

# Predictors of global methylation levels in blood DNA of healthy subjects: a combined analysis

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**Accepted** 4 August 2010

**Background** Estimates of global DNA methylation from repetitive DNA elements, such as Alu and LINE-1, have been increasingly used in epidemiological investigations because of their relative low-cost, high-throughput and quantitative results. Nevertheless, determinants of these methylation measures in healthy individuals are still largely unknown. The aim of this study was to examine whether age, gender, smoking habits, alcohol drinking and body mass index (BMI) are associated with Alu or LINE-1 methylation levels in blood leucocyte DNA of healthy individuals.

**Methods** Individual data from five studies including a total of 1465 healthy subjects were combined. DNA methylation was quantified by PCR-pyrosequencing.

**Results** Age [ $\beta = -0.011\%$  of 5-methyl-cytosine (%5mC)/year, 95% confidence interval (CI)  $-0.020$  to  $-0.001\%$ 5mC/year] and alcohol drinking ( $\beta = -0.214$ , 95% CI  $-0.415$  to  $-0.013$ ) were inversely associated with Alu methylation. Compared with females, males had lower Alu methylation ( $\beta = -0.385$ , 95% CI  $-0.665$  to  $-0.104$ ) and higher LINE-1 methylation ( $\beta = 0.796$ , 95% CI  $0.261$  to  $1.330$ ). No associations were found with smoking or BMI. Percent neutrophils and lymphocytes in blood counts exhibited a positive ( $\beta = 0.036$ , 95% CI  $0.010$  to  $0.061$ ) and negative ( $\beta = -0.038$ , 95% CI  $-0.065$  to  $-0.012$ ) association with LINE-1 methylation, respectively.

**Conclusions** Global methylation measures in blood DNA vary in relation with certain host and lifestyle characteristics, including age, gender,

alcohol drinking and white blood cell counts. These findings need to be considered in designing epidemiological investigations aimed at identifying associations between DNA methylation and health outcomes.

**Keywords** Blood, DNA methylation, epigenetics, meta-analysis, repetitive elements

## Introduction

DNA methylation is a well-defined epigenetic mechanism involved in the regulation of a wide variety of biological processes, including gene expression, genomic stability and parental imprinting.<sup>1</sup> In mammals, methylation involves addition of methyl groups to cytosine to form 5-methyl-cytosine (5mC). It is estimated that more than one-third of DNA methylation occurs in repetitive elements,<sup>2,3</sup> which represent a large portion of the human genome.<sup>4</sup> Among these repetitive sequences, Alu and LINE-1 are the most plentiful families representing ~30% of the human genome.<sup>5–7</sup> Because of their high representation throughout the genome, Alu and LINE-1 have been used as surrogate markers for estimating global DNA methylation levels.<sup>8,9</sup> Methodologically, a high-throughput quantitative method based on bisulphite treatment of DNA and subsequent PCR pyrosequencing<sup>9</sup> or real-time PCR<sup>8</sup> has been developed for estimating global DNA methylation levels of Alu and LINE-1 elements. This method is amenable to use in screening large sets of samples because it is cost-effective and requires relatively small amounts of genomic DNA. As a result, DNA methylation analysis of Alu and/or LINE-1 methylation has been used in a number of epidemiological investigations.<sup>10–27</sup> Because of the growing interest in DNA methylation, as well as the wide availability of the technology necessary to conduct DNA methylation analyses, the number of epidemiological investigations involving DNA methylation measures will increase rapidly in the next few years. Information about how DNA methylation measures vary in relation with subjects' characteristics and other information commonly collected in epidemiological investigations will be relevant for effective design and statistical analysis of such studies.

Abnormal DNA methylation patterns have been associated with various human diseases, including cancer, cardiovascular disease and autoimmune disease.<sup>28–30</sup> In healthy populations, inter-individual methylation variations at Alu and LINE-1 elements from blood DNA have also been associated with risk factors for cancer and neurological and cardiovascular diseases.<sup>10–13</sup> As recently discussed by Foley *et al.*,<sup>31</sup> the identification and validation of epigenetic markers measured in easily obtainable tissues will be required for epidemiologic studies to benefit from

incorporation of epigenetics. Among the biospecimens suitable for DNA methylation analysis, blood DNA has been the most widely collected in epidemiology investigations. Although global DNA methylation levels have been proposed to be influenced by a number of endogenous and exogenous parameters,<sup>32</sup> determinants of blood DNA methylation in repetitive elements in healthy individuals are still largely unexplored.

Although a number of demographic and lifestyle factors have been associated with global hypomethylation, the results have been inconsistent, including those from our own studies.<sup>12–14</sup> Because of the moderate inter-individual differences in global methylation measures in blood leucocyte DNA, the limited sample size of each investigation may have contributed to the inconsistencies. In a study of elderly individuals in the VA Normative Aging Study (NAS), we have shown that repetitive element methylation was cross-sectionally associated with age, particularly in the Alu element.<sup>14</sup> In the present work on a combined analysis of 1465 subjects from five investigations, we sought to determine the association of age, gender, smoking habits, alcohol drinking and body mass index (BMI) with the methylation status of Alu and LINE-1 elements among healthy individuals. Because DNA methylation was analysed on DNA from white blood cells in all studies, whether differences in white blood cell count were associated with Alu and LINE-1 methylation was also explored.

## Methods

### Study populations

Individual data from five studies were combined, including a total of 1465 healthy subjects: (i) 722 subjects from the VA NAS in Eastern Massachusetts, USA; (ii) 421 subjects from controls of a population-based case-control study of gastric cancer conducted in Warsaw, Poland; (iii) 211 subjects from a cross-sectional study of low benzene exposure conducted in Milan, Italy; (iv) 63 healthy workers from a steel plant in Brescia, Italy and (v) 48 healthy workers from a perfluorooctanoic acid (PFOA) production facility in Trissino, Italy. All participants in Studies 2, 3, 4 and 5, and 98.2% in Study 1 were Caucasians. Detailed information about gender, age, height, weight, drinking and smoking was obtained by structured questionnaires, either self-administered (Studies

1, 3 and 4) or through in-person interviews (Studies 2 and 5). White blood cell counts were performed on fresh blood using automated methods (Coulter Cell Counter, Abbott or Bayer) within 3 h from the time of blood drawing for all studies. Informed consent was obtained from all participants, and the ethical committees of all participating centres approved the studies. Details on each of the studies are provided below.

Study 1 included 722 men who were evaluated between March 1999 and October 2007 as part of the NAS, a longitudinal study of normal ageing established in 1963 by the US Veterans Administration.<sup>33</sup> The men, in the age range of 55–100 years during 1999–2007, are given a health examination every 3–5 years and asked to donate a 7-ml blood sample at each visit. DNA methylation data from only the first blood sample of each study participant was included in our analysis.

Study 2 was a population-based case–control study of gastric cancer conducted in Warsaw, Poland, during 1994–96.<sup>34</sup> Four hundred and twenty-one subjects included in the present analysis were non-cancer controls randomly selected from a computerized registry of the Warsaw population, frequency matched by age and gender to the cases.

Study 3 was carried out among residents of Milan, Italy, from October 1999 to June 2000.<sup>12</sup> This study included 77 gasoline-station attendants, 77 traffic-control officers (both groups exposed to low benzene levels) and 57 office workers. All subjects were free of major illnesses.

Study 4 included 63 healthy male workers from a steel production plant in Brescia, Italy.<sup>17</sup> Between April and May 2006, every subject was asked to donate a blood sample at two different times. In the current study, only blood samples of every participant collected in the morning of the first work week day (after 2 days off work) before the beginning of any work activity were analysed.

Study 5 included 48 male workers who were employed in PFOA production during 1978–2007.<sup>35</sup> Blood samples were collected in 2007, when 35 were still active workers in the PFOA department, whereas 13 were no longer exposed after retirement or being transferred to other departments.

### Completeness of the data

Some of the variables evaluated in our analysis were not available in all studies. BMI of the 211 subjects from Study 3 and information on alcohol drinking about the 63 subjects from Study 4 were not recorded. Detailed information on smoking except for smoking status (non-smoker, former and current smoker) was not collected from the 48 subjects from Study 5. In addition, white blood cell count data were not available on the 421 subjects from Study 2, and only data on lymphocyte and monocyte counts, but

not on neutrophils, eosinophils and basophils, were available on the 63 subjects from Study 4.

### Definition of the variables of interest

All variables used in the present analysis were defined for all studies using the same criteria. An ever smoker was defined as a smoker of at least one cigarette per day for 6 months or longer. Pack-years of smoking were calculated as the product of packs of cigarettes smoked per day and total years of smoking. An ever drinker was defined as a person who reported drinking alcoholic beverage at least once per month for 6 months or longer. The age and BMI at blood draw were used for all analyses.

### Alu and LINE-1 methylation analyses

Alu and LINE-1 methylation analyses were conducted using the method developed by Yang *et al.*<sup>9</sup> for all the studies, as previously described.<sup>12,14,17</sup> One of the study collaborators (V.B.) participated in all DNA methylation analyses, either by directly performing them or supervising the laboratory-protocol application. Blood leucocyte DNA was extracted, bisulphite treated and PCR amplified. Pyrosequencing was done using the PSQHS96 Pyrosequencing System (Pyrosequencing). The degree of methylation was expressed for both Alu and LINE-1 as percentage of methylated cytosines (%5mC). For all assays, built-in controls were used to verify bisulphite conversion. Each marker was tested in at least two replicates and their average was used in the statistical analysis. The within-sample coefficient variations in duplicate runs were 7.0 and 5.3% for Alu and LINE-1, respectively. Samples were dropped from analysis when replication failed or replicates were not within a specified range (5%). Pyrosequencing data for each marker were successfully obtained for  $\geq 98.6\%$  of the samples.

### Statistical methods

Multivariable linear regression models were used to evaluate Alu and LINE-1 methylation levels in relation to (i) subjects' characteristics (age, gender, BMI, smoking status, current cigarettes/day, past cigarettes/day, total smoking years, pack-years, age smoking started, age smoking stopped and alcohol drinking), with adjustment for age (as a continuous variable), gender (male vs female) and study (using indicator variables), and to (ii) total number of white blood cells and the proportions of white blood cell types (neutrophils, lymphocytes, monocytes, eosinophils and basophils) with adjustment for age (as a continuous variable), gender (male vs female), alcohol drinking (ever drinker vs non-drinker) and study (using indicator variables). To evaluate whether differences in differential blood counts confounded the potential associations between subjects' characteristics and DNA methylation, multivariable models were fitted

adjusting for percent lymphocytes, in addition to age, gender and study. Since blood count data were missing in Study 2 (Warsaw, Poland), percent lymphocyte data were imputed using linear prediction from a multiple-equation (ME) regression model<sup>36</sup> that included age, gender, smoking status, current cigarettes/day, pack-years and alcohol drinking. All statistical analyses were conducted using Stata 10.1 (Stata Corporation, College Station, TX).

## Results

The characteristics of the study populations, as well as of the combined data, are shown in Table 1. In the combined data, mean blood DNA methylation levels, expressed as percentage of methylated cytosines, were 26.0 [standard deviation (SD) = 1.8] for Alu, and 76.2 (SD = 6.2) for LINE-1.

The associations between the subjects' characteristics and Alu and LINE-1 methylation are shown in combination, as well as within each of the studies (Table 2). In the combined data, age ( $\beta = -0.011\%$  5mC/year, 95% CI  $-0.020$  to  $-0.001\%$  5mC/year) was negatively associated with DNA methylation in Alu elements. Compared with females, males had lower Alu methylation levels ( $\beta = -0.385$ , 95% CI  $-0.665$  to  $-0.104$ ) but higher LINE-1 methylation levels ( $\beta = 0.796$ , 95% CI  $0.261$  to  $1.330$ ). As Studies 1, 4 and 5 contained males only, further analyses of gender in relation to Alu and LINE-1 methylation were repeated using only subjects from Studies 2 and 3. In this analysis (Supplementary Table S1 available at *IJE* online), no major differences in effect estimates were observed from the results reported above. In addition, alcohol drinkers tended to have lower Alu methylation levels than non-drinkers ( $\beta = -0.214$ , 95% CI  $-0.415$  to  $-0.013$ ). Age and alcohol drinking showed no association with LINE-1 methylation level. DNA methylation in both Alu and LINE-1 elements was not associated with BMI, smoking status (Table 2), current cigarettes/day, past cigarettes/day, total smoking years, pack-years, age smoking started or age smoking stopped (data not shown). Further analyses on the associations of age, gender and BMI with Alu and LINE-1 methylation were conducted on subsets of the study population by including alcohol drinkers only ( $n = 246$ ), smokers only ( $n = 371$ ) or individuals who were both alcohol drinkers and smokers ( $n = 481$ ). These sets of analyses produced comparable results (data not shown). As smoking habits, alcohol drinking, and BMI differed between males and females ( $P < 0.001$  for all, Table 1), we also performed gender-stratified analyses of smoking habits, alcohol drinking and BMI, which showed no major differences in their associations with Alu or LINE-1 methylation (data not shown). Since 265 subjects (18.1% of the total number of subjects) were exposed to certain occupational pollutants, including benzene,<sup>12</sup> particulate matter<sup>17</sup> and PFOA,<sup>35</sup>

which may exert some effects on global DNA methylation and thus modify the effects of characteristics on global DNA methylation, further association analyses of subjects' characteristics with DNA methylation were repeated by excluding these exposed subjects. In this analysis (Supplementary Table S2 available at *IJE* online), only minor departures of the effect estimates were observed from the results based on the total number of subjects.

As DNA methylation was measured on white blood cells, whether the differential white blood cell count was associated with Alu and LINE-1 element methylation was examined (Table 3). The total number of white blood cells was not associated with either Alu or LINE-1 methylation. Percent neutrophils and lymphocytes, the two major types of white blood cells, were inversely correlated with each other ( $r = -0.936$ ,  $P < 0.001$ ) and exhibited a positive ( $\beta = 0.036$ , 95% CI  $0.010$  to  $0.061$ ) and negative ( $\beta = -0.038$ , 95% CI  $-0.065$  to  $-0.012$ ) association with LINE-1 methylation, respectively. No association between the differential blood count and Alu element methylation was found. Adding percent lymphocytes into multivariable linear regression models produced no major difference in the effects of characteristics on Alu and LINE-1 methylation level (Table 4). When these analyses were repeated without imputation of percent lymphocytes for Study 2 (i.e. by excluding Study 2), the results were generally similar to the ones reported (data not shown). The only noticeable difference was that alcohol drinking was not associated with Alu methylation in this set of models ( $\beta = -0.178$ , 95% CI  $-0.433$  to  $0.076$ ). However, this appeared to result from the exclusion of Study 2, which was the study with the highest number of ever drinkers ( $n = 283$ ), rather than from adjustment for percent lymphocytes, as also demonstrated in a model adjusting for age, gender and study, but not for percent lymphocytes, fitted without including Study 2 ( $\beta$  for alcohol drinking =  $-0.177$ , 95% CI  $-0.428$  to  $0.073$ ).

## Discussion

In a combined analysis of blood DNA methylation from five investigations, we showed that age, gender and alcohol drinking are predictors for global methylation levels in blood DNA from healthy subjects. In particular, age and alcohol were inversely associated with Alu element methylation. Gender had opposite associations with Alu and LINE-1 methylation levels, with males having lower Alu and higher LINE-1 methylation levels than females. We also showed that the neutrophil and lymphocyte proportions of white blood cell types modified LINE-1 methylation levels measured in blood DNA but did not confound the association between global methylation levels and subjects' age, gender and alcohol drinking. Although Alu and LINE-1 methylation

**Table 1** Subject characteristics of the five studies included in a combined analysis of determinants of blood DNA methylation in repetitive elements in healthy individuals [mean or *n* (%)]

Variable	Study 1 Boston, USA ( <i>n</i> =722)	Study 2 Warsaw, Poland ( <i>n</i> =421)	Study 3 Milan, Italy ( <i>n</i> =211)	Study 4 Brescia, Italy ( <i>n</i> =63)	Study 5 Trissino, Italy ( <i>n</i> =48)	All studies ( <i>n</i> =1465)
Age, years (min-max)	72 (55-100)	63 (28-80)	37 (19-74)	44 (27-55)	43 (26-62)	62 (19-100)
Gender, <i>n</i> (%)						
Female	0 (0.0)	149 (35.4)	58 (27.5)	0 (0.0)	0 (0.0)	207 (14.1)
Male	722 (100.0)	272 (64.6)	153 (72.5)	63 (100.0)	48 (100.0)	1258 (85.9)
BMI, kg/m <sup>2</sup> (SD)	28.2 (4.1)	25.7 (3.7)	NA	26.5 (2.7)	25.5 (2.9)	27.2 (4.0)
Smoking status, <i>n</i> (%)						
Non-smoker	212 (29.4)	169 (40.1)	95 (45.0)	20 (33.3)	28 (58.3)	524 (35.8)
Former smoker	482 (66.8)	143 (34.0)	33 (15.6)	15 (25.0)	2 (4.2)	675 (46.2)
Current smoker	28 (3.9)	109 (25.9)	83 (39.3)	25 (41.7)	18 (37.5)	263 (18.0)
Current cigarettes, <i>n</i> /day (min-max)	20 (3-40)	18 (2-97)	15 (1-40)	13 (1-30)	NA	17 (1-97)
Past cigarettes, <i>n</i> /day (min-max)	26 (1-144)	21 (2-97)	19 (2-60)	17 (5-50)	NA	24 (1-144)
Total smoking years (min-max)	24 (1-63)	30 (1-59)	19 (1-48)	21 (3-38)	NA	25 (1-63)
Pack-years of smoking (min-max)	32 (0.1-267)	31 (0.1-162)	17 (0.3-82)	16 (0.7-50)	NA	29 (0.1-267)
Age smoking started, years (min-max)	18 (6-44)	20 (11-73)	17 (13-28)	18 (10-30)	NA	18 (6-73)
Age smoking stopped, years (min-max)	42 (13-84)	49 (19-75)	33 (19-56)	34 (20-53)	NA	43 (13-84)
Alcohol drinking, <i>n</i> (%)						
Non-drinker	390 (58.4)	138 (32.8)	77 (36.8)	NA	14 (29.2)	619 (46.0)
Ever drinker	278 (41.6)	283 (67.2)	132 (63.2)	NA	34 (70.8)	727 (54.0)
Blood count						
White blood cells, 10 <sup>3</sup> cell/mm <sup>3</sup> (min-max)	6.6 (1.8-16.4)	NA	7.1 (3.5-18.5)	7.3 (3.6-10.4)	7.0 (4.1-12.6)	6.6 (1.8-18.5)
Neutrophils, % (min-max)	62.2 (31-85)	NA	54.5 (33.7-84.3)	NA	53.3 (34.7-87.9)	60.1 (31-87.9)
Lymphocytes, % (min-max)	25.5 (5-65)	NA	34.3 (8.5-55.5)	30.7 (15.4-44.1)	36.1 (7.7-60.1)	28.2 (5-65)
Monocytes, % (min-max)	8.7 (2-17)	NA	8.0 (2.6-14.5)	10.4 (4.5-19.4)	9.1 (4.2-18.7)	8.7 (2-19.4)
Eosinophils, % (min-max)	3.3 (0-22)	NA	2.9 (0.1-9.2)	NA	2.8 (0.1-7.1)	3.2 (0-22)
Basophils, % (min-max)	0.6 (0-2)	NA	0.3 (0-1.5)	NA	0.4 (0-1.4)	0.5 (0-2)
DNA methylation, %5mC (SD)						
Alu	26.3 (1.1)	25.1 (1.4)	27.1 (3.4)	25.8 (0.7)	24.9 (1.0)	26.0 (1.8)
LINE-1	76.9 (2.0)	80.2 (3.2)	71.7 (5.9)	78.8 (1.0)	78.7 (3.2)	76.2 (6.2)

%5mC, percentage of 5-methyl cytosine; max, maximum; min, minimum; NA, not available; SD, standard deviation.

**Table 2** Association of Alu and LINE-1 methylation with the characteristics of the study subjects, in combination as well as within each of the five studies

Variable	Alu				LINE-1			
	N	%5mC <sup>a</sup>	95% CI <sup>a</sup>	$\beta$ (95% CI) <sup>a</sup>	N	%5mC <sup>a</sup>	95% CI <sup>a</sup>	$\beta$ (95% CI) <sup>a</sup>
<b>All studies</b>								
Age, years								
<48	285	26.1	25.8–26.4		264	77.2	76.7–77.8	
48–63	279	26.0	25.8–26.2		271	77.4	77.0–77.8	
64–69	314	26.0	25.8–26.2		307	77.2	76.8–77.6	
70–74	267	25.9	25.7–26.1		263	77.1	76.7–77.6	
≥75	320	25.9	25.7–26.1	−0.011 (−0.020 to −0.001) <sup>b</sup>	313	77.2	76.8–77.6	0.003 (−0.016 to 0.021) <sup>b</sup>
Gender								
Female	206	26.3	26.1–26.6		202	76.6	76.1–77.0	
Male	1238	25.9	25.8–26.0	−0.385 (−0.665 to −0.104)	1216	77.4	77.2–77.5	0.796 (0.261 to 1.330)
BMI, kg/m <sup>2</sup>								
<25.3	413	25.8	25.7–25.9		408	78.0	77.8–78.3	
25.3–28.5	415	25.8	25.6–25.9		415	78.3	78.1–78.5	
≥28.6	410	25.9	25.7–26.0	0.012 (−0.005 to 0.030) <sup>b</sup>	408	78.2	78.0–78.4	0.003 (−0.033 to 0.040) <sup>b</sup>
Alcohol drinking								
Non-drinker	609	26.1	26.0–26.3		604	77.2	76.9–77.4	
Ever drinker	717	25.9	25.8–26.0	−0.214 (−0.415 to −0.013)	700	77.1	76.9–77.3	−0.053 (−0.430 to 0.323)
Smoking status								
Non-smoker	519	26.0	25.8–26.1		504	77.2	77.0–77.5	
Former smoker	665	26.0	25.9–26.1		659	77.3	77.0–77.5	
Current smoker	257	26.0	25.8–26.2		252	77.2	76.7–77.6	
Trend statistics				0.018 (−0.107 to 0.143)				−0.025 (−0.263 to 0.214)
<b>Study 1</b>								
Age, years								
<48	0	NA	NA		0	NA	NA	
48–63	63	26.5	26.2–26.7		63	77.4	77.0–77.9	
64–69	199	26.5	26.3–26.6		196	76.9	76.6–77.1	
70–74	185	26.3	26.1–26.4		186	76.8	76.5–77.1	
≥75	261	26.2	26.1–26.3	−0.022 (−0.034 to −0.010) <sup>b</sup>	258	76.9	76.6–77.1	−0.011 (−0.033 to 0.010) <sup>b</sup>
Gender								
Female	0	NA	NA		0	NA	NA	
Male	708	26.3	26.2–26.4	NA	703	76.9	76.8–77.0	NA
BMI, kg/m <sup>2</sup>								
<25.3	160	26.3	26.1–26.4		156	76.9	76.6–77.2	
25.3–28.5	251	26.3	26.1–26.4		252	77.0	76.7–77.2	
≥28.6	297	26.4	26.2–26.5	0.021 (0.001 to 0.041) <sup>b</sup>	295	76.9	76.6–77.1	0.005 (−0.032 to 0.042) <sup>b</sup>

(continued)

Table 2 Continued

Variable	Alu				LINE-1			
	N	%5mC <sup>a</sup>	95% CI <sup>a</sup>	$\beta$ (95% CI) <sup>a</sup>	N	%5mC <sup>a</sup>	95% CI <sup>a</sup>	$\beta$ (95% CI) <sup>a</sup>
Alcohol drinking								
Non-drinker	383	26.3	26.2–26.5		381	76.7	76.5–76.9	
Ever drinker	271	26.3	26.2–26.4	–0.023 (–0.188 to 0.143)	272	76.9	76.7–77.1	0.239 (–0.037 to 0.515)
Smoking status								
Non-smoker	208	26.3	26.2–26.5		206	76.7	76.5–77.0	
Former smoker	473	26.3	26.2–26.4		470	76.9	76.8–77.1	
Current smoker	27	26.2	25.8–26.6		27	77.4	76.7–78.2	
Trend statistics				–0.015 (–0.173 to 0.143)				0.252 (–0.033 to 0.536)
<b>Study 2</b>								
Age, years								
<48	41	25.0	24.6–25.5		40	79.4	78.4–80.4	
48–63	141	25.1	24.8–25.3		141	80.5	79.9–81.0	
64–69	109	24.9	24.7–25.2		108	80.2	79.6–80.9	
70–74	75	24.9	24.6–25.3		75	80.2	79.5–80.9	
≥75	55	25.4	25.0–25.8	0.004 (–0.009 to 0.017) <sup>b</sup>	55	80.2	79.4–81.1	0.017 (–0.012 to 0.047) <sup>b</sup>
Gender								
Female	149	25.2	25.0–25.4		148	79.6	79.1–80.1	
Male	272	25.0	24.8–25.1	–0.201 (–0.486 to 0.084)	271	80.6	80.2–80.9	0.951 (0.304 to 1.597)
BMI, kg/m <sup>2</sup>								
<25.3	206	25.1	24.9–25.3		205	80.1	79.6–80.5	
25.3–28.5	126	25.0	24.7–25.2		125	80.4	79.8–81.0	
≥28.6	88	25.0	24.7–25.3	–0.013 (–0.051 to 0.025) <sup>b</sup>	88	80.3	79.6–81.0	–0.024 (–0.110 to 0.062) <sup>b</sup>
Alcohol drinking								
Non-drinker	138	25.2	24.9–25.5		138	80.4	79.8–81.0	
Ever drinker	283	25.0	24.8–25.2	–0.227 (–0.567 to 0.112)	281	80.2	79.8–80.6	–0.218 (–0.991 to 0.554)
Smoking status								
Non-smoker	169	24.9	24.7–25.1		168	80.3	79.7–80.8	
Former smoker	143	25.1	24.9–25.4		143	80.3	79.7–80.8	
Current smoker	109	25.2	24.9–25.5		108	80.1	79.5–80.8	
Trend statistics				0.136 (–0.046 to 0.317)				–0.053 (–0.466 to 0.361)
<b>Study 3</b>								
Age, years								
<48	164	27.2	26.7–27.7		150	71.8	70.8–72.7	
48–63	36	26.7	25.6–27.8		31	71.3	69.2–73.4	
64–69	3	26.8	23.0–30.7		3	72.7	65.9–79.4	
70–74	2	27.4	22.7–32.1		2	69.5	61.1–77.8	
≥75	0	NA	NA	–0.027 (–0.069 to 0.014) <sup>b</sup>	0	NA	NA	0.007 (–0.071 to 0.084) <sup>b</sup>

(continued)

**Table 2** Continued

Variable	Alu				LINE-1			
	N	%5mC <sup>a</sup>	95% CI <sup>a</sup>	$\beta$ (95% CI) <sup>a</sup>	N	%5mC <sup>a</sup>	95% CI <sup>a</sup>	$\beta$ (95% CI) <sup>a</sup>
Gender								
Female	57	27.6	26.8–28.5		54	71.4	69.8–73.0	
Male	148	26.9	26.3–27.4	–0.782 (–1.811 to 0.247)	132	71.8	70.8–72.8	0.397 (–1.500 to 2.294)
BMI, kg/m <sup>2</sup>								
<25.3	NA	NA	NA		NA	NA	NA	
25.3–28.5	NA	NA	NA		NA	NA	NA	
≥28.6	NA	NA	NA	NA	NA	NA	NA	NA
Alcohol drinking								
Non-drinker	74	27.6	26.7–28.4		71	72.3	70.8–73.8	
Ever drinker	129	26.8	26.2–27.4	–0.756 (–1.831 to 0.319)	113	71.2	70.0–72.3	–1.164 (–3.128 to 0.800)
Smoking status								
Non-smoker	94	27.2	26.5–27.8		82	72.0	70.7–73.3	
Former smoker	32	26.9	25.7–28.1		29	71.2	69.0–73.4	
Current smoker	79	27.1	26.3–27.8		75	71.5	70.2–72.9	
Trend statistics				–0.051 (–0.554 to 0.451)				–0.232 (–1.171 to 0.707)
<b>Study 4</b>								
Age, years								
<48	43	25.8	25.5–26.0		43	78.8	78.5–79.1	
48–63	19	26.0	25.7–26.3		19	78.9	78.4–79.3	
64–69	0	NA	NA		0	NA	NA	
70–74	0	NA	NA		0	NA	NA	
≥75	0	NA	NA	0.014 (–0.010 to 0.039) <sup>b</sup>	0	NA	NA	–0.006 (–0.040 to 0.027) <sup>b</sup>
Gender								
Female	0	NA	NA		0	NA	NA	
Male	62	25.8	25.7–26.0	NA	62	78.8	78.6–79.1	NA
BMI, kg/m <sup>2</sup>								
<25.3	21	25.7	25.4–26.0		21	79.1	78.7–79.5	
25.3–28.5	26	25.8	25.5–26.1		26	78.8	78.4–79.2	
≥28.6	15	26.0	25.6–26.4	0.035 (–0.034 to 0.104) <sup>b</sup>	15	78.4	77.9–78.9	–0.108 (–0.201 to –0.016) <sup>b</sup>
Alcohol drinking								
Non-drinker	NA	NA	NA		NA	NA	NA	
Ever drinker	NA	NA	NA	NA	NA	NA	NA	NA
Smoking status								
Non-smoker	20	26.2	25.9–26.5		20	78.8	78.3–79.2	
Former smoker	15	25.5	25.1–25.8		15	78.8	78.3–79.4	
Current smoker	24	25.9	25.6–26.1		24	78.9	78.4–79.3	
Trend statistics				–0.162 (–0.380 to 0.055)				0.057 (–0.259 to 0.373)

(continued)

Table 2 Continued

Variable	Alu				LINE-1			
	N	%5mC <sup>a</sup>	95% CI <sup>a</sup>	$\beta$ (95% CI) <sup>a</sup>	N	%5mC <sup>a</sup>	95% CI <sup>a</sup>	$\beta$ (95% CI) <sup>a</sup>
<b>Study 5</b>								
Age, years								
<48	31	24.9	24.6–25.3		31	79.1	77.9–80.2	
48–63	17	24.8	24.3–25.3		17	78.1	76.6–79.7	
64–69	0	NA	NA		0	NA	NA	
70–74	0	NA	NA		0	NA	NA	
≥75	0	NA	NA	0.006 (–0.025 to 0.037) <sup>b</sup>	0	NA	NA	–0.061 (–0.161 to 0.039) <sup>b</sup>
Gender								
Female	0	NA	NA		0	NA	NA	
Male	48	24.9	24.6–25.2	NA	48	78.7	77.8–79.7	NA
BMI, kg/m <sup>2</sup>								
<25.3	26	25.0	24.6–25.4		26	77.6	76.4–78.8	
25.3–28.5	12	24.6	24.1–25.2		12	79.7	77.9–81.5	
≥28.6	10	24.8	24.1–25.5	–0.093 (–0.198 to 0.011) <sup>b</sup>	10	80.5	78.5–82.5	0.386 (0.058 to 0.714) <sup>b</sup>
Alcohol drinking								
Non-drinker	14	25.4	24.8–25.9		14	77.6	75.8–79.5	
Ever drinker	34	24.7	24.3–25.0	–0.687 (–1.379 to 0.005)	34	79.2	78.0–80.3	1.557 (–0.722 to 3.836)
Smoking status								
Non-smoker	28	24.9	24.5–25.3		28	79.1	77.9–80.3	
Former smoker	2	25.3	23.8–26.8		2	74.5	70.0–79.1	
Current smoker	18	24.8	24.3–25.3		18	78.6	77.1–80.2	
Trend statistics				–0.027 (–0.341 to 0.287)				–0.290 (–1.300 to 0.719)

%5mC, percentage of 5-methyl cytosine; NA, not available.

<sup>a</sup>Adjusted for age, gender and study.

<sup>b</sup> $\beta$  for age and BMI were obtained using continuous variables.

Table 3 Effect of blood count on Alu and LINE-1 methylation (combined analysis of the five studies)

Blood count	Alu		LINE-1	
	N	$\beta$ (95% CI) <sup>a</sup>	N	$\beta$ (95% CI) <sup>a</sup>
White blood cells, 10 <sup>3</sup> cells/mm <sup>3</sup>	1013	0.001 (–0.060 to 0.062)	991	0.077 (–0.034 to 0.187)
Neutrophils, %	939	0.008 (–0.006 to 0.022)	917	0.036 (0.010 to 0.061)
Lymphocytes, %	1001	–0.009 (–0.023 to 0.006)	979	–0.038 (–0.065 to –0.012)
Monocytes, %	994	0.001 (–0.040 to 0.042)	972	–0.032 (–0.105 to 0.042)
Eosinophils, %	932	–0.012 (–0.070 to 0.047)	910	0.010 (–0.094 to 0.114)
Basophils, %	932	0.008 (–0.254 to 0.270)	910	–0.198 (–0.668 to 0.272)

<sup>a</sup>Adjusted for age, gender, alcohol drinking and study.

levels were shown to be correlated with each other in tumour tissue DNA,<sup>26</sup> no such correlation has been found in surrounding normal tissues<sup>26</sup> or in non-target tissues such as blood and buccal

cells.<sup>12,13,37</sup> In this respect, the differences between Alu and LINE-1 in methylation-regulation mechanisms,<sup>38</sup> responses to cellular stressors and environmental exposures<sup>12,13,37</sup> and average levels of DNA

**Table 4** Effects of age, gender and alcohol drinking on Alu and LINE-1 methylation in multivariable models including percent lymphocytes in blood count, age, gender and study as independent variables (combined analysis of the five studies)

Variable	Alu				LINE-1			
	N	%5mC <sup>a</sup>	95% CI <sup>a</sup>	$\beta$ (95% CI) <sup>a</sup>	N	%5mC <sup>a</sup>	95% CI <sup>a</sup>	$\beta$ (95% CI) <sup>a</sup>
Age, years								
<48	285	26.2	25.9–26.5		264	77.4	76.8–77.9	
48–63	279	26.0	25.8–26.2		271	77.5	77.1–77.9	
64–69	314	26.0	25.8–26.2		307	77.2	76.8–77.6	
70–74	267	25.9	25.7–26.1		263	77.1	76.7–77.5	
≥75	320	25.9	25.7–26.1	−0.012 (−0.022 to −0.002) <sup>b</sup>	313	77.1	76.7–77.5	−0.003 (−0.022 to 0.016) <sup>b</sup>
Gender								
Female	206	26.3	26.0–26.6		202	76.5	76.0–77.0	
Male	1238	25.9	25.8–26.0	−0.361 (−0.642 to −0.079)	1216	77.4	77.2–77.5	0.874 (0.339 to 1.409)
Alcohol drinking								
Non-drinker	609	26.1	26.0–26.3		604	77.2	76.9–77.4	
Ever drinker	717	25.9	25.8–26.0	−0.208 (−0.409 to −0.007)	700	77.1	76.9–77.3	−0.049 (−0.425 to 0.327)

%5mC, percentage of 5-methyl cytosine.

<sup>a</sup>Adjusted for age, gender, percent lymphocytes in blood count and study.

<sup>b</sup> $\beta$  for age were obtained using continuous variables.

methylation<sup>9,13</sup> may account for the different findings for Alu and LINE-1 methylation in association with the potential determinants evaluated in the present study, such as age, gender, alcohol drinking and the proportions of white blood cell types.

The effect of age on global DNA methylation has been widely discussed.<sup>39,40</sup> In analysis of blood DNA derived from healthy subjects, several studies based on relatively small study samples (between 76 and 237 subjects) reported an inverse association between age and genomic 5mC content,<sup>41,42</sup> concluding that age is an independent predictor for genomic 5mC content. However, several other similarly sized or larger studies (between 32 and 526 samples) reported no association of age with genomic 5mC content<sup>43</sup> or other estimates of global DNA methylation obtained from various genomic components, including LINE-1, Alu and CCGG sequences.<sup>13,44–46</sup> Our finding that Alu, but not LINE-1, methylation levels decreased in association with age suggests that age-related decreases in DNA methylation are not occurring homogeneously across the human genome. Also, our recent longitudinal analysis in the VA NAS,<sup>14</sup> along with analyses in the present study and in a previous investigation,<sup>41</sup> showed that age-related methylation alteration are small, particularly compared with the inter-individual variability in DNA methylation. Thus, the lack of association with age in several studies<sup>13,44–46</sup> could be partially due to smaller sample size, insufficient age-range evaluated and/or limitations of the analytical methods used.

We found that gender had opposite associations with Alu and LINE-1 methylation levels, with males having lower Alu but higher LINE-1 methylation levels. Previous studies have also observed that males, compared with females, had elevated LINE-1 methylation in blood DNA,<sup>15,45</sup> consistent with our data for LINE-1. Yet, our observation that males had lower Alu methylation levels may seem paradoxical. One of the two X chromosomes in females is transcriptionally inactive and heavily methylated. This, together with differences in Alu element density and composition between chromosome X and Y,<sup>5</sup> may partly account for the lower Alu methylation levels observed in males. Two investigations of global 5mC content, reflecting a net effect of increase and decrease of methylation of various components in genomic DNA,<sup>47</sup> revealed a higher global 5mC content of blood DNA in males than in females.<sup>41,42</sup> Our data seemed to be consistent with these findings, since male gender was associated with higher  $\beta$  estimates for LINE-1 ( $\beta=0.796$ ) than for Alu ( $\beta=-0.385$ ), which may contribute to an elevated net global methylation levels in males.

Smoking has been associated with a state of global hypomethylation in genomic DNA derived from tumour tissues in head and neck squamous cell carcinoma (HNSCC).<sup>19,45,48,49</sup> Vaissiere *et al.*<sup>50</sup> found that smoking was associated with increased methylation in lung cancer tissues of *MTHFR*, a gene participating in the methyl donor pathway, and that, in turn, *MTHFR* methylation showed a marked inverse

correlation with LINE-1 methylation. We hypothesized that smoking would exert effects on global methylation levels in genomic DNA derived from blood of healthy subjects, but we failed to find any association between smoking habits (smoking status, current cigarettes/day, past cigarettes/day, total smoking years, pack-years, age smoking started and age smoking stopped) and Alu or LINE-1 methylation levels. Consistent with our data, other studies of smoking effects on global methylation in blood DNA of healthy subjects also reported negative results.<sup>13,43,45</sup> The lack of association between smoking habits and global methylation in genomic DNA from blood of healthy subjects, which are at variance with inverse associations found in tumour tissues,<sup>19,45,48,49</sup> may suggest that smoking acts differently in different tissue types, or acts differently in healthy vs tumour tissues. Although we did not observe a direct effect of smoking on global DNA methylation among healthy subjects, a possible involvement of smoking in modifying global DNA methylation cannot be excluded. Hillemecher *et al.*<sup>51</sup> recently reported that smoking modifies the correlation between paternal and offspring DNA methylation. Although neither paternal smoking nor offspring smoking had any effect on global DNA methylation estimated in CCGG sequences, correlation between offspring and paternal DNA methylation was strongest when both were non-smokers, and absent when the offspring smoked.<sup>51</sup> In addition, Breton *et al.*<sup>52</sup> reported that prenatal exposure to tobacco smoke was associated with decreased global methylation level in buccal cell DNA in children. Because DNA methylation is largely established *in utero* or in early life,<sup>53</sup> these findings may reflect higher susceptibility to smoking in specific periods of life.

Several studies have examined the association between alcohol drinking and global 5mC content or LINE-1 element methylation in both normal and tumour tissue DNA, with most studies reporting no association.<sup>43,45,48,49</sup> Only one study of HNSCC tumour tissues reported that alcohol use was inversely associated with LINE-1 methylation levels in univariate analysis, but this significance disappeared in multivariate analysis.<sup>19</sup> In our data, no association was found between alcohol drinking and LINE-1 methylation, whereas we showed for the first time that drinking was inversely associated with Alu methylation levels. Alcohol drinkers might have lower intakes as well as lower serum levels of vitamin B<sub>12</sub> and folate<sup>54</sup> and thus have lower availability of methyl sources, as well as decreased efficiency of the enzymatic pathways responsible for DNA methylation.<sup>54,55</sup> In addition, animal models have shown that chronic alcohol exposure can decrease cytosine methyltransferase mRNA levels in sperm<sup>56</sup> and DNA methylation in tissues of liver and colon mucosa.<sup>57</sup> It should be noted that most of the studies included in the present analysis did not have detailed data on

alcohol drinking, which hindered our ability to further evaluate alcohol dose-related effects on global DNA methylation. Moreover, our present analysis, together with all other studies on the association between alcohol drinking and global DNA methylation,<sup>19,43,45,48,49</sup> mostly included social drinkers. Additional studies on alcohol abusers and dependence are required.

Our data showed that the proportions of white blood cell subsets affected LINE-1 methylation levels measured in blood DNA, with percent neutrophils and lymphocytes, the major types of white blood cells, exhibiting opposite effects on LINE-1 methylation levels. Previous studies have shown that there exist between-tissue methylation variations, which contribute to regulating functions that are specific to each tissue or cell types.<sup>58</sup> In the present work, further analysis showed that the addition in multivariable regression models of percent lymphocytes did not modify the associations of the subjects' characteristics we evaluated with repetitive-element methylation levels. However, the association we observed between differential white blood count and LINE-1 methylation indicates that findings from epidemiological studies based on DNA methylation analyses on blood DNA might be confounded by differences in the proportion of white blood cell types. This would be a concern for exposures or disease states that are associated with inflammatory responses that may produce shifts in white blood cell type proportions.<sup>59,60</sup>

Our study had the advantages of being based on a large sample size and accurate quantitative analysis using pyrosequencing methodology, which is suitable for measuring subtle changes in DNA methylation. In the present work, all DNA methylation analyses were performed using the same laboratory protocol, and each variable used in the present analysis was defined using the same criteria. To account for potential confounding due to differences between the five studies, all our analyses were adjusted by study using indicator variables in the regression models, thus also minimizing the potential effect on methylation caused by between-study differences in ethnic background, which has been shown to be associated with global DNA methylation levels,<sup>18,61</sup> as well as potential analytical batch effects. One limitation of our analysis is that results on the association of gender with LINE-1 or Alu methylation could be confounded by the origin of the study and by the difference in lifestyle factors between males and females. Only two (Studies 2 and 3) of the five studies used in the combined analysis included females (only 14.1% of the study subjects were females). In addition, smoking habits, alcohol drinking and BMI differed between males and females. However, similar effect estimates were observed after excluding studies containing males only (Studies 1, 4 and 5) from the analyses (Supplementary Table S1 available at *IJE* online), or by further adjusting for variables in multivariable

analyses that might have confounded the associations, including smoking habits, alcohol drinking, BMI and percent lymphocytes (data not shown). Nonetheless, it cannot be excluded that other unmeasured lifestyle or personal factors might underline the gender-related differences in DNA methylation levels we observed. Secondly, dietary differences were not investigated here, which may also influence methylation levels in genomic DNA.<sup>62</sup> Lastly, we assumed that DNA methylation in Alu and LINE-1 repetitive elements may be used as a surrogate for global DNA methylation content. However, methylation levels of both repetitive elements are not equivalent to, albeit vastly represents, global DNA methylation content.<sup>9</sup> Also, measures of repetitive element-based methylation analyses as used in the present study, representing a pool of multiple unique Alu or LINE-1 repeats in the entire genome, are different from measures of gene-specific or genome-wide array-based (genomic site-specific) methylation analyses, and thus the extent to which our conclusions apply to site-specific methylation measures remains to be determined. In particular, whereas the present associations of the variables we evaluated with Alu and/or LINE-1 methylation might suggest that there may also exist associations with gene-specific methylation, lack of association with Alu and LINE-1 methylation does not exclude associations with specific loci. Both Alu and LINE-1 methylation levels represent an average measure of methylation at multiple sites across the genome. Opposite concurrent changes of hypo- and hypermethylation might offset each other without being reflected in these average measures of methylation.

In conclusion, this combined analysis of blood DNA methylation showed that study participant data that are routinely collected in most epidemiological investigations, including age, gender and alcohol drinking,

are predictors of global DNA methylation levels. We also showed that the neutrophil and lymphocyte proportions of white blood cell types modified LINE-1 methylation level measured in blood DNA. These findings provide valuable information that can be used in planning future epidemiological studies, as well as in analysing existing data sets.

## Supplementary Data

Supplementary Data are available at *IJE* online.

## Funding

Study 1: National Institute of Environmental Health Sciences [ES015172-01] and Environmental Protection Agency [R83241601, R827353]. The VA Normative Aging Study is supported by the Cooperative Studies Program/Epidemiology Research and Information Center of the U.S. Department of Veterans Affairs and is a component of the Massachusetts Veterans Epidemiology Research and Information Center (MAVERIC). Study 2: Intramural Research Program (Division of Cancer Epidemiology and Genetics, NCI) of the National Institutes of Health, Diane Belfer Program for Human Microbial Diversity and the National Institutes of Health [R01GM63270]. Study 3: Italian Association for Cancer Research (AIRC) (2008–10) [6016]. Study 4: Cariplo Foundation [2007-5469] and Italian Ministry of Scientific Research (MIUR) [PRIN-20072S2HT8]. Study 5: Milan University intramural funding.

**Conflict of interest:** None declared.

### KEY MESSAGES

- Information on how global methylation measured in blood leucocyte DNA varies in relation with subjects' characteristics and other factors commonly collected in epidemiological investigations will be relevant for effective study design and statistical analysis.
- We showed that study participant data that are generally collected in most epidemiological investigations, including age, gender, alcohol drinking and blood neutrophil and lymphocyte proportions, are predictors of global DNA methylation levels.
- These findings need to be considered in designing epidemiological investigations aiming at identifying associations between DNA methylation and health outcomes.

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