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ABSTRACT

Some retrospective studies suggest an association between infection with GB-virus C (GBV-C) and non-Hodgkin lymphoma (NHL). We evaluated this association prospectively in a nested case-control study within the U.S. Prostate, Lung, Colorectal and Ovarian Cancer Screening Trial (PLCO). Cases (N=658) and controls (N=1,316) were individually-matched by age, sex, race/ethnicity, timing of study entry and sample selection. Pre-diagnostic PLCO serum samples were tested for GBV-C RNA (as a measure of active infection) and E2 antibody (active or resolved infection). Logistic regression was used to estimate odds ratios (ORs) for the association between GBV-C and NHL overall and NHL subtypes. Twelve cases (1.8%) and 7 controls (0.5%) were GBV-C RNA positive. GBV-C RNA positivity was associated with NHL overall (OR=3.43, 95% CI=1.35-8.71) and, based on small numbers, diffuse large B-cell lymphoma (OR=5.31, 95% CI=1.54-18.36). The association with NHL persisted when the interval between testing and selection was greater than 4 years (OR=6.00, 95% CI=1.21-29.73). In contrast, E2 antibody-positivity was not associated with NHL risk (OR=1.08, 95% CI=0.74-1.58). Our study demonstrates that GBV-C infection precedes development of NHL. GBV-C infection may play an etiologic role in a small proportion of NHL cases, perhaps by causing chronic immune stimulation or impaired immunosurveillance.
INTRODUCTION

Discovered in the mid-1990s, GB virus-C (GBV-C, also known as hepatitis G virus) is a single-stranded RNA virus belonging to the Pegivirus genus within the family Flaviviridae (1-3). GBV-C is the most closely related human virus to hepatitis C virus (HCV) (2-4). GBV-C is transmissible through blood and sexual exposure, particularly through blood transfusions and injection drug use (4). Following initial infection, most people clear GBV-C within a few years, but the virus can cause chronic infection in an estimated 20-30% of people (5, 6). The prevalence of detectable GBV-C viremia is 1-2% among U.S. blood donors (4).

Non-Hodgkin lymphoma (NHL) is the sixth most common cancer in U.S. men and women (7). Severe immune dysregulation due to AIDS, organ transplantation, or primary immune deficiencies strongly increases NHL risk, but it only accounts for a fraction of NHL cases (8). Direct transformation by infectious agents including Epstein-Barr virus and human herpesvirus 8, or chronic immune stimulation by HCV and Helicobacter pylori, are thought to play a role in some NHL subtypes (9).

Several considerations support the fact that GBV-C could also contribute to development of NHL. GBV-C RNA is commonly detected in bone marrow and spleen tissue (10, 11), and GBV-C has been demonstrated to replicate in vitro in peripheral blood mononuclear cells, particularly B and T lymphocytes (12, 13). Chronic GBV-C infection has been associated with decreased apoptosis of T cells, impaired T cell activation and proliferation, and changes in immune responsiveness which may contribute to lymphomagenesis (14-16).
A recent Canadian case-control study of 553 cases and 438 controls evaluated the association of GBV-C and NHL, reporting a significantly higher prevalence of GBV-C viremia in cases compared to controls (4.5% vs. 1.8%; adjusted odds ratio (aOR)=2.7, 95% CI=1.2-6.7) (17). Prior case-control studies had fewer cases and widely varying results (overall ORs 1.1 to 14.4), although most studies suggested an association (18-24). Notably, these previous studies tested for GBV-C infection retrospectively, after development of NHL, which could have led to bias. Along these lines, blood transfusion is a possible route of transmission for GBV-C infection, so assessment of exposure in NHL cases who previously received blood transfusions (e.g., as therapy for anemia arising during chemotherapy) could have been a major source of confounding. It is also possible that as people develop NHL, weakened immunity could lead to GBV-C reactivation, causing an increase of detectable viremia. If such a disease effect were present, it could lead to an artifactual association in a retrospective study design. Additionally, controls were often drawn from non-representative convenience groups (i.e., blood donors, cancer patients).

We evaluated NHL risk associated with GBV-C infection in a case-control study nested in a large, U.S. general population cohort. Our study is the first to prospectively assess GBV-C status using pre-diagnostic serum specimens for the NHL cases. We tested subjects both for active infection as indicated by viremia (i.e., the presence of GBV-C RNA in serum) and for either active or resolved infection (as indicated by the presence of antibodies to the E2 viral capsid protein).

MATERIALS AND METHODS
Study design, study population, and subject selection

The Prostate, Lung, Colorectal and Ovarian (PLCO) Cancer Screening Trial cohort consists of approximately 150,000 men and women between the ages of 55-74, who were randomized to enter either a screening program for several cancers (~75,000 subjects) or usual care, with the goal of determining the effects of screening on cancer-related mortality (25). Subjects were enrolled in 10 U.S. sites between 1993 and 2001. Screening arm participants received annual examinations for up to 6 years, including blood draws at baseline and 5 subsequent years (T0-T5), and were then followed for up to 12 additional years. All participants provided informed consent. For the present study, we excluded participants having a prior history of cancer, no follow-up time contributed to PLCO, a rare non-NHL cancer (as defined by PLCO), no baseline questionnaire, no consent for etiology research, or inadequate stored serum.

Cases were defined as participants diagnosed with pathologically confirmed NHL occurring after enrollment and through April 30, 2011. Controls were eligible if they had not developed NHL at the time the case was diagnosed (measured from baseline) and were individually matched to cases 2:1 by age at baseline (5-year age groups), sex, race/ethnicity, calendar year of entry, time on study, and study year of blood draw.

Biological specimen testing

PLCO serum samples selected for testing for GBV-C RNA (to detect viremia, or active infection) and E2 antibody (to detect active or resolved infection) were closest in time to, but preceding, NHL diagnosis or control selection (i.e., proximal samples). Testing was performed at one site (University of Iowa) and laboratory personnel were blinded to case-control status. The
testing of PLCO samples was approved by the Institutional Review Boards of the National Cancer Institute and the University of Iowa.

Due to the lack of approved or commercial tests, the University of Iowa laboratory developed and optimized methods for detecting GBV-C RNA and antibodies (26). RNA was extracted from 20 µl of serum using the QIAamp Viral RNA Mini kit for amplification by a one-step reverse transcription real-time polymerase chain reaction (RT-PCR) as described (16, 26). RNA was amplified using 5’NTR primers and a 6-FAM/TAMRA labeled probe using the SuperScript II Platinum One-step Quantitative RT-PCR System (Invitrogen). Oligonucleotide primers were: sense 5’ GGCGACCGGCCAAAA 3’ (nucleotide [nt] 96-110); antisense 5’ CTTAAGACCCACCTATAGTGCTACC (nt 163-188); and probe 5’ FAM-TGACCGGGATTTACGACCTACCAACCCT-TAMRA (nt 131-158). Samples were amplified in an ABI Prism 7700 sequence detector at 50°C x 50 minutes, 95°C x 2 minutes, followed by 40 cycles (58°C x 15 seconds, 72°C x 1 minutes). Four negative control wells (two blanks and two water controls) were included with each set of samples, and a standard curve was generated using synthetically transcribed GBV-C RNA (26-28). If the calculated RNA concentration was 50,000 copies/ml or greater, then the result was considered positive.

Additional quality control measures were taken to ensure validity and reproducibility of GBV-C RNA testing. On all experiments, the standard curve for 8 positive controls utilizing the synthetic GBV-C RNA was reviewed; the cycle threshold (C_T) for the highest concentration was required to be within 1.0 C_T of the mean value (17.5), and the linear regression analysis of the standard curve values was required to have an R^2 ≥ 0.98 before the experiment was accepted.
addition, the 4 negative control samples were required to be negative. If these criteria were not met, the RNA samples were re-tested. In addition to these known laboratory controls, a blinded set of positive and negative controls, provided by the testing laboratory, were aliquoted by a different laboratory and incorporated randomly into the tested batches (1 set for each of 25 batches). To account for possible batch effects, cases and their matched controls were tested together, in a random order within the matching group.

Positive and negative results were initially based on an algorithm that incorporated both RT-PCR (as described above) and 4 nested PCR assays (using 5’NTR and three E2 primer sets) in efforts to detect additional GBV-C infections. We assessed the reproducibility of this approach by retesting a set of PLCO samples (10 control subjects GBV-C RNA positive according to this algorithm, and 10 control subjects GBV-C RNA negative according to the algorithm) in a subsequent run. This duplicate testing revealed that this algorithm using the additional nested PCR primers was unreliable (data not shown), so we defined GBV-C positivity based on RT-PCR only. Positivity based on RT-PCR was reliable: all 3 positive control samples that were selected for retesting tested positive again, and 16 of 17 negative control samples retested negative. Thus, all of the GBV-C results reported in this paper are based on the RT-PCR testing only.

Samples testing GBV-C RNA-positive at the proximal timepoint (indicating active infection) were further tested using another PLCO sample at the earliest available (i.e., most distal pre-diagnostic) timepoint to determine whether these infections were persistent. Because the selection was based on positivity as defined by the nested PCR algorithm, 5 samples (all NHL
cases) that were positive based only on RT-PCR, but negative based on the algorithm, were not selected for testing at the distal timepoint.

To measure GBV-C antibodies, a solid-phase enzyme-linked immunosorbent assay (ELISA) based on a recombinant GBV-C E2 protein expression system was developed. Briefly, recombinant E2-Fc fusion protein (29) (2 µg/ml in carbonate buffer) was used to coat ELISA plates, which were stored at 4°C until use. Following washing, patient samples (diluted 1:200) were added to the wells for 1 hour at 37°C. Plates were washed, then alkaline phosphatase conjugated, anti-human lambda/kappa immunoglobulin light chain was added for 1 hour at 37°C. The reaction was developed with addition of para-nitrophenylphosphate substrate (incubated at 37°C), and absorbance determined at A405 nanometers. All samples were tested in duplicate, and wells coated with E2-Fc protein were compared to wells coated with bovine serum albumin (BSA). A positive result was defined as absorbance values for the E2 well greater than 1.00 ELISA unit and 2.5 times that of the control BSA well.

Because GBV-C shares at least one transmission route with HCV and HIV (i.e., injection drug use) and both other viruses are associated with NHL (8, 9), we also tested for HCV and HIV infection in the proximal samples using clinically licensed antibody tests. Positive results were confirmed or evaluated for active infection by measuring viral RNA. HCV and HIV testing was performed on anonymized samples, limited to GBV-C RNA positive cases and controls.

Statistical analysis
Odds ratios (OR) and 95% confidence intervals (CI) for the association between GBV-C and NHL overall were calculated using conditional logistic regression to adjust for the matching factors using PROC PHREG (SAS version 9.3, Cary, NC). Using the measurements from the proximal timepoint, we first examined NHL risk related to GBV-C RNA positivity (i.e. active infection) as well as E2 antibody positivity (i.e. active or resolved infection). We also examined risk in relation to combinations of viremia and antibody positivity relative to negative status for both markers.

The risk of specific NHL subtypes was examined, since the Canadian study reported a particularly strong association for diffuse large B-cell lymphoma (DLBCL) (17). We broke the individual matching of cases and controls and used polytomous regression (PROC LOGISTIC) to maximize the power by comparing each subgroup with all of the controls. In an additional analysis, we examined whether associations differed by latency, i.e., the time between the proximal timepoint assessed for GBV-C infection and NHL diagnosis/selection. We also compared the mean viral RNA levels (log10 copies/ml) between viremic cases and controls using PROC TTEST.

To evaluate the potential confounding effect of HIV and HCV on the association between GBV-C viremia and NHL, we excluded co-infected people in a sensitivity analysis. Specifically, given the anonymized nature of the HCV and HIV testing, only grouped data were used in the sensitivity analysis. A 2x2 table showing the relationship between GBV-C viremia and NHL was created, and the number of GBV-C viremic cases and GBV-C viremic controls who tested
positive for HCV or HIV was subtracted from the corresponding cells. Finally, the crude odds ratio corresponding to this revised table was calculated.

To estimate the proportion of NHL cases that might be linked to GBV-C infection, the population attributable risk (PAR) was calculated based on the formula: \( PAR = \frac{P_e \times (RR-1)}{P_e \times (RR-1) + 1} \) where \( P_e = \) the prevalence of the exposure (GBV-C viremia) in controls, and \( RR = \) the relative risk (odds ratio) associating GBV-C viremia and NHL (30).

RESULTS

The characteristics of the cases (\( N=658 \)) and individually-matched controls (\( N=1,316 \)) are presented in Table 1. The cases and controls were largely male (60.6%), age 60-69 years at randomization into the PLCO trial (57.6%), and white (94.1%). NHL developed 7.0 years on average after randomization, and the mean number of years from the proximal serum sample to NHL diagnosis was 3.7 years.

Overall, there were a total of 19 GBV-C RNA-positive cases and controls. Among the blinded positive and negative control samples incorporated into each batch, 92% (23 of 25 samples) of positive controls and 92% (23 of 25) of negative controls were correctly classified based on RT-PCR testing. Twelve cases (1.8%) and 7 controls (0.5%) were GBV-C RNA positive. GBV-C RNA positivity was thus associated with NHL overall (OR=3.43, 95% CI=1.35-8.71; \( p=0.010 \)) (Table 2). Risks of each NHL subtype were all elevated, but the association was statistically significant only for DLBCL (OR=5.31, 95% CI=1.54-18.36).
An association was apparent when the interval between GBV-C RNA measurement and case/control selection was greater than 4 years (mean interval=7.3 years) (OR=6.0, 95% CI=1.21- 29.73) (Table 3). Among the GBV-C RNA positive subjects who were also tested at a distal timepoint (i.e., earlier in time), there was a suggestion that cases were more frequently positive at both timepoints than controls (4 of 7 [57%] vs. 2 of 7 [29%]), although this difference was not significant (p=0.280). As mentioned in the Methods, 5 positive cases were not selected for testing at the distal timepoint.

Based on the 7 positive controls and 12 positive cases, viral RNA levels were higher in controls than cases (log_{10} copies/ml=7.8 vs. 5.9, p= 0.006). Furthermore, based on small numbers, the viral load varied across NHL subtypes (mean log_{10} copies/ml ranging from 5.2 to 8.1), with the lowest levels observed among DLBCL cases (mean log_{10} copies/ml=5.2).

There were no differences in the prevalence of E2 antibody between cases and controls, with 45 (6.8%) and 84 (6.4%) testing positive respectively (p=0.694). Among E2 antibody-positive subjects, 1 (0.8%) was also GBV-C RNA positive; among E2 antibody-negative subjects, 18 (1.0%) were also GBV-C RNA positive. E2 antibody positivity was not associated with NHL overall (OR=1.08, 95% CI=0.74-1.58), but was significantly associated with “other” NHL subtypes (OR=1.96, 95% CI=1.07-3.56) (Table 2). NHL was not associated with E2 antibody status in any of the follow-up periods (Table 3).

Using GBV-C uninfected subjects (i.e., negative for both GBV-C RNA and E2 antibody) as the reference group, resolved infection (i.e., GBV-C RNA-negative but E2 antibody-positive) was
not associated with NHL (OR=1.07, 95% CI=0.73, 1.58). In contrast, active infection (GBV-C RNA-positive) was significantly associated with NHL (OR=3.45, 95% CI=1.36, 8.76) (Table 4).

None of the GBV-C RNA-positive cases or controls was HIV antibody-positive. One GBV-C RNA-positive case was HCV antibody-positive; however, this sample did not have HCV RNA detected. Therefore, the antibody test represented either resolved HCV infection or a false positive test. After subtracting the HCV-positive NHL case from the exposed group, the association between GBV-C infection and NHL remained (crude OR=3.18, 95% CI=1.23-8.25).

Based on the prevalence of GBV-C infection and the magnitude of association with NHL in our study (where Pe = 0.005 and RR=3.43 from our results), we estimate that 1.2% of NHL cases might be linked to GBV-C infection, i.e., 0.005 (3.43-1) / [0.005 (3.43-1) + 1] = 0.012.

DISCUSSION
In the present U.S. case-control study, active GBV-C infection, as indicated by GBV-C RNA positivity, was associated with an increased risk of NHL overall (OR=3.43). Risk was elevated across all subtypes, but estimates were imprecise due to small numbers and statistically significant only for DLBCL (OR=5.31). Of note, we show for the first time that GBV-C infection precedes the development of NHL by several years, and that the association with NHL risk appeared strongest at the longest latency (4 years or more after testing, OR=6.00). In contrast, resolved infection (antibody positivity in the absence of viremia) was not associated with NHL risk.
Our findings are consistent with the findings of the large, population-based Canadian case-control study in which associations of GBV-C viremia with NHL overall (OR=2.7) and with DLBCL (OR=5.2) were also reported (17). The consistency of the findings is remarkable considering the differences between the two studies. First, while both were matched case-control studies, the Canadian study obtained samples from NHL cases after they were diagnosed, while our samples were obtained before NHL diagnosis. Second, the prevalence of GBV-C viremia was higher among the Canadian controls (1.8%) compared to ours (0.5%), which may in part be explained by the differences in age distribution. Canadian controls were aged 20-79 years compared with our controls aged 55 years and older, and previous studies found an inverse relationship between GBV-C viremia prevalence and age among adults (31, 32). Finally, the real-time PCR assays used to detect GBV-C infection used different primers and were performed in different laboratories. Thus, the differences in the prevalence of GBV-C viremia may reflect the different methodologies (in addition to differences in study populations), and it is possible our PCR assay was less sensitive than that of the Canadian study. The positive associations observed in the Canadian study and ours are consistent with results from previous but less definitive case-control studies (18-24). Some of these studies included NHL cases coinfected with HCV (18, 21, 24), and the controls in some studies were drawn from convenience groups (blood donors, cancer patients) which were not representative of the source population giving rise to the NHL cases (18, 20, 21, 23).

We found that among the GBV-C RNA positive subjects who were also tested at a distal timepoint (i.e., earlier in time), there was a suggestion that cases were more frequently positive at both timepoints than controls (4 of 7 [57%] vs. 2 of 7 [29%]), although this difference was not
significant (p=0.280). Following transfusion acquired infection, the majority of infected people clear viremia within two years, although viremia lasting for decades has been described (33, 34). GBV-C viremia has been documented to persist for more than 5 years in both HIV-uninfected people and HIV coinfected people (5, 6). We therefore expected that some people with viremia would have had persistence at two timepoints separated by up to several years, while others with viremia would have had a new infection.

Of further interest, among the 19 subjects with viremia, viral RNA levels were higher in controls than cases (mean log_{10} copies/ml=7.8 vs. 5.9, p = 0.006). Also, based on small numbers, the mean log_{10} viral load across NHL subtypes varied, with lower levels among diffuse large B-cell lymphoma cases. We speculate that the higher viral loads among controls may indicate acute infection, while the lower viral loads in cases may indicate a chronic, persistent infection that would increase risk of NHL. HIV serves as a well-documented example of high viral load during acute infection with a reduction over time (35).

While serum GBV-C RNA is a marker of active viremia, serum E2 antibody is generally thought to serve as a marker of a resolved infection. Unfortunately, the lack of a standardized E2 antibody assay, and the fact that E2 antibody may fade to levels below the limit of detection over time, limit the usefulness of E2 antibody as an accurate marker of resolved infection. The E2 antibody detection method used in the current study has been shown to detect antibody elicited by recombinant E2 protein in mice and rabbits (36). However, it has not been directly compared with previously available assays that found an inverse relationship between viremia and E2 antibodies in humans (37, 38). Our finding of a high rate of concurrent GBV-C viremia and E2
antibody differs from those prior reports. Although further studies are needed to better characterize the humoral response to GBV-C, the lack of association between E2 antibody positivity and risk of NHL may not be surprising. One possibility is that resolved infection may indicate an ability to normalize lymphoma risk, whereas persistently active infection indicates chronic immune disturbances and elevated NHL risk.

Our study has several important strengths. Cases and controls were drawn from a prospective cohort, therefore minimizing potential for selection bias. We had a relatively large sample size (658 cases, 1,316 controls), necessary to examine with good precision the association of a rare exposure such as GBV-C with NHL. Because NHL subtypes are increasingly recognized as distinct entities, our data regarding NHL subtypes were a further strength, and we identified a significant association between GBV-C infection and DLBCL.

Additionally, we evaluated GBV-C infection status using pre-diagnostic samples in cases, obtained on average 3.7 years before NHL. This aspect of our study design is unique among studies that have assessed the association between GBV-C and NHL, and it was critical for minimizing potential disease or treatment effects on GBV-C status. Also, the availability of serial samples in the PLCO cohort enabled us to assess GBV-C persistence. The findings here were based on small numbers, but they suggested an association between persistent viremia and NHL. Finally, we assessed the possibility of confounding by HIV and HCV by testing for these infections in the GBV-C infected cases and controls.
The main limitation of our study was the small number of people with active GBV-C infection, which limited the precision of our estimates. In particular, although we observed a significantly elevated risk of DLBCL associated with GBV-C viremia, the confidence intervals were quite wide. We also observed elevated, but not statistically significant ORs across the other NHL subtypes. It is notable that the OR for DLBCL was still statistically significant among samples collected 4+ years prior to NHL diagnosis (OR=13.6, 95% CI=2.2-83.4), though this was based on only 3 exposed DLBCL cases (data not shown). Larger studies are needed to determine if GBV-C viremia is more strongly associated with DLBCL than other NHL subtypes. Another limitation, noted above, is the lack of standard, commercially available RNA and E2 antibody assays. In particular, E2 antibody positivity was not associated with NHL overall but was associated with “other” (miscellaneous or unspecified) NHL subtypes. Because the sensitivity and specificity of the antibody test are unknown, it is difficult to interpret this result, and we put greater emphasis on the associations with viremia. Indeed, the results for the RNA testing were strengthened because we incorporated a number of quality control measures to confirm the reliability and reproducibility of the RNA assay (i.e. known positive and negative controls, masked PLCO duplicates).

The association between HCV and NHL can serve as a model for understanding a possible etiologic relationship between GBV-C and NHL. HCV is an established NHL risk factor (39). While HCV has been reported to infect lymphocytes, the virus neither integrates into the host genome nor contains a known oncogene, and HCV RNA is not detectable in NHL tumors (40). HCV is thought to increase risk of NHL through chronic host infection and long-term immune stimulation (40, 41), although direct effects on B-cells are possible (42-44). GBV-C is
structurally similar to HCV, and the mechanism by which it might cause NHL could be similar. Furthermore, GBV-C infection has been associated with decreased apoptosis of T cells which may contribute to the prolonged survival of HIV-infected patients coinfected with GBV-C (14). Recent data showing that GBV-C infection reduces T cell activation and proliferation in HIV-infected individuals suggests that GBV-C infection may impair immune surveillance and immune responsiveness, which may lead to lymphomagenesis (15, 45, 46).

In conclusion, our prospective study adds support that GBV-C infection is a risk factor for NHL. Further research is needed to confirm the GBV-C association with NHL in diverse populations. Additionally, future studies should be conducted to understand immune-related mechanisms related to persistent GBV-C infection, which would inform a mechanistic understanding and assessment of whether the association is causal. The GBV-C association with NHL may have public health implications because the blood supply is not screened for GBV-C, and an estimated 1,000 units of GBV-C RNA-containing blood products are transfused daily in the United States (47). Based on our calculations, we estimate that about 1.2% of NHL cases might be linked to GBV-C infection. Ultimately, demonstration of a causal association with cancer would provide the rationale for a formal evaluation of the costs and benefits of screening donors for GBV-C and eliminating contaminated units of blood.

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AUTHORSHIP CONTRIBUTIONS: C.M.C, E.A.E., and J.T.S. designed the study; J.T.S., D.K., and J.H.M. generated the data; C.M.C. and H.A.K. designed and performed the statistical analysis; C.M.C., E.A.E., J.T.S., M.P.P., and H.A.K. interpreted the data; C.M.C, E.A.E., and J.T.S wrote the manuscript. All authors reviewed and approved the manuscript.
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Table 1. Comparison of NHL cases and controls

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</table>

*aFollowing prior PLCO methods, year of randomization was defined according to fiscal year, defined as the 1-year period starting October 1st of the previous calendar year.*

*bNo serum was collected in study year 3.*
Table 2. Associations of GBV-C infection with NHL overall and NHL subtypes

<table>
<thead>
<tr>
<th></th>
<th>GBV-C RNA Positivity&lt;sup&gt;a&lt;/sup&gt;</th>
<th>E2 Antibody Positivity&lt;sup&gt;b&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Total N</td>
<td>N</td>
</tr>
<tr>
<td>Controls</td>
<td>1,316</td>
<td>7</td>
</tr>
<tr>
<td>All NHL cases</td>
<td>658</td>
<td>12</td>
</tr>
<tr>
<td>NHL cases, by subtype</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Diffuse large B-cell lymphoma</td>
<td>145</td>
<td>4</td>
</tr>
<tr>
<td>Follicular lymphoma</td>
<td>88</td>
<td>2</td>
</tr>
<tr>
<td>CLL/SLL</td>
<td>249</td>
<td>4</td>
</tr>
<tr>
<td>Other NHL</td>
<td>119</td>
<td>1</td>
</tr>
<tr>
<td>Unknown NHL subtype</td>
<td>52</td>
<td>1</td>
</tr>
</tbody>
</table>

Abbreviations: OR, odds ratio; CI, confidence interval; NHL, non-Hodgkin lymphoma; CLL/SLL, chronic lymphocytic leukemia/
small lymphocytic lymphoma

<sup>a</sup>Referent group is RNA-negative subjects.

<sup>b</sup>Referent group is E2 antibody-negative subjects.
Table 3. Latency analysis of GBV-C infection and NHL

<table>
<thead>
<tr>
<th>Latency</th>
<th>GBV-C RNA Positivitya</th>
<th>E2 Antibody Positivityb</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Controls</td>
<td>Cases</td>
</tr>
<tr>
<td>0-0.99 year</td>
<td>2 0.58</td>
<td>3 1.73</td>
</tr>
<tr>
<td>1-3.99 years</td>
<td>3 0.64</td>
<td>3 1.28</td>
</tr>
<tr>
<td>4.00+ yearsc</td>
<td>2 0.40</td>
<td>6 2.39</td>
</tr>
</tbody>
</table>

aReferent group is RNA-negative subjects.
bReferent group is E2 antibody-negative subjects.
cMean=7.3 years (range 4.0 to 14.6 years)
Table 4. Association of GBV-C infection with NHL based on combined RNA and E2 antibody testing

<table>
<thead>
<tr>
<th>GBV-C Infection Status</th>
<th>Cases N</th>
<th>%</th>
<th>Controls N</th>
<th>%</th>
<th>OR</th>
<th>95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Uninfected: RNA negative, E2 negative</td>
<td>602</td>
<td>91.49</td>
<td>1225</td>
<td>93.09</td>
<td>1.00</td>
<td>(reference)</td>
</tr>
<tr>
<td>Resolved: RNA negative, E2 positive</td>
<td>44</td>
<td>6.69</td>
<td>84</td>
<td>6.38</td>
<td>1.07</td>
<td>(0.73 , 1.58)</td>
</tr>
<tr>
<td>Active: RNA positive</td>
<td>12</td>
<td>1.82</td>
<td>7</td>
<td>0.53</td>
<td>3.45</td>
<td>(1.36 , 8.76)</td>
</tr>
</tbody>
</table>


GBV-C infection and risk of NHL among U.S. adults


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