

Association of Killer Cell Immunoglobulin-Like Receptors With Endemic Burkitt Lymphoma in Kenyan Children

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Abstract

Endemic Burkitt lymphoma (eBL) is an aggressive pediatric B cell lymphoma, common in Equatorial Africa. Co-infections with Epstein-Barr virus (EBV) and *Plasmodium falciparum*, coupled with *c-myc* translocation are involved in eBL etiology. Infection-induced immune evasion mechanisms to avoid T cell cytotoxicity may increase the role of Natural killer (NK) cells in anti-tumor immunosurveillance. Killer immunoglobulin-like receptor (KIR) genes on NK cells exhibit genotypic and allelic variations and are associated with susceptibility to diseases and malignancies. However, their role in eBL pathogenesis remains undefined. This retrospective study genotyped sixteen KIR genes and compared their frequencies in eBL patients (n=104) and healthy geographically-matched children (n=104) using sequence-specific primers polymerase chain reaction (SSP-PCR) technique. The relationship between KIR polymorphisms with EBV loads and eBL pathogenesis was investigated. Possession of ≥ 4 activating KIRs predisposed individuals to eBL (OR=3.340; 95% CI 1.530-7.825; $p=0.004$). High EBV levels were observed in Bx haplogroup ($p=0.016$) and AB genotypes ($p=0.049$) relative to AA haplogroup and AA genotype respectively, in eBL patients but not in healthy controls. Our results suggest that KIR-mediated NK cell stimulation could mute EBV control, contributing to eBL pathogenesis.

Introduction

Endemic Burkitt lymphoma (eBL) is the quintessential Epstein-Barr Virus (EBV)-associated B cell malignancy in pediatric patients within Africa and Papua New Guinea¹. In Africa, eBL has the highest incidence in areas where *Plasmodium falciparum* (*Pf*) malaria is common, hence repeated interaction of *Pf*-infected red blood cells with EBV-infected B cells is postulated to result in eBL oncogenesis¹⁻³. The proposed mechanism of eBL development involves a combination of activation-induced cytidine deaminase (AID)-associated *c-myc* chromosomal translocation, modulation of host T cell immunity to EBV antigens, monoclonal expansion of B cells infected with EBV, and reactivation of EBV, resulting in increased viremia⁴⁻⁸. Cells infected with EBV down-regulate the expression of human leukocyte antigen (HLA) to evade recognition by HLA-restricted cytotoxic CD8+ T cells⁹. However, this immune evasion mechanism, i.e. 'loss-of-self' should render them susceptible to killing by natural killer (NK) cells⁹. NK cells constitute the body's first line of defense against viral infections and tumor cells^{10,11}. They are identified by the expression of CD56, a neural cell adhesion molecule 1 (NCAM-1) belonging to the immunoglobulin supergene family. This molecule mediates cell to cell interactions and its surface expression levels vary with cell maturation¹². Consequently, there are two major NK cell populations: CD56^{bright} are mainly cytokine-producing¹³, while CD56^{dim} acquire additional CD16 and killer immunoglobulin-like receptors (KIRs) receptors, which enhance their cytolytic activities^{13,14}. Other studies have reported accumulation of CD56^{negative} CD16^{positive} NK cell subsets in eBL patients¹⁵, and in HIV-infected individuals¹⁶. NK cell anti-viral and anti-tumor activities are partly regulated by inhibitory and activating KIRs, which interacts with various human leukocyte antigen (HLA) class I ligands on target cells¹⁷. Tumor cells lacking ligands for inhibitory and activating KIRs, do not stimulate NK cells response¹⁸. Additionally, NK cells do not kill

healthy cells when only the inhibitory receptors are ligated to HLA-I ligands on the target cells, since there is no activating signal generated¹⁸.

Down-regulation of HLA-I in target cells by viral infections or neoplastic transformation results in a lack of ligation of inhibitory NK cell receptors to their ligands, hence the absence of NK cell inhibition. Instead, only the activating NK cell receptors are ligated to activating ligands, resulting in NK cell stimulation to kill target cells¹⁹. The outcome of the interaction of NK cells with tumor cells containing ligands for both inhibitory and activating receptors depends on the balance of the strength of signals generated¹⁸.

The KIR gene family comprise of rapidly evolving genes present in all primates^{20,21}. KIRs are coded by inhibitory genes (2DL1, 2DL2/2DL3, 2DL4, 2DL5, 3DL1, 3DL2, and 3DL3), activating genes (2DS1, 2DS2, 2DS4, 2DS3/2DS5, and 3DS1) and two pseudogenes (2DP1 and 3DP1)²² (Figure 1). These genes are arranged in a head-to-tail order in the long arm of chromosome 19 (19q13.4), within the Leukocyte Receptor Complex (LRC)²³. Each KIR gene is 10-16kb in length, with a 2kb sequence separating each gene pair, except a 14kb sequence that occurs upstream of KIR2DL4²². The expression of KIR genes varies between NK cell subsets and is controlled by four types of promoters²⁴. CD56^{dim} NK cells express all KIR genes except 3DL3²⁴. 2DL4 occur on both CD56^{bright} and ^{-dim} NK cells in a non-variegated manner^{24,25}, and can transmit both activating and inhibitory signals²⁶⁻²⁸. Some KIR genes demonstrate variations in their sequences, for example, KIR2DS4 has a 22 base pair (bp) deletion in the second extracellular domain which results in a non-functional gene^{22,29}. A deletion of one base-pair in exon 4 of KIR2DP1 introduces a stop codon, resulting in a pseudogene³⁰. Another pseudogene, KIR3DP1 has a deletion of 1.5 kb that removes exon 2. There are no transcripts for the 2 pseudogenes³⁰. KIR2DL5 has two variants A and B, encoded by different loci³¹. 2DL5B is in the centromeric region, while 2DL5A occurs in the telomeric region.

Polymorphisms within the KIR locus result from gene content, allelic, and copy number variations³². Based on gene content and copy number, KIRs are grouped into inhibitory haplotype A and activator haplotype B. The haplotypes are further subdivided into AA and Bx genotypes, where x can be A or B³³. There are more than 500 different Bx groups in the database (<http://www.allelefreqencies.net>)³⁴. KIR genotype AA is homozygous for the haplotype A and contains 3DL3, 2DL3, 2DP1, 2DL1, 3DP1, 2DL4, 3DL1, 2DS4, and 3DL2 genes²². Activator haplotype B comprise of 2DS2, 2DL2, 2DL5B, 2DL1, 2DP1, 3DP1, 3DL3, 2DL4, 3DS1, 2DL5A, 2DS3/2DS5, 2DS1, 2DS4, 2DS3/2DS5 and 3DL2 genes²². This haplotype has a Bx group containing one (AB heterozygous) or two (BB homozygous) genotypes. Genotype BB does not have one or more of the group A KIR genes. All the remaining genotypes in haplotype B are defined as AB³⁵. 3DL3, 3DL2, 2DL4, and 3DP1 are framework genes, hence they appear in all haplotypes^{30,36}. KIR haplotypes are split into centromeric A or B (cA, cB) and telomeric A or B (tA, tB) halves^{37,38}. Classification of KIR based on presence/absence of a gene generate eight telomeric regions (tA01, tB01, tB02, tB03, tB04, tB05, tB06 and tB07) and nine centromeric regions (cA01, cA02, cA03, cB01, cB02, cB03, cB04, cB05 and cB06)^{37,39}. KIR2DL5, 2DS5, and 2DS3 can occur in centromeric and telomeric

locations. The cB region is abundant in East Africa, relative to tB⁴⁰. The B content score is the sum of cenB and/or telB motifs in each genotype⁴¹. The Bx group can be classified further into four subsets, by considering two gene clusters; T4, containing KIR2DL5-3DS1-2DS1-2DS5 genes, and C4, which has KIR2DL2-2DS2-2DS3-2DL5 genes. The C4T4 contains both C4 and T4 genes, while the C4Tx subset has C4 but lack T4 genes. CxT4 lacks C4 genes, thus it contains T4 genes. The absence of both C4 and T4 genes results in CxTx subset^{35,36}. The Bx subsets have a variable number of activating KIRs³⁶.

Studies have suggested that specific KIRs influence the generation of either inhibitory versus activating signals. A balance between these signals determines whether NK cells bypass or kill viral-infected or tumor cells²⁸. Consequently, these signals can influence an individual's susceptibility to diseases and malignancies^{29,37,42-44}. The presence of certain KIRs has been associated with cancer pathogenesis. For instance, an increased number of activating KIRs predispose individuals to EBV-related nasopharyngeal carcinoma (NPC)⁴², whereas the presence of genotype B, which mainly contains activating KIRs is associated with gastric cancer lesions³⁷. In contrast, the presence of Bx provides protection against colorectal adenocarcinoma⁴⁵. However, there is little understanding of the impact of KIR polymorphisms on eBL pathogenesis. Therefore, to improve our understanding of how KIR genes may contribute to eBL pathology, we performed KIR genotyping using commercially available kits and analyzed the haplotype, genotypes, centromere-telomere regions, Bx subsets, and B score contents in eBL patients and healthy controls. Given the strong link between EBV and eBL^{6,46}, we further evaluated the association of haplogroups AA/Bx and genotypes AA, AB, and BB with EBV loads, to determine viral control.

Results

KIR genes. To characterize the frequencies of KIR genes in the study population, we genotyped the genes responsible for inhibitory signals (2DL1, 2DL2/2DL3, 2DL4, 2DL5, 3DL1, 3DL2, and 3DL3), activating signals (2DS1, 2DS2, 2DS4, 2DS3/2DS5, and 3DS1) and the two pseudogenes (2DP1 and 3DP1) from genomic DNA using sequence-specific primers polymerase chain reaction (SSP-PCR) technique. KIR genotypes were classified based on the presence or lack of each gene locus and were analyzed to determine differences in their frequencies between eBL patients and healthy controls (HC). The pseudogenes (KIR3DP1, KIR2DP1) and the inhibitory genes (KIR2DL1, KIR2DL4, KIR3DL2 and KIR3DL3) occurred at a frequency $\geq 99\%$ and were excluded from the association analysis. The KIR genes were not statistically different between the study groups hence were not associated with eBL (Table 1).

Table 1. Analysis of the association of KIR genes with endemic Burkitt lymphoma by multivariate logistic regression. Comparisons were made with healthy control as the reference group. $p \leq 0.05$ is considered statistically significant. $p \leq 0.05$ and the OR (95% CI) were adjusted by age and sex.

Genes	eBL n=104 (%)	HC n=104 (%)	Odds Ratio (95%Confidence Interval)	p-value
Inhibitory genes				
2DL2	64 (61.5)	54 (51.9)	1.246 (0.641-2.427)	0.516
2DL3	90 (86.5)	91 (87.5)	1.267 (0.447-3.737)	0.658
2DL5All	70 (67.3)	60 (57.7)	1.283 (0.654-2.532)	0.468
2DL5A	16 (15.4)	11 (10.6)	1.762 (0.699-4.540)	0.232
2DL5B	61 (58.7)	55 (52.9)	1.118 (0.580-2.154)	0.738
3DL1	102 (98.1)	102 (98.1)	0.303 (0.013-3.412)	0.345
Activating genes				
2DS1	27 (26.0)	18 (17.3)	1.383 (0.633-3.040)	0.416
2DS2	54 (51.9)	47 (45.2)	1.136 (0.589-2.190)	0.702
2DS3	20 (19.2)	21 (20.2)	0.840 (0.341-2.023)	0.699
3DS1	16 (15.4)	17 (16.3)	1.124 (0.472-2.657)	0.790
2DS5	58 (55.8)	44 (42.3)	1.394 (0.718-2.704)	0.324
2DS4ins	68 (65.4)	70 (67.3)	0.887 (0.444-1.773)	0.733
2DS4del	67 (64.4)	67 (64.4)	1.364 (0.689-2.748)	0.378

KIR haplotypes and genotypes. In the studied population, the haplotypes A and B occurred at frequencies of 56.7% vs. 60.6% and 43.3% vs 39.4% in eBL patients and HC respectively. The haplotypes were grouped into haplogroup AA (27.9% vs. 34.6%) and Bx (72.1% vs. 65.4%) for eBL patients and HC respectively (Table 2). There were 35 different haplogroups in the study population, based on the allele frequencies database (<http://www.allelefreqencies.net>)³⁴ (Figure 2). Out of these, 15 were identified in both cases and controls, fourteen had frequencies >1.0 %; representing 88.5 % of the population, while eighteen had frequencies >1.0 % representing 94.2 % of the healthy controls and eBL patients respectively. The remaining haplogroups (17 in eBL and 21 in HC) were rare, with frequencies ≤ 1.0 %. The haplogroups were subdivided further into genotypes AA, AB, or BB according to the gene content. Among 104 eBL patients, 29 were genotypes AA (27.9%), 60 were AB (57.7%) while 15 were BB (14.4%). All the AA genotypes had ID 1. Among 104 HC, 36 were genotypes AA (34.6%), 54 were AB (51.9%) while 14 were BB (13.5%). The distribution of the KIR genotypes among the study groups were not statistically significant (Table 2).

KIR centromeric and telomeric distribution. The KIR gene contents vary in the centromeric and telomeric regions. To investigate these differences in our study population, genotypes AA and Bx were grouped into

centromeric and telomeric contents³⁸. A total of 6 centromeric and 2 telomeric region genes were reported. There were no significant differences in the centromeric and telomeric genes when comparing eBL patients with the control group (Supplementary Table S1).

KIR B score. To evaluate the involvement of B motifs in eBL development, the AA and Bx genotypes were investigated according to the distribution of B content in the centromeric (cB) and telomeric (tB) regions. A score of zero was more common in healthy controls while a score of one was frequent in eBL patients (44.2% vs. 38.5 and 43.3 vs. 50.0% respectively) (Supplementary Table S2). The results obtained from this study demonstrate that B score is not associated with the risk of eBL

Bx Subsets and the number of activating KIRs: We observed that all the four Bx subsets (C4T4, CxT4, C4Tx, CxTx) were present in the study population (Table 2). C4T4 had the least frequency, with no representation among the healthy individuals. CxTx had the highest frequency in both eBL patients and healthy controls. Further, in order to investigate possible differences in the number of KIRs, we compared the iKIRs and aKIRs in cases and controls. There was an increased proportion of eBL patients with ≥ 4 aKIRs relative to HC.

Table 2. Comparison of haplotypes, genotypes, linkage groups, and the number of activating KIRs between endemic Burkitt lymphoma patients and healthy controls. $p \leq 0.05$ are considered statistically significant; based on the two-tailed Fisher's exact test. The haplotype A and B were obtained as follows; haplotype A = $2NAA+NAB/2n$ and haplotype B = $2NBB+NAB/2n$. The NAA, NAB, and NBB are the numbers of AA, AB, and BB genotypes, n = total number of individual^{36,47,48}.

Gene	eBL n=104	HC n=104	OR (95% CI)	p-value
	N(%F)	N(%F)		
Haplotype				
A	118(56.7)	126(60.6)	0.8533(0.487-1.487)	0.673
B	90(43.3)	82(39.4)		
KIR Haplogroup and Genotype Frequencies				
AA	29(27.9)	36 (34.6)	0.730 (0.400-1.308)	0.370
KIR Bx Subgroup (Linkage group) Frequencies				
Bx	75(72.1)	68 (65.4)		
AB	60(57.7)	54(51.9)	1.263(0.733-2.190)	0.486
BB	15(14.4)	14(13.5)	1.083(0.511-2.297)	1.000
KIR Bx Subgroup (Linkage group) Frequencies				
C4T4	4(3.8)	0	NA	NA
CxT4	10(9.6)	7(6.7)	1.474(0.554-3.818)	0.614
C4Tx	14(13.5)	17(16.3)	0.796(0.386-1.716)	0.698
CxTx	76(73.1)	80(76.9)	0.814(0.431-1.510)	0.631
C4 gene-cluster	18(17.3)	17(16.3)	1.071(0.533-2.178)	1.000
T4 gene-cluster	14(13.5)	7(6.7)	2.156(0.807-5.495)	0.166
Number of activating KIRs				
≥4	25(24.0)	9(8.7)	3.340(1.530-7.825)	0.004
<4	79(76.0)	95(91.3)		

KIR haplotypes, genotypes, and EBV Viral loads. We compared EBV viral loads and observed significantly higher viremia in children with eBL (median 6,496.571 EBV copies/μg of DNA) compared to healthy children from the malaria holoendemic region (median 202.697 EBV copies/μg of DNA) (p -value <0.0001). Next, we investigated whether the EBV loads differed between the haplotypes and genotypes. Considering the KIR haplotypes and genotypes, we observed significant differences in EBV load in eBL patients but not in healthy controls (Figure 3).

Discussion

KIR gene polymorphisms predispose individuals to various malignancies associated with viruses. However, few studies have evaluated the role of such polymorphisms in eBL etiology. To address this issue, we evaluated the association of KIR genes with eBL development. The most common KIR genotype in our study population was homozygous A, with the genotype id AA1. This genotype has previously been shown to be the most frequent in all worldwide populations, including Africans^{40,49}. Interestingly, while its frequency in healthy controls was consistent with the expected frequency in African populations (35.6%)⁴⁹, the representation was lower in eBL patients (27.9%). However, such variations have been reported in a few African populations, from 12.0% in the Xhosa population of South Africa, 28.1% in the Ugandan population, and 42.0% in Senegal^{40,50,51}. In our study, the Bx genotype was highly variable, with a frequency range of 0.0%-10.6%. This genotype consists of two haplotypes; AB and BB. Most of the study participants were heterozygous AB, and there was a very low frequency of homozygous BB. The considerable diversity for Bx but not AA genotypes may be a result of copy number variation³⁹ due to selection pressure from environmental, climatic, chronic, and infectious diseases that have prevailed in our study population for many years⁴⁴. In our study, there were more eBL patients carrying ≥ 4 aKIRs compared to healthy controls; therefore individuals with ≥ 4 aKIRs had a high risk of developing eBL. Consistent with our findings, an increased number of aKIRs predispose individuals to viral-associated cancers, including human papillomavirus-associated cervical cancer and EBV-associated nasopharyngeal carcinoma^{19,43}. The role of the number of aKIRs in the etiology of cancers is explained by two hypotheses⁴³. First, an increased number may protect individuals against cancers, due to enhanced cytotoxicity of tumor cells, resulting from increased NK cell activation³⁷. In contrast, increased immune activation of NK cells by aKIRs may cause non-specific inflammatory responses, such as oxidative DNA damage^{19,37}. Such responses may increase the risk of cancer development³⁷. Therefore, considering the second hypothesis in our study, an increasing number of aKIRs coupled with repeated infections with *Plasmodium falciparum* in our study population⁵² could be associated with increased NK cell activation resulting in inflammation-associated oncogenesis.

The study participants had a higher frequency of centromeric B region and a lower frequency of telomeric B region. Similar observations were reported in a Ugandan population⁴⁰. Generally, cenB region is common in the African population relative to telB region⁴⁰. The number of B motifs in the centromere and telomere regions influences NK cell activation³⁷. Subsequently, the B motif is associated with disease outcome³⁷. In this study, we evaluated how the number of KIR B gene motifs of centromeric or telomeric origin influences eBL development. We report here that the B score does not increase the risk of eBL.

Previous studies have reported that children living in malaria holoendemic areas experience primary EBV infection at an early age compared to children residing in areas with lower incidences of malaria^{8,53}. In addition, repeated exposure to malaria is associated with poor viral control, hence higher viremia^{4,7,54}. Consistent with these findings, we observed that eBL patients had higher median EBV loads relative to healthy controls (6,496.571 versus 202.697 EBV copies/ μ g of DNA), respectively, p -value <0.0001). The EBV levels were significantly different when considering the KIR haplogroup and genotypes in children

with eBL but not in healthy controls, with higher EBV loads observed in Bx relative to AA haplogroup. Considering the genotypes, EBV load differed between AA and AB. NK cells are essential in the control of infections associated with viruses⁵⁵. Their subsets expand upon infection with herpes viruses⁵⁶, and the proliferation positively correlates with EBV viral loads⁵⁶. Individuals deficient in NK cells are predisposed to herpes viruses-associated infections⁵⁷. The persistence of viruses in an individual may cause chronic recruitment and activation of NK cells, up to when in some individuals; the NK cell activation is deregulated. Therefore, increased viral load in Bx relative to AA haplogroup in eBL could be related to continuous stimulation and subsequent loss of NK cell control of EBV. A previous study reported the accumulation of dysfunctional CD56 negative CD16 positive subset of NK cells in eBL patients¹⁵. Consistent with these findings, our results raise the possibility that activation of NK cells that is mediated by KIRs may impair NK cell functions in our study population¹⁵. Further studies are required to confirm this observation.

A limitation of our study was the small sample size and convenience sampling of healthy controls which led to them being younger than eBL cases. However, since KIR genotypes do not change with age, we don't believe this biased our findings. In addition, our conclusion is restricted by a lack of HLA ligands data, as KIR/HLA combinations influence NK cell activity. As KIRs can vary at the gene or allele level, we only investigated the presence or absence of each KIR gene, and we could not evaluate allelic and copy number variations that can impact NK cell functions. A previous study reported decreased expression of KIR2DL1/S1 inhibitory/activation marker and increased expression of KIR3DL1 in children exposed to malaria and eBL patients relative to healthy children¹⁵, hence future studies will assess the mechanistic implications of KIRs protein and gene expression profiles in eBL pathogenesis. This study presents the first attempt to define the role of KIRs in eBL pathogenesis and demonstrates that the Bx haplogroup and increased number of aKIRs are associated with EBV load and eBL pathogenesis.

Materials And Methods

Ethical approval. This research was approved by the Scientific and Ethical Review Unit (SERU) at the Kenya Medical Research Institute (KEMRI), and the Institutional Review Board at the University of Massachusetts Medical School (UMMS), Worcester, USA. Study participants were informed about the study and since they were all below 18 years, the parent and/or legal guardian provided written informed consent, before enrollment. In addition, children aged 13 years and above provided assent as per the requirements of the local IRB.

Study site and subjects. The study enrolled 208 children; 104 eBL patients, and 104 healthy individuals. Patients with eBL were children aged 0-14 years old, who were enrolled at Jaramogi Oginga Odinga Teaching and Referral Hospital (JOOTRH), located in Kisumu County, western Kenya. JOOTRH is one of the two regional referral centers for childhood cancer cases in western Kenya. Morphologic diagnosis of eBL was performed by staining fine-needle aspirates (FNA) with Giemsa/May-Grunwald and observed under a microscope⁵⁸. The control group comprised of convenience samples selected from healthy non-

eBL children, aged 0-12 years old, living in the same malaria-holoendemic regions of western Kenya as the eBL patients. Convenience sampling did not affect our results since KIR genotypes do not differ by age.

DNA extraction and KIR genotyping. Genomic DNA was isolated from 200µl of blood using QIAGEN QIAamp® (Valencia, CA, USA), following the manufacturer's instructions, and frozen at -20 °C until genotyping. The samples were analyzed for KIR gene content⁵⁹. A commercially available KIR genotyping sequence-specific Primers (SSP) kit (Miltenyi, Biotec, Inc, Germany), was used to test for the presence or absence of KIRs generating inhibitory signals (KIR2DL1, 2DL2, 2DL3, 2DL4, 2DL5A, 2DL5B, 2DL5 (A and B) 3DL1, 3DL2, 3DL3), activating KIRs (2DS1, 2DS2, 2DS3, 2DS4del, 2DS4ins, 2DS5, and 3DS1) and the two pseudogenes (2DP1 and 3DP1) following the manufacturer's recommendations. The amplified sequences were examined by electrophoresis in 2% agarose gel stained with SYBR Safe (Invitrogen, Burlington, ON, Canada) and visualized on a UV transilluminator using a gel documentation system (ChemiDoc, BioRad) for the presence or lack of amplicons specific to each gene(See full-length gel in Supplementary Fig. 1 online).

Definitions for KIR gene content polymorphisms. KIR polymorphisms were analyzed by determining the presence or absence of 16 KIRs genes; 2 pseudogenes, 8 inhibitory, and 6 activating KIR genes. The KIR haplotypes were classified into AA (inhibitory) and Bx (activator), where x can be A or B. The homozygote AA genotype was defined by the absence of KIR2DL2, 2DL5 (2DL5A and B, 2DL5A, 2DL5B) 2DS1, 2DS2, 2DS3, 2DS5, and 3DS1 genes. Individuals in the Bx genotype contained at least one of the genes above³⁴. The genes 2DL4, 3DP1, 3DL2, and 3DL3 are framework genes³⁰. The genotypes AA and Bx were evaluated according to the distribution of the centromeric and telomeric genes and the B content score as previously reported³⁸.

EBV Load. Epstein-Barr virus load was determined by quantitative Polymerase Chain Reaction (qPCR)⁶⁰. Briefly, amplification of genomic DNA was done in a Bio-Rad CFX96 Real-Time System with C1000 Thermocycler base for the primers and probes. The PCR amplification conditions were: 180s at 95°C, 10s at 95°C, 30s at 63.5°C- plate read, 10s at 95°C (39 times).

Statistical Analysis. The frequencies of KIR genes, haplotypes, genotypes, B score, and centromere-telomere gene content in eBL patients were compared with the healthy controls. Differences between KIR genes and EBV loads were assessed by Fisher's exact test using Graphpad Prism version 8.0.2 software (GraphPad Software, La Jolla, CA). Comparisons of log-transformed EBV load between the genotypes were performed using the Mann-Whitney test and one way Kruskal-Wallis statistic. When the *p*-value in the Kruskal-Wallis test was statistically significant, pair-wise comparisons were assessed by Dunn's test. Multivariable logistic regression analyses were performed in R, controlling for age and sex as variables influencing the risk of eBL etiology. The statistical significance of associations was assessed using odds ratios (OR) with 95% confidence intervals (CI). A $p \leq 0.05$ was considered significant.

Data Availability. The datasets evaluated in this study are available in supplementary data online).

Declarations

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Authors Contribution

BMM conceived, participated in the design, performed KIR genotyping, performed statistical analyses, prepared and edited the manuscript. JMO, AMM, JAB, and AG conceived, designed and coordinated assay performance, prepared, and edited the manuscript. CSF and POO edited the manuscript and participated in statistical analysis.

Competing Interests

The authors declare no competing interests.

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Figures

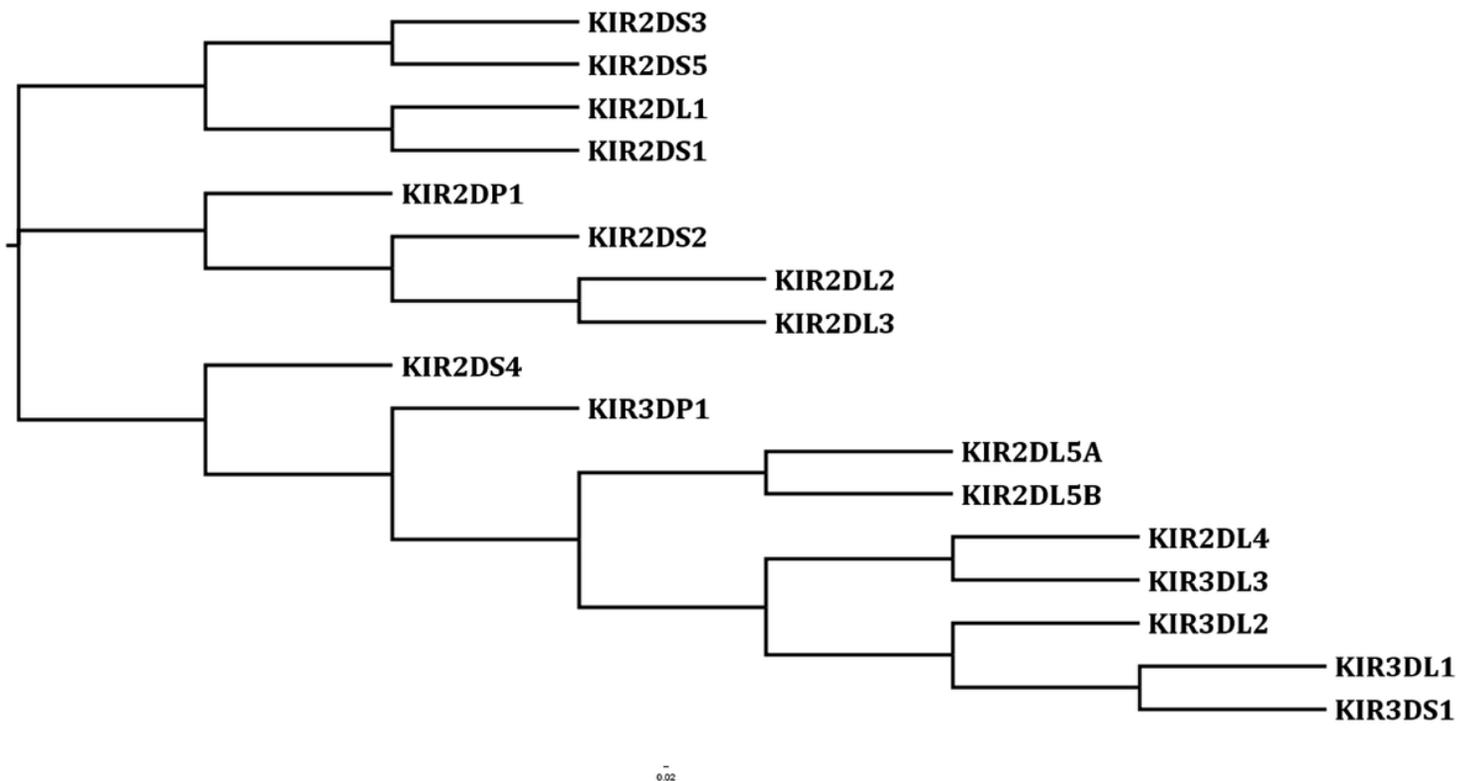


Figure 1

Phylogenetic relationship of human killer immunoglobulin-like receptor gene showing three clades. The Neighbor-Joining (NJ) tree was generated using publicly available KIR DNA sequences in Clustal Omega (EMBL-EBI) with default settings.

ID	Haplotype	Genotype	Bx Subset	Activating genes						Inhibitory genes					Framework/Pseudogenes					%BL	%HC		
				2DS1	2DS2	2DS3	2DS4	2DS5	3DS1	2D11	2D12	2D13	2D15	3D11	2D14	3D12	3D13	2D11	3D11				
1	AA	AA	CxTx																		27.9	34.6	
6	Bx	AB	C4T4																			1.9	0.0
3	Bx	AB	CxT4																			3.8	1.0
22	Bx	AB	C4Tx																			1.0	0.0
9	Bx	AB	CxTx																			7.7	5.8
2	Bx	AB	CxT4																			4.8	4.8
24	Bx	AB	CxTx																			0.0	1.0
271	Bx	AB	CxTx																			0.0	1.0
21	Bx	AB	CxTx																			10.6	8.7
5	Bx	AB	C4Tx																			7.7	10.6
35	Bx	AB	CxTx																			1.0	1.0
680	Bx	AB	CxTx																			1.0	1.0
17	Bx	AB	CxTx																			0.0	1.9
27	Bx	AB	CxTx																			0.0	1.9
267	Bx	AB	CxTx																			0.0	1.0
587	Bx	AB	CxTx																			0.0	1.0
20	Bx	AB	CxTx																			6.7	3.8
4	Bx	AB	CxTx																			2.9	2.9
32	Bx	AB	CxTx																			2.9	1.0
10	Bx	AB	CxTx																			1.9	1.0
31	Bx	AB	CxTx																			1.0	0.0
51	Bx	AB	CxTx																			1.0	0.0
14	Bx	AB	CxTx																			0.0	1.9
19	Bx	AB	CxTx																			1.9	0.0
38	Bx	AB	CxTx																			0.0	1.0
73	Bx	BB	C4T4																			1.9	0.0
82	Bx	BB	C4Tx																			1.9	0.0
86	Bx	BB	CxT4																			1.0	0.0
92	Bx	BB	CxTx																			2.9	2.9
112	Bx	BB	C4Tx																			2.9	2.9
77	Bx	BB	CxTx																			0.0	1.0
80	Bx	BB	CxT4																			0.0	1.0
228	Bx	BB	CxTx																			1.9	2.9
71	Bx	BB	C4Tx																			0.0	2.9
175	Bx	BB	CxTx																			1.9	0.0

Figure 2

The occurrence of KIR genotypes in the study population. Thirty-five different KIR genotypes were observed in the 208 persons. The genotypes differed from each other by the presence of (black box) or absence (open box) of KIR genes. The variants KIR2DL5A and 2DL5B were considered as KIR2DL5 while KIR2DS4 mutant and 2DS4 full length were considered as KIR2DS4, we analyzed a total of 16 KIR genes. The data are expressed as percentage frequency, obtained by dividing the number of individuals having the genotype by the number of individuals in the studied group. Genotype ID reference numbers were acquired from the KIR genotype database (<http://www.allelefreqencies.net>).

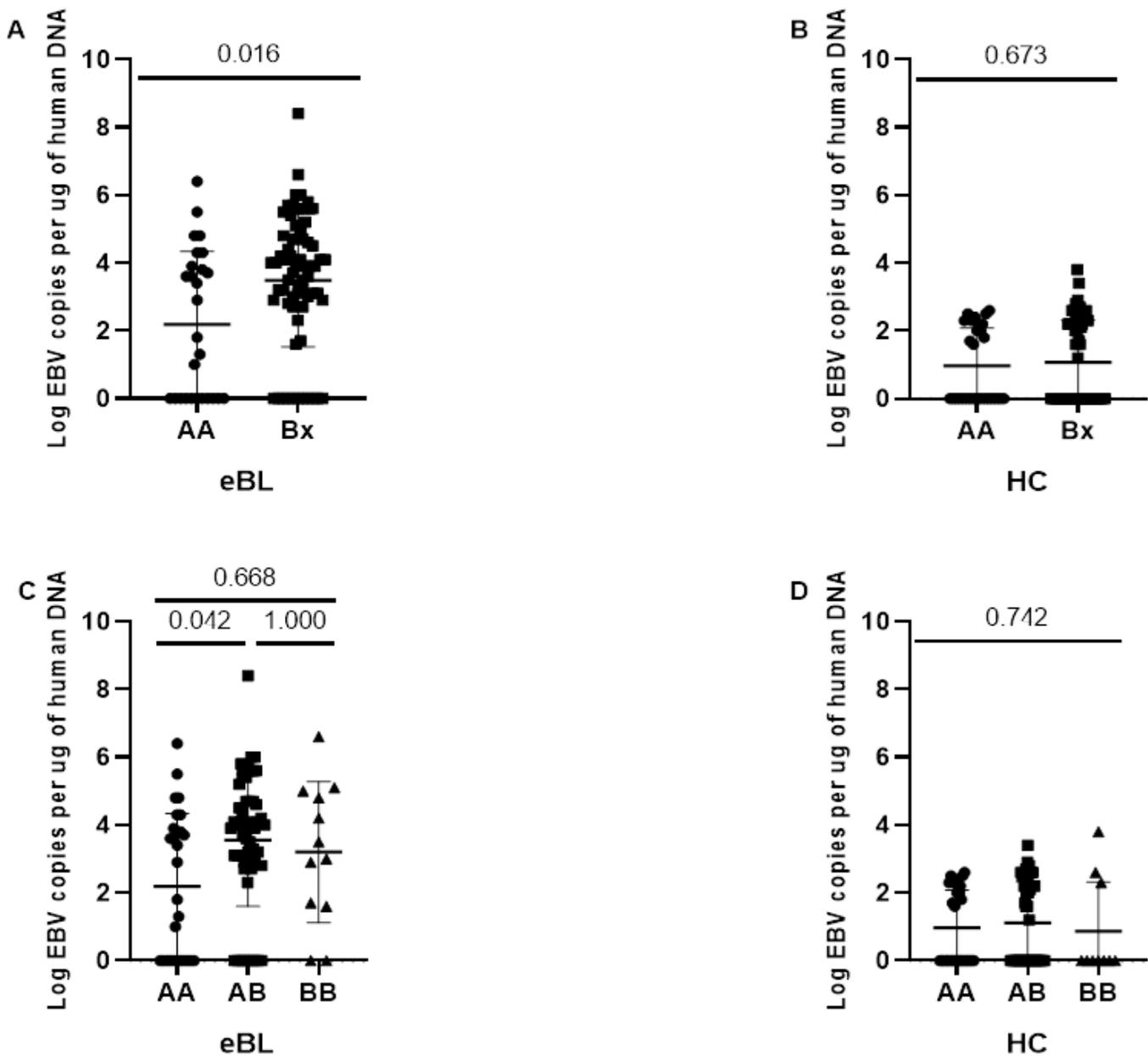


Figure 3

EBV load stratified by AA/Bx haplogroups and AA, AB, and BB genotypes. The EBV levels were compared for eBL patients (n=93), and healthy controls (n=80) after stratification by AA/Bx haplogroups A and B and AA, AB and BB genotypes C and D. Significant differences in EBV viral loads were associated with AA/Bx haplogroups and AA/AB genotypes in eBL patients but not in healthy controls; based on Mann-Whitney test and one way Kruskal-Wallis statistic respectively (*p<0.05).

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [KIRGenecontentSupplimentaryRawData.xlsx](#)
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