Research Article

Plasma Cytokines and Future Risk of Non-Hodgkin Lymphoma (NHL): A Case-Control Study Nested in the Italian European Prospective Investigation into Cancer and Nutrition

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Abstract

Background: Recently, biological markers related to the immune system such as cytokines have been studied to further understand the etiology of non-Hodgkin Lymphoma (NHL). However, to date, there are no studies that have studied cytokine levels prospectively in relation to NHL risk in the general population.

Methods: Using bead-based immunoassays, plasma levels of 11 cytokines, 4 chemokines, and 1 adhesion molecules were measured in prediagnostic blood samples of 86 NHL cases and 86 matched controls (average time between blood collection and diagnosis, 4.5 y). Conditional logistic regression adjusted for body mass index and alcohol consumption was used to analyze the association between individual plasma cytokine levels and the risk of developing NHL.

Results: In multivariate models, excluding cases diagnosed within 2 years after inclusion, we observed a significant association for interleukin 2 (IL2; *P* trend = 0.004), interferon (IFN)- γ (*P* trend = 0.05), and intercellular adhesion molecule (ICAM) (*P* trend = 0.04). Subanalyses of B-cell NHL patients showed a significant association with IL2 (*P* trend = 0.003), tumor necrosis factor- α (TNF- α ; *P* trend = 0.03), and ICAM (*P* trend = 0.04) and a borderline association with IL5 (*P* trend = 0.07) and IFN- γ (*P* trend = 0.08).

Conclusions: The results of this study suggest, in a prospective setting, a possible association between plasma levels of IL2, ICAM, IFN- γ , and TNF- α with NHL risk and provide some evidence that risk of NHL might be related to a downregulation of T helper 1 cytokines.

Impact: Identification of subtle changes in immune response regulation quantified by plasma cytokine levels possibly provides new insights in the etiology of NHL. *Cancer Epidemiol Biomarkers Prev;* 19(6); 1577–84. ©2010 AACR.

Introduction

Non–Hodgkin lymphomas (NHL) are a heterogeneous disease group belonging to malignancies of the lymphoid tissue, which vary in histologic characteristics, clinical manifestations, and etiologic factors (1-5).

Note: P. Vineis and R. Vermeulen are co-senior authors.

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Incidence rates of NHL have shown a significant rise especially in highly aggressive subtypes during the past several decades worldwide (6). In European countries, an overall increase in NHL incidence of 4.2% per annum was observed from 1985 to 1992 (7) and there is still a small (3%) but continuing increase in incidence (8). Despite extensive research in recent years, reasons for this increase are still largely unknown (9).

The most established risk factors of NHL are those related to severe immunocompromised individuals such as genetically determined or acquired immune deficiencies, including HIV infection or iatrogenically induced immune suppression after transplantation (3-5). As an extension of this observation, it has been hypothesized that many of the known and unknown NHL risk factors might influence NHL risk through (subtle) modulations of the immune system (10). A possible role of cytokines in the development of NHL is supported by recent reports on NHL risk related to genetic variation in genes encoding proinflammatory and antiinflammatory cytokines [tumor necrosis factor (TNF), LTA, IL10, and IL4; refs. 11-13]. These reports offer important evidence linking immune function to NHL

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among nonimmunocompromised individuals. However, functional relevance of the found single-nucleotide polymorphisms (SNP) is still unclear. Therefore, studies incorporating direct measurements of the immune environment, in addition to investigation of genetic polymorphisms, are needed to further elucidate the role of immunomodulatory factors in lymphomagenesis.

Biological markers related to the immune system such as cytokines have been studied to explain the etiology of NHL (14-16). However, there are only few studies that have studied cytokine levels prospectively in relation to NHL risk and none have been in the general population. In a study nested within the Multicenter AIDS Cohort Study (17) in which serum samples were obtained preceding a diagnosis of AIDS lymphoma, Breen et al. reported an increased serum level of IL6 in Burkitt's lymphoma patients compared with CD4-matched AIDS controls who did not have lymphoma. In another study (18), a significant increase in detectable serum levels of IL10 in AIDS lymphoma patients was found compared with HIV⁺/ HIV⁻ subjects. However, in this study, >81% of the cases developed NHL within 1 year of blood collection, and as such, it can be questioned if the observed increases in IL10 were a result of the disease itself or the cause of the disease. Furthermore, as this study was conducted among HIV⁺ subjects, it is questionable if these results can be extrapolated to the general population.

We hypothesize that given the pivotal role of cytokines in immune function, blood levels of multiple cytokines collectively might reflect the subtle status of a deregulated immune response or a failure to modulate the immune response appropriately. To illustrate innate and acquired variations in immune responses that affect the risk of developing NHL, a prospective study is the only appropriate epidemiologic design. Only in this way factors related to disease can be studied years before the onset of the disease, excluding the possibility that the measured response is actually caused by the disease and not the cause of the disease itself. We therefore did a casecontrol study nested within the Italian contribution to the European Prospective Investigation into Cancer and Nutrition (EPIC) on plasma cytokine and chemokine levels potentially related to NHL risk.

Materials and Methods

Study population

The EPIC project is a European network of prospective cohorts that was set up to examine relationships of cancer risk with nutrition and metabolic risk factors (19). In the period 1993 to 1998, EPIC Italy completed the recruitment of 47,749 volunteers (15,171 men and 32,578 women, ages 35-65 y) in four different areas covered by cancer registries: Varese (12,083 volunteers) and Turin (10,604) in the northern part of the country and Florence (13,597) and Ragusa (6,403) in central and southern Italy, respectively. An associated center in Naples enrolled 5,062 women. The present study included incident cases of NHL until the end of 2004 according to the International Classification of Diseases for Oncology, third edition.

For each case subject, one random control was selected among all cohort members alive and free of cancer at the time of diagnosis of the index case matched by center, gender, date of recruitment, age at diagnosis, and age at recruitment $(\pm 3 \text{ y})$.

A total of 91 patients with NHL were eligible to be included in the study. Excluded were cases without suitable control samples (n = 2) and cases for whom plasma specimen was missing (n = 3), so a total of 86 pairs entered the study. NHL diagnosis was the second malignancy for five cases. Analyses excluding these cases did not change the results of the study.

Laboratory assay

Blood samples collected from EPIC participants were stored at -196°C in liquid nitrogen until they were pulled for laboratory analysis. None of the plasma specimens were thawed before the analyses. We measured 11 cytokines [interleukin (IL) 1a, IL1B, IL2, IL4, IL5, IL6, IL10, IL12, IL13, IFN- γ , and TNF- α], 4 chemokines (IL8, RANTES, eotaxin, and IP10), and 1 adhesion molecules (ICAM) in stored citrate plasma samples (50 µL) of all cases and controls using the Luminex multianalyte profiling technology (Lab-MAP) according to the protocol described by de Jager et al. (20), except that, instead of a 1-hour incubation, an overnight incubation at 4°C was used (21). The Luminex multianalyte assay has been validated previously against standard ELISA tests (20). In a recent study, we showed that this assay provides reproducible results in plasma and serum samples and that the rank correlations between measured and analyte levels in serum and plasma were relatively high (Spearman rank correlation, 0.74-0.98) for most of the analytes (21). All laboratory personnel were blinded with regard to case-control status. Median time interval between sample collection and freezing was 4 hours for both cases and controls (Table 1). All samples were run in duplicate with matched case-control sets assayed in the same batch. Quality control sets (low- and high-concentration cytokine quality control samples) were run in duplicate with the case-control sets in each batch. The median intrabatch coefficient of variation for all of cytokines based on these quality control duplicate sets was 6.7% (4.3-30), and the median interbatch coefficient of variation was 30.7% (9.6-110). The lower limits of detection (LOD) based on the standard curve were 0.24 pg/mL for IL4; 0.61 pg/mL for IL12; 1.22 pg/mL for IL1 β , IL2, IL5, IL6, IL8, IL10, IL13, IFN- γ , and TNF- α ; 2.44 pg/mL for IL1 α , RANTES, and eotaxin; 4.88 pg/mL for IP10; and 73.24 pg/mL for ICAM.

Statistical analysis

Values of cytokine levels below the LOD or above the maximum range of detection were imputed based on a

| | Case (n = 86) | Control (<i>n</i> = 86) | P_{diff} |
|------------------------------------------------|----------------------------|--------------------------|---------------------|
| Matching variables | | | |
| Age at recruitment, y* | 55 (36-74) | 54 (35-73) | 0.845 |
| Age at diagnosis, y* | | | |
| Male (%), y* | 39.5%; 60 (41-69) | — | |
| Female (%), y* | 60.5%; 59.5 (41-77) | — | |
| Center (%) | | | |
| Florence | 20.9% | 20.9% | |
| Naples | 7% | 7% | |
| Ragusa | 5.8% | 5.8% | |
| Turin | 20.9% | 20.9% | |
| Varese | 45.3% | 45.3% | |
| Other variables | | | |
| BMI* | 24.8 (17.8-36.6) | 25.3 (18.8-35.3) | 0.896 |
| Physical activity (sex-specific quartiles), % | | | 0.665 |
| Qrt1 | 14% | 15.1% | |
| Qrt2 | 27.9% | 20.9% | |
| Qrt3 | 45.3% | 52.3% | |
| Qrt4 | 9.3% | 10.5% | |
| Missing | 3.5% | 1.2% | |
| Education | | | 0.241 |
| None | 4.8% | 0 | |
| Primary school completed | 53% | 55.3% | |
| Technical/professional school | 10.8% | 16.5% | |
| Secondary school | 22.9% | 18.8% | |
| Longer education (including University degree) | 8.4% | 9.4% | |
| Ethanol intake at recruitment (g/d) | 12.3 (0-104.4) | 11.7 (0-93.9) | 0.685 |
| Storage time of samples (h)* | 4 (1:30-30:07) | 4 (1:30-74:23) | 0.216 |
| Histologic subtype of NHL (%) | | | |
| B-NHL | 92% | — | |
| Follicle center cell | 29.1% (31.6%) [†] | — | |
| Diffuse large B cell | 16.3% (17.7%) [†] | — | |
| Marginal zone B-cell lymphoma | 11.6% (12.7%) [†] | — | |
| Chronic lymphocytic leukemia | 10.5% (11.4%) [†] | — | |
| Mantle cell lymphoma | 4.7% (5.1%) [†] | — | |
| Miscellaneous nodal lymphomas | 19.8% (21.5%) [†] | — | |
| T-cell NHL | 8% | — | |
| Extranodal T cell | 4.7% | — | |
| Nodal peripheral T-cell lymphoma | 3.5% | _ | |

*Median (range); for individuals without self-report and measured anthropometric data, center, age, and gender-specific average values of anthropometric variables have been imputed. [†]Percentage of B-NHL subjects.

maximum likelihood estimation method (22). In all analyses, levels of cytokines were log transformed to normalize their distributions. For individuals without self-reported and measured anthropometric data, center/age/gender-specific average values of anthropometric variables have been imputed (n = 7). Differences between cases and controls in mean plasma concentrations of cytokines and baseline covariates were assessed using paired *t* test. For categorical variables, the statistical significances of case-control differences were tested by the χ^2 test.

Odds ratios (OR) and 95% confidence intervals (95% CI) for NHL in relation to plasma cytokine concentrations (as continuous variables) were calculated by conditional logistic regression (CLR) using the PHREG procedure (SAS statistical software, version 9.1; SAS Institute). Risk estimates were computed both as crude and with additional adjustments for potential confounders, including body mass index (in kg/m²; continuous) and alcohol intake (g/d; continuous). The effect of physical activity (sex-specific quartiles of combined recreational, household, and occupational physical activity) and educational level (indicator of socioeconomic status, categorical) as potential confounding variable was examined, but they did not appreciably change the risk estimates and therefore were not included in the models. Tertiles of plasma cytokine concentrations were calculated based on the distribution in control subjects, and CLR models were used to estimate the association between tertiles of cytokine levels and risk of NHL. We also investigated the possible associations by histologic subtype of B-cell NHL (B-NHL) and by excluding samples that were not stored within 12 hours of collection and cases diagnosed with <2 years of follow-up. The latter exclusion was made to remove the possibility that cytokine levels may have been changed in cases compared with control subjects due to preclinical disease status (n = 18 cases). In addition, potential modification of the effect of cytokines by gender and centers was tested.

Statistical analyses were done using SPSS software (version 11.5; SPSS, Inc.) and SAS (version 9.1; SAS institute). All P values are two-sided, with P < 0.05 considered as statistically significant.

Results

Description of the study population

This study included 86 cases and an equal number of controls (68 men and 104 women). The median age at cancer diagnosis was 60 (range, 41-69) and 59.5 (range, 41-77) years for men and women, respectively (Table 1). Median time between recruitment (i.e., blood collection) in the study and diagnosis of NHL was 4.5 years (range, 0.12-10.4). Of all NHL cases, 92% were diagnosed with B-NHL, with the most common diagnosed subtypes being follicular lymphoma (31.6%), miscellaneous nodal lymphomas (21.5%), and diffuse large B-cell lymphoma (17.7%). Cases and control subjects did not differ considerably with regard to most risk factors and covariates (Table 1).

Plasma cytokine concentration

Geometric mean and SD for plasma levels of individual cytokines are shown in Table 2. Cytokine levels for cases seemed to be lower than for controls. For chemokines, this seemed to be reversed. Cases and controls showed small differences in mean level of IFN- γ (P = 0.05), IP10 (P = 0.07), TNF- α (P = 0.07), and ICAM (P =0.07) in the paired t test. By excluding case patients (n = 18) diagnosed within <2 years of follow-up, significant differences between levels of TNF- α (*P* = 0.04) and ICAM (P = 0.02) and borderline significant differences for IFN- γ (P = 0.06) and IL5 (P = 0.06) between cases and controls were found (data not shown).

Risk estimation

CLR analyses based on tertiles of cytokine levels showed a significant inverse association for IL2 and a borderline significant association for IFN-y and ICAM with

To date, little is known about blood immune marker changes that may be related to the development of NHL, except for a few small studies among HIV patients (17, 18). In several studies, it has been documented that an immunosuppressed state plays a key role in development of lymphomas (3-6). Of the many mechanisms contributing to immune suppression, much attention was recently given to inflammatory cells and to inflammatory mediators in general. Adhesion molecules and their ligand(s) such as ICAM-1 play an important regulatory role in the inflammatory process. It is shown that ICAM can be upregulated on many cell types during an inflammatory or immune response, particularly under the influence of various cytokines (23, 24). Interaction of all activated leukocytes with ICAM-1 may be a crucial step in the induction and protraction of an inflammatory response (23). In the multivariate CLR model, we found that increased levels of ICAM were associated with higher NHL risk. Several clinical studies have shown that blood level of ICAM is increased in NHL patients; however, to our knowledge, there are no reports until now relating this adhesion molecule prospectively to the risk of NHL.

Discussion

As immune dysfunction is thought to be the underlying basis of lymphomagenesis, an imbalance in the regulation and expression of T helper 1 (Th1) and Th2 cytokines could play an important role in the etiology of NHL and its major subtypes (9, 25). Th1 cytokines generate and activate CTLs and natural killer cells, which play crucial roles in antitumor immune responses. Mori et al. (25) studied CD4⁺ cells of diffuse large B-cell lymphoma patients and concluded that the Th1/Th2 balance was polarized to Th2 in untreated patients and to Th1 in patients in complete remission. We found similar results in that a lower risk of NHL with increasing IL2, IFN- γ , and TNF- α (Th1) plasma levels was observed. It should be noted, however, that reevaluation of the Th1 and Th2 paradigm and discovery of other Th cells, such as Th3 and Th17, have led to the realization that a number of inflammatory conditions in which Th1 was previously considered central may actually be related to other types of Th cells. So, although the Th1/ Th2 model still provides a valuable framework to describe the immune changes found in this study, the actual regulatory mechanisms involved are likely more complicated.

Recent genetic studies showed that SNPs from candidate genes, including TNF (10, 12-14); LTA (10); IL4, IL5, and IL6 (11); and IL10 (10-12, 14), may be risk factors for NHL overall or for certain NHL subtypes. Our study showed evidence of a possible role of TNF- α in lymphomagenesis, particularly B-NHL. Based on laboratory evidence, both TNF G308A and IL10 T357A polymorphisms result in overall elevated expression of TNF- α and thus contribute to a shift in the Th1/proinflamatory immune response (13), whereas our results showed low expression of Th1 cytokines (IL2, IFN- γ , and TNF- α) in prospective NHL cases compared with controls. Lan et al. (12), in a study of cytokine polymorphisms in the Th1/Th2 pathway, documented that SNPs in Th2 cytokine genes may be associated with risk of NHL. These findings raise the possibility that a shift in the balance of the Th1/Th2 response could have crucial consequences for lymphomagenesis. However, it should be considered that malignant diseases develop and progress as a result of multifactorial processes, in which genomic alterations and modifications in gene expression in premalignant cells are joined by a tumor-supporting microenvironmental setting (23). Further, functional significance of cytokine SNPs is not clear, as genotypephenotype correlation studies have shown conflicting results possibly due to the extensive networks of gene products regulating the production, modulation, and decay of cytokines. It is therefore likely that any influence of individual cytokine genes on respective phenotypes will be relatively minor.

Our study is one of the first studies that used prospectively collected samples, thus avoiding inverse causation bias that may occur when variation in blood level of cytokines is induced by the disease or by cancer treatments or lifestyle changes after cancer diagnosis. There were, however, several limitations in our study. First, we only had one blood sample for each individual to characterize their immune profile. There are little data on the interindividual and intraindividual variation of cytokines. However, in a previous study (21), we looked at the interindividual and intraindividual variability of cytokines measured in this study. Intraclass correlation coefficients for most cytokines, based on two repeated blood samples collected 1 to 2 weeks apart and tested on two different days, were generally above 0.8, indicating that cytokine levels did not vary much in time within a

| | | | | | | | | · · · · · | | | |
|---------|--------------------------|-----------------|----------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------|--------|-----------------------|-----------------|----------------------|------------------------------------------------|--------|------|
| | Control (<i>n</i> = 86) | | | | | Case (<i>n</i> = 86) | | | | | |
| | Geometric mean | Geometric SD | Min-max | <lod< th=""><th>>Range</th><th>Geometric mean</th><th>Geometric SD</th><th>Min-max</th><th><lod< th=""><th>>Range</th><th></th></lod<></th></lod<> | >Range | Geometric mean | Geometric SD | Min-max | <lod< th=""><th>>Range</th><th></th></lod<> | >Range | |
| IL1β | 1.65 | 3.39 | 0.14-71.95 | 28 | | 1.51 | 3.422 | 0.07-51.2 | 23 | | 0.75 |
| IL1α | 67.56 | 8.97 | 0.46-32,976.9 | 3 | | 48.62 | 9.89 | 0.7-29,806.4 | 4 | 2 | 0.24 |
| IL2 | 70.61 | 8.76 | 0.16-3,854.4 | 5 | 2 | 41.13 | 12.63 | 0.0004- 18,044.2 | 4 | | 0.11 |
| IL4 | 0.71 | 4.17 | 0.02-25.8 | 7 | | 0.59 | 4.44 | 0.02-45.45 | 5 | | 0.39 |
| IL5 | 27.84 | 6.78 | 0.2-3,640.1 | 9 | | 18.23 | 6.38 | 0.19-5,509.4 | 13 | | 0.09 |
| IL6 | 58.38 | 6.04 | 0.61-7,122.8 | 5 | | 61.73 | 6.28 | 0.25-2,785.1 | 3 | | 0.56 |
| IL8 | 6.97 | 6.16 | 0.37-951.8 | 14 | | 5.31 | 7.29 | 0.16-1,474.9 | 16 | | 0.35 |
| IL10 | 46.44 | 6.8 | 0.77-7,117.2 | 1 | | 42.39 | 7.58 | 0.38-8,754.2 | 2 | 1 | 0.76 |
| IL12 | 14.91 | 7.05 | 0.17-1,931.2 | 3 | 1 | 11.77 | 8.04 | 0.23-3,395.9 |) 1 | 1 | 0.40 |
| IL13 | 1.88 | 4.69 | 0.06-199.3 | 24 | | 1.45 | 5.23 | 0.09-103.01 | 24 | | 0.21 |
| IFN-γ | 6.81 | 7.97 | 0.16-702.7 | 21 | | 3.47 | 13.9 | 0.0002- 2,539.6 | 29 | | 0.05 |
| TNF-α | 1.03 | 4.42 | 0.04-208.1 | 32 | | 0.65 | 6.47 | 0.001-76.21 | 30 | | 0.07 |
| RANTES | 9,459.68 | 2.51 | 1,237- 16,581,337 | 1 | 30 | 9,981.54 | 2.09 | 1,320-74,929 |) | 31 | 0.38 |
| ICAM | 117,761.8 | 1.66 | 28,986- 179,640 | | | 128,143.4 | 1.4 | 38,274.8- 210,085 | | | 0.07 |
| Eotaxin | 74.34 | 2.16 | 8.9-837.5 | 1 | | 83.82 | 2.15 | 22.24-985.7 | | | 0.28 |
| IP10 | 40.54 | 1.68 | 10.9-180.1 | 1 | | 46.95 | 1.97 | 13.01-397.9 | | | 0.07 |

Table 2. Descriptive statistics of plasma cytokine levels for cases and control subjects

NOTE: Number of samples with cytokine value lower than LOD (<LOD) and higher than maximum value (>Range) were imputed. Abbreviations: Min, minimum values of cytokine concentration; Max, maximum values of cytokine concentration; RANTES, regulated on activation, normal T cell expressed and secreted; IP10, IFN-inducible protein 10.

*P value of paired t test (two-sided) based on log-transformed values of cytokine concentrations.

Cytokine Univariate model Multivariate model More than *n* = 172 n = 1722 y of follow-up (n = 136)Tertile OR P* Ρ OR P* Ρ OR P* Р No. cases/ trend[†] limits no. controls (95% CI) trend[†] (95% CI) trend[†] (95% CI) IL1β 0.91 0.7 0.98 0.98 0.8 0.5 <-0.242 31/29 1.00 (reference) 1.00 (reference) 1.00 (reference) -0.242 to 0.848 29/29 0.94 (0.46-1.92) 0.93 (0.44-1.96) 0.85 (0.39-1.86) >0.848 26/28 0.83 (0.36-1.93) 0.97 (0.39-2.45) 0.73 (0.25-2.07) IL1α 0.98 0.8 0.86 0.9 0.5 0.4 <3.078 29/28 1.00 (reference) 1.00 (reference) 1.00 (reference) 3.078-4.896 29/29 0.95 (0.44-2.04) 0.8 (0.36-1.82) 0.5 (0.21-1.42) >4.896 28/29 0.92 (0.41-2.07) 0.8 (0.33-1.98) 0.6 (0.23-1.66) 0.02 0.004 IL2 0.05 0.01 0.05 0.04 <3.524 43/28 1.00 (reference) 1.00 (reference) 1.00 (reference) 3.524-5.166 0.17 (0.04-0.6) 21/29 0.39 (0.16-0.91) 0.34 (0.14-0.86) >5.166 22/29 0.41 (0.18-0.96) 0.38 (0.14-1) 0.23 (0.07-0.78) IL4 0.59 0.5 0.9 0.9 0.9 0.7 <-1.129 32/29 1.00 (reference) 1.00 (reference) 1.00 (reference) -1.129 to -0.115 22/28 0.68 (0.29-1.59) 0.83 (0.34-2.06) 0.8 (0.28-2.32) >-0.115 32/29 0.95 (0.19-2.24) 1.04 (0.41-2.54) 0.8 (0.29-2.23) IL5 0.25 0.2 0.15 0.1 0.1 0.08 <2.639 40/29 1.00 (reference) 1.00 (reference) 1.00 (reference) 0.38 (0.15-0.98) 2.639-3.742 21/290.57 (0.28-1.15) 0.46 (0.2-1.07) >3.742 25/28 0.67 (0.30-1.45) 0.61 (0.27-1.38) 0.52 (0.2-1.3) IL6 0.85 0.8 0.77 0.5 0.9 0.8 <3.906 28/29 1.00 (reference) 1.00 (reference) 1.00 (reference) 3.906-4.620 27/29 0.99 (0.44-2.23) 1.2 (0.51-2.79) 1.17 (0.45-3.05) >4.620 1.24 (0.50-3.1) 1.42 (0.54-3.72) 1.00 (0.33-3.04) 31/28 0.15 0.3 IL8 0.32 0.2 0.1 0.06 1.00 (reference) <1.021 37/29 1.00 (reference) 1.00 (reference) 1.021-2.546 20/28 0.55 (0.25-1.19) 0.43 (0.18-1) 0.35 (0.13-0.95) >2.546 29/29 0.79 (0.36-1.73) 0.73 (0.3-1.77) 0.58 (0.21-1.58) IL10 0.74 0.7 0.5 0.3 0.4 0.3 33/29 <2.912 1.00 (reference) 1.00 (reference) 1.00 (reference) 2.912-4.512 25/29 0.73 (0.34-1.59) 0.61 (0.26-1.42) 0.48 (0.18-1.27) >4.512 28/28 0.87 (0.38-1.98) 0.71 (0.28-1.8) 0.62 (0.22-1.7) IL12 0.54 0.3 0.42 0.3 0.3 0.2 <1.845 35/29 1.00 (reference) 1.00 (reference) 1.00 (reference) 1.845-3.146 23/28 0.63 (0.28-1.43) 0.58 (0.25-1.35) 0.47 (0.17-1.26 >3.146 28/29 0.76 (0.35-1.67) 0.64 (0.27-1.55) 0.61 (0.23-1.61) IL13 0.52 0.3 0.2 0.6 0.4 0.4 1.00 (reference) <-0.049 36/29 1.00 (reference) 1.00 (reference) 0.82 (0.33-2.03) -0.49 to 1.125 0.7 (0.32-1.56) 25/29 0.67 (0.31-1.43) >1.125 25/28 0.70 (0.33-1.48) 0.7 (0.32-1.55) 0.53 (0.22-1.3) IFN-γ 0.17 0.06 0.13 0.04 0.1 0.05 <1.019 39/29 1.00 (reference) 1.00 (reference) 1.00 (reference) 1.019-2.910 28/29 0.69 (0.33-1.44) 0.64 (0.28-1.44) 0.61 (0.24-1.56) >2.910 19/28 0.44 (0.19-1.03) 0.38 (0.15-0.97) 0.34 (0.12-0.96) (Continued on the following page)

Table 3. Crude and multivariable-adjusted ORs and 95% Cls of NHL cases by tertiles of plasma cytokine concentrations in EPIC Italy

| Cytokine | e | Univariate model | | | | | Multivariate model | | | | | |
|----------|-------------------|----------------------------|------------------|------------|-------------------------|------------------|--------------------|-------------------------|--------------------------------------------|------------|-------------------------|--|
| | | n = 172 | | | | n = 172 | | | More than 2 y of follow-up (n = 136) | | | |
| | Tertile limits | No. cases/ no. controls | OR (95% CI) | P * | P trend [†] | OR (95% CI) | P * | P trend [†] | OR (95% CI) | P * | P trend [†] | |
| TNF-α | | | | 0.38 | 0.2 | | 0.41 | 0.18 | | 0.3 | 0.1 | |
| | <-0.928 | 36/28 | 1.00 (reference) | | | 1.00 (reference) | | | 1.00 (reference) | | | |
| | -0.928 to 0.3 | 27/29 | 0.71 (0.34-1.47) | | | 0.73 (0.33-1.62) | | | 0.66 (0.27-1.59) | | | |
| | >0.3 | 23/29 | 0.58 (0.26-1.28) | | | 0.56 (0.24-1.31) | | | 0.46 (0.18-1.17) | | | |
| RANTES | 5 | | | 0.34 | 0.2 | | 0.28 | 0.16 | | 0.09 | 0.1 | |
| | <8.828 | 24/29 | 1.00 (reference) | | | 1.00 (reference) | | | 1.00 (reference) | | | |
| | 8.828-9.145 | 25/29 | 1.06 (0.46-2.46) | | | 0.98 (0.39-2.47) | | | 0.57 (0.2-1.71) | | | |
| | >9.145 | 37/28 | 1.69 (0.76-3.74) | | | 1.81 (0.78-4.2) | | | 2.1 (0.8-5.46) | | | |
| ICAM | | | | 0.15 | 0.06 | | 0.14 | 0.05 | | 0.1 | 0.04 | |
| | <11.675 | 19/28 | 1.00 (reference) | | | 1.00 (reference) | | | 1.00 (reference) | | | |
| | 11.675-11.887 | 27/29 | 1.40 (0.64-3.09) | | | 1.36 (0.6-3.15) | | | 1.68 (0.64-4.41) | | | |
| | >11.887 | 40/29 | 1.25 (0.99-5.12) | | | 2.44 (0.98-6.08) | | | 3.1 (1.08-8.92) | | | |
| Eotaxin | | | | 0.61 | 0.6 | | 0.5 | 0.8 | | 0.7 | 0.9 | |
| | <4 | 28/28 | 1.00 (reference) | | | 1.00 (reference) | | | 1.00 (reference) | | | |
| | 4-4.435 | 24/29 | 0.78 (0.35-1.73) | | | 0.64 (0.28-1.48) | | | 0.67 (0.26-1.73) | | | |
| | >4.435 | 34/29 | 1.16 (0.58-2.31) | | | 0.91 (0.43-1.94) | | | 0.91 (0.42-2) | | | |
| IP10 | | | | 0.23 | 0.4 | | 0.18 | 0.3 | | 0.4 | 0.8 | |
| | <3.537 | 29/28 | 1.00 (reference) | | | 1.00 (reference) | | | 1.00 (reference) | | | |
| | 3.537-3.907 | 20/29 | 0.61 (0.24-1.55) | | | 0.56 (0.19-1.66) | | | 0.52 (0.16-1.65) | | | |
| | >3.907 | 37/29 | 1.27 (0.53-3.05) | | | 1.32 (0.51-3.44) | | | 0.97 (0.35-2.73) | | | |

Table 3. Crude and multivariable-adjusted ORs and 95% CIs of NHL cases by tertiles of plasma cytokine concentrations in EPIC Italy (Cont'd)

NOTE: ORs estimated by CLR models for tertiles of plasma cytokine concentrations (tertile cut points based on the distribution of cytokine levels for control subjects). P trend = P value (two-sided) were calculated by including the median of each tertile of cytokine concentrations as continuous variables in addition to all covariates to the multivariate models. *Type III P value.

[†]*P* value of Wald χ^2 test.

subject compared with the variance between subjects at least in a 2-week period. It was concluded that, therefore, a single plasma or serum cytokine measurement possibly could be used to characterize an individual's immune profile.

We had a relatively high interbatch coefficient of variation (~30%) in the current study. However, as the case-control pair samples were analyzed next to each other (randomized order) in the same batch, the interbatch variability will not have affected the case-control comparisons. In contrast, the intrabatch coefficient of variation was on average small (~7%). Another potential limitation is that after blood collection cytokines are being excreted from cells as an emergency response. Therefore, the time between blood collection and storage can be important. In our study, the time between blood collection and storage was relatively short (median, 4 h) and did not differ between cases and controls. We explored this issue further by excluding samples that

were not stored within 12 hours of collection. These analyses resulted in observations similar to the main analyses. Although we could not control for some of the known risk factors for NHL (i.e., occupation exposures, viral infections, or some previous immune diseases), they are unlikely to have confounded our results, as the prevalence of these risk factors is low in the general population. Previous studies on polymorphisms in cytokine genes have shown that the effects of these genes were related to specific NHL subtypes. Unfortunately, our study was too small to investigate the association of cytokines with specific subtypes of NHL.

Blood cytokines are produced not only by those cell types considered to play pivotal roles in the immune system as well as in inflammatory responses, including lymphocytes, monocytes, and mast cells, but also by macrophages and, for some cytokines, also fibroblasts, neutrophils, and endothelial cells (26). So, it should be noted that plasma level of cytokines may not necessarily reflect activity in the target tissue (lymph nodes). Lastly, although we found some evidence of cytokine levels being associated with NHL risk, it is important to notice that analyses of a large number of cytokines may produce statistically significant associations simply by chance. Moreover, due to small sample size of the study, it is possible that some associations between these immune system molecules and NHL were missed. It is therefore important that our findings are replicated in larger studies.

In conclusion, our findings suggest a possible association between plasma levels of IL2, ICAM, IFN- γ , and TNF- α with NHL risk and provided some evidence that risk of NHL might be related to a chronic inflammatory environment as well as a shift in the balance of Th1/Th2 cytokines.

References

- Harris NL, Jaffe ES, Diebold J, Flandrin G, Muller-Hermelink HK, Vardiman J. Lymphoma classification—from controversy to consensus: the R.E.A.L. and WHO classification of lymphoid neoplasms. Ann Oncol 2000;11:3–10.
- Skibola CF. Obesity, diet and risk of non-Hodgkin lymphoma. Cancer Epidemiol Biomarkers Prev 2007;16:392–5.
- Grulich AE, Vajdic CM, Cozen W. Altered immunity as a risk factor for non-Hodgkin lymphoma. Cancer Epidemiol Biomarkers Prev 2007; 16:405–8.
- Engels EA, Cerhan JR, Linet MS, et al. Immune-related conditions and immune-modulating medications as risk factors for non-Hodgkin's lymphoma: a case-control study. Am J Epidemiol 2005; 162:1153–61.
- Engels E. Infectious agents as causes of non-Hodgkin lymphoma. Cancer Epidemiol Biomarkers Prev 2007;16:401–4.
- Muller AM, Ihorst G, Mertelsmann R, Engelhardt M. Epidemiology of non-Hodgkin lymphoma (NHL): trends, geographic distribution, and etiology. Ann Hematol 2005;84:1–12.
- Cartwright R, Brincker H, Carli PM, et al. The rise in incidence of lymphomas in Europe 1985-1992. Eur J Cancer 1999;35:627–33.
- Morgen G, Vornanen M, Puitinen J, Naukkarinen A, Brincker H, Oslen J. Changing trends in the incidence of non-Hodgkin's lymphoma in Europe. Ann Oncol 1997;8:S49–54.
- Chiu BC, Weisenburger DD. An update of the epidemiology of non-Hodgkin lymphoma. Clin Lymphoma 2003;4:161–8.
- Vineis P, D'Amore F, Working Group on the Epidemiology of Hematolymphopoietic Malignancies in Italy. The role of occupational exposure and immunodeficiency in B-cell malignancies. Epidemiology 1992;3:266–70.
- Rothman N, Skibola CF, Wang SS, et al. Genetic variation in TNF and IL10 and risk of non-Hodgkin lymphomas: a report from InterLymph Consortium. Lancet Oncol 2006;7:27–38.
- Lan Q, Zheng T, Rothman N, et al. Cytokine polymorphisms in the Th1/Th2 pathway and susceptibility to non-Hodgkin lymphoma. Blood 2006;107:4101–8.
- Wang SS, Cozen W, Cerhan JR, et al. Immune mechanisms in non-Hodgkin lymphoma: joint effects of the TNF G308A and IL10 T3575A polymorphisms with non-Hodgkin lymphoma risk factors. Cancer Res 2007;67:5042–54.
- 14. Bel Hadj Jrad B, Chatti A, Laatiri A, et al. Tumor necrosis factor promoter gene polymorphism associated with increased susceptibility to non-Hodgkin's lymphomas. Eur J Haematol 2006;78:117–22.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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- Purdue MP, Lan Q, Kricker A, et al. Polymorphisms in immune function genes and risk of non-Hodgkin lymphoma: finding from the New South Wales non-Hodgkin Lymphoma Study. Carcinogenesis 2007; 28:704–12.
- Cerhan JR, Ansell SM, Fredericksen ZS, et al. Genetic variation in 1253 immune and inflammation genes and risk of non-Hodgkin lymphoma. Blood 2007;110:4455–63.
- Breen EC, van der Meijden M, Cumberland W, Kishimoto T, Detels R, Martinez-Maza O. The development of AIDS-associated Burkitt's/ small non-cleaved lymphoma is preceded by elevated serum levels of interleukin 6. Clin Immunol 1999;92:293–8.
- Breen EC, Boscardin WJ, Detels R, et al. Non-Hodgkin's B cell lymphoma in persons with acquired immunodeficiency syndrome is associated with increased serum levels of IL10, or the IL10 promoter-592 C/C genotype. Clin Immunol 2003;109:119–29.
- Riboli E, Hunt KJ, Slimani N, et al. European Prospective Investigation into Cancer and Nutrition (EPIC): study populations and data collection. Public Health Nutr 2002;5:1113–24.
- de Jager W, te Velthuis H, Prakken BJ, Kuis W, Rijkers GT. Simultaneous detection of 15 human cytokines in a single sample of stimulated peripheral blood mononuclear cells. Clin Diagn Lab Immunol 2003;10:133–9.
- Saberi Hosnijeh F, Krop EJM, Portengen L, et al. Stability and reproducibility of simultaneously detected plasma and serum cytokine levels in asymptomatic persons. Biomarkers 2010;15:140–8.
- Lubin JH, Colt JS, Camann D, et al. Epidemiologic evaluation of measurement data in the presence of detection limits. Environ Health Prospect 2004;112:1691–6.
- 23. Rothlein R, Cajkowski M, O'neill MM, Marlin SD, Mainolfi E, Merluzzi VJ. Induction of intercellular adhesion molecule 1 on primary and continuous cell lines by pro-inflammatory cytokines. Regulation by pharmacologic agents and neutralizing antibodies. J Immunol 1988;141:1665–9.
- Roos E. Adhesion molecules in lymphoma metastasis. Cancer Metastasis Rev 1991;10:33–48.
- Mori T, Takada R, Watanabe R, Okamoto S, Ikeda Y. T-helper (Th) 1/(Th)2 imbalance in patients with previously untreated B-cell diffuse large cell lymphoma. Cancer Immunol Immunother 2001;50: 566–8.
- Jason J, Archibald LK, Nwanyanwu OC, et al. Comparison of serum and cell-specific cytokines in humans. Clin Diagn Lab Immunol 2001; 8:1097–103.