Prognostic implications of circulating Epstein–Barr virus DNA for extranodal natural killer/T-cell lymphoma, nasal type: a meta-analysis

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Introduction: To evaluate the prognostic value of circulating Epstein-Barr virus DNA for extranodal natural killer/T-Cell lymphoma, nasal type (ENKTL), we performed a meta-analysis of published studies that provided survival information with pre-/post-treatment circulating EBV DNA.

Methods: Eligible studies that discussed prognostic significance of circulating EBV DNA in ENKTL were included. Random effects models were applied to obtain the estimated hazard ratios and 95% confidence intervals to evaluate prognostic significance (OS and DFS/PFS). Eleven studies covering a total of 562 subjects were included in this analysis.

Results: The summary HRs and 95% CIs of pre-treatment EBV DNA for OS and PFS/DFS were 4.43 (95% CI 2.66–7.39, \( P = 0.0001 \)) and 3.12 (95% CI 1.42–6.85, \( P = 0.005 \)), respectively. The corresponding HRs and 95% CIs of post-treatment EBV DNA for OS and PFS/DFS were 6.28 (95% CI 2.75–14.35, \( P = 0.0001 \)) and 6.57 (95% CI 2.14–20.16, \( P = 0.001 \)). Subgroup analyses indicated a strong trend of prognostic powers with pre-/post-treatment EBV DNA.

Conclusion: With the present evidence, circulating EBV DNA consistently correlated with poorer prognosis in patients with ENKTL which need further investigation in large-scale clinical studies.

Keywords: circulating EBV DNA, ENKTL, prognosis

Introduction

Extranodal natural killer (NK)/T-cell lymphoma, nasal type (ENKTL-NT) is an aggressive malignancy of putative NK-cell origin, with a minority deriving from the T-cell lineage, which presents peculiar clinicopathological features, including angioinvasion, prominent necrosis, and close association with Epstein–Barr virus (EBV).1,2 It occurs most commonly (80%) in the nose and upper aerodigestive tract, and less commonly (20%) in the non-nasal areas (skin, gastrointestinal tract, testis, salivary gland). It generally pursues an aggressive clinical course and has a poor outcome.3 Despite recent application of PET/CT in diagnosis,4 concurrent chemoradiotherapy in early-stage patients,5–7 and newly developed chemotherapy regimen containing L-asparaginase,8,9 it still presents a poor prognosis without an established standard therapy.

Previous studies have identified several prognostic clinicopathological features of ENKTL, including age, primary sites, Ann Arbor stage,10 International prognostic index,11 and Korea-developed NK/T-cell prognostic index.12 However, varying outcomes have been observed in patients with similar prognostic features and undergoing similar therapies, suggesting inherent heterogeneity of tumor and insufficiency of existing prognostication.13 Although several biomarkers have been reported as a prognostic

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surrogate, prognostic prediction in ENKTL is still dismal. Therefore, it is of great clinical value to identify novel biomarkers, which could be utilized as effective prognostic predictors or possible therapeutic targets, in order to optimize the treatment of patients with ENKTL.

EBV is a human herpes virus that has been confirmed to be in close association with several lymphoid and epithelial malignancies.\textsuperscript{14,15} It has been reported that inappropriate expression of EBV latent genes combined with environment and genetic cofactors may result in virus-associated malignancies.\textsuperscript{16} In EBV-associated nasopharyngeal carcinoma (NPC), the putative tumorigenic role has been thoroughly studied and revealed in large-scale studies that circulating EBV DNA is correlated with tumor load and disease prognosis.\textsuperscript{17–19} Circulating EBV DNA has been detected in plasma or serum in lymphomas, including ENKTL, Hodgkin’s disease, AIDS-related lymphoma, and diffuse large B-cell lymphoma.

Due to the rarity of ENKTL, there is only several small series of studies that reported the prognostic effect of circulating EBV DNA, with various clinical stages, primary locations and treatment regimens.

Hence, we conducted the present meta-analysis to comprehensively explore the potential prognostic impact of circulating EBV DNA in ENKTL.

Materials and methods

Search strategy
We searched systematically PubMed, Embase, the Science Citation Index, Cochrane databases, and the Ovid Database for studies discussed prognostic significance of circulating EBV DNA in ENKTL, with no restrictions on language, place of publication, or date of publication (up to June 2017). The main search terms explored were “Epstein-Barr virus”, “EBV”, “EBV load”, “Natural killer/T-cell lymphoma”, “NK/T-cell lymphoma”, and “ENKTL”.

Eligibility criteria
To yield potential relevant publications, we screened the titles and abstracts and author information. Full texts were considered for detailed assessment according to the following inclusion criteria: 1) containing patient cases of ENKTL, 2) measuring the titer of circulating EBV DNA in either plasma or whole blood, and 3) investigating the prognostic significance of EBV DNA titers in ENKTL patients with at least one of the outcome measures of interest. Studies excluded from our study were those that: 1) were duplicated publications, and 2) showed no survival data or insufficient data to be extracted.

Data extraction
Two investigators (CW and YZ) independently evaluated each paper and extracted data, and any discrepancy between the 2 researchers was resolved via discussion, with a third investigator if necessary. The following information was extracted: first author, publication year, type of studies, population characteristics (i.e., country, number of patients), clinicopathological characteristics (i.e., anatomical sites, tumor stage), sampling time (pre-treatment, intra-treatment, or post-treatment), detection methods (reverse transcription-polymerase chain reaction [RT-PCR]), EBV DNA positive rate, median EBV DNA copies, end points, and survival data. For 1 study using 2 different primer sets for LMP1 and Bam HI W fragment by RT-PCR, each of the cohorts was considered an independent data set.

Statistical approaches
Statistical analysis was performed using Review Manager 5.2 (Copenhagen: The Nordic Cochrane Centre; The Cochrane Collaboration, 2012).\textsuperscript{22} The estimated hazard ratio (HR) and associated 95% CI were used to evaluate prognostic significance (overall survival [OS] and disease-free survival/progression-free survival [DFS/PFS]). If the HR and its variance were not reported directly in the original study, these values were calculated based on survival data or survival curves using software designed by Tierney.\textsuperscript{20} The random-effects model was explored to perform the analyses, because this model obtained more conservative results than the fixed-effect model.\textsuperscript{21} Heterogeneity among the studies was tested using the $\chi^2$ test and $I^2$ statistic. A value of $I^2<$25%, within 25%–50%, or $>50%$ was regarded as low, moderate, or significant heterogeneity, respectively. We then evaluated the potential publication bias with funnel plots. The quality of the included studies was assessed with the Newcastle–Ottawa scale (NOS) for cohort studies.\textsuperscript{22}

Results

Baseline characteristics
The comprehensive literature search was performed till June 2017, yielding a total of 406 studies. Among these studies, 356 publications were identified as non-English publications, duplicates, or laboratory researches. The remaining 50 studies were thoroughly reviewed, of which 11 studies were appropriate for the meta-analysis (Figure 1).

Eleven studies (sample size from 15 to 120) with 562 patients, basically located in East Asia, were published between 2002 and 2016.\textsuperscript{21–33} All the included publications provided data on the correlation between circulating EBV
DNA and prognosis in patients with ENKTL. There were 4 studies designed prospectively and the remaining retrospectively. The most employed detection methods were RT-PCR, with 1 study from Japan using 2 different primer sets for LMP1 and Bam HI W fragment, which was considered as 2 independent data sets. For the sample types of included studies, 5 studies used EBV DNA detection in plasma, 1 study used serum, 3 studies from whole blood, 1 study from plasma/MNC, and 1 study from plasma/whole blood. Positive rates of detected EBV DNA irrespective of methods and time points varied from 4.20% to 100% in extracted studies. The characteristics of the included studies are summarized in Table 1. The quality of the included studies was evaluated with NOS and summarized in Table 2.

Correlation between EBV DNA and survival outcome

Pre-treatment EBV DNA and OS

A total of 10 cohorts evaluated the relationship between pre-treatment EBV DNA and OS, with 7 cohorts giving the HRs and 95% CIs for OS directly; the HRs in the remaining studies were extracted using the survival curves with $P$-values. The $\chi^2$ test showed low heterogeneity among the studies ($P=0.34; I^2=11\%$). The combined pooled HR of the aforementioned studies by a random-effects model was 4.43 (95% CI: 2.66–7.39, $P<0.00001$), indicating that high EBV DNA load was significantly associated with a poor OS in patients with ENKTL (Figure 2A).

Post-treatment EBV DNA and OS

A total of 6 cohorts evaluated the relationship between post-treatment EBV DNA. The $\chi^2$ test showed high heterogeneity among the studies ($P=0.04; I^2=57\%$). The combined pooled HR of the aforementioned studies by a random-effects model was 6.28 (95% CI: 2.75–14.35, $P<0.0001$), indicating that high post-treatment EBV DNA load was significantly associated with a poor OS in patients with ENKTL (Figure 3A).

Subgroup analysis

To clarify the intra-study inconsistencies, we further evaluated the relationship between pre-/post-treatment EBV DNA and OS in the following subgroup analysis (Table 3).
Table 1 Baseline characteristics of the enrolled studies

<table>
<thead>
<tr>
<th>References</th>
<th>Country</th>
<th>No of patients</th>
<th>Type of study</th>
<th>Clinical stage</th>
<th>Primary site</th>
<th>Detection of EBV DNA</th>
<th>Outcomes</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Time</td>
<td>Sample type</td>
</tr>
<tr>
<td>Lei et al 200323</td>
<td>HK</td>
<td>15</td>
<td>Retrospective</td>
<td>I–IV/recurrent</td>
<td>All sites</td>
<td>Pre/intra Plasma</td>
<td>25 (96.2%)</td>
</tr>
<tr>
<td>Ishii et al 200724</td>
<td>Japan</td>
<td>20</td>
<td>Retrospective</td>
<td>I–IV</td>
<td>UNKTL</td>
<td>Pre/intra/post Serum</td>
<td>20/19 (100%/95%)</td>
</tr>
<tr>
<td>Suzuki et al 201125</td>
<td>Japan</td>
<td>32</td>
<td>Prospective</td>
<td>I–IV</td>
<td>All sites</td>
<td>Pre/intra/post Plasma/MNC</td>
<td>14 (43.75%)/6 (18.75%)</td>
</tr>
<tr>
<td>Wang et al 201226</td>
<td>China</td>
<td>69</td>
<td>Retrospective</td>
<td>I–II</td>
<td>UNKTL</td>
<td>Pre/post Plasma</td>
<td>58 (84.1%)/27 (85%)</td>
</tr>
<tr>
<td>Ito et al 201227</td>
<td>Japan 26</td>
<td>Prospective</td>
<td>I–IV/recurrent</td>
<td>ENKTL</td>
<td>Pre/post Plasma/whole blood</td>
<td>15 (5%)/22 (85%)</td>
<td>500</td>
</tr>
<tr>
<td>Kwong et al 201428</td>
<td>HK 56</td>
<td>Retrospective</td>
<td>I–IV</td>
<td>All sites</td>
<td>Plasma</td>
<td>Pre/intra/post Plasma</td>
<td>41 (73.2%)/9 (1.9×10^9)</td>
</tr>
<tr>
<td>Kim et al 201529</td>
<td>Korea</td>
<td>27</td>
<td>Prospective</td>
<td>IV</td>
<td>ENKTL</td>
<td>Pre Whole blood</td>
<td>17 (63%)/15 (22.1%)</td>
</tr>
<tr>
<td>Wang et al 201530</td>
<td>China</td>
<td>68</td>
<td>Prospective</td>
<td>I, II</td>
<td>All sites</td>
<td>Pre/post Plasma</td>
<td>43 (63.2%)/15 (22.1%)</td>
</tr>
<tr>
<td>Kim et al 201531</td>
<td>Korea 102</td>
<td>Retrospective</td>
<td>I–IV</td>
<td>ENKTL</td>
<td>Pre/post Whole blood</td>
<td>48 (47%)/30 (29.4%)</td>
<td>60 (19.3–165.5)</td>
</tr>
<tr>
<td>Liang et al 201632</td>
<td>China</td>
<td>120</td>
<td>Retrospective</td>
<td>I–IV</td>
<td>ENKTL</td>
<td>Pre Whole blood</td>
<td>5 (4.2%)/12 (44.4%)</td>
</tr>
<tr>
<td>Lim et al 201633</td>
<td>Korea 27</td>
<td>Retrospective</td>
<td>I–IV</td>
<td>ENKTL</td>
<td>Pre Whole blood</td>
<td>5 (4.2%)/12 (44.4%)</td>
<td>NR</td>
</tr>
</tbody>
</table>

Abbreviations: DFS, disease-free survival; EBV, Epstein–Barr virus; ENKTL, extranodal NK/T-cell lymphoma; HK, Hongkong; Intra, Intra-treatment; MNC, mononuclear cells; No, number; NR, not reported; OS, overall survival; PFS, progression-free survival; post, post-treatment; pre, pre-treatment; UNKTL, upper aerodigestive tract NK/T cell lymphoma.
Type of samples: plasma/serum and whole blood/mononuclear cell (MNC)

Pre-treatment EBV DNA is significantly correlated with OS in both plasma/serum and whole blood/MNC subgroups. The HR and 95% CI for OS in plasma/serum and whole blood/MNC subgroups were 5.30 (95% CI: 3.01–9.33, P<0.00001) and 5.30 (95% CI: 1.68–16.75, P=0.005), respectively. The same relationship was found between post-treatment EBV DNA and OS in subgroup analysis.

Tumor sites: upper aerodigestive tract NK/T-cell lymphoma (UNKTL) and others

When considering primary tumor sites, we further evaluated combined HR and 95% CI for OS in separated subgroups.
In UNKTL subgroup, the HR and 95% CI for OS was 7.24 (95% CI: 1.24–42.10, P=0.03). Meanwhile, in the subgroup in which the primary tumor was not limited to UNKTL, the HR and 95% CI for OS was 4.15 (95% CI: 2.40–7.17, P=0.0001).

In included studies evaluating the relationship between post-treatment EBV DNA and OS, the HR and 95% CI for OS was 4.68 (95% CI: 1.66–13.19, P=0.003) in ENKTL subgroup, and 7.29 (95% CI: 2.13–24.91, P=0.002) in the subgroup in which the primary tumor was not limited to ENKTL.

**Type of study: prospective and retrospective**

Prospective and retrospective cohorts were both enrolled in this meta-analysis. In further subgroup analysis, the relationship between EBV DNA and OS remains statistically significant in either prospective or retrospective subgroups.

The HR and 95% CI for OS in prospective and retrospective subgroups were 7.53 (95% CI: 3.60–15.78, P<0.00001) and 3.05 (95% CI: 1.52–6.11, P=0.002), respectively. Similar result was found between post-treatment EBV DNA and OS in subgroup analysis.

**Sample sizes: N>30 and N<30**

In subgroup with large patient number, the HR and 95% CI for OS was 4.81 (95% CI: 2.15–10.79, P=0.0001). Meanwhile, in the subgroup with patient number <30, the HR and 95% CI for OS was 4.43 (95% CI: 1.96–10.06, P=0.0004). When considering the relationship between post-treatment EBV DNA and OS in this subgroup.
EBV DNA and OS, the HR and 95% CI for OS was 7.75 (95% CI: 2.54–23.61, \( P=0.0003 \)) in subgroup with large patient number and 3.92 (95% CI: 1.20–12.86, \( P=0.02 \)) in subgroup with patient number <30.

**Sensitivity analysis and publication bias**
There was no obvious publication bias seen in this meta-analysis (Figure 4A and B)

**Discussion**
The standard of care for patients with ENKTL remains controversial. Concurrent chemoradiotherapy, chemotherapy regimen containing L-asparaginase, and stem cell transplantation\(^1^4\) have been proposed for patients with ENKTL. However, these high-dose, aggressive therapy strategies do not always translate into survival benefits, with the cumulative probability of 5-year survival ranging from 10% to 55%.\(^{35–37}\) The optimal treatment strategies and prognostic prediction have not been completely defined yet.

To our knowledge, this is the first meta-analysis to assess the prognostic value of circulating EBV DNA load in patients with ENKTL. Previous small-scale (\( N<60 \)) studies have showed that high load of circulating EBV DNA is associated with a poorer survival in ENKTL patients. Hence, a quantitative meta-analysis is urgently required for individualized cancer treatment. Our meta-analysis, which

![Funnel plots of the enrolled studies.](image)

**Notes:** (A) OS in pre-treatment group. (B) OS in post-treatment group.
**Abbreviation:** OS, overall survival.
involved a relatively large series of patients, provided robust evidence that circulating EBV DNA load in peripheral blood is significantly associated with poor OS and PFS/DFS in patients with ENKTL.

As a well-known EBV-associated malignancy, the invariably association with episomal infection of EBV in ENKTL cells has strongly implied its tumorigenic role. Fragmented viral DNA has also been found in peripheral blood from EBV-associated malignancies, which was mostly <500 bp in length. It is reasonable to speculate that measurement of the circulating EBV DNA level may be used as a marker for diagnosis, monitoring treatment response, and prognostication of these EBV-associated malignancies. Previous reports had shown that EBV DNA load has predictive and prognostic significance for EBV-associated malignancies, including NPC and Hodgkin’s disease. The diagnostic and prognostic impact has also been evaluated in patients with ENKTL in relatively small-scale studies, suggesting a favorable prognosis with low EBV DNA level. Due to the rarity of the disease, the scales of these cohorts remained relatively small with heterogeneous primary locations, clinical stages, sampling time, and treatment regimens. The present meta-analyses provide stronger evidence that the quantification of EBV DNA level is effective in prognostication in patients with ENKTL.

Besides the potential prognostic impact, other clinical applications of circulating EBV DNA in ENKTL have been evaluated in previous small cohorts of publications, including its diagnostic significance, relationship with clinicopathological features, and predication of therapy response. Due to the limited data, we did not discuss the aforementioned clinical applications in the present meta-analysis. Large-scale investigation is needed to confirm these potential correlations, which may hypothetically help for patient stratification and personalized therapy.

Circulating EBV DNA can be detected from peripheral plasma, serum, whole blood, or peripheral blood mononuclear cells (PBMCs). There is still controversy regarding selection of the most suitable blood compartment for the detection of EBV DNA. Previous studies suggested that whole blood compartments and PBMCs demonstrated a higher sensitivity in diagnosis and prognosis than plasma. However, the exact patient number, which might include rare pediatric cases. Therefore, the current meta-analysis included rare pediatric cases that were not enough for further analysis. Considering the rarity of ENKTL worldwide, it is difficult to conduct large prospective studies. High-quality meta-analysis may provide more reliable evidence to guide treatment and predict prognosis. Third, the cut-off value of EBV DNA in our enrolled publications varies from 349.9 copies/mL to 6.1×10^7 copies/mL, implying that there was not a uniform cut-off value to define the high load of circulating EBV DNA in patients with ENKTL, which might lead to heterogeneity.

**Conclusion**

In summary, our meta-analysis provides convincing evidence supporting the proposition that circulating EBV
DNA consistently correlated with prognosis of patients with ENKTL, regardless of primary tumor locations, sampling times, or sample types. However, to confirm this conclusion as well as derived speculations, high-quality, well-designed, and large-scale clinical studies of ENKTL are urgently needed.

**Novelty and impact statements**

In this work, we have for the first time investigated the prognostic value of circulating EBV DNA for ENKTL by meta-analysis based on published data. Our meta-analysis provides convincing evidence supporting the proposition that circulating EBV DNA consistently correlated with prognosis of patients with ENKTL, regardless of primary tumor locations, sampling times, or sample types. To confirm this conclusion, high-quality, well-designed, and large-scale clinical studies of ENKTL are urgently needed.

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**Disclosure**

The authors report no conflicts of interest in this work.

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