Hardie[5](http://orcid.org/0000-0002-0056-7547)

Received: 24 October 2024 / Accepted: 15 November 2024 © The Author(s) 2024

Abstract

South Africa has a high burden of human immune defciency virus (HIV)-associated Hodgkin lymphoma (HL) which is typically Epstein–Barr virus (EBV) infected, detected by histological stains. Circulating plasma EBV derived from apoptotic EBV infected tumour cells is a potential biomarker. This study aimed to evaluate the role of plasma EBV load testing in newly diagnosed HL patients and correlate pretreatment plasma EBV levels, HIV status and EBV tumour status with overall survival (OS). Untreated HL patients were prospectively included. Polymerase chain reaction measured EBV plasma viral loads. Kaplan–Meier curves with log-rank tests estimated the impact of HIV, EBV tumour status and plasma EBV viral loads on OS. Multivariable analysis was performed using a Cox proportional hazards model. Receiver operative characteristic curve analysis determined cutoff plasma EBV DNA levels with optimal sensitivity, specificity and concordance with tumour EBV status. The 68 patients included 21 (31%) HIV +ve and 33 (49%) EBV tumour +ve. EBV plasma $\geq 10\,000$ IU/ ml ($P=0.008$), EBV +ve tumour ($P=0.014$), HIV +ve status ($P=0.009$) and age \geq 45 years ($P=0.018$) predicted poorer OS on univariate analysis. Plasma EBV levels >762 IU/ml had 89.29% sensitivity and 96.77% specifcity for detecting EBV +ve HL. High plasma EBV levels ≥10 000 IU/ml, HIV +ve status and EBV tumour +ve status predicted poorer OS. Plasma EBV levels >762 IU/ml predicted EBV +ve tumour status with high sensitivity and specifcity. Plasma EBV viral DNA testing is a promising biomarker for EBV +ve HL.

Keywords Hodgkin lymphoma · EBV · HIV · Plasma EBV · DNA · Overall survival

 \boxtimes J. Opie Jessica.opie@uct.ac.za

- ¹ Department of Pathology, Division of Haematology, Groote Schuur Hospital, University of Cape Town and National Health Laboratory Service, Cape Town, South Africa
- ² Department of Radiation Oncology, University of Cape Town and Groote Schuur Hospital, Cape Town, South Africa
- Department of Pathology, Division of Anatomical Pathology, Groote Schuur Hospital, University of Cape Town and National Health Laboratory Service, Cape Town, South Africa
- ⁴ Department of Medicine, Division of Clinical Haematology, University of Cape Town and Groote Schuur Hospital, Cape Town, South Africa
- ⁵ Department of Pathology, Division of Virology, Groote Schuur Hospital, University of Cape Town and National Health Laboratory Service, Cape Town, South Africa

Introduction

In 2022 sub-Saharan Africa had the highest global burden of human immunodefciency virus (HIV), and South Africa had more than 8 million people living with HIV (PLWH) [[1\]](#page-5-0). Hodgkin lymphoma (HL) is a high-grade lymphoma of B cell origin, with increased incidence in PLWH [\[2](#page-5-1)[–4](#page-5-2)]. Even in the era of antiretroviral therapy, the risk of HL in PLWH is 7.7-fold higher than in HIV negative (−ve) populations. HL has good therapeutic outcomes in well-resourced settings; however, in resource-restricted settings, outcomes are often poorer, and patients present with disseminated disease and bone marrow infltration [\[5](#page-5-3)]. With the increase in the rollout of antiretroviral therapy in sub-Saharan Africa, the impact of HIV status on survival in HL has been less clear with some studies reporting that HIV +ve status does not negatively impact overall survival (OS) [[6,](#page-5-4) [7\]](#page-5-5).

The pathogenesis of HL in PLWH includes reduced immune surveillance, chronic antigen B cell stimulation and concomitant oncogenic viral infection with enhanced risk for

virus-induced oncogenesis [\[8\]](#page-5-6). Epstein–Barr virus (EBV) is a ubiquitous virus which establishes lifelong latent infection in the host. EBV is known to immortalise human B lymphocytes in culture and may lead to EBV-associated lymphoma, particularly in the setting of immunodefciency [[9](#page-5-7)]. Hodgkin tumour cells are known to be EBV infected in 30–40% of HIV −ve HL patients; however, in PLWH, 95% or more HL cases are EBV infected which suggests cooperative oncogenesis between HIV and EBV. The gold standard for assessment of EBV status in tumour cells is by pathologist morphological review of EBV-encoded small RNA in situ hybridization (EBERish) or EBV-encoded latent membrane protein (LMP-1) stains of histological tissue [[10](#page-5-8)].

Peripheral blood EBV DNA viral loads measured by real time polymerase chain reaction (RT-PCR) have been used as a non-invasive biomarker for EBV-associated lymphoma to measure EBV tumour status, tumour burden, prognosis and treatment response $[11-14]$ $[11-14]$ $[11-14]$. Plasma EBV DNA contains only cell free (cf) EBV, which is derived from apoptotic EBV infected tumour cells [\[15\]](#page-6-0). Whole blood includes latent EBV infected B lymphocytes, and therefore, healthy individuals may have low measurable whole blood EBV DNA levels potentially confounding interpretation [\[16\]](#page-6-1). EBV DNA loads in whole blood are higher in PLWH than in the general population and are restricted to the whole blood compartment which may increase the risk of EBV-associated malignancies [\[17](#page-6-2)]. Plasma EBV is therefore generally preferred to whole blood as a biomarker in EBV-associated malignancies [[11](#page-5-9), [13,](#page-5-11) [15,](#page-6-0) [18–](#page-6-3)[20\]](#page-6-4). The role of EBV biomarkers in HIV-associated HL has not been clearly established, and hold promise in view of the high clinical burden of EBV-associated HL in HIVendemic populations in sub-Saharan Africa [[15,](#page-6-0) [21](#page-6-5)[–25](#page-6-6)]. A technological challenge is that EBV viral load reporting is poorly standardised despite the development of international EBV DNA standards by the World Health Organization in 2016 [\[26\]](#page-6-7).

Resource restricted settings typically have poor access to pathologists and the functional imaging required for staging and monitoring in HL [[25](#page-6-6), [27\]](#page-6-8). This study aimed to investigate the clinical utility of plasma EBV DNA viral load testing, and to evaluate the impact of EBV +ve tumour status and HIV in newly diagnosed HL. We aimed to establish cutoff plasma EBV DNA values with optimal sensitivity and specifcity for EBV +ve tumour status, and to correlate the impact of high plasma EBV DNA levels ≥ 10000 IU/ml, HIV +ve and EBV +ve tumour status on OS.

Patients and methods

Patients

Newly diagnosed HL patients presenting to Groote Schuur Hospital (GSH) were prospectively enrolled from 2019 to 2023. GSH is a large tertiary academic hospital in Cape Town, South Africa. Staging was performed according to the Lugano classifcation using positron-emission tomography combined with computed tomography (PET-CT), CT and/or bone marrow fndings [[28\]](#page-6-9). Clinical and laboratory data were extracted from medical and laboratory records. Information collected included age, sex, stage at diagnosis (I–IV), histological subtype, EBV tumour status by EBERish or LMP-1 stains, bone marrow infltration by HL, coronavirus disease 2019 (COVID) status, HIV status, CD4 counts, antiretroviral therapy, chemotherapy received and survival (alive/dead) at 6 months and 24 months after diagnosis. Standard frst-line chemotherapy was doxorubicin, bleomycin, vinblastine and dacarbazine (ABVD). Second-line therapy decisions were made on an individual patient basis at multidisciplinary team meetings. Patients found eligible for transplant were treated with high dose salvage chemotherapy regimens followed by autologous stem cell transplant if they achieved remission. The study was approved by the Human Research Ethics Committee (Number 376/2019) at the University of Cape Town.

EBV DNA viral load testing

Peripheral blood was collected in EDTA prior to commencement of therapy. EBV DNA viral loads were measured using the Abbott 2000 Real Time system (Chicago, USA) on paired whole blood and plasma samples for each patient. This assay targets the *BLLF1* gene, which encodes the gp350/220 envelope glycoprotein of EBV. The lower quantifable limit of the assay was 150 IU/ml. Samples with a detectable viral load <150 IU/ml were assigned a value of 100 IU/ml for analytical purposes. Histopathological diagnoses of classical HL were made by qualifed pathologists in laboratories accredited according to International Standard Organization (ISO) quality standards. Diagnostic formalin fixed paraffin embedded tissue blocks were stained with EBERish or LMP-1 to establish EBV infection status of Hodgkin tumour cells.

Statistical analysis

Categorical variables were described using frequencies and percentages and compared using Pearson Chi-squared or Fisher's exact tests. Numerical variables were described using medians and interquartile ranges (IQR) and compared using Wilcoxon rank-sum tests, as data were nonparametric. The Kaplan–Meier method was used to estimate OS which was defned as the time from date of diagnosis to date of death from any cause or date last seen (censored) at a public health facility in the Western Cape Province of South Africa. Kaplan–Meier curves were compared using log-rank tests to determine associations between predictor variables and OS (univariate analysis). Predictor variables with a P value $\lt 0.2$ in univariate analysis were considered most appropriate for multivariate analysis. A Cox proportional hazards model was used to assess the association between predictor variables and OS. Predictor variables with a P value $\lt 0.2$ in univariate analysis selected for multivariable analysis included age \geq 45 years, HIV status and EBV plasma viral load >10 000 IU/ml. Receiver operative characteristic curve (ROC) analysis was used to determine the cutoff value for plasma EBV DNA giving optimal sensitivity, specifcity and concordance with tumour EBV status. Statistical analyses were performed using STATA version 18.0 (Stata corporation, College

Table 1 Baseline characteristics of Hodgkin lymphoma patients

Station, Texas, USA), and 2-sided *P* values < 0.05 were considered statistically signifcant.

Results

Baseline characteristics of the study population are presented in Table [1.](#page-2-0) The study enrolled 68 patients with a median age of 36 years [Interquartile range (IQR) 26–52 years]. 34 (51%) were female, and 21 (31%) were PLWH, of which 18 (86%) were receiving antiretroviral therapy. Tumours were EBV +ve in 33 (49%) of all HL patients; 20 (95%) PLWH and 13 (28%) of HIV −ve (*P*<0.001). Overall, 54 (80%) presented with advanced disease, defned as Stage III or IV [[28\]](#page-6-9). The most frequent histological subtype was nodular sclerosing in 37 (54%) of all HL patients; 6 (29%) of HIV +ve and 31 (66%) of HIV −ve patients. 7 (33%) of HIV +ve HL cases could not be histologically subclassifed as they were diagnosed on bone marrow biopsy.

One patient died before treatment. 52 (76%) patients received frst-line chemotherapy only and 15 (22%) patients

ART antiretroviral therapy; *CHL* classical Hodgkin lymphoma; *PLWH* people living with HIV; *IQR* interquartile range

*1 patient did not have a CD4 count available

**Detected by EBERish (for lymph node and tissue) and LMP-1 staining (for bone marrow biopsies)

***All CHL unclassifed cases were diagnosed on bone marrow biopsy

required second-line chemotherapy, with no signifcant difference in chemotherapy treatment according to HIV status $(P=0.244)$. There was no correlation between advanced disease at diagnosis and HIV +ve status $(P=1.000)$ nor EBV +ve tumour status ($P = 0.282$). Of the twelve HL patients in the cohort who died, four had documented COVID +ve tests in the 14 days prior to death. In two of these, their deaths were regarded as likely COVID related.

Kaplan–Meier survival curves are provided in Fig. [1.](#page-3-0) The total cohort survival probability was 91% [95% confdence

Fig. 1 Kaplan–Meier survival curves in Hodgkin lymphoma patients

interval (CI) 81–96%] at 6 months, and 81% (95% CI 68–89%) at 24 months. PLWH had poorer OS ($P = 0.009$), and a survival probability of 85.5% (95% CI 61.3–95.1%) at 6 months compared to 93.5% (95% CI 81.2–97.9%) for HIV −ve HL. The survival probabilities at 24 months were 58.9% (95% CI 30.9–78.7%) for PLWH compared to 89.6% (95% CI 73.6–96.2%) for HIV −ve HL patients. EBV tumour +ve status also correlated with signifcantly poorer survival $(P=0.014)$, and a 6-month survival probability of 84.53% (95% CI 66.71 -93.32%) compared to 97.1% (95% CI 80.94- 99.6%) for EBV −ve. The 24-month survival probability for EBV tumour +ve was 67.3% (95% CI 45.1–82.2%) versus 92.7% (95% CI 72.9–98.2%) for EBV tumour −ve patients. There was a signifcant diference between survival distributions when HIV and EBV tumour status were com-bined (Fig. [1A](#page-3-0), $P = 0.016$). Specifically, EBV +ve PLWH had signifcantly poorer survival than those who were HIV −ve and EBV −ve (*P*=0.004). No signifcant diferences were noted for the other comparisons $(HIV + EBV + vs.$ HIV−EBV+, *P*=0.221 and HIV−EBV+vs. HIV–EBV−, *P*=0.278). Comparing the survival by HIV and EBV tumour status, those that were both $HIV+$ and EBV tumour + did not show a signifcant diference in survival compared to $HIV-EBV+(p=0.221)$.

A high plasma EBV viral load level at diagnosis $(>10$ 000 IU/ml) was associated with a lower survival probability at 6 months of 76.9% (95% CI 44.2–91.9%) versus 89.4% (95% CI 63.8–97.3%) for plasma viral loads < 10 000 IU/ml. At 24 months the survival probability for those with EBV viral loads ≥ 10000 IU/ml was 58.6% (95% CI 26.7–80.6%) compared to 73.4% (95% CI 40.7–89.9%) for those with a plasma EBV viral load $<$ 10 000 IU/ml. Patients aged \geq 45 years had a significantly shorter survival time than younger patients $(P = 0.018)$. Patients with any detectable plasma EBV DNA also had a significantly shorter survival time compared to their EBV plasma DNA −ve counterparts $(P=0.021)$. There was no significant difference in OS for early-stage I and II versus advanced stage III and IV disease ($P = 0.258$) nor for males versus females ($P = 0.777$). Predictor variables selected for multivariable analysis included age, HIV status and EBV tumour status (Table [2](#page-3-1)). Age \geq 45 years was associated with a poorer prognosis

Table 2 Multivariable analysis for the outcome death from any cause^{*}

Covariate	Hazard ratio (95% CI)	P value
Age \geq 45	$4.2(1.2-14.1)$	0.022
$HIV + ve$	$3.2(1.0-10.3)$	0.056
EBV plasma viral load > 10000 IU/ml	$3.4(1.0-11.5)$	0.051

*Multivariable Cox proportional hazards model

Fig. 2 Plasma log EBV viral loads in Hodgkin lymphoma

Table 3 Plasma EBV DNA viral loads in newly diagnosed Hodgkin lymphoma

EBV tumour status [#]	Positive	negative
Number of patients	$n = 33$	$n = 35$
EBV DNA plasma +ve*	$n = 31/33(94\%)$	$n = 6/35$ (17%)
Median viral load,	8912	0
Range IU/ml	0-997 237	$0 - 7585$
Viral load IU/ml IOR	1496-25118	$0 - 0$
Median Log IU/ml	3.950	0
Range IU/ml	$0 - 5.990$	$0 - 3.880$
Log viral load IQR	3.175-4.40	$0 - 0$

Determined by EBERish or LMP-1 histological stains

*+ve defned as any detectable EBV DNA, IQR, interquartile range

(hazard ratio (HR) 4.2, 95% CI 1.2–14.1) (*P*=0.022). HIV +ve status (HR 3.2, 95% CI 1.0–10.3, $P = 0.056$) and a EBV plasma viral load ≥ 10000 IU/ml (HR 3.4, 95% CI 1.0–11.5, $P = 0.051$) trended towards poorer OS.

Plasma EBV viral loads were significantly higher in EBV tumour +ve HL compared to EBV tumour −ve HL $(P=0.002)$ $(P=0.002)$ $(P=0.002)$ (Fig. 2). Median log viral loads in EBV +ve cases in whole blood and plasma were 4.010 IU/ml (IQR 3.465–4.530) and 3.950 IU/ml (IQR 3.175–4.40), respectively. In EBV tumour −ve cases, median log viral loads in whole blood and plasma were both 0 IU/ml with an IQR of $0-2.170$ and $0-0$, respectively. In patients with EBV +ve tumours, the EBV viral load values in paired whole blood and plasma samples were similar, difering by an average of 0.32 log IU/ml, with levels marginally higher in whole blood (supplementary Fig. 1).

Table [3](#page-4-1) stratifes plasma EBV DNA viral loads in newly diagnosed HL according to EBV tumour status.

 $31/33$ (94%) EBV tumour + ve cases had detectable plasma EBV DNA. Two EBV tumour + ve cases tested plasma EBV −ve. The viral loads were repeated to confrm the fndings in both cases. The frst patient was a PLWH and advanced stage HL with bone marrow infltration. The second patient was HIV −ve and had early-stage disease (stage II). Six EBV tumour −ve patients had detectable plasma EBV DNA. Using ROC curve analysis, a cutoff value of >762 IU/ml EBV DNA plasma viral load had a sensitivity of 89.29% (CI 72.80–96.29) and specifcity of 96.77% (CI 83.81–99.83) for detecting EBV +ve HL.

Discussion

We found that the EBV plasma viral load was a valuable prognostic test with values ≥ 10000 IU/ml associated with poorer survival $(P=0.008)$. HIV +ve status significantly correlated with poorer OS ($P = 0.009$) in univariate analysis and was associated with a 3.2-fold increased risk of death in multivariate analysis ($P = 0.056$). EBV tumour +ve HL patients had significantly poorer OS $(P=0.014)$ than EBV tumour −ve patients, which aligns with the fndings of a large recent meta-analysis [[29\]](#page-6-10). Our fndings are noted to confict with a recent local study which reported better survival in EBV tumour +ve HL, possibly due to less EBV +ve HIV −ve HL cases in their cohort [[7](#page-5-5)]. We found age ≥45 years was associated with a 4.2-fold increased risk of death $(P=0.022)$ and high plasma EBV DNA viral loads \geq 10 000 IU/ml with a 3.4-fold increased risk of death $(P=0.051)$. Our findings contrast with previous publications reporting no prognostic value for EBV DNA viral load testing in HIV-associated HL [\[21,](#page-6-5) [22\]](#page-6-11) and support reports that high pretreatment levels of plasma EBV DNA are associated with inferior outcomes [[11,](#page-5-9) [30](#page-6-12)].

Almost a third of this study cohort were PLWH, and 95% of them were EBV tumour +ve. Half our total cohort, 49%, were EBV tumour +ve, confrming the potential utility of an EBV biomarker for HL in our HIV-endemic setting. In view of limited resources in sub-Saharan Africa including pathologists and advanced imaging such as PET-CT scanning, this novel biomarker should be considered to assist with diagnosis, prognostication and monitoring of EBV-associated lymphomas. Using ROC curve analysis, a cutoff value of >762 IU/ml plasma EBV DNA provided high sensitivity (89.29%) and specificity (96.77%) for EBV tumour +ve status. Future research directions include confrming these fndings in larger patient cohorts and monitoring plasma EBV DNA viral load testing at treatment follow-up milestones and after completion of therapy to assess utility in our setting.

Most of our cohort, 79%, presented with advanced stage disease (Stage III and IV), irrespective of HIV status, which is known to negatively impact survival [\[31](#page-6-13)]. Unexpectedly,

we did not fnd stage of disease to statistically correlate with survival, likely due to the small number of patients in the early-stage disease group. Total survival probability of the whole cohort was at 91% (CI 81–96%) at 6 months and 81% (CI 68- 89%) at 24 months, which is poorer than in well-resourced settings where there is a lower burden of HIV-associated HL, and more patients present with earlystage disease [[32](#page-6-14)]. An important contributing factor to our patient's late presentation is likely diagnostic delay due to the overlapping clinical symptoms and signs of tuberculosis (TB) and lymphoma. South Africa is a TB-endemic area, and diagnostic biopsies are difficult to access; thus, patients often receive empiric therapy for TB before an alternative diagnosis is considered or a biopsy obtained [\[33](#page-6-15)]. Furthermore, the COVID pandemic negatively impacted survival in our cohort, with several documented COVID-related deaths.

Conclusion

This study assessed the prognostic role of pretreatment plasma EBV DNA viral loads, tumour EBV status and HIV status in HL patients in an HIV-endemic setting, where a high proportion of HL cases are EBV-associated. EBV tumour + ve status ($P = 0.014$), HIV + ve status ($P = 0.009$) and EBV DNA plasma levels \geq 10 000 IU/ml ($P = 0.008$) were all significantly associated with poorer OS. A cutoff value of >762 IU/ml EBV plasma DNA had high sensitivity and specifcity for detecting EBV tumour +ve HL. EBV plasma DNA testing is a useful biomarker with potential to assist with early diagnosis and prognosis in EBV-associated HL.

Supplementary Information The online version contains supplementary material available at<https://doi.org/10.1007/s10238-024-01524-8>.

Acknowledgements Patients and clinical staff at Clinical Haematology and Radiation Oncology, Groote Schuur Hospital. Cylene Seaton and Jihaan Isaacs for sample collection and distribution.

Author contributions JO wrote the main manuscript and performed data collection. KB and JB performed data collection and statistical analysis. DH performed EBV testing, data collection and statistical analysis. All authors reviewed the manuscript.

Funding Open access funding provided by University of Cape Town. National Health Laboratory Service, 9473, Fogarty International Centre of the National Institutes of Health, D43TW010345.

Data availability The raw data are available in redcap and excel spreadsheets and can be provided if requested.

Declarations

Conflict of interest The authors declare that they have no confict of interest.

Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit<http://creativecommons.org/licenses/by/4.0/>.

References

- 1. UNAIDS. Global HIV and AIDS statistics—fact sheet 2023 2 November 2023.
- 2. Yarchoan R, Uldrick TS. HIV-associated cancers and related diseases. N Engl J Med. 2018;378(22):2145.
- 3. Phillips L, Opie J. The utility of bone marrow sampling in the diagnosis and staging of lymphoma in South Africa. Int J Lab Hematol. 2018;40(3):276–83.
- 4. Wiggill T, Mayne E, Perner Y, Vaughan J. Changing patterns of lymphoma in the antiretroviral therapy era in Johannesburg, South Africa. J Acquir Immune Defc Syndr. 2021;88(3):252–60.
- 5. Swart L, Novitzky N, Mohamed Z, Opie J. Hodgkin lymphoma at Groote Schuur Hospital, South Africa: the efect of HIV and bone marrow infltration. Ann Hematol. 2019;98(2):381–9.
- 6. Moahi K, Ralefala T, Nkele I, Triedman S, Sohani A, Musimar Z, et al. HIV and Hodgkin lymphoma survival: a prospective study in Botswana. JCO Glob Oncol. 2022;8:e2100163.
- 7. Antel K, Chetty D, Oosthuizen J, Mohamed Z, Van der Vyver L, Verburgh E. CD68-positive tumour associated macrophages, PD-L1 expression, and EBV latent infection in a high HIV-prevalent South African cohort of Hodgkin lymphoma patients. Pathology. 2021;53(5):628–34.
- 8. Carbone A, Volpi CC, Gualeni AV, Gloghini A. Epstein-Barr virus associated lymphomas in people with HIV. Curr Opin HIV AIDS. 2017;12(1):39–46.
- 9. Thorley-Lawson DA, Gross A. Persistence of the Epstein-Barr virus and the origins of associated lymphomas. N Engl J Med. 2004;350(13):1328–37.
- 10. Swerdlow SH CE, Harris NL, Jafe ES, Pileri SA, Stein H, Thiele J. WHO classifcation of tumours of haematopoietic and lymphoid tissues: international agency of research on cancer. 2017.
- 11. Kanakry JA, Li H, Gellert LL, Lemas MV, Hsieh WS, Hong F, et al. Plasma Epstein-Barr virus DNA predicts outcome in advanced Hodgkin lymphoma: correlative analysis from a large North American cooperative group trial. Blood. 2013;121(18):3547–53.
- 12. Welch JJG, Schwartz CL, Higman M, Chen L, Buxton A, Kanakry JA, et al. Epstein-Barr virus DNA in serum as an early prognostic marker in children and adolescents with Hodgkin lymphoma. Blood Adv. 2017;1(11):681–4.
- 13. Kanakry JA, Hegde AM, Durand CM, Massie AB, Greer AE, Ambinder RF, et al. The clinical signifcance of EBV DNA in the plasma and peripheral blood mononuclear cells of patients with or without EBV diseases. Blood. 2016;127(16):2007–17.
- 14. Liang WS, Vergilio JA, Salhia B, Huang HJ, Oki Y, Garrido-Laguna I, et al. Comprehensive genomic profling of Hodgkin

lymphoma reveals recurrently mutated genes and increased mutation burden. Oncologist. 2019;24(2):219–28.

- 15. Kimura H, Kwong YL. EBV viral loads in diagnosis, monitoring, and response assessment. Front Oncol. 2019;9:62.
- 16. Smatti MK, Yassine HM, AbuOdeh R, AlMarawani A, Taleb SA, Althani AA, et al. Prevalence and molecular profling of Epstein Barr virus (EBV) among healthy blood donors from diferent nationalities in Qatar. PLoS ONE. 2017;12(12):e0189033.
- 17. Stevens SJ, Blank BS, Smits PH, Meenhorst PL, Middeldorp JM. High Epstein-Barr virus (EBV) DNA loads in HIV-infected patients: correlation with antiretroviral therapy and quantitative EBV serology. AIDS. 2002;16(7):993–1001.
- 18. Alberti A, Stocker G, Lordick F, Hacker UT, Kobitzsch B, Haffner I, et al. Plasma EBV DNA as a prognostic factor in EBV associated gastric cancer: a multicenter, prospective study (EBV PRESAGE study). Front Oncol. 2023;13:1276138.
- 19. Chen J, Zhou J, Cheng F, Chen D, Guan F, Zhang E, et al. Role of plasma EBV-DNA load and EBER status on newly diagnosed peripheral T-cell lymphoma. J Cancer Res Clin Oncol. 2024;150(4):181.
- 20. Meyer RM. EBV DNA: a Hodgkin lymphoma biomarker? Blood. 2013;121(18):3541–2.
- 21. Ul-Haq I, Dalla Pria A, Suardi E, Pinato DJ, Froeling F, Forni J, et al. Blood Epstein-Barr virus DNA does not predict outcome in advanced HIV-associated Hodgkin lymphoma. Med Oncol. 2018;35(4):53.
- 22. Lupo J, Germi R, Lancar R, Algarte-Genin M, Hendel-Chavez H, Taoufk Y, et al. Epstein-Barr virus biomarkers have no prognostic value in HIV-related Hodgkin lymphoma in the modern combined antiretroviral therapy era. AIDS. 2019;33(6):993–1000.
- 23. Yu S, Yang Q, Wu J, Zhu M, Ai J, Zhang H, et al. Clinical application of Epstein-Barr virus DNA loads in Epstein-Barr virusassociated diseases: a cohort study. J Infect. 2021;82(1):105–11.
- 24. Shen Z, Hu L, Yao M, He C, Liu Q, Wang F, et al. Disparity analysis and prognostic value of pretreatment whole blood Epstein-Barr virus DNA load and Epstein-Barr encoding region status in lymphomas: a retrospective multicenter study in Huaihai lymphoma working group. Int J Cancer. 2022;150(2):327–34.
- 25. Tomoka T, Montgomery ND, Powers E, Dhungel BM, Morgan EA, Mulenga M, et al. Lymphoma and pathology in Sub-Saharan Africa: current approaches and future directions. Clin Lab Med. 2018;38(1):91–100.
- 26. Fryer JF, Heath AB, Wilkinson DE, Minor PD. A collaborative study to establish the 1st WHO international standard for Epstein-Barr virus for nucleic acid amplifcation techniques. Biologicals. 2016;44(5):423–33.
- 27. Zaucha JM, Chauvie S, Zaucha R, Biggii A, Gallamini A. The role of PET/CT in the modern treatment of Hodgkin lymphoma. Cancer Treat Rev. 2019;77:44–56.
- 28. Cheson BD, Fisher RI, Barrington SF, Cavalli F, Schwartz LH, Zucca E, et al. Recommendations for initial evaluation, staging, and response assessment of Hodgkin and non-Hodgkin lymphoma: the Lugano classifcation. J Clin Oncol. 2014;32(27):3059–68.
- 29. Hu J, Zhang X, Tao H, Jia Y. The prognostic value of Epstein-Barr virus infection in Hodgkin lymphoma: a systematic review and meta-analysis. Front Oncol. 2022;12:1034398.
- 30. Qin JQ, Yin H, Wu JZ, Chen RZ, Xia Y, Wang L, et al. Pretreatment whole blood Epstein-Barr virus DNA predicts prognosis in Hodgkin lymphoma. Leuk Res. 2021;107:106607.
- 31. Brice P, de Kerviler E, Friedberg JW. Classical Hodgkin lymphoma. Lancet. 2021;398(10310):1518–27.
- 32. Driessen J, Visser O, Zijlstra JM, Lugtenburg PJ, Plattel WJ, Kersten MJ, et al. Primary therapy and relative survival in classical Hodgkin lymphoma: a nationwide population-based study in the Netherlands, 1989–2017. Leukemia. 2021;35(2):494–505.
- 33. Antel K, Oosthuizen J, Brown K, Malherbe F, Loebenberg P, Seaton C, et al. Focused investigations to expedite cancer diagnosis among patients with lymphadenopathy in a tuberculosis and HIVendemic region. AIDS. 2023;37(4):587–94.

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.