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Multi-Vitamins, Folate, and Green Vegetables Protect Against Gene Promoter Methylation in the Aerodigestive Tract of Smokers

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Abstract

The detection of gene promoter hypermethylation in sputum is a promising molecular marker for early lung cancer detection. Epidemiologic studies suggest that dietary fruits and vegetables and the micronutrients they contain may reduce risk of lung cancer. This investigation evaluated whether diet and multi-vitamin use influence the prevalence for gene methylation in the cells exfoliated from the aerodigestive tract of current and former smokers. Members (n = 1101) of the Lovelace Smokers Cohort completed the Harvard Food Frequency Questionnaire and provided a sputum sample that was assessed for promoter methylation of eight genes commonly silenced in lung cancer and associated with risk for this disease. Methylation status was categorized as low (< 2 genes methylated) or high (≥ 2 genes methylated). Logistic regression models were used to identify associations between methylation status and 21 dietary variables hypothesized to affect the acquisition of gene methylation. Significant protection against methylation was observed for leafy green vegetables (OR = 0.83 per 12 monthly servings, CI: 0.74, 0.93) and folate (OR = 0.84 per 750 mcg/day, CI: 0.72, 0.99). Protection against gene methylation was also seen with current use of multi-vitamins (OR = 0.57, CI: 0.40, 0.83). This is the first cohort-based study to identify dietary factors associated with reduced promoter methylation in cells exfoliated from the airway epithelium of smokers. Novel interventions to prevent lung cancer should be developed based on the ability of diet and dietary supplements to affect reprogramming of the epigenome.

Keywords

gene methylation; folate; multi-vitamins; green vegetables; smokers

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Introduction

Lung cancer, the leading cause of cancer-related death in the U.S., occurs largely from chronic exposure to tobacco carcinogens (1). The development of this disease over 30–40 years involves field cancerization, characterized as the acquisition of genetic and epigenetic changes throughout the respiratory epithelium (2,3). The silencing of genes through promoter hypermethylation is now recognized as a major and causal epigenetic event that occurs during lung cancer initiation and progression to affect the function of hundreds of genes. Gene silencing involves methylation of cytosines in the gene promoter region, recruitment of transcriptional co-repressors, and modification of histone tails that culminate in the establishment of chromatin modifications that block transcription (4,5). Genes involved in all aspects of normal cell function such as regulating the cell cycle, differentiation, adhesion, and death are silenced in lung tumors (3). Importantly, the tumor suppressor gene p16, which plays a critical role in regulating the cell cycle, is not only commonly silenced by methylation in lung cancer, but is also inactivated early in the development of this disease. Silencing of p16 and other genes are detected in bronchial epithelium of smokers and in precursor lesions to adenocarcinoma and squamous cell carcinoma and increase during disease progression, substantiating a vital role for gene silencing in lung cancer etiology (6–8).

Based on the silencing of key tumor suppressor genes in the lungs of smokers, we hypothesized that the detection of gene-specific promoter hypermethylation in exfoliated cells in sputum would provide an assessment of the extent of field cancerization that in turn may predict early lung cancer. This hypothesis has been validated in two studies, the first detecting methylation of the p16 and MGMT genes in sputum up to 3 years prior to clinical diagnosis of squamous cell carcinoma (9). The second study, a nested, case-control study of incident lung cancer cases from a high-risk cohort identified six genes associated with > 50% increased lung cancer risk. Importantly, concomitant methylation of three or more of these six genes was associated with a 6.5-fold increased risk of incident lung cancer and sensitivity and specificity both at 64% (10). These studies suggested that gene promoter hypermethylation in sputum could be used as a molecular marker for identifying people at high risk for cancer incidence (11). However, the precise mechanism by which carcinogens disrupt the capacity of cells to maintain the epigenetic code during DNA replication and repair are largely unknown.

The fact that gene promoter methylation is a promising marker for lung cancer makes understanding factors that influence the propensity for this epigenetic process throughout the respiratory epithelium a high priority, because such knowledge could be used not only for early detection, but to identify persons who would benefit most from chemoprevention. The precise mechanism by which carcinogens disrupt the capacity of cells to maintain the epigenetic code during DNA replication and repair are largely unknown. Carcinogens within tobacco induce single- and double-strand breaks in DNA and reduced DNA repair capacity (DRC) has been associated with lung cancer (12). Accumulating evidence from our group suggests that extensive DNA damage could be responsible for acquisition of gene promoter hypermethylation during lung carcinogenesis (3,13). Strong support for this supposition was provided through a recent community-based study in which a highly significant association was seen between DRC and sequence variants within specific DNA repair genes and the propensity for methylation of genes detected in sputum from cancer-free smokers from the Lovelace Smokers Cohort (14). Specifically, smokers with a high methylation index (defined by having ≥ 3 genes methylated from an 8-gene panel in sputum) had a 50% reduction in DRC compared to smokers with no genes methylated in sputum. Single nucleotide polymorphisms within five double-strand break DNA repair genes were also highly associated with methylation index. This study suggests that chronic DNA damage

coupled with reduced DRC could be an important determinant for inducing gene promoter hypermethylation.

Epidemiological studies suggest that select dietary nutrients and vitamin supplements might protect against lung cancer (15). Fruits, vegetables, and multi-vitamins all possess antioxidant activity that should reduce tobacco-induced DNA damage. In addition, folate, a B vitamin is metabolized to 5-methyltetrahydrofolate that provides methyl groups for S-adenosyl methionine, a universal donor for reactions that include methylation of DNA (16). Low folate has been associated with reduced DRC and an increase in prevalence for gene promoter methylation (17,18). The purpose of the current investigation was to determine whether diet and multi-vitamin use influence the presence of methylation in cells exfoliated from the aerodigestive tract of current and former smokers. Composite variables were selected based on our hypotheses that fruits, tomatoes, cruciferous vegetables, leafy vegetables, yellow vegetables, and vitamin intake will be associated with a reduction in number of genes methylated in sputum, while animal fat, red and processed meat will be associated with increased methylation.

Materials and Methods

Study Population

The Lovelace Smokers Cohort began recruitment of female smokers in 2001 and expanded to include male smokers in 2004 (14). Enrollment, which is still ongoing, is restricted to current and former smokers aged 40 to 75 with a minimum of 15 pack years of smoking. Participants primarily are residents of the Albuquerque, New Mexico metropolitan area. Participants complete a standard questionnaire covering demographics, smoking history, personal, and family health and a food frequency questionnaire. Weight and height are measured. Participants provide both blood and sputum samples and undergo standard pulmonary function testing. A total of 1145 people completed a food frequency questionnaire and were assessed for prevalence for methylation of eight genes in sputum. Those with caloric intake outside of gender specific bounds ($n = 44$) were excluded, resulting in a total of 1101 participants (845 women and 256 men) in this study. All participants signed a consent form, and the Western Institutional Review Board approved this project.

Dietary Questionnaire

Participants completed the adult version of the Harvard University Food Frequency Questionnaire Dietary Assessment form, a self-administered instrument that includes approximately 150 food items (19). The participant indicates consumption frequency for most food items by choosing one of five to ten categories that vary depending on the food item, and can range from never to six or more servings per day. A food group analysis was conducted to combine food items to obtain estimates of intake of macro and micronutrients. We focused on factors known or suspected of being associated with lung cancer or methylation. Thus, the macronutrients animal fat and total fat, and the micronutrients vitamin C, vitamin E, folate (that included supplements and fortified foods), carotene, alpha carotene, beta-carotene, lycopene, lutein and zeaxanthin, and retinol were examined. Alcohol, multi-vitamins, and cod liver oil intake were also assessed as categorical variables. In a study of eating patterns, Fung *et al.* (20) created a set of 38 composite variables using the food frequency questionnaire. Six of these composite variables, red and processed meats, fruit, tomatoes, cruciferous vegetables, leafy green vegetables and yellow vegetables, were related to our hypotheses, so we calculated these variables.

Total caloric intake was assessed. People with either extremely low ($n = 8$) or extremely high ($n = 36$) intake were excluded. Cut-offs for extremely low intake were < 500 calories and < 800 calories for women and men, respectively. Extremely high intake was defined as > 3500 and > 4200 calories for women and men, respectively. It is standard to exclude participants with at least 70 missing items on the food frequency questionnaire, but none of our participants met this criterion. Participants with missing data on individual food items were excluded from analyses of these items.

Methylation-Specific PCR (MSP)

Eight genes (p16, MGMT, DAPK, RASSF1A, PAX5 α , PAX5 β , GATA4 and GATA5) were selected for analysis of methylation in sputum based on our previous studies establishing their association with risk for lung cancer (10,21). DNA was isolated from sputum and modified with bisulfite as described (10). Nested MSP was used to detect methylated alleles from individual genes in DNA recovered from the sputum samples as described (21). Methylation index, the number of genes methylated in a sputum sample, was also defined. Sputum from males and females was randomly selected and included in batches of 96 samples for assessment of gene methylation. A Hamilton robot was used to assemble PCR reactions in 96 well plates.

Covariates

The questionnaire included questions on gender, age, ethnicity, and smoking. Cigarette smoking history included current status (former or current), pack years, and duration of smoking. Body mass index (BMI) was calculated from measured height and weight and categorized as normal ($< 25 \text{ kg/m}^2$), overweight ($25 - 29.9 \text{ kg/m}^2$) and obese ($\geq 30 \text{ kg/m}^2$). Age was categorized as 40 to 54, 55 to 64 and ≥ 65 years. Pack years of smoking were categorized as light (< 29), moderate (30 to 49), and heavy (≥ 50).

Statistical Methods

Demographic, dietary, and methylation variables were summarized overall and by gender. Proportions were used for categorical variables and medians with the interquartile range (IQR) for continuous variables. Differences between men and women in clinical covariates and categorical dietary variables were assessed with Fisher's exact test. For continuous dietary variables, a two-step linear regression analysis was used to account for differences in total caloric intake between genders. In the first step, the dietary variable was regressed on the total caloric intake. In the second step the residuals from the first analysis were regressed on gender, which resulted in an estimate of the differences in the mean dietary variable after adjustment for total caloric intake, along with 95% confidence intervals (CI).

The total number of methylated genes in the eight-gene panel was dichotomized into low (< 2 genes methylated) and high (≥ 2 genes methylated). This binary outcome, methylation status, was modeled with logistic regression. Initially only the clinical covariates gender, age, BMI, and three smoking variables (status, packyears and duration) were assessed. Interactions among the covariates, including interactions with gender, were evaluated. After the development of a model with only clinical covariates, individual dietary variables were included, along with adjustment for total caloric intake. Continuous variables such as total fat intake were included as a continuous variable or were categorized into quartiles, with the quartiles defined by gender and the quartile medians used as the predictor values. Interactions between dietary variables and clinical covariates were assessed. Only the 21 dietary variables specific to our hypothesis were examined to reduce the potential for false positive results. In addition, no formal adjustment for multiple comparisons was made to reduce the chance of false negative results since this is one of the first studies to examine the association between dietary factors and methylation. However, the issue of examining

multiple predictor variables is considered in the interpretation of the results. Methylation index was also used as the outcome variable to further assess the association between methylation and dietary factors. Since the methylation index could theoretically take on nine values, but actually took on only seven, it was unclear that linear regression would be appropriate. Thus, results obtained from linear and ordinal logistic regression were compared. The association between significant dietary factors and each of the individual genes was explored using logistic regression models, but viewed as secondary analyses to reduce the issue of multiple comparisons. All statistical analyses were conducted in SAS 9.2.

Results

Population Characteristics

The demographics and smoking history of the 1101 participants are described in Table 1. The Lovelace Smokers Cohort is largely comprised of females (76.7%) and non-Hispanic Whites (77.8%). Median age was 56 years, with males slightly older than females. Over half of the participants currently smoked and median duration of smoking was 33 years. There was no difference between men and women with regard to smoking status or duration, but men had significantly higher pack years of smoking (median = 39 pack-years for men versus 34 pack-years for women).

Summary of Dietary Intake

The completion rate of the food frequency questionnaire was excellent, as only 2.7% of participants failed to respond to more than 10 items. Dietary information was compiled for the 21 items of particular interest to this study and included three macronutrients, nine micronutrients, six serving variables and three categorical variables (Table 2). The selection of these variables was based on our hypotheses that fruits, tomatoes, cruciferous vegetables, leafy vegetables, yellow vegetables and vitamin intake will be associated with a reduction in number of genes methylated in sputum, while animal fat and red and processed meat will be associated with increased methylation. On average, men had higher intake of total calories, but after adjustment for caloric intake, women generally had higher consumption of micronutrients, and men had higher consumption of red meat. There was no difference in vitamin usage, but men were more likely to report having at least one alcoholic drink per day.

Prevalence for Gene Promoter Hypermethylation in Sputum

Methylation of an eight-gene panel that included *p16*, *MGMT*, *DAPK*, *RASSF1A*, *GATA4*, *GATA5*, *PAX5 α* , and *PAX5 β* was evaluated. Methylation of these genes is associated with increased risk for lung cancer (10,21). The prevalence of methylation ranged from 1.1% and 0.0% for *RASSF1A* to 33.8% and 51.2% for *GATA4* for women and men, respectively (Table 3). Three genes, *MGMT*, *GATA4* and *PAX5 α* , were more frequently methylated among men than women ($p < 0.01$). Methylation index, the number of methylated genes in each sputum sample, was higher in men than women (median = 2 and 1, respectively; $p < 0.001$). Our previous study was comprised largely of male participants and dichotomized methylation index as < 3 or ≥ 3 genes methylated in sputum (10). However, since this study is comprised of 77% women who have a lower prevalence for gene methylation, high methylation index was defined as ≥ 2 genes methylated and was present in sputum from 36.6% of women and 50.4% of men ($p < 0.001$).

Association of Clinical Covariates with Gene Methylation

Gender, age, BMI, and cigarette smoking history were assessed in a multivariate model for association with methylation status. Meaningful interactions, including interactions between gender and all of the other covariates, were assessed. There were significant interactions between gender and both BMI ($p = 0.04$) and pack years of smoking ($p = 0.05$). There were relatively more women with high methylation among obese participants than among both normal weight and overweight individuals, while for men the association was less consistent. The odds of high methylation increased with pack years among men, but there was no association among women. Age and duration of smoking were not associated with methylation, after adjustment for the other clinical covariates, but age was retained in the model. With two other smoking variables included in the model (pack years and current status), duration was excluded. Thus, the clinical covariates that were included in the modeling with the nutritional variables were gender, pack years of smoking, current smoking status, BMI, age and interactions between gender and both pack years and BMI.

Association of Dietary Factors with Gene Methylation

Each dietary factor was assessed for association with methylation status (≥ 2 genes methylated vs < 2 genes) using logistic regression. A total of 21 variables were examined: three macronutrients, nine micronutrients, six serving variables and three categorical variables (consumption of alcohol, vitamins, and cod liver oil; Table 4, Table S1). Leafy green vegetable consumption was significantly associated with reduced risk for high methylation status (OR = 0.83, CI: 0.74, 0.93), as was higher folate (OR = 0.84, CI: 0.72, 0.99) (Table 4). The most striking effect seen was the association between current multi-vitamin use and methylation status (OR = 0.57, CI: 0.40, 0.83) (Table 4). The duration of vitamin use was not associated with methylation (data not shown). Moreover, since folate levels were higher for participants taking multi-vitamins, stratification by vitamin use was also conducted and folate remained significantly associated with methylation. There was a marginal increase in odds for methylation associated with total fat and animal fat that did not reach statistical significance (Table S1). None of the other dietary or nutrient predictor variables analyzed were associated with methylation (Table S1). Interactions between each dietary variable and gender were assessed, but none were significant. The association between these dietary variables and methylation of the individual genes also was examined, but because of the number of tests (8 genes \times 3 dietary variables = 24 tests), these results were viewed as exploratory. Associations with at least one of the three significant dietary variables were observed for *DAPK*, *GATA4*, *PAX5 α* and *PAX5 β* (Table S2).

A further analysis was conducted to assess whether any extreme outliers influenced the observed results for continuous variables by defining quartiles by gender and then using the medians within the quartiles as predictors in logistic regression modeling. Similar results were obtained as in the initial analysis, except that total fat was associated with marginal increased methylation (OR=1.43 per 40 gm/day; CI: 1.03, 1.99). The same dietary variables were identified to be significant in analyses that used the continuous methylation index as the outcome. In addition, vitamin E showed a protective effect for methylation per gene (OR = 0.98 per 20 mg/day; CI: 0.96, 1.00, $p = 0.04$).

Discussion

This is the first cohort-based study to systematically evaluate the association between dietary factors and risk for methylation in cells exfoliated from the aerodigestive tract of smokers and former smokers. Our findings support a significant, biologically plausible role for leafy green vegetables, folate, and multi-vitamin use in protection against the acquisition of gene promoter methylation.

There has been considerable interest and debate for decades regarding the impact of diet and vitamins on the risk for cancer. Recent large epidemiological studies along with functional investigations are beginning to provide a clearer picture as to the dietary variables which may influence risk for cancers such as lung where a clear causative environmental exposure in the form of smoking has been established. Reduced folate intake has been associated with increased risk for lung cancer in current and former smokers (22). A link between folate and gene methylation exists through the role of 5-methyltetrahydrofolate in providing methyl groups for S-adenosyl methionine (SAM), a key methyl donor in the methylation of DNA. Higher folate has been associated with a lower prevalence for methylation of individual and total number of genes in colorectal tumors (17). This finding was validated in a second study of colorectal tumors in which folate was inversely associated with gene-specific promoter hypermethylation (23). Our study shows for the first time, the acquisition of gene promoter methylation throughout the airway epithelium is influenced by folate. The biological mechanisms related to low folate and hypermethylation are still unclear; however, Jhaveri *et al.* (24) suggested that folate deficiency leads to increased levels of SAM and S-adenosyl-homocysteine (SAH), an inhibitor of SAM. The increase in free intracellular SAM could contribute to gene specific hypermethylation if an absolute level of SAH needed to regulate SAM is not maintained. Folate is also involved in DNA repair through *de novo* synthesis of purines and pyrimidines and low dietary folate has been associated with reduced DRC (18). This observation, combined with our recent study identifying reduced DRC as a determinant for gene promoter methylation in sputum (14) suggests that folate may directly, through affecting the one carbon pool, and indirectly by impacting DRC, affect the propensity for methylation.

Green leafy vegetables were the only food item in this analysis to exhibit protection against methylation status. Leafy vegetables are rich in phytochemicals such as vitamin C, carotenoids, lutein, and folic acid in addition to vitamins A and K. A comprehensive and systematic review of the literature up to 2007 by the World Cancer Research Fund concluded that probable evidence existed for reduction of lung cancer risk among persons with higher intake of fruits, while evidence was inconclusive regarding green, leafy vegetables (15). However, a recent hospital-based case-control study of lung cancer (25) demonstrated a strong protective effect of green leafy vegetables (OR = 0.5, CI: 0.3, 0.81). The lack of an effect of cruciferous vegetable on methylation status in our study is not surprising since lung cancer observational studies report only modest effects that may be influenced by genetic variation (26). In addition, the lack of association with red meat and processed meat intake is consistent with the inconclusive evidence, as summarized by the WCRF (15). However, a recent cohort study has observed increased risk for lung cancer among those consuming meats prepared in ways that would be expected to have increased their carcinogenicity (27).

In our study, strong protection against gene methylation was also associated with the use of multi-vitamins that contain some of the same agents as leafy green vegetables. While a clear connection between vitamin supplements and risk of lung cancer has not been established (28), vitamin supplementation has been associated with reduction in DNA damage by benzo(a)pyrene, a major tobacco carcinogen (29–32).

The silencing of genes by promoter hypermethylation is now well established as a major component of lung cancer initiation and progression and has emerged as a potential disease marker for early detection. The ability to impact reprogramming of the epigenome through diet and chemopreventive supplements could significantly impact mortality from lung cancer. This study has identified two dietary variables, leafy green vegetables and folate, along with multi-vitamin use that could help reduce the incidence of lung cancer by reducing the induction of methylation in the aerodigestive tract of smokers.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Table 1
 Characteristics of Study Participants Overall and by Gender: Frequencies (%)

Demographic characteristic	Overall	Females	Males	p-value*
Sample size	1101	845	256	
Age				
40–54	46.0	46.7	43.4	0.06
55–64	31.8	32.7	28.9	
65+	22.3	20.6	27.5	
Ethnicity#				
NHW	77.8	77.5	78.7	0.36
Hispanic	16.8	17.5	14.6	
Other	5.4	5.0	6.7	
Smoking status				
Current	56.7	56.7	56.6	1.00
Duration of smoking				
< 30	35.0	35.9	32.0	
30–40	38.7	38.1	40.6	
40+	26.3	26.0	27.3	0.53
Pack years of smoking				
15–29	35.6	38.7	25.4	
30–49	40.7	40.4	41.8	
50+	23.7	20.9	32.8	<0.001
BMI				
< 25	31.7	32.5	28.9	0.40
25–29.9	37.7	36.7	41.0	
30.0+	30.6	30.8	30.1	

* Comparison of females and males, from Fisher's exact test.

Ethnicity is not reported for 6 participants.

Table 2

Summary and Differences of Dietary Intake by Gender

Dietary Factor	Females (n=845) *	Males (n=256) *	Adjusted Difference (95% CI) †	p-value ‡
Macronutrients¹				
Total caloric intake (kcal)	1688 (1312, 2121)	1975 (1517, 2600)		<0.001
Total fat (gm)	69 (52, 91)	78 (60, 104)	3.5 (1.1, 5.9)	0.004
Animal fat (gm)	323 (23, 45)	38 (26, 53)	0.9 (-0.9, 2.6)	
Micronutrients¹				
Vitamin C (mg)	185 (88, 668)	181 (84, 623)	71 (3, 140)	0.04
Folate (mcg)	985 (423, 1298)	1038 (479, 1408)	28 (57, 112)	0.52
Vitamin E (mg)	23 (8, 191)	21 (8, 40)	23 (8, 38.5)	0.003
Carotene (IU)	5599 (3419, 9921)	5334 (3026, 8510)	1568 (761, 2374.)	<0.001
Alpha Carotene (mcg)	357 (176, 641)	370 (146, 585)	127 (50, 1349)	0.001
Beta Carotene (mcg)	3095 (1912, 5518)	2925 (1592, 4621)	891 (432, 1349)	<0.001
Lycopene (mcg)	4991 (3242, 8283)	5968 (3655, 9665)	-320 (-968, 328)	0.33
Lutein and Zeaxanthin (mcg)	2315 (1326, 3612)	2059 (1138, 3097)	844 (476, 1213)	<0.001
Retinol (IU)	3736 (1512, 6072)	3683 (1613, 6106)	505 (-120, 1129)	0.11
Food Groups²				
Red and processed meats	20 (12, 34)	28 (16, 50)	-4.1 (-6.4, -1.9)	<0.001
Fruit	19 (9, 37)	19 (8, 38)	5.3 (1.1, 9.6)	0.01
Tomatoes	12 (5, 17)	13 (5, 17)	0.5 (-1.0, 1.9)	0.54
Cruciferous vegetables	5.0 (3, 9)	5.0 (3, 9)	1.5 (0.3, 2.8)	0.01
Leafy green vegetables	13 (5, 25)	10.0 (5, 18)	5.7 (3.6, 7.9)	<0.001
Yellow vegetables	5 (3, 12)	4 (2, 9)	3.1 (1.8, 4.4)	<0.001
Alcohol				
Drinks per day (%)	None	30	22	<0.001
	0.1 – 1.0	57	48	
	> 1	13	31	
Multi-vitamin use (%)				
Never	13	18		0.19
Past	24	21		
Current	63	61		
Current cod liver oil use (%)	1.7	2.0		0.78

¹ Daily intake.

² Servings per month

* Summary statistics are medians (IQRs) for continuous variables and percents for categorical variables.

† Differences are calculated as mean for females minus mean for males, after adjustment for total caloric intake.

‡ P-values are obtained from linear regression after adjustment for total caloric intake, or, for those variables without adjustment, from linear regression for total caloric intake and from Fisher's exact test for categorical variables.

Table 3

Prevalence of gene methylation in sputum

Gene	Overall (n=1101)	Females (n=845)	Males (n=256)	p-value*
	(% positive)			
P16	16.6	16.2	18.0	0.50
MGMT	26.3	24.4	32.8	0.009
RASSF1A	0.8	1.1	0.0	0.13
DAPK	17.8	16.7	21.5	0.09
GATA4	37.9	33.8	51.2	<0.001
GATA5	18.0	17.0	21.1	0.14
PAX5 α	15.3	13.1	22.3	<0.001
PAX5 β	9.6	9.5	10.2	0.72
≥ 2 genes methylated	39.8	36.6	50.4	<0.001

* Comparison of females and males, from Fisher's exact test.

Table 4

Dietary variables significantly associated with methylation status in the Lovelace Smokers Cohort

Dietary Predictor Variable	OR ⁺ (95% CI)	p-value
Leafy green vegetables (per 12 monthly servings)	0.83 (0.74, 0.93)	< 0.001
Folate (per 750 mcg/day)	0.84 (0.72, 0.99)	0.04
Multi-vitamin use versus never		
Current	0.57 (0.40, 0.83)	0.01
Past	0.68 (0.45, 1.03)	

⁺ Odds ratios are obtained from models with a single dietary variable, but including adjustment for gender, age, BMI, pack years of smoking, current smoking status, total caloric intake and interactions between gender and both BMI and pack years of smoking.