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Is prenatal diet associated with the composition of the vaginal microbiome?

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Abstract

Background: The vaginal microbiome has been associated with adverse pregnancy outcomes, but information on the impact of diet on microbiome composition is largely unexamined.

Objective: To estimate the association between prenatal diet and vaginal microbiota composition overall and by race.

Methods: We leveraged a racially diverse prenatal cohort of North Carolina women enrolled between 1995-2001 to conduct this analysis using cross-sectional data. Women completed food frequency questionnaires about diet in the previous 3 months and foods were categorized into subgroups: fruits, vegetables, nuts/seeds, whole grains, low-fat dairy, sweetened beverages, and red meat. We additionally assessed dietary vitamin D, fiber, and yogurt consumption. Stored vaginal swabs collected in mid-pregnancy were sequenced using 16S taxonomic profiling. Women were categorized into 3 groups based on predominance of species: *Lactobacillus iners, Lactobacillus* miscellaneous, and Bacterial Vaginosis (BV)-associated bacteria. Adjusted Poisson models with robust variance estimators were run to assess the risk of being in a specific vagitype compared to the referent. Race-stratified models (Black/White) were also run.

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Results: In this study of 634 women, higher consumption of dairy was associated with increased likelihood of membership in the *L. crispatus* group compared to the *L. iners* group in a dose-dependent manner (RR quartile 4 vs. 1: 2.01 [95% CI: 1.36, 2.95]). Increased intake of fruit, vitamin D, fiber, and yogurt was also associated with increased likelihood of membership in *L. crispatus* compared to *L. iners,* but only among black women. Statistical heterogeneity was only detected for fiber intake. There were no detected associations between any other food groups or risk of membership in the BV-group.

Conclusions: Higher consumption of low-fat dairy was associated with increased likelihood of membership in a beneficial vagitype, potentially driven by probiotics.

Keywords

microbiota; diet; bacterial vaginosis; pregnancy

Introduction

The vaginal microbiome is a constellation of bacterial species whose balance helps maintain a woman's health. Though women have unique patterns, evidence suggests that a shift towards anaerobic microbes coupled with a decrease in *Lactobacillus* species is associated with higher risk of adverse pregnancy outcomes like preterm birth and miscarriage.[1-3] These studies examined associations with individual species or a diagnosis of Bacterial Vaginosis (BV), a dysbiotic vaginal state characterized by pH >4.5 and increased levels of anaerobic species including *Gardnerella vaginalis*, *Atopobium vaginae,* and *Mycoplasma hominis*.[4] Up to 40% of preterm births are thought to be caused by intrauterine infection and subsequent inflammation, potentially resulting from pathogenic organisms gaining access to the amniotic cavity through the vagina.[5,6] Bacteria of the *Lactobacillus* genus serve as physiological barriers to these pathogens by producing lactic acid and lowering vaginal pH.[7] Lowered pH also helps promote "healthy" bacteria, thereby preventing colonization by pathologic organisms.[8,9]

Known influences on the vaginal microbiome include douching, sexual activity, race, and smoking.[10] Effects of diet on vaginal microbiota remain largely unexamined. Previous studies have examined associations between diet and BV, but there are very few studies on diet and microbiome composition beyond a BV diagnosis, or studies examining specific dietary subgroups and vaginal microbiota. Prior literature found that BV risk increases with deficiencies in iron and vitamin D during pregnancy,[11,12] as well as higher levels of dietary fat, glycemic load, and a diet consisting of low nutritional density foods.[13,14]

Despite a clear scientific gap in the relationship between diet and vaginal microbiota, many lay articles discuss the impact of foods on vaginal health.[15,16] Frequently mentioned is the benefit of probiotic foods, most commonly yogurt, which contains active cultures. While yogurt is often discussed as an important food for maintaining vaginal health, there have been no scientific studies examining its effects, or dairy consumption generally, on the vaginal microbiome beyond a BV diagnosis.

Mounting literature suggests that there may be racial/ethnic differences in vaginal microbiome compositions.[8,17] Dietary patterns, behavioral practices, and sociodemographic factors also differ by race/ethnicity.[18,19] Additionally, it is well established that there are significant racial disparities in preterm birth such that black women are at substantially higher risk than White women.[20,21] Because of these important racial differences, we examined the association between diet and microbiome by maternal race.

Disentangling diet from other underlying determinants of vaginal microbiome composition will better inform our understanding of modifiable routes to optimal vaginal microbial community patterns. Our study objective was to measure the association between diet and vaginal microbiome composition in a racially diverse prenatal cohort.

Methods

Cohort selection

The Pregnancy, Infection, and Nutrition (PIN) study enrolled pregnant women with singleton pregnancies in the central North Carolina region between August 1995 and February 2001. Women were recruited from prenatal care clinics at the University of North Carolina Hospitals, Wake County Human Services, and the Wake Area Health Education Center. Women were eligible if they were between 24- and 29-weeks' gestation, had a singleton pregnancy, able to communicate in English, >16 years old, had phone access, and planned to deliver at the recruitment site. Of the 5,196 women eligible for participation, 3,163 were recruited successfully (61%).[22]

The PIN study was structured to enable a nested case-cohort design, such that a random subset of the cohort was identified at enrollment to serve as a reference population for nested studies that is representative of the exposure distribution in the larger cohort, referred to as "subcohort". This random subcohort was sampled irrespective of pregnancy outcome. For the current study, we included women who were sampled into this nested subcohort (n = 855). Of these women, 723 had information on both dietary consumption and taxonomic profiling. We further excluded women who did not self-identify as Black or White (Figure 1).

Exposure

Women completed a self-administered Block food frequency questionnaire (FFQ) between 26- and 29-weeks' gestation. The questionnaire was modified to reflect the previous 3-month period and to include "southern" foods.[23] Women recorded both frequency of intake and portion sizes using a serving-size visual, allowing for the calculation of total servings consumed. Using relevant food items from the FFQ, we constructed 7 sub-categories of intake: fruits, vegetables, nuts/legumes, low-fat dairy, whole grains, red meats, and sweetened beverages, expressed in servings consumed per day. These categorizations, known as the DASH diet, reflect previously established components of a healthy diet.[24,25] Studies have found that this diet is associated with reduced risk of pregnancy complications.[26,27] Our objective was to understand the role that the DASH diet played as an upstream predictor of vaginal microbiome. We additionally examined fiber and

vitamin D based on associations with the vaginal microbiome and BV in prior literature[28,29] and yogurt due to its probiotic content.

The fruit category included whole fruits only and excluded 100% fruit juices. Whole grain foods included whole wheat bread and high fiber cereals. The red meat category included pork and beef products. Sweetened beverages included soft drinks, Snapple, KoolAid, drinks with some juice (Sunny D), or the addition of sugar to coffee/tea. In addition, the FFQ was used to calculate dietary intake of various nutrients and specific food items expressed in nutrient specific units or grams/day.

Outcome

DNA extraction and sequencing—Self-collected vaginal swabs were obtained between 24- and 29 weeks' gestation. Samples were collected using cotton swabs from the posterior vaginal apex. Frozen swabs were thawed on ice and processed using the PowerSoil DNA Isolation Kit from MO BIO Laboratories, Inc. as described by the Vaginal Microbiome Consortium at Virginia Commonwealth University.[30] DNA samples were eluted with 100 μL buffer into tubes and quantitated using PicoGreen.

Extracted DNA was amplified with barcoded primers targeting the V1–V3 hypervariable regions of the bacterial 16S rRNA gene.[31,32] Samples are multiplexed (384 samples/run) using a sample-specific dual-index strategy and sequenced using 2 x 300 b PE technology on Illumina MiSeq sequencers. The paired-end quality-aware raw sequence files (.fastq) are demultiplexed into sample-specific data using custom scripts. The raw paired-end sequencing data is subjected to merging and quality-filtering using MeFiT,[33] our software package that invokes CASPER for merging paired-end sequences and quality filters them using their maximum expected error rate. Of the 1,077 samples, seven samples with <1,000 high-quality reads were excluded. High-quality sequences were then identified to species-level taxonomy using STIRRUPS with a 97% identity cutoff.[1]

Comprehensive 16S rRNA gene-based taxonomic survey yielded a mean count of 43,276 reads/sample with minimum and maximum counts of 1,824 and 186,784. Over 99.9% of the high-quality single reads generated overlapping pair-end reads. High-quality sequences were then assigned to the species-level taxonomic assignments for vaginal samples using STIRRUP,[31] an analysis platform that employs the USEARCH algorithm[34] combined with a curated 16S rRNA sequence database. Paired reads which did not align to the same reference sequence were discarded as chimeras.

Vagitype clusters—Because previous research has found that vaginal microbial community patterns cluster within groups,[1,8] we applied the clustering algorithm of Fettweis et al.[1] to the current cohort. Women were classified based on their most abundant species, if detected at >30%. If no species was detected >30% abundance, women were classified "no type." We created vagitypes by combining women with similar dominant species. The BV-mix vagitype was characterized by species associated with BV (*Gardnerella vaginalis, Atopobium vaginae, Lachnospiraceae BVAB1).* The *L. crispatus* vagitype was characterized by the predominance of *Lactobacillus* species: *Lactobacillus crispatus cluster, Lactobacillus gasseri cluster, Lactobacillus jensenii/fornicalis/psittaci,* and *Lactobacillus*

delbrueckii. Lastly, the *Lactobacillus iners* vagitype was characterized by the predominance of *Lactobacillus iners*, which is hypothesized as a transitional species between healthy and a BV-like microbiome. 36 women did not fall into the aforementioned vagitypes and were excluded from analyses due to heterogeneity.

Covariates

Trained staff members interviewed participants within two weeks of recruitment. Women were asked about demographics, sexual behaviors, and behaviors like smoking, alcohol and drug use. Maternal self-reported race/ethnicity was categorized into White, Black, or other. "Other" was excluded due to small sample size (n=45). Women completed a Life Experiences Survey[35] in which they indicated if they experienced any of a listed 39 life events since the beginning of pregnancy, with the option to write in additional events. Examples of events on the questionnaire include job loss, illness/injury of family members, and relationship difficulties.

Statistical analysis

Demographic characteristics were assessed in a univariate analysis, and additionally stratified on vagitype assignment. We then examined the distribution of our exposures (food group and specific nutrients/food item) in the population and stratified on race and vagitype. For fruit, vegetables, nuts, red meat, and sweetened beverages, each component was divided into equal quartiles based on the distribution of daily servings in the entire population. The distributions of low-fat dairy and whole grains were right skewed, so quartiles were created by examining the distributions and selecting interpretable cut-points. Red meats and sweetened beverages were reverse coded so that the highest quartile represents the fewest servings. Thus, for all components, the 4th quartile indicates the most beneficial consumption, following current and previous scores of a good quality diet.[36] Fiber was modeled in quartiles based on distributions in the total population. The distributions of dietary vitamin D and yogurt were right-skewed so exposure was modeled using tertiles. For yogurt, many women (n=332) reported no daily intake so tertiles were created using 0 grams/day as a referent, and the upper two tertiles created by halving the number of women who consumed any yogurt. A sensitivity analysis was conducted which excluded women with reported calorie intakes <2.5th percentile or >97.5th percentile.

Covariates were selected *a priori* using a Directed Acyclic Graph (eFigure 1). Poisson models with robust variance estimators were run to assess the risk of being in a specific vagitype compared to the referent. Due to sample size considerations, the referent was the *L. iners* vagitype. Each category of food was run in an independent model that adjusted for race (White, Black), parity (0, 1-2, 3+), maternal age (continuous), pre-pregnancy BMI (continuous), and maternal stress (continuous count of stressful events during pregnancy). Fiber, vitamin D, and yogurt were adjusted for the same covariates.

We additionally stratified analyses on race to examine race-specific associations, given the heterogeneity in both microbiome composition and diet. We considered $p<0.1$ evidence of statistically significant interaction.

Missing data

Our analysis restricted to those with both exposure and outcome data. Missing values for covariates selected for the final model were multiply imputed using chained equations. Prior to imputation, the only covariate in our minimally sufficient set with missing >5% was negative life events ($n_{missing}$ = 148).

Ethics approval

All procedures were approved by the University of North Carolina's Institutional Review Board.

Results

The largest vagitype was *L. iners* (n=308), followed by the *L. crispatus*-dominated vagitype (n=250), and the smallest retained vagitype was the BV-mix species (n=76). Most women in this population were aged 20-34, had normal pre-pregnancy BMI, and were non-smokers (Table 1).

Of the food groups examined, women consumed the fewest daily servings of nuts/legumes, red meat, and whole grains (mean servings/day: 0.59, 0.69, 0.72, respectively) (Table 2). On average, Black women consumed more servings of fruits, vegetables, nuts, red meat, and sweetened beverages than White women. Black women also had more servings of dietary fiber (median grams/day: 22.8 vs. 19.2). White women consumed considerably more low-fat dairy and yogurt than Black women (median yogurt grams/day: 8.16 vs. 0).

Women in the *L. crispatus* vagitype reported more servings of low-fat dairy, yogurt, and dietary vitamin D than women in the other two vagitypes. When specifically examining yogurt consumption, women in the *L. crispatus* vagitype reported a median consumption of 9.4 grams/day, as compared to 0 grams/day in the *L. iners* and BV-mix vagitypes. Women in *L. crispatus* group consumed less red meat and sweetened beverages.

In adjusted models, we found a dose-dependent relationship between quartiles of low-fat dairy servings and risk of membership in the *L. crispatus* vagitype compared to the *L. iners* vagitype (Table 3). Women in the highest quartile were more likely to be classified into the *L. crispatus* vagitype than women in the lowest quartile (RR 1.58, 95% confidence interval [CI]: 1.17, 2.15). Associations were slightly stronger among Black women although not statistically heterogeneous by race. We also detected beneficial effects of higher fruit consumption, wherein women who were in the top quartiles of consumption were 1.39 and 1.34 times as likely to belong to *L. crispatus* vagitype (CIs: 1.05, 1.83; 1.00, 1.80). For consumption of vegetables, whole grains, and sweetened beverages, being in the 4th quartile (i.e., highest consumption of vegetables and whole grains and lowest consumption of sweetened beverages) was suggestively associated with increased membership in the *L. crispatus* vagitype. We found no associations between diet and likelihood of membership in the BV-mix vagitype. Sample sizes and cutpoints for each quartile are displayed in eTable 1.

We found some evidence that dietary vitamin D intake was associated with membership in the *L crispatus* vagitype, more so among Black women (Table 4). Overall, women with the

highest dietary vitamin D intake were 1.21 times as likely (95% CI: 0.98 1.50) to belong to *L. crispatus* vagitype compared to the *L. iners* vagitype. In multivariable models, yogurt intake was suggestively associated with vagitype overall, driven by the association among Black women (RR: 1.54, 95% CI: 0.99, 2.42). The relationship between dietary fiber intake and vagitype was heterogeneous by race (p = 0.06); associations were generally null for White women and an increased likelihood of belonging to *L. crispatus* vagitype was only seen in the highest quartiles of intake for Black women (RR: 2.10, 95% CI: 1.19, 3.72). There was statistically significant heterogeneity noted in the association between yogurt intake and membership in BV-mix vagitype, but no individual associations were non-null. Sample sizes in each tertile were notably low and imbalanced in the BV-mix vs. *L. iners* comparison (eTable 2). Results were similar when restricting our sample to those with energy intakes between 2.5th percentile and 97.5th percentile of the population (eTables 3 and 4).

Comment

Principal findings—We leveraged a diverse cohort of pregnant women to investigate the relationship between dietary intake and vaginal microbial community patterns, allowing for potential racial heterogeneity. Higher consumption of low-fat dairy and fruit were associated with membership in the *L. crispatus* cluster. While associations were somewhat stronger among Black women, overall effects were not heterogeneous by race. Similarly, higher vitamin D, yogurt, and fiber intake was associated with membership in the more favorable *L. crispatus* vagitype, with somewhat stronger associations among Black women, although associations were only significantly heterogenous for fiber.

Strengths of the study—Our study had many strengths. We used a valid and reliable FFQ to capture food intake; moreover, our specific FFQ was modified to reflect local foods to better capture women's complete intake. Compared to studying individual food items, examining dietary subgroups offers multiple benefits: it reduces the number of comparisons made to avoid statistically spurious associations, provides effects that are sufficiently large to detect, and allows for synergistic effects of nutrients within food groups. Additionally, our population was large and racially diverse, allowing us to meaningfully investigate population-specific differences in associations. Lastly, our study is the first to consider dietary intake in relation to microbiome composition, not just a diagnosis of BV. This improved resolution of vaginal microbial community types better reflects current research linking vagitypes with risk for adverse pregnancy outcomes. Vaginal microbial community patterns dominated by *L. crispatus* have been associated with lower risk of preterm birth,[1,37-39] which may be due to beneficial effects on cervical health.[40] Identifying factors potentially amenable to intervention/modification, including diet, may help reduce adverse pregnancy outcomes.

Limitations of the data—Our study has several limitations. The FFQ asked women to reflect on the past 3 months, however it was intended to reflect usual dietary patterns. The vaginal microbiota composition may shift over time and that these temporal shifts were not captured. However, previous data suggest that the vaginal microbiome is relatively stable across pregnancy, more so than in non-pregnant women.[41,42] Furthermore, prior

literature suggests that diet generally remains stable across pregnancy and thus risk of misclassification is mitigated.[43] However, due to the cross-sectional nature of our study, we must be cautious about assuming causal relations between diet and vagitype. Additionally, we did not have information on vitamin D supplementation. Total vitamin D is comprised of dietary vitamin D, sunlight exposure, and supplementation; our study only examined dietary vitamin D and associations with total vitamin D may differ. Lastly, by limiting dairy to low-fat, not all dietary constituents of probiotics are captured. However, potential probiotic benefits of full-fat products must be balanced against a healthy diet and thus we opted to limit our assessment to healthy intake.

Interpretation—There have been few studies on diet and the vaginal microbiome and most examine nutrients rather than food groups. One previous study found no significant associations between sugar, fiber, protein, or fat intake and membership into one of five vagitypes using daily swabs from college-aged women, but they only examined 26 women.[44] Additionally, most studies focused on general dysbiosis and BV as the outcome rather than community patterns. Some studies have found that suboptimal levels of vitamin D are associated with BV risk,[11,13,45] while another found no association using season as a proxy for vitamin D.[46] One study surveying 104 reproductive-aged women found that diets richer in fiber were associated with decreased BV risk; however, they could not isolate the source of fiber driving this association as results were null when examining fiber from beans, grains, and fruits/vegetables.[29] In this same population, there were no associations between fat, protein, or carbohydrate intake and BV. Studies of probiotics, including trials, have examined preterm birth and/or BV but yielded mixed results.[47-51] Results from randomized trials suggest that probiotic supplementation via oral pills during pregnancy had no effect on microbiome composition, although all three studies supplemented with different probiotics.[50-52]

Our findings that higher low-fat dairy, yogurt, and vitamin D consumption were associated with more favorable vagitype membership is consistent with our hypothesis. Yogurt has the highest volume of production among cultured dairy products in the U.S., and regulations stipulate that *Steptococcus thermophilus* and *Lactobacillus bulgaricus* be used in the starter culture in yogurt production.[53] Additionally, *Lactobacillus acidophilus*, a taxonomically-similar species to *L. crispatus,* is often added.[53] *Lactobacillus* species, including *L. acidophilus*, confer benefits by lowering the vaginal pH through production of lactic acid.[8,54] The acidity promotes the establishment and growth of “healthy” bacteria and prevents colonization by pathologic organisms, serving as a barrier to infection.[8,9] However, it is important to note that yogurt consumption in our population was low: women in the highest tertile of intake consumed >34 grams/day, approximately 20% of one recommended serving.

Although the relationship between yogurt intake and vaginal community pattern did not meet our criteria for heterogeneity, associations appeared to be largely driven by elevated effect estimates among Black women. The prevalence of lactose intolerance is higher in the Black community[55] and yogurt is a dairy product often tolerated by those who are lactose intolerant due to its low lactose content.[56] In our population, yogurt represented a slightly larger percentage of total dairy intake in Black women compared to White women. The

association with fruit may be driven by mechanisms including antioxidants and prebiotics and/or improved immune function. It is well established that cranberries reduce risk of vaginal infections and a trial found that ascorbic acid pills can halve the risk of recurrent BV.[57] Additionally, certain fruits such as watermelons and bananas contain prebiotics, specialized fibers that stimulate growth of beneficial bacteria.

Dietary vitamin D was associated with increased membership in the *L. crispatus* cluster among Black women with the highest intake. A trial of pregnant women in South Carolina found similar results: using plasma 25(OH)D levels, women with >40 ng/mL had vaginal microbiomes with greater abundances of *Lactobacillus* species compared to women with <30 ng/mL, with results stronger among women of African ancestry.[28]

Fortified milk and cereals are a major source of dietary vitamin D in the US. Therefore, our associations with dairy and fiber intake may be partly attributable to fortified foods. It should be noted, however, that dietary intake of vitamin D contributes only minimally to total circulating 25-hydroxyvitamin D.[59] For light-skinned women, circulating levels are largely driven by sun exposure; however, among women with darker skin, higher levels of melanin reduce the skin's ability to generate vitamin D from sunlight.[60] Therefore, diet may represent a more important source of vitamin D among women with darker skin. Despite observing no significant differences in the effect of vitamin D consumption on vagitype by race, fiber intake was one of the few associations that was heterogeneous by race, which may be in part due to heterogeneous sources of fiber across populations. Total fiber levels reflect intake from various dietary components, including whole grains, fruits, and vegetables. There may be differences in predominant source of fiber across race and subsequent differences in the underlying nutrient contributions, potentially explaining the racial heterogeneity we observed.

Conclusions

In this cohort of pregnant women, we found that fruit, dairy, vitamin D, yogurt, and fiber intake was associated with the *L. crispatus* vagitype. While our results should be interpreted cautiously given the cross-sectional nature of our design, they may be used to generate hypotheses informing accessible and low risk intervention studies. Determining the relationship between dietary intake and vaginal health has important public health implications as well as substantial interest by the lay public and yet high-quality scientific evidence is lacking. More research is needed to disentangle these complex associations, ideally addressing the potential for longitudinal variability in vaginal microbial composition over time.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Synopsis:

Study question:

Is diet during pregnancy associated with composition of the vaginal microbiome, and do associations differ by maternal race?

What's already known:

Diet is associated with Bacterial Vaginosis and there is lay literature suggesting a benefit of probiotics on vaginal health, but scientific studies on this question are limited.

What this study adds:

This study provides evidence that certain components of diet are associated with membership in more beneficial vagitype clusters, and that findings are stronger among Black women.

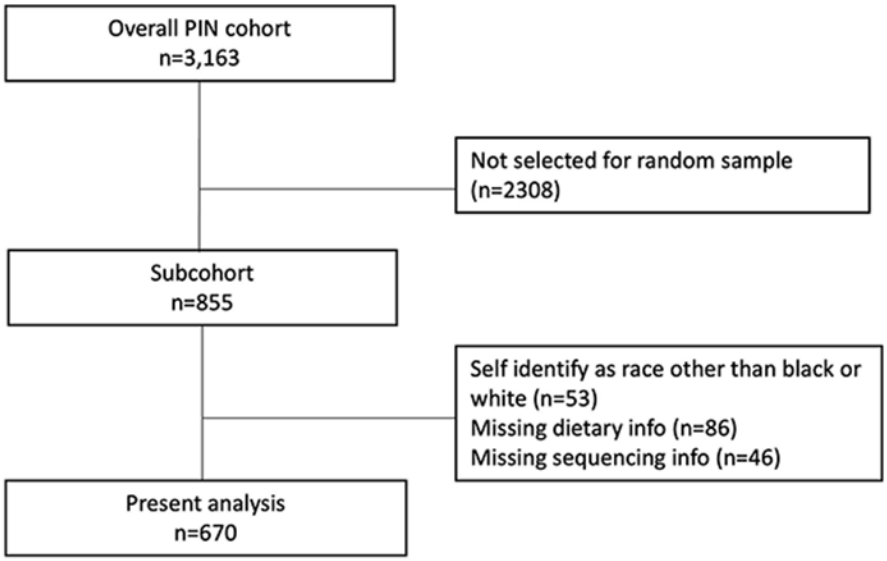

Figure 1.

Flow chart diagramming selection from overall cohort to present analytic sample

Abbreviations: Pregnancy, Infection, and Nutrition (PIN)

Table 1.

Demographics of study population stratified on sequencing vagitype, N (%) or mean (std)

	Overall (n=634)	***L. iners* vagitype (n=308)**	***L. crispatus* vagitype (n=250)**	**BV-mix vagitype (n=76)**
Maternal age (years)				
<20	122 (19.2)	78 (25.3)	30 (12.0)	14 (18.4)
20-34	437 (68.9)	208 (67.5)	182 (72.8)	47 (61.8)
35+	75 (11.8)	22 (7.1)	38 (15.2)	15 (19.7)
Mean (SD)	26.1 (6.1)	24.6 (5.6)	27.8 (6.1)	26.6 (6.9)
Race				
White	370 (58.4)	152 (49.4)	176 (70.4)	42 (55.3)
Black	264 (41.6)	156 (50.6)	74 (29.6)	34 (44.7)
Maternal education (years)				
<12	135 (21.3)	84 (27.3)	30 (12.0)	21 (27.6)
12	198 (31.2)	108 (35.1)	65 (26.0)	25 (32.9)
13-15	136 (21.5)	73 (23.7)	53 (21.2)	10 (13.2)
16+	165 (26.0)	43 (14.0)	102 (40.8)	20 (26.3)
Pre-pregnancy BMI (kg/m^2)				
<18.5	33 (5.2)	17 (5.5)	10 (4.0)	5 (6.6)
18.5 – 24.9	300 (47.3)	137 (44.5)	133 (53.2)	30 (39.5)
25.0 – 29.9	125 (19.7)	60 (19.5)	49 (19.6)	16 (21.1)
≥30	176 (27.8)	94 (30.5)	58 (23.2)	25 (32.9)
Mean (SD)	26.4 (7.5)	26.7 (7.5)	25.8 (7.5)	27.2 (7.1)
Parity				
0	289 (45.6)	142 (46.1)	125 (50.0)	23 (30.3)
1-2	295 (46.5)	141 (45.8)	112 (44.8)	41 (53.9)
>2	50 (7.9)	25 (8.1)	13 (5.2)	12 (15.8)
Smoked months 1-6				
Any	154 (24.3)	83 (27.0)	52 (20.8)	19 (25.0)
None	480 (75.7)	225 (73.0)	198 (79.2)	57 (75.0)
Negative life events	3.8 (3.2)	3.9 (3.1)	3.5 (3.1)	3.9 (3.4)
Income, % of 1996 poverty level				
<50	77 (12.1)	48 (15.6)	19 (7.6)	11 (14.5)
50-99	128 (20.2)	78 (25.3)	33 (13.2)	17 (22.4)
100-199	184 (29.0)	101 (32.7)	57 (22.8)	25 (32.0)
≥200	245 (38.6)	81 (26.3)	141 (56.4)	23 (30.2)

Table 2.

Distribution of servings per day of diet components and selected nutrients and foods

	Min-max	Mean (sd)	Median (25th, 75th)					
			Total population (n=634)	**White women (n=370)**	**Black women (n=264)**	***L. iners* vagitype (n=308)**	***L. crispatus* vagitype (n=250)**	**BV-mix vagitype (n=76)**
Fruit	0 – 22.9	2.52 (2.8)	1.8 (0.8, 3.2)	1.5 (0.7, 2.8)	2.3 (0.9, 4.4)	1.5 (0.7, 3.1)	2.0 (1.0, 3.4)	1.5 (0.7, 2.9)
Veg	0 – 15.9	2.45 (2.3)	1.8 (0.9, 3.2)	1.7 (0.9, 3.0)	1.9 (1.0, 3.8)	1.7 (0.8, 2.9)	1.9 (1.1, 3.7)	1.5 (0.9, 2.7)
Nuts	0 – 6.81	0.59 (0.7)	0.4 (0.2, 0.7)	0.4 (0.2, 0.6)	0.4 (0.2, 0.9)	0.4 (0.2, 0.8)	0.4 (0.2, 0.7)	0.4 (0.2, 0.8)
Whole grains	0 – 22.2	0.72 (1.3)	0.4 (0.1, 1.0)	0.5 (0.1, 1.1)	0.3 (0, 0.8)	0.3 (0, 0.8)	0.5 (0.1, 1.2)	0.4 (0, 1.1)
Low-fat dairy	0 – 21.9	2.05 (2.8)	1.0 (0, 3.0)	1.5 (0.2, 3.9)	0.3 (0, 1.4)	0.4 (0, 2.1)	1.7 (0.3, 4.0)	0.7 (0, 2.8)
Red meat	0 – 4.00	0.69 (0.6)	0.5 (0.3, 0.9)	0.4 (0.2, 0.7)	0.8 (0.4, 1.2)	0.6 (0.3, 1.0)	0.4 (0.3, 0.8)	0.5 (0.3, 1.0)
Sweetened beverages	0 – 33.3	2.48 (4.1)	1.2 (0.2, 3.0)	0.9 (0.1, 2.5)	1.2 (0.3, 3.7)	1.2 (0.3, 3.3)	0.7 (0.1, 2.1)	1.3 (0.3, 4.1)
Selected nutrients/food								
Yogurt (grams/day)	0 – 682	33.3 (69.7)	0 (0, 32.4)	8.16 (0, 48.4)	0 (0, 16.1)	0 (0, 30.3)	8.16 (0, 56.8)	0 (0, 32.4)
Dietary vit D (micrograms/day)	2.07 – 801	55.2 (111)	15.4 (10.7, 26.2)	15.2 (10.0, 28.3)	16.4 (11.5, 25.1)	14.7 (10.5, 22.9)	16.6 (11.0, 33.7)	14.8 (11.0, 24.5)
Dietary fiber (grams/day)	2.42 – 111	23.7 (13.7)	20.1 (14.7, 29.6)	19.2 (14.0, 25.8)	22.8 (16.4, 35.3)	19.5 (14.1, 27.1)	20.5 (15.7, 31.2)	20.6 (15.7, 32.3)

Table 3.

Adjusted risk ratios (95% confidence intervals) for risk of being in select vagitype by quartile of daily servings of dietary components

	L. crispatus **vs.** ***L. iners***	***L. crispatus*** **vs.** ***L. iners,*** **White women**	***L. crispatus*** **vs.** ***L. iners,*** **Black women**	**P for interaction**	**BV-mix vs.** ***L. iners***	**BV mix vs.** ***L. iners,*** **White women**	**BV-mix vs.** ***L. iners,*** **Black women**	**P for interaction**
Fruit								
2 vs. 1	1.25 (0.93, 1.67)	1.22 (0.89, 1.68)	1.25 (0.66, 2.37)		1.10 (0.64, 1.90)	0.97 (0.50, 1.88)	1.16 (0.41, 3.27)	
3 vs. 1	1.39 (1.05, 1.83)	1.40 (1.03, 1.90)	1.24 (0.66, 2.34)		1.11 (0.62, 1.96)	0.88 (0.42, 1.86)	1.41 (0.55, 3.61)	
4 vs. 1	1.34 (1.00, 1.80)	1.15 (0.82, 1.62)	1.77 (1.01, 3.11)	0.22	1.10 (0.63, 1.91)	0.48 (0.17, 1.32)	1.98 (0.86, 4.57)	0.10
Vegetables								
2 vs. 1	1.14 (0.87, 1.49)	1.24 (0.92, 1.66)	0.87 (0.49, 1.56)		1.18 (0.69, 2.02)	1.35 (0.66, 2.73)	0.94 (0.42, 2.15)	
3 vs. 1	1.01 (0.77, 1.34)	1.12 (0.83, 1.53)	0.73 (0.50, 1.35)		1.02 (0.58, 1.77)	0.95 (0.44, 2.05)	1.05 (0.48, 2.34)	
4 vs. 1	1.22 (0.94, 1.59)	1.19 (0.88, 1.60)	1.24 (0.75, 2.03)	0.30	0.78 (0.42, 1.47)	0.83 (0.36, 1.93)	0.67 (0.27, 1.67)	0.84
Nuts								
2 vs. 1	0.96 (0.77, 1.21)	0.95 (0.74, 1.21)	1.07 (0.61, 1.88)		1.11 (0.61, 2.04)	1.61 (0.68, 3.81)	0.81 (0.31, 2.10)	
3 vs. 1	0.90 (0.71, 1.14)	0.99 (0.78, 1.25)	0.74 (0.40, 1.38)		1.17 (0.63, 2.14)	1.38 (0.53, 3.59)	1.21 (0.56, 2.58)	
4 vs. 1	0.91 (0.70, 1.19)	0.78 (0.56, 1.10)	1.16 (0.70, 1.92)	0.17	0.90 (0.48, 1.69)	1.46 (0.60, 3.56)	0.63 (0.25, 1.62)	0.45
Whole grains								
2 vs. 1	1.16 (0.79, 1.40)	1.09 (0.79, 1.51)	0.93 (0.55, 1.57)		0.86 (0.49, 1.49)	0.87 (0.38, 1.97)	0.76 (0.34, 1.72)	
3 vs. 1	1.01 (0.73, 1.39)	0.85 (0.59, 1.23)	1.35 (0.76, 2.39)		0.88 (0.44, 1.76)	0.42 (0.14, 1.29)	1.80 (0.80, 4.08)	
4 vs. 1	1.31 (0.99, 1.73)	1.20 (0.87, 1.67)	1.44 (0.87, 2.40)	0.26	1.35 (0.76, 2.39)	1.03 (0.42, 2.53)	1.32 (0.56, 3.11)	0.16
Low-fat dairy								
2 vs. 1	1.32 (0.96, 1.83)	1.26 (0.85, 1.88)	1.43 (0.83, 2.47)		0.77 (0.43, 1.36)	1.14 (0.49, 2.65)	0.55 (0.24, 1.23)	
3 vs. 1	1.47 (1.07, 2.00)	1.30 (0.90, 1.89)	1.70 (0.99, 2.93)		1.00 (0.58, 1.73)	1.44 (0.64, 3.25)	0.61 (0.24, 1.53)	
4 vs. 1	1.58 (1.17, 2.15)	1.43 (1.01, 2.05)	1.89 (1.01, 3.55)	0.85	1.22 (0.69, 2.17)	1.35 (0.58, 3.15)	1.48 (0.64, 3.40)	0.31
Red meat								
2 vs. 1	1.02 (0.75, 1.38)	1.42 (0.88, 2.30)	0.76 (0.47, 1.24)		0.86 (0.49, 1.53)	1.07 (0.43, 2.67)	0.78 (0.35, 1.75)	
3 vs. 1	1.12 (0.83, 1.51)	1.45 (0.91, 2.32)	0.92 (0.56, 1.52)		1.25 (0.72, 2.15)	1.45 (0.62, 3.40)	1.12 (0.50, 2.59)	
4 vs. 1	1.03 (0.75, 1.40)	1.32 (0.83, 2.12)	0.82 (0.44, 1.54)	0.28	0.86 (0.45, 1.64)	0.88 (0.34, 2.32)	0.95 (0.34, 2.60)	0.92
Sweetened beverages								
2 vs. 1	1.13 (0.85, 1.51)	1.14 (0.81, 1.60)	1.11 (0.66, 1.85)		0.92 (0.54, 1.57)	0.92 (0.46, 1.85)	0.94 (0.40, 2.22)	

	L. crispatus* vs. *L. iners	***L. crispatus* vs. *L. iners*, White women**	***L. crispatus* vs. *L. iners*, Black women**	**P for interaction**	**BV-mix vs. *L. iners***	**BV mix vs. *L. iners*, White women**	**BV-mix vs. *L. iners*, Black women**	**P for interaction**
3 vs. 1	1.18 (0.89, 1.57)	1.26 (0.91, 1.75)	0.98 (0.57, 1.71)		0.85 (0.48, 1.52)	0.73 (0.34, 1.57)	0.92 (0.41, 2.07)	
4 vs. 1	1.23 (0.93, 1.61)	1.21 (0.89, 1.66)	1.26 (0.73, 2.18)	0.77	0.87 (0.49, 1.54)	0.62 (0.30, 1.27)	1.37 (0.57, 3.29)	0.58

All models adjusted for maternal age, parity, pre-pregnancy BMI, and number of stressful life events. Models for total population additionally adjusted for race.

Table 4.

Adjusted risk ratios (95% confidence intervals) for risk of being in select vagitype for dietary vitamin D, yogurt, and fiber quantiles

	L. crispatus* vs. *L. iners			**BV-mix vs. *L. iners***		
	Total population	**White women**	**Black women**	**Total population**	**White women**	**Black women**
Dietary vitamin D						
2 vs. 1	1.14 (0.91, 1.44)	1.15 (0.90, 1.48)	1.11 (0.66, 1.88)	1.08 (0.68, 1.76)	0.99 (0.52, 1.89)	1.16 (0.56, 2.44)
3 vs. 1	1.21 (0.98, 1.50)	1.13 (0.90, 1.42)	1.43 (0.87, 2.33)	1.20 (0.73, 1.97)	1.13 (0.60, 2.13)	1.20 (0.54, 2.65)
P for interaction		0.48			0.94	
Yogurt						
2 vs. 1	1.05 (0.84, 1.33)	0.90 (0.70, 1.16)	1.36 (0.86, 2.17)	0.75 (0.44, 1.29)	0.97 (0.50, 1.87)	0.18 (0.03, 1.33)
3 vs. 1	1.18 (0.95, 1.46)	1.00 (0.80, 1.26)	1.54 (0.99, 2.42)	0.97 (0.67, 1.68)	0.86 (0.42, 1.77)	1.11 (0.51, 2.43)
P for interaction		0.15			0.05	
Fiber						
2 vs. 1	1.15 (0.88, 1.51)	1.13 (0.85, 1.50)	1.07 (0.52, 2.20)	1.07 (0.59, 1.95)	0.93 (0.45, 1.93)	1.52 (0.54, 4.30)
3 vs. 1	1.06 (0.80, 1.40)	0.98 (0.73, 1.32)	1.16 (0.59, 2.30)	1.06 (0.59, 1.88)	0.79 (0.38, 1.64)	1.53 (0.58, 3.99)
4 vs. 1	1.42 (1.09, 1.86)	1.13 (0.82, 1.55)	2.10 (1.19, 3.72)	1.49 (0.87, 2.55)	0.99 (0.49, 1.98)	2.39 (0.97, 5.89)
P for interaction		0.06			0.45	

All models adjusted for maternal age, parity, pre-pregnancy BMI, and impact of life events. Models for total population additionally adjusted for race.