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RESEARCH ARTICLE

Obesity and the gut microbiota in the Middle East: a cross-cultural study of Lebanese and Emirati adults

M. Ali Ahmad[1,#], *M. Abou-Samra*[1,#], *E. Blaak*[1], *M. Karavetian*[2*], *C. Ayoub Moubareck*[3] *and K. Venema*[4*]

[1]Department of Human Biology, NUTRIM Institute of Nutrition and Translational Research in Metabolism, Maastricht University Medical Centre, 6200 MD Maastricht, the Netherlands; [2]Faculty of Kinesiology and Physical Education, University of Toronto, Toronto, ON M5S2C9, Canada; [3]College of Natural and Health Sciences, Zayed University, Dubai 19282, United Arab Emirates; [4]Wageningen Food & Biobased Research, Wageningen University, Bornse Weilanden 9, 6708 WG Wageningen, the Netherlands; *mirey.karavetian@utoronto.ca; koen.venema@wur.nl

[#]These authors share first authorship

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Abstract

Obesity is a growing public health concern in the Middle East and North Africa (MENA) region, yet limited research has explored how gut microbiota varies between Arab populations. This study compared the gut microbiota composition and diversity of Emirati and Lebanese adults with obesity and assessed the role of age and nationality in shaping microbial variation. A total of 43 Emirati and 30 Lebanese individuals with obesity (body mass index (BMI) ≥35 kg/m^2) were recruited. Participants provided anthropometric and biochemical data, dietary records, and stool samples for 16S rRNA sequencing. The analysis revealed significantly higher BMI, weight, and fat mass in Emirati participants, while Lebanese individuals reported higher fibre intake. Taxonomic profiling showed higher relative abundances of *Pseudomonadota*, *Mycoplasmatota*, *Cyanobacteriota*, and *Lentisphaerota* in the Lebanese group, whereas *Bacteroidota* was more abundant among Emiratis. Lebanese participants also exhibited significantly greater microbial alpha-diversity. Beta-diversity analysis confirmed clear distinctions in microbial community structure between the two groups. Linear Discriminant Analysis Effect Size (LefSe) (LDA score >^{10}log2) and regression models ($P < 0.05$) identified specific bacterial genera associated with nationality, although these associations were attenuated after adjusting for age. These findings suggest that gut microbiota in Arab populations is influenced by demographic, dietary, and environmental factors, emphasising the need for culturally tailored microbiota-based strategies to manage obesity and related metabolic conditions.

Keywords

gut microbiota – 16S rRNA – microbial diversity – ethnicity – anthropometrics

1 Introduction

Obesity has emerged as one of the most pressing global health challenges of the 21st century. According to the World Health Organization (2024), more than one billion people – approximately one in eight worldwide – are currently living with obesity (WHO, 2024). The World Obesity Federation (2025) projects that by 2030, adult obesity prevalence will have increased by over 115% compared with 2010, reaching roughly 1.13 billion individuals globally. Furthermore, long-term forecasts from the Global Burden of Disease (GBD) BMI Collaborators (2025) suggest that by 2050, around 60% of adults (nearly 3.8 billion people) and one-third of children and adolescents (≈ 746 million) will be overweight or obese worldwide (IHME, 2025). These trends are particularly concerning in the Middle East and North Africa, where obesity rates are among the fastest rising. Obesity rates have been steadily rising in Gulf countries, with prevalence increasing from 6.5% in 1975 to 20% in 2016 (Ritchie, 2017; WHO, 2016). According to the United Arab Emirates (UAE)'s 2017–2018 National Health Survey, obesity affected 27.8% of the UAE population, while in Lebanon, the prevalence was 30.8% as reported by the World Health Organization in 2016 (WHO, 2016). Without effective prevention and policy interventions, obesity-related diseases – including type 2 diabetes, cardiovascular disease, and other metabolic complications – are expected to increase substantially, especially in low- and middle-income settings (GBD 2021 Adult BMI Collaborators, 2025; IHME, 2025; WHO, 2024; World Obesity Federation, 2025).

Genetic predisposition, lifestyle and environmental factors contribute to obesity, whilst emerging evidence highlights the gut microbiota as a key regulator of in particular, environmental and diet-related effects on metabolism and energy homeostasis (Patrone *et al.*, 2016; Turnbaugh *et al.*, 2006). The gut microbiota comprises not only bacterial phyla but also fungi, archaea, viruses, and protozoa, with its bacterial component being primarily composed of *Bacillota*, *Bacteroidota*, *Actinomycetota*, *Pseudomonadota*, *Fusobacteriota*, and *Verrucomicrobiota* (Oren and Garrity, 2021), with *Bacillota* and *Bacteroidota* accounting for nearly 90% of microbial communities (Arumugam *et al.*, 2011; Rinninella *et al.*, 2019).

An imbalance in gut microbiota, commonly referred to as dysbiosis, remains a debated concept, as microbial composition varies considerably among individuals, making it difficult to establish universal criteria for distinguishing a dysbiotic state from a healthy profile. Nevertheless, variations in gut microbiota have been linked to several metabolic and inflammatory disorders, including obesity, diabetes, and allergies (Gupta *et al.*, 2017). Early animal studies suggested a strong relationship between the *Bacillota*/*Bacteroidota* ratio and obesity (Turnbaugh *et al.*, 2006), but subsequent findings in humans have been inconsistent (Magne *et al.*, 2020; Sze and Schloss, 2016). Beyond this ratio, specific bacterial phyla and genera have also been associated with obesity (OB) (Crovesy *et al.*, 2020). Individuals with obesity, insulin resistance (IR), and type 2 diabetes mellitus (T2DM) frequently exhibit altered gut microbiota compared to lean counterparts, characterised by reduced microbial richness and diversity as well as lower levels of butyrate-producing bacteria, changes that have been linked to metabolic impairments (Jardon *et al.*, 2022). Increasingly, researchers emphasise that definitions of dysbiosis should account not only for taxonomic shifts but also for functional consequences on host metabolism and health.

The composition of gut microbiota varies among individuals and across populations, influenced by lifestyle, genetics, age, diet, medication use, geography, ethnicity, and environment (Crovesy *et al.*, 2020; Deschasaux *et al.*, 2018; Gupta *et al.*, 2017; Jardon *et al.*, 2022; Pinart *et al.*, 2021). Advances in high-throughput sequencing technology have enhanced our understanding of population-specific differences in gut microbiota (Yasir *et al.*, 2015).

While the Lebanese and Emirati populations share some environmental and cultural similarities, variations in dietary patterns, lifestyle habits, and genetic backgrounds may shape distinct gut microbiota profiles. These differences raise concerns about the universality of microbiome-based therapies, emphasising the need for geographically tailored, community-specific approaches to microbiome research (Gupta *et al.*, 2017).

Although multiple studies have explored the relationship between gut microbiota and obesity in different populations (Escobar *et al.*, 2014; Jain *et al.*, 2018), comparative research in Middle Eastern populations remains scarce (Yasir *et al.*, 2015). Furthermore, data on ethnicity-driven gut microbiota differences in Arab populations remain inconsistent (Brooks *et al.*, 2018).

This study aims to bridge this research gap by analysing gut microbiota composition and diversity in Lebanese and Emirati individuals with OB using high throughput 16S ribosomal RNA (rRNA) gene amplicon sequencing and assessing whether age or other factors contribute to these observed variations. Identifying population-specific microbiota signatures associ-

ated with OB will provide valuable insights for developing targeted interventions to manage and prevent obesity-related complications in the Middle East, where research remains limited.

2 Materials and methods

Study design

We conducted a cross-sectional design among Lebanese and Emirati subjects with OB living in the UAE and Lebanon, respectively. The present study was conducted in accordance with the Declaration of Helsinki and approved by the Institutional Review Board of Middle East Institute of Health University Hospital (MEIH-UH) in Lebanon (AL-04-02/2018-IRB/MEIH) and by the Research Ethics Committee of the Ministry of Health and Prevention of UAE (MOHP/DXB-REC-52/2018), the Dubai Health Care Regulatory Research Ethics Committee (DHCR-REC), and the Zayed University Ethical Committee Board (ZU19_51_F) in UAE.

Study population

Recruitment took place from October 2019 until April 2021. Sample size was determined by following standard calculations based on normal distributions. The current study utilised data from a mother study designed to investigate gut microbiota profiles in Lebanese and Emirati participants, both with OB and of normal weight, as well as changes following bariatric surgery. The present analysis was restricted to obese participants from these larger cross-sectional studies that included both obese and normal-weight adults from Lebanon and the UAE. The current manuscript focuses solely on the obese subgroup to assess ethnicity-related microbial differences within obesity. In the mother study, the primary outcome was the change in the *Bacillota* /*Bacteriodota* ratio. Sample size calculation was based on expected changes in this ratio before and after bariatric surgery, referencing findings from Damms-Machado *et al.* (2015), which reported a significant increase in the faecal *Bacillota* /*Bacteriodota* ratio from 5.9 (SD 2.1) to 10.4 (SD 1.4) three months post-surgery. Based on these values, a minimum of two participants was required to achieve 80% power at a two-sided 5% significance level (Ali Ahmad *et al.*, 2025). To account for protocol deviations and anticipated reductions in effect size (~30%), researchers conservatively multiplied the required sample by a factor of 15. This adjustment yielded a final target of 30 participants per group. Accordingly, we aimed to recruit 30 Emirati and 30 Lebanese adults with OB, including both sexes, residing in the UAE and Lebanon, respectively.

Inclusion and exclusion criteria

Participants were eligible if they were adults between 18 and 60 years of age, had a body mass index (BMI) ≥ 35 kg/m^2, and had maintained stable body weight (no fluctuation greater than 5%) during the three months prior to recruitment. Eligibility was restricted to Emirati and Lebanese nationals with both parents of the same nationality. Additional requirements included absence of antibiotic use in the previous three months and willingness to complete a 3-day 24-hour food diary (two weekdays and one weekend) to assess habitual energy and fibre intake. For Emirati participants, dietary intake was analysed using the Middle Eastern food composition database available in the Nutritics software, whereas for Lebanese participants, food reference tables from *Understanding Nutrition* (Whitney and Rolfes, 2002) were used. All participants provided written informed consent before enrolment. Eligibility was assessed through a structured screening questionnaire (Supplementary Materials and methods S1), which captured information on general health, weight history, alcohol intake, physical activity, smoking, medication use, and supplement intake (including probiotics, fibre, and prebiotics).

Participants were excluded if they had experienced weight loss ≥5% within the last three months, were pregnant, reported excessive alcohol consumption (>1/2 ounce/day for females; >1 ounce/day for males) (Snetselaar *et al.*, 2021), or were unwilling or unable to provide informed consent.

Recruitment

Lebanese participants with obesity were recruited from the weight-loss program at the Middle East Institute of Health University Hospital (MEIH-UH), while Emirati participants with obesity were recruited from hospitals in Dubai and Sharjah. Recruitment took place between October 2019 and April 2021.

Anthropometric measurements

Eligible subjects were asked to arrive at the testing site after a 12 h fast and were asked to avoid alcohol and caffeine consumption, as well as any unusual strenuous exercise 24 h prior to the screening. While subjects wore light clothes and no shoes, height and weight were measured using the 'SECA 700' balance and BMI was calculated as the ratio of weight (kg) to height (m) squared (kg/m^2). Waist circumference (WC) (cm) was measured

to the nearest 0.1 cm using a flexible, non-stretchable measuring tape at the umbilicus level midway between the lower ribs and the upper iliac crest while standing (Alberti *et al.*, 2006). WC was defined as normal or 'at risk' according to the International Diabetes Federation (IDF) using Europids cutoff values for normal of <94 cm for males and <80 cm for females (Alberti *et al.*, 2006). Waist-to-height ratio (WtHR) was calculated as the ratio of the waist circumference divided by height (both in cm). A cut-off of 0.5 was used to define abdominal obesity, whereby a WtHR <0.5 was considered normal (Gibson and Ashwell, 2020).

The percentage of body fat (PBF) was measured using a bioelectrical impedance analyzer 200 (BC-420 MA, Tanita Corporation, Tokyo, Japan) for Emiratis and an InBody composition analyzer 720 (InBody Co., Ltd., Seoul, Korea) for Lebanese participants, according to the manufacturer's instructions. Cutoffs of ≥25% and ≥35% were used to define elevated PBF among males and females, respectively (Nuttall, 2015).

Biochemical analyses

After a 12 h fast, on-site, venous blood samples were collected by a registered nurse for the analyses of fasting blood glucose (FBG, mg/dl), total cholesterol (TC, mg/dl), low-density lipoprotein cholesterol (LDL-C, mg/dl), high-density lipoprotein cholesterol (HDL-C, mg/dl), and triglyceride (TG, mg/dl) that were analysed via an enzymatic colorimetric method using the Roche/Hitachi Cobas® 6000 analyzer (Roche, Basel, Switzerland) and insulin via the Enzyme-Linked Immunosorbent Assay (ELISA) principle using the Elecsys insulin kit (Roche) for Lebanese participants. As for Emirates, the former were measured via the portable Lux Meter Blood Test (Biochemical Systems International, S.p.A; Arezzo, Italy) following the manufacturer's instructions. As for insulin: one 5 ml venous blood sample was drawn into an ethylenediaminetetraacetic acid (EDTA) tube and analysed by using ELISA kits (Diametra Millipore, St. Louis, MO, USA).

Insulin resistance was calculated using the Homeostatic Model Assessment for Insulin Resistance (HOMA-IR), defined as (fasting immunoreactive insulin (μU/ml) × fasting plasma glucose (mg/dL))/ 405 (Vaccaro *et al.*, 2004). HOMA-IR values exceeding 1.8 for Emirati participants (Esteghamati *et al.*, 2009) and 2.32 for Lebanese participants (Chedid *et al.*, 2009) were considered indicative of insulin resistance.

Stool collection

Stool was collected using a faecal specimen collector along with the Zymo DNA/RNA Shield™ Faecal Collection tube which was pre-filled with DNA/RNA Shield™ (9 ml) (Zymo Research Corp., Irvine, CA, USA). Subjects were asked to follow the instructions by the developer of the tubes, where two samples were collected from each participant, one of which was analysed, and the second was held for accurate verification. Collection tubes had a spoon attached to the cap for collecting 1 g of faeces. The nucleic acids (DNA & RNA) in the samples were preserved by DNA/RNA Shield™ at room temperature (DNA > 1 year, RNA up to 1 month).

DNA isolation and sequencing of the V3–V4 region of the 16S rRNA gene

DNA isolation and sequencing of the barcoded amplicons of the V3–V4 region of the 16S rRNA gene were performed according to the Illumina protocols (Illumina, Eindhoven, the Netherlands) which involved PCR amplification using region-specific primers, followed by indexing, purification, and paired-end library preparation (Surono *et al.*, 2022). Sequencing was conducted on the Illumina MiSeq platform (San Diego, CA, USA) using barcodes and the paired end 2 × 300 bp protocol. Raw reads were processed and demultiplexed using (QIIME 2, version 2023.2) (Bolyen *et al.*, 2019), and taxonomic classification was performed using the SILVA 16S rRNA gene reference database, version 132 (Quast *et al.*, 2013; Yilmaz *et al.*, 2014).

Diversity analyses

The alpha-diversity metrics used in this study included Faith's phylogenetic diversity (PD) (Faith, 1992), observed features (DeSantis *et al.*, 2006), Chao1 index (Chao, 1984), Pielou's evenness (Pielou, 1966) and Shannon's indices (Shannon and Weaver, 1949). These indices were calculated using QIIME 2 and visualised in RStudio (version 4.2.1) using the phyloseq and ggplot2 packages (Wickham, 2016). Rarefaction curves were also generated using the ggplot2 package, with rarefication depth set at 3800. Beta-diversity was assessed using Bray–Curtis dissimilarity (Bray and Curtis, 1957), Jaccard similarity (Jaccard, 1908), unweighted UniFrac, and weighted UniFrac (Lozupone and Knight, 2005) and visualised through Principal Coordinate Analysis (PCoA) plots using the vegan and phyloseq packages in R.

Statistical analyses

Statistical analyses were performed using the Statistical Package for the Social Sciences software version 20 (SPSS Inc. Chicago, IL, USA) and software package R (4.2.1) (R Core Team, http://www.R-project.org) in RStudio. The normality of data using SPSS was tested using the skewness and kurtosis. Normally distributed data is expressed as mean (M) ± standard deviation (SD), and skewed data as median (Mdn) and interquartile range (IQR). Depending on the data distribution, differences between the groups were assessed using an independent samples t-test for normally distributed continuous variables or a nonparametric test using the Mann–Whitney U-test for skewed continuous variables and chi-square for categorical values. The value of $P < 0.05$ was used to denote statistical significance.

Comparisons of relative abundances at the phylum and genus levels were performed using the nonparametric Kruskal–Wallis H-test corrected with the Benjamini–Hochberg false discovery rate (FDR) for multiple comparisons by using the software package R in RStudio. Although only two groups were compared, the Kruskal–Wallis test was retained for the microbiota data to maintain consistency with the LEfSe workflow and because its distribution-free properties are well suited to highly skewed genus-level abundance data. In contrast, Mann–Whitney U-tests were used for clinical variables, as this is the standard non-parametric method for two-group comparisons. Spearman's rank correlation coefficient was used to evaluate associations between microbial taxa and clinical variables. In addition, linear regression models were applied to examine the relationship between microbial composition and nationality, with age assessed as a potential confounder. Both unadjusted and age-adjusted models were reported. For each genus-level analysis, the relative abundance of the bacterial genus was used as the dependent variable in separate linear regression models, and nationality (Lebanese *vs*. Emirati) served as the main independent variable (coded 1 and 0, respectively). Relative abundances were analysed as proportional values without transformation (e.g. no log, arcsine-square-root, or CLR transformation), as exploratory inspection indicated that model residuals met acceptable assumptions for linear regression. Zero values were retained as observed without imputation. Age was added as a covariate in adjusted models to assess confounding, applying a ≥10% change-in-estimate criterion for identifying meaningful confounding effects (Skelly *et al*., 2012). Model assumptions – including linearity, homoscedasticity, multicollinearity, and normality of residuals – were evaluated using residual plots and diagnostic checks. No additional covariates met criteria for inclusion.

Taxonomic composition was summarised using stacked bar plots at the phylum and genus levels, illustrating the relative abundance of dominant microbial taxa across study groups.

The statistical significance of beta-diversity between the two groups with OB (Emirati *vs*. Lebanese) was determined using Permutational Multivariate Analysis of Variance (PERMANOVA) using the software package R in RStudio.

Linear discriminant analysis (LDA) effect size (LEfSe) was done using the R software in RStudio to explore microbial taxa with differential abundance between Lebanese and Emirati individuals with OB. Genera enriched in each group with an LDA score $>^{10}\log 2$ at a value of $P < 0.05$ were considered (Segata *et al*., 2011).

3 Results

Participant characteristics

The participant characteristics are presented in Table 1. A total of 43 Emirati and 30 Lebanese individuals with OB (BMI ≥35 kg/m^2) were enrolled in the study. The difference in sample sizes between the two groups was mainly due to recruitment challenges in Lebanon. While the broader study initially aimed to enrol participants undergoing bariatric surgery from both countries, enrolment in Lebanon was hindered by financial constraints and disruptions caused by the COVID-19 pandemic.

Most of the subjects were females including 62.8 and 66.7% of the Emirati and Lebanese participants, respectively ($P = 0.807$). Anthropometric measurements showed that weight ($P = 0.015$), BMI ($P = 0.002$), WtHR ($P < 0.001$), fat mass (FM) ($P < 0.011$), and probiotic food consumption ($P = 0.001$) were significantly higher in the Emirati group. As for fibre intake ($P < 0.001$), total cholesterol ($P = 0.02$), dyslipidaemia ($P = 0.017$), and alcohol consumption ($P < 0.001$), these were significantly higher in the Lebanese subjects. There was no significant difference between the two groups with respect to WC, PBF, energy intake (EI), FBG, insulin, HOMA-IR, HDL-C, LDL-C, TG, fibre supplement, smoking, diabetes, cardiovascular disease, irritable bowel syndrome, hypertension, and cancer. None of the participants were on probiotic or prebiotic supplements. Lebanese participants were significantly older than Emirati participants (41.0 ± 10.7 vs 29.9 ± 9.1 years, $P < 0.001$; Table 1).

TABLE 1 Demographic, anthropometric, and biochemical parameters between Lebanese and Emirati individuals with obesity

Variable[1]	Emirati n = 43	Lebanese n = 30	*P*-value[2]
Age (years)	29.9 ± 9.1	41.0 ± 10.7	<0.001*
Female (n (%))	27 (62.8)	20 (66.7)	0.807
Weight (kg)	119.0 (98.8 –133.2)	101.1 (98.4-112.0)	0.015*
Height (cm)	165.2 ± 9.8	164.06 ± 8.07	0.062
BMI (kg/m^2)	42.8 (37.8-46.1)	38.4 (35.7-41.7)	0.002*
WC (cm)	123.3 ± 17.8	118.7 ± 8.5	0.149
WtHR	0.74 ± 0.08	0.63 ± 0.07	<0.001*
PBF (%)	46.1 ± 5.3	45.4 ± 5.79	0.596
FM (kg)	53.8 ± 13.3	47.4 ± 7.3	<0.011*
EI (Kcal)	2075 ± 738	1822 ± 746	0.157
Fibre (g)	10 (7.8-13.8)	17.3 (13.1-21)	<0.001*
Fibre (g)/1000 Kcal	4.9 (4.0-7.3)	10.5 (6.4-14.3)	<0.001*
FBG (mg/dL)	97 (93.6-104.0)	98.5 (95.0-107.3)	0.346
Insulin	22.0 ± 14.0	20.9 ± 10.3	0.716
HOMA-IR	4.78 (3.08-7.59)	5.24 (3.47-6.73)	0.771
HDL-C (mg/dl)	41.7 ± 11.1	44.6 ± 11.3	0.279
LDL-C (mg/dl) (Mdn (IQR))	93 (75-118)	109 (81-136)	0.115
TG (mg/dl) (M ± SD)	128.5 ± 62.1	149.7 ± 50.2	0.127
TC (mg/dl) (Mdn (IQR))	161.6 (143.0-181.7)	177.0 (159.3-218.3)	0.020*
Lifestyle factors	Yes, n (%)	Yes, n (%)	
Probiotic supplement	0 (0)	0 (0)	–
Fiber supplement	2 (4.7)	0 (0)	0.509
Probiotic food consumption	29 (67.4)	8 (26.7)	0.001*
Probiotic food consumption frequency			
None	15 (34.9)	22 (73.3)	<0.001*
2 or less/week	13 (30.2)	7 (23.3)	
3 to 6/week	11 (25.6)	1(3.3)	
7 or more/week	4 (9.3)	1 (3.3)	
Prebiotic supplement	0 (0)	0 (0)	–
Smoker	12 (27.9)	14 (46.7)	0.137
Alcohol consumption	2 (4.7)	12 (40)	<0.001*
Diabetes	0 (0)	2 (6.7)	0.166
Cardiovascular disease	0 (0)	3 (10)	0.065
Dyslipidaemia	1 (2.3)	6 (20)	0.017*
Hypertension	5 (11.6)	8 (26.7)	0.125
Irritable bowel syndrome	0 (0)	3 (10)	0.065
Cancer	0 (0)	0 (0)	–

1 BMI: body mass index, WC: waist circumference, PBF: percentage body fat, FM: fat mass, WtHR: waist-to-height ratio, FBG: fasting blood glucose, HOMA-IR: homeostatic model assessment for insulin resistance, HDL-C: high- density lipoprotein cholesterol, LDL-C: low-density lipoprotein cholesterol, TG: triglycerides, TC: total cholesterol, M ± SD: Mean ± standard deviation, Mdn (IQR): median (interquartile range).

2 Statistical significance * (P <0.05) between groups. Independent-sample t-test was used for normally distributed continuous variables with mean, and SD (Age, Height, WC, WtHR, PBF, FM, EI, insulin, HDL-C, TG), Mann-Whitney U-test for skewed continuous variables (Weight, BMI, Fiber, Fiber/ 1000 kcal; FBG, HOMA-IR, LDL-C and TC) with medians and IQR, and Chi-square test was used for categorical variables.

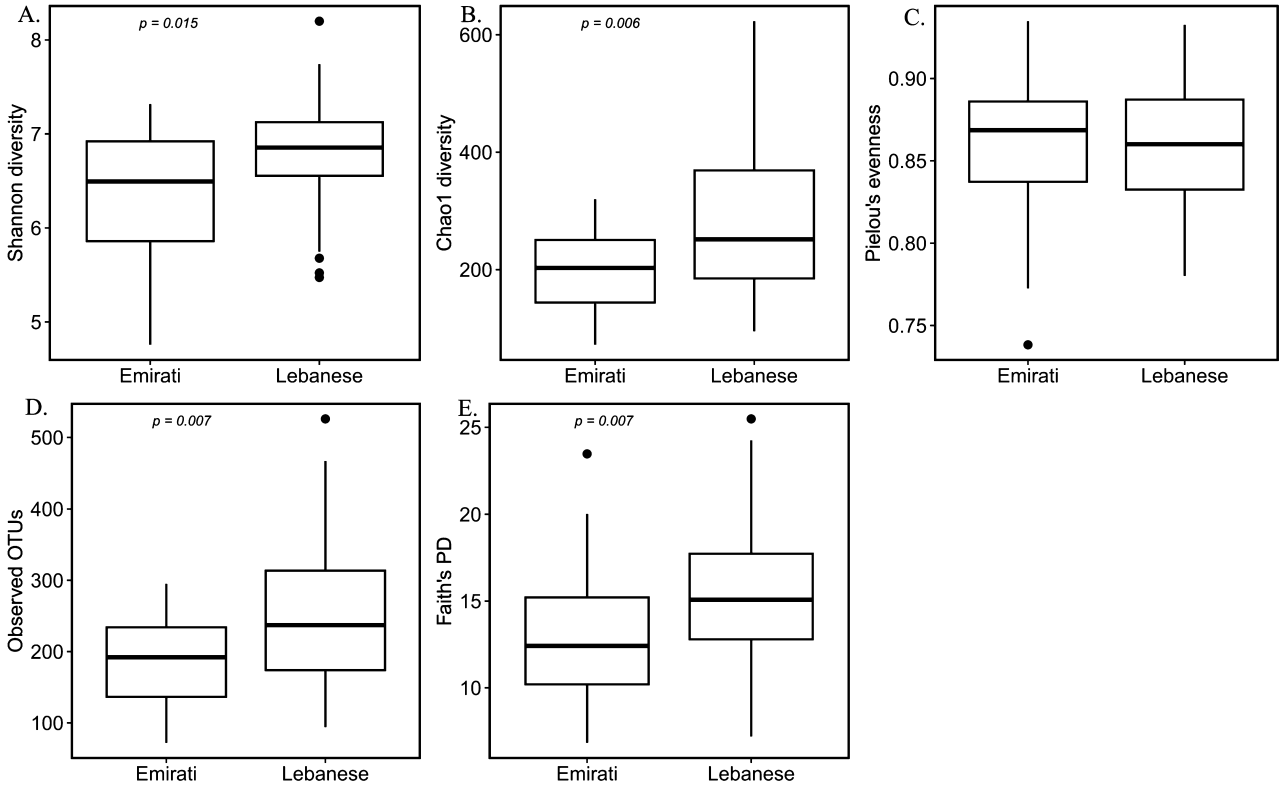

FIGURE 1 Alpha-diversity of Lebanese and Emirati individuals with obesity. Alpha-diversity boxplot showing Shannon diversity (A), Chao1 diversity (B), Pielou's evenness (C), Observed operational taxonomic unit (OTU)(D), and Faith's Phylogenetic Diversity (PD) (E) of Lebanese and Emirati individuals with obesity. For each sample, the alpha-diversity indices are shown on the y-axis, and the groups (Emirati or Lebanese) are on the x-axis. Boxes denote the interquartile range (IQR) between the first and third quartiles, and the horizontal line defines the median. Whiskers represent the smallest (ymin) and largest (ymax) values. Outliers are indicated by black circles. Kruskal Wallis test was performed. A P-value <0.05 denotes a significant difference between Lebanese and Emirati individuals with obesity.

Alpha- and beta-diversity

According to the alpha-diversity metrics (Figure 1), Lebanese adults with OB showed significantly higher diversity (Shannon index, P = 0.015), coinciding with the higher observed operational taxonomic unit (OTU) (P = 0.007), higher Chao1 richness (p = 0.006), and higher Faith's phylogenetic diversity (PD) (P = 0.007) compared to the Emirati group, but no statistically significant difference in evenness (Pielou's evenness, P = 0.964). Microbial composition as reflected by the beta-diversity measures including unweighted UniFrac, weighted UniFrac, Bray–Curtis dissimilarity, and Jaccard similarity showed a marked separation between the gut microbiota community of Lebanese and Emirati with OB. Pairwise PERMANOVA analysis indicated a significant difference in beta-diversity between the two groups (Figure 2); (P = 0.001; P = 0.008; P = 0.001; P = 0.001, respectively).

Taxonomic analysis

Taxonomic profiling of the gut microbiota was conducted and visualised using stacked bar plots. At the phylum level (Figure 3A), the microbial communities of both Lebanese and Emirati participants with obesity were dominated by *Bacillota* and *Bacteroidota*, which together accounted for nearly 90% of the total bacterial abundance. In the Lebanese group, *Bacillota* represented approximately 49% of the community, followed by *Bacteroidota* (41%), while *Pseudomonadota* (about 9%) and *Verrucomicrobiota* (<1%) were detected in lower proportions. Similarly, in the Emirati group, *Bacillota* (47%) and *Bacteroidota* (49%) were the most abundant phyla, with smaller contributions from *Pseudomonadota* (3%) and other phyla such as *Actinomycetota*, *Mycoplasmatota*, *Cyanobacteriota*, and *Lentisphaerota*, each present at very low levels.

At the genus level (Figure 3B), the gut microbiota composition included a range of taxa commonly reported in obese populations. The most represented genera included *Bacteroides*, *Prevotella*, *Faecalibacterium*, *Ruminococcus*, *Lachnospira*, *Blautia*, and *Alloprevotella*, reflecting their contribution to carbohydrate fermentation and short-chain fatty acid production. Additional taxa such as *Collinsella*, *Parapre-*

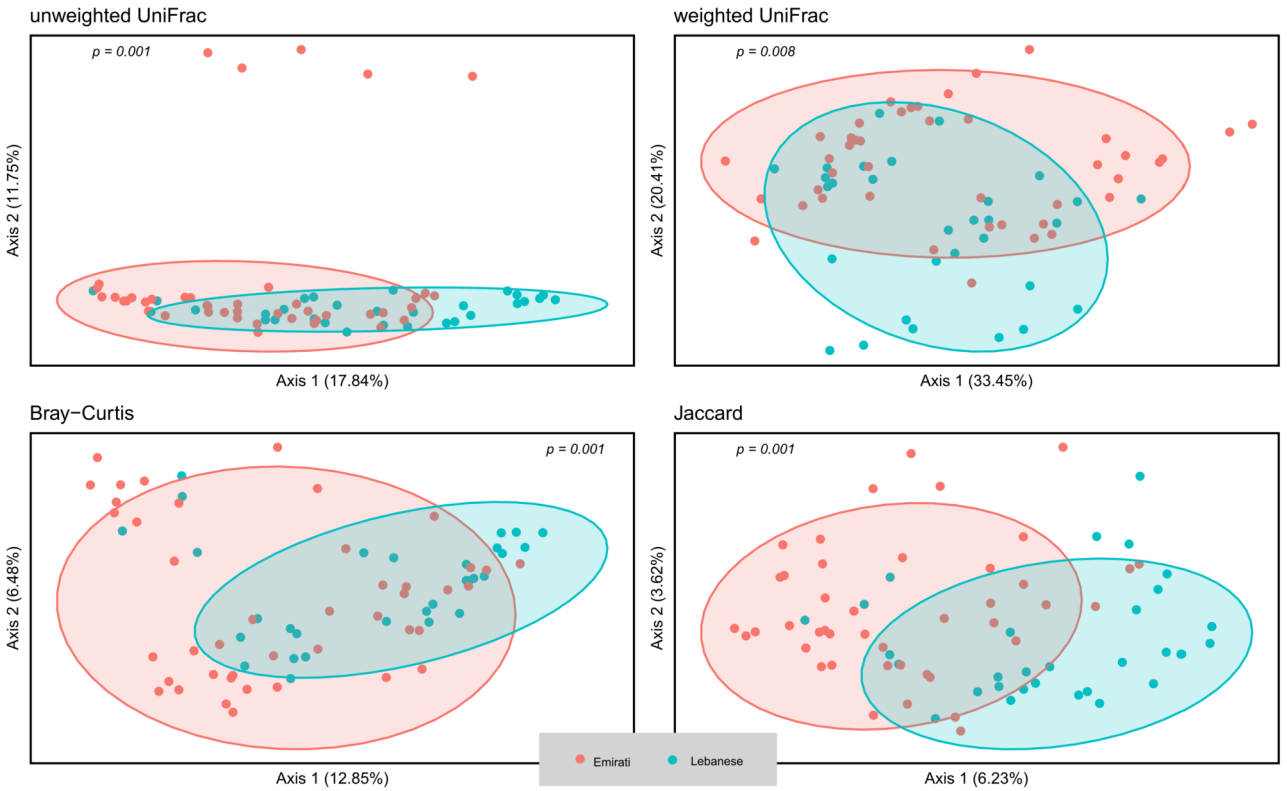

FIGURE 2 Beta-diversity of Lebanese and Emirati individuals with obesity. Principal coordinate analysis (PCoA) plot of unweighted Unifrac, weighted Unifrac, Bray-Curtis dissimilarity, and Jaccard similarity index between Lebanese (blue) and Emirati individuals (red) with OB. A *P*-value <0.05 denotes a significant difference between the two groups.

votella, *Dialister*, *Eubacterium ruminantium* group, *Intestinimonas*, and *Caproiciproducens* were also present, alongside multiple low-abundance genera distributed across individuals.

It is noteworthy that several taxa were completely absent in one group but present in the other at phylum (Figure 4A) and genus level (data not shown). For example, *Allisonella*, *Howardella*, *Intestinimonas*, and *Caproiciproducens* were detected in the Lebanese cohort but absent in Emiratis, whereas other genera such as *Bacteroides* and *Parabacteroides* were enriched in Emiratis but nearly absent in Lebanese participants.

Taken together, these findings indicate that the gut microbiota in both Lebanese and Emirati individuals with obesity was shaped by a limited number of dominant phyla and genera, complemented by a broad range of low-abundance taxa that added to inter-individual variability within each population.

Differences in gut microbial genera between Lebanese and Emirati individuals with obesity

Based on the relative abundances of the gut microbiota in the Lebanese *vs*. Emirati individuals with OB, LEfSe identified several genera that differed significantly between Lebanese and Emirati individuals, with only taxa exceeding the LDA threshold (>10 $\log_2$) and $P < 0.05$ reported.

In the Emirati group, *Bacteroides*, *Parabacteroides* (both of the *Bacteroidota* phylum), *Blautia*, *Acidaminococcus*, *Subdoligranulum*, *Phascolarctobacterium*, and *Lachnospiraceae UCG-004* (all *Bacillota* phylum) were enriched. In contrast, Lebanese participants showed higher abundances of 22 bacterial genera: *Unchar.taxon Clostridiales vadinBB60* group 1, *Tyzzerella*, *Streptococcus*, *Anaerotruncus*, *Erysipelotrichaceae UCG-003*, *Ruminiclostridium 6*, *Ruminococcaceae NK4A214* group, *Ruminococcaceae UCG-010*, *Eubacterium ruminantium* group, *Ruminococcaceae UCG-005*, *Christensenellaceae R-7* group, *Dialister*, *Ruminococcaceae UCG-002*, *Lachnospiraceae NK4A* 136 group (all *Bacillota* phylum); *Rikenellaceae RC9* gut group, *Paraprrevotella*, *Prevotellaceae NK3B31* group, *Unchar.taxon in Prevotellaceae*, and *Alloprevotella* (all *Bacteroidota* phylum); *Desulfovibrio*, *Sutterella*, and *Succinivibrio* (all *Pseudomonadota* phylum) (Figure 5).

According to the Kruskal-Wallis analysis with Benjamini–Hochberg correction at the genus level, as seen in Figure 6, there is an overlap with some of the results from the LEfSe. For the Lebanese group with OB, in accordance with the LEfSe results, there

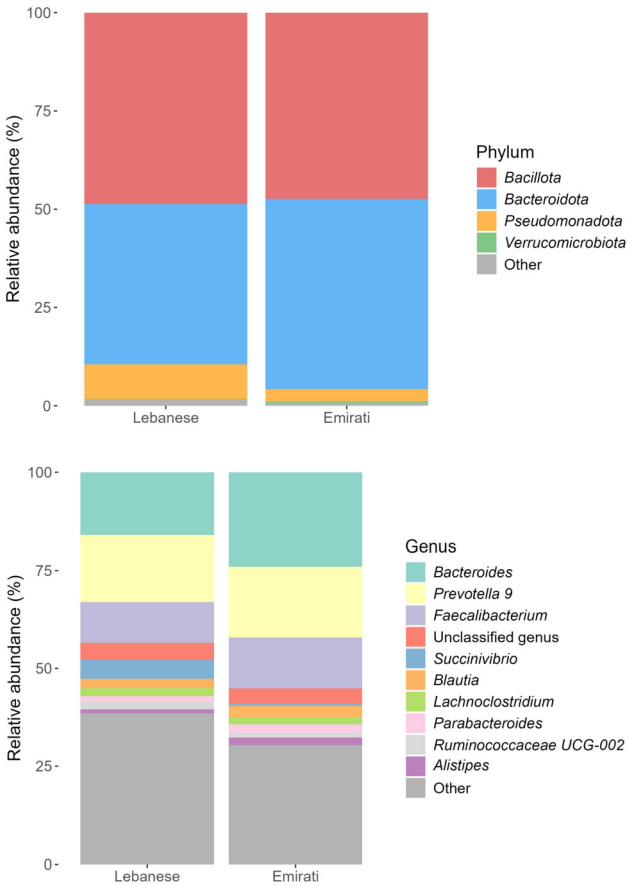

FIGURE 3 Stacked bar plots. (Top) Stacked bar plots of phylum-level and (Bottom) at genus level composition detected in datasets of Lebanese *vs*. Emirati individuals with obesity. Relative abundances (percentages) of the phyla are displayed.

is an increased relative abundance of 14 out of the 22 microbial taxa, which are *Alloprevotella* (q <0.001), *Lachnospiraceae* NK4A136 group (q <0.001), *Ruminococcaceae* UCG-005 (q = 0.002), *Eubacterium ruminantium* group (q = 0.003), *Sutterella* (q = 0.006), *Ruminococcaceae* UCG-002 (q = 0.010), *Unchar.taxon Clostridiales vadin* BB60 group 1 (q = 0.013), *Paraprevotella* (q = 0.016), *Dialister* (q = 0.020), *Ruminiclostridium* 6 (q = 0.021), *Rikenellaceae* RC9 gut group (q = 0.022), *Anaerotruncus* (q = 0.029), *Erysipelotrichaceae* UCG-003 (q = 0.035), and *Christensenellaceae* R-7 group (q = 0.037). None of the results for LEfSe and Kruskal-Wallis overlapped for the Emirati subjects.

Spearman correlation between gut microbiota and age in Lebanese and Emirati individuals with obesity

There was on average more than 10-year difference between Lebanese and Emirati participants (Table 1). Spearman correlation analysis with FDR correction (Figure 7 and Table 2) identified several bacteria that were significantly positively associated with age (q < 0.01). The most pronounced correlation was observed for *Ruminococcaceae* NK4A214 (rho = 0.397, q = 0.0014), followed by *Prevotellaceae D_5* uncultured (rho = 0.386, q = 0.002), *Ruminococcaceae* UCG-005 (rho = 0.364, q = 0.004), and *Anaerotruncus* (rho = 0.359, q = 0.005). Additional significant associations were found for *Alloprevotella* (rho = 0.358, q = 0.005), *Ruminococcaceae* UCG-002 (rho = 0.358, q = 0.005), *Clostridiales vadin BB60* group (rho = 0.354, q = 0.005), and *Ruminococcaceae* UCG-010 (rho = 0.347, q = 0.006). Among all clinical and demographic variables assessed, age was the only factor significantly correlated with specific bacterial genera after FDR correction (Figure 7). Collectively, these findings indicate that age plays a substantial role in shaping gut microbiota composition, particularly influencing members of the *Ruminococcaceae* family and other bacteria such as *Prevotellaceae D_5* uncultured and *Anaerotruncus*. The uniformity of positive associations suggests a gradual, age-related enrichment of these bacteria. None of the other clinical parameters were significantly correlated with any of the taxa.

Linear regression analysis

The relationship between microbial composition and nationality was subsequently examined, comparing Lebanese and Emirati individuals with OB, while accounting for age as a potential confounder. Linear regression models were used (Table 3) to assess these associations, with both unadjusted and adjusted models reported. A change-in-estimate criterion with a cut-off of 10% was used to identify the confounder (Skelly *et al*., 2012).

In the unadjusted model, Lebanese individuals had a significantly higher relative abundance of *Alloprevotella* compared to Emiratis (β = 0.0109, P = 0.007). However, after adjusting for age, the effect size decreased (β = 0.0084) and was no longer statistically significant (P = 0.067), with a 22.9% reduction in effect size, suggesting that age may be a confounder.

For *Prevotellaceae D_5*, Lebanese nationality remained significantly associated with higher bacterial abundance in both unadjusted (β = 0.0057, P = 0.012) and adjusted models (β = 0.0055, P = 0.037). The 5% reduction in effect size suggests that age had minimal confounding influence.

In *Clostridiales vadin BB60*, a strong association was observed in the unadjusted model (β = 0.0012, P < 0.001). After adjusting for age, the effect size decreased by 38.9% (β = 0.0007, P = 0.047), indicating that age played a significant role as a confounder. Additionally,

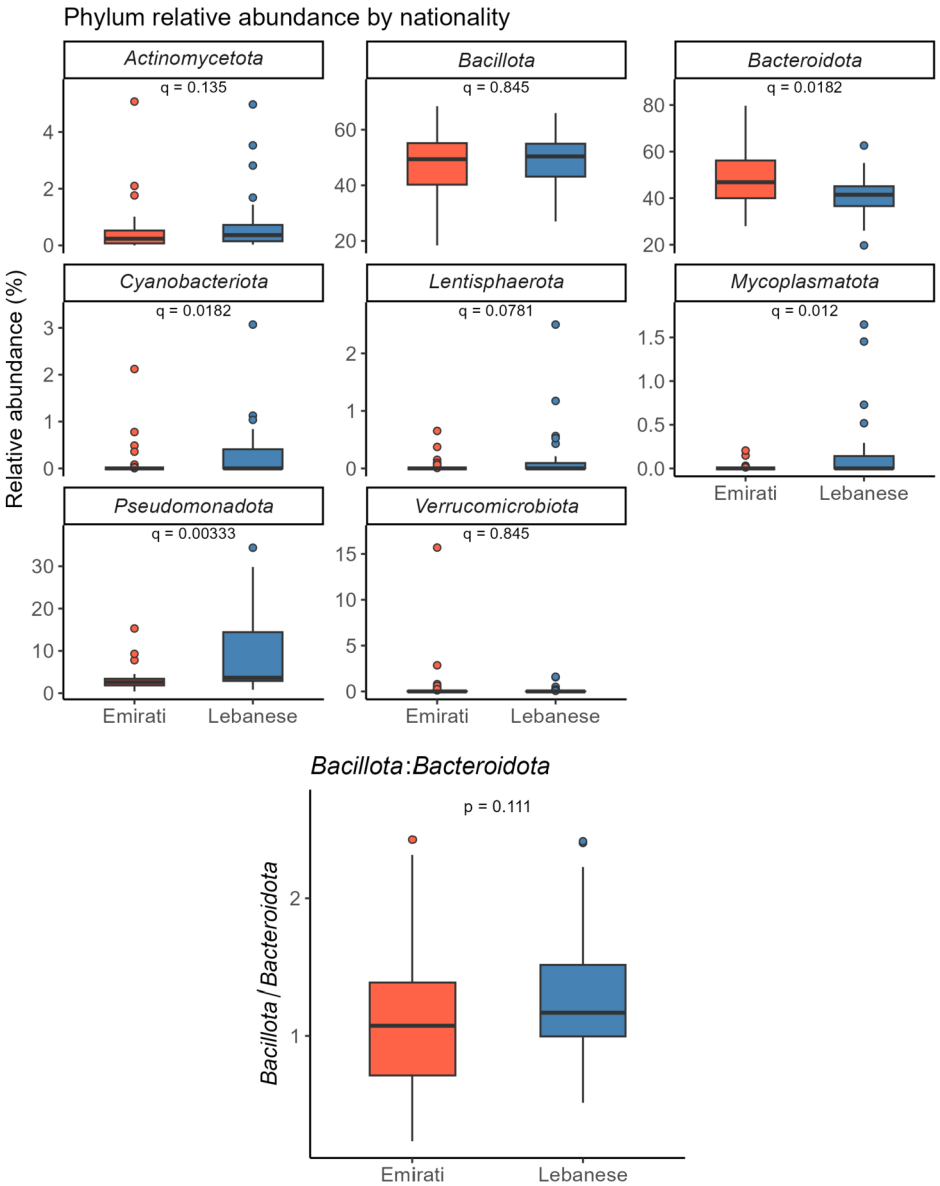

FIGURE 4 Comparative relative abundance of selected bacterial phyla and *Bacillota*/*Bacteroidota* ratio in Lebanese and Emirate participants with obesity. (Top panels) Boxplots showing relative abundance (%) of selected phyla, stratified by nationality with q-values. (Bottom panel) Boxplot of *Bacillota*/*Bacteroidota* ratio stratified by nationality. Differences between groups were assessed using the Kruskal-Wallis test followed by false discovery rate (FDR). Adjusted *q*-values are indicated where applicable. A *q*-value of ≤ 0.05 was considered statistically significant, as determined by the Kruskal-Wallis test with FDR correction.

TABLE 2 Correlation analysis between gut microbiota and age in Lebanese and Emirati individuals with obesity

Bacteria	q-value[1]	rho
Ruminococcaceae.NK4A214.group	0.0014*	0.397
Prevotellaceae.D_5__uncultured	0.0022*	0.386
Ruminococcaceae.UCG.005	0.0040*	0.364
Anaerotruncus	0.0046*	0.359
Alloprevotella	0.0046*	0.358
Ruminococcaceae.UCG.002	0.0046*	0.358
Clostridiales.vadinBB60. group. D_5__uncultured. bacterium	0.0052*	0.354
Ruminococcaceae.UCG.010	0.0064*	0.3467

1 Indicates significant correlation * $q < 0.05$ for Spearman correlation analysis with FDR correction.

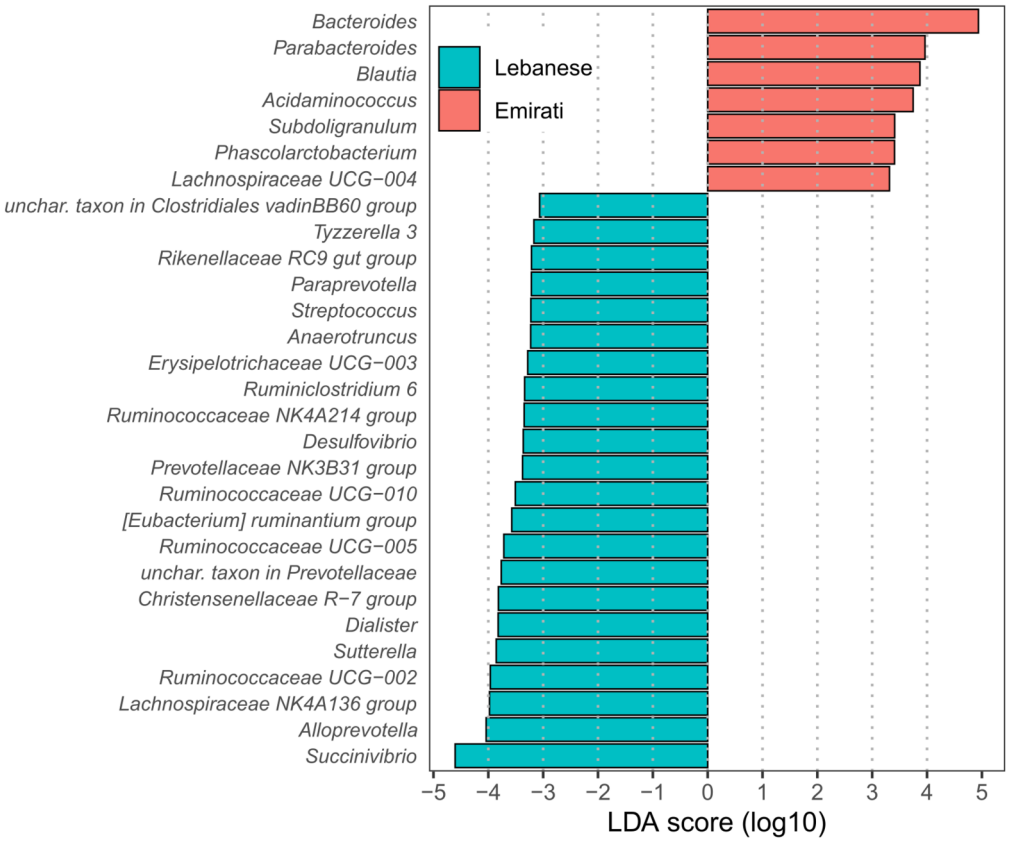

FIGURE 5 Linear discriminant analysis effect size (LEfSe) plot. The genera enriched in Lebanese and Emirati individuals with OB are coloured by blue and red, respectively. Histogram of the LDA scores computed for features differentially abundant among Lebanese and Emirati individuals with obesity. Only class meetings with an LDA significant threshold $>^{10}\log 2$ and $P < 0.05$ are shown.

age was a significant predictor of bacterial abundance ($P = 0.011$).

For *Anaerotruncus*, Lebanese nationality was significantly associated with bacterial abundance in the unadjusted model ($\beta = 0.0015$, $P = 0.036$). However, after adjusting for age, the effect size declined by 35.3% ($\beta = 0.00097$) and was no longer significant ($P = 0.229$), further indicating confounding by age.

The unadjusted model for *Ruminococcaceae NK4A214* showed a weak association ($\beta = 0.0019$, $P = 0.073$), and in the adjusted model, the effect size further decreased ($\beta = 0.0006$, $P = 0.613$), indicating that age largely explained the observed relationship.

For *Ruminococcaceae UCG* – 002, Lebanese individuals exhibited significantly higher levels in the unadjusted model ($\beta = 0.0079$, $P = 0.030$). However, after adjustment, the effect size decreased by 46.97% ($\beta = 0.0042$) and lost statistical significance ($P = 0.301$), suggesting that age was a strong confounder.

No significant association was found for *Ruminococcaceae UCG* – 005 in either the unadjusted ($P = 0.284$) or adjusted model ($P = 0.599$).

Finally, for *Ruminococcaceae UCG* – 010, the unadjusted model showed a strong association ($\beta = 0.00297$, $P < 0.001$). After adjusting for age, the effect size decreased by 22.73% but remained statistically significant ($\beta = 0.0023$, $P = 0.018$), indicating that the association persisted but was partially influenced by age.

Overall, the regression analyses revealed a consistent pattern across taxa: several nationality–microbiota associations observed in the unadjusted models were attenuated after controlling for age, indicating that age acted as a meaningful confounder for many genera. However, a subset of taxa – including *Prevotellaceae D_5*, *Clostridiales vadinBB60*, and *Ruminococcaceae UCG-010* – remained significantly associated with nationality even after adjustment, suggesting a robust nationality-linked microbial signature. In addition, age itself showed positive associations with several genera, reinforcing its influential role in shaping gut microbial composition within this cohort.

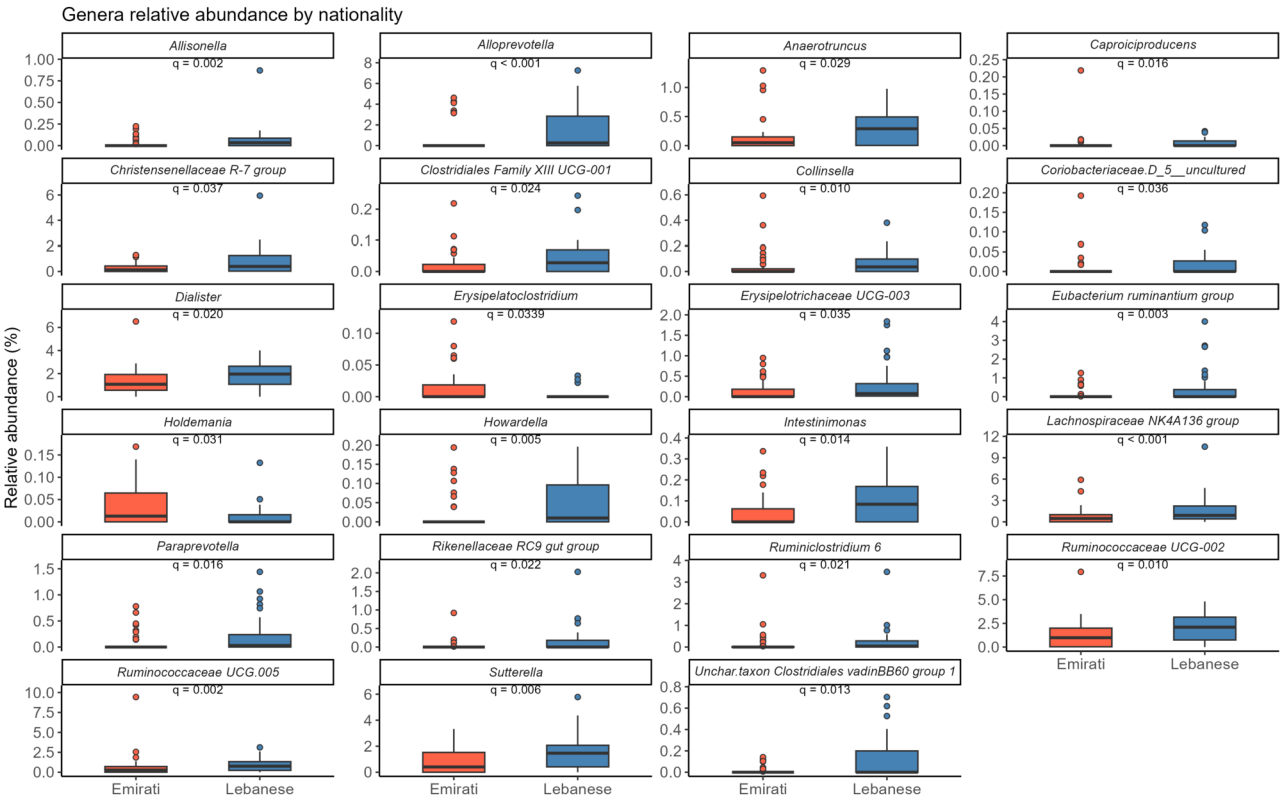

FIGURE 6 Relative abundance of selected gut bacterial genera by nationality. Boxplots depict the relative abundance (%) of selected bacterial genera in Lebanese and Emirati participants with obesity. Group comparisons were performed using the Kruskal–Wallis test, with false discovery rate (FDR) correction applied to account for multiple testing. Adjusted q-values are displayed for each genus.

4 Discussion

This study contributes to the growing body of research exploring how geography, culture, and ethnicity shape gut microbiota and its relationship with obesity. By comparing obese individuals from two Arab nationalities – Lebanese and Emirati residing in their respective countries, we highlight distinct microbial patterns potentially driven by regional dietary and lifestyle habits. Existing studies, such as comparisons between French and Saudi individuals, have shown that dietary and cultural factors can significantly influence microbial composition (Yasir *et al.*, 2015). Despite global interest in ethnic differences in microbiota composition, data from Middle Eastern populations remain limited. Our findings emphasise the need for more inclusive studies in this region to better understand how cultural and environmental factors influence metabolic health and to inform tailored intervention strategies.

The comparison of Lebanese and Emirati individuals with OB provides a meaningful framework to explore how cultural norms shape gut microbiota and potentially affect metabolic outcomes. The predominance of female participants 62.8 to 66.7% reflects a broader regional trend of higher obesity prevalence among ciswomen in the Middle East and North Africa (MENA), a phenomenon attributed to sociocultural perceptions associating larger body size with beauty and affluence (Mallat *et al.*, 2016; Naja *et al.*, 2011; Sibai *et al.*, 2003). These findings suggest that public health strategies targeting obesity in MENA countries should consider the cultural contexts influencing body image and dietary behaviours, alongside biological factors such as the gut microbiota.

Despite overall dietary similarities, Lebanese participants reported significantly higher fibre intake. While no direct correlations between fibre intake and microbial taxa were observed after FDR correction, fibre's known role in modulating gut microbiota may partly explain the distinct microbial profiles observed. In contrast, Emirati individuals exhibited higher anthropometric measures – including weight, BMI, WtHR, and fat mass – although these were not significantly associated with specific bacterial genera in our dataset. These differences align with previous studies linking higher fibre intake to greater gut microbial diversity

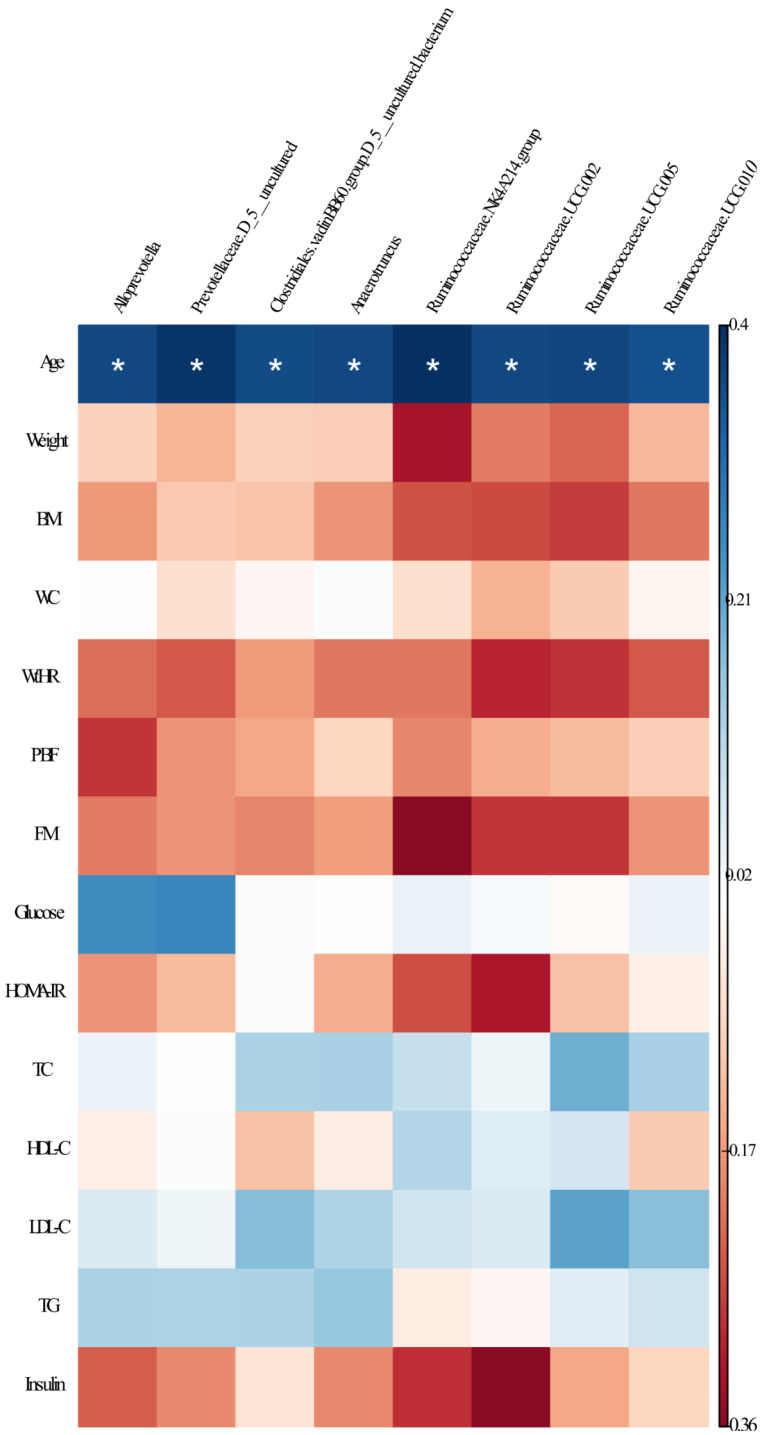

FIGURE 7 Spearman correlation analysis between gut microbiota and clinical variables in Lebanese and Emirati individuals with obesity. In the heatmap, blue squares indicate significant positive correlations, and red squares indicate significant negative correlations. * Significant correlation at q <0.05 (FDR-correction). Only age showed significant correlations with gut microbial taxa after FDR correction. Abbreviations: BMI: Body mass index; WC: waist circumference; WtHR: waist to height ratio, PBF: percent body fat; FM: fat mass; HOMA-IR: homeostatic model assessment for insulin resistance LDL-C: low density lipoprotein cholesterol, HDL-C: high density lipoprotein cholesterol; TG: triglyceride.

and improved metabolic health (Nasreddine *et al.*, 2012, 2014). Comparable patterns have been observed in other cross-cultural comparisons, such as between French and Saudi populations, where differences in fibre consumption and traditional *versus* Westernised diets influenced microbial composition (Yasir *et al.*, 2015). Another important demographic difference in our cohort was age, with Lebanese participants being on average more than 10 years older than Emiratis (Table 1). Since age is a well-recognised determinant of gut microbiota com-

TABLE 3 Linear regression analysis between gut microbiota and age among Lebanese and Emirati individuals with obesity.[1]

Gut microbiota	Model	Intercept estimate	Nationality (Lebanese) estimate	Age estimate	R^2 (Adj.)	*P*-value (Nationality)	*P*-value (Age)	Confounding (%)
Alloprevotella	Unadj.	5.00×10^{-3}	1.09×10^{-2}	–	0.085	0.007 **	–	–
	Adj.	-1.30×10^{-3}	8.40×10^{-3}	2.2 × 10-4	0.089	0.067	0.263	22.9
Prevotellaceae D_5	Unadj.	8.00×10^{-4}	5.70×10^{-3}	–	0.074	0.012 *		–
	Adj.	-1.00×10^{-5}	5.50×10^{-3}	3 × 10-5	0.061	0.037 *	0.821	5.0
Clostridiales vadinBB60	Unadj.	1.00×10^{-4}	1.20×10^{-3}	–	0.147	<0.001*	–	–
	Adj.	-1.10×10^{-3}	7.00×10^{-4}	4 × 10-5	0.213	0.047 *	0.011*	38.9
Anaerotruncus	Unadj.	1.50×10^{-3}	1.50×10^{-3}	–	0.048	0.036 *	–	–
	Adj.	6.00×10^{-5}	9.7 × 10-4	5.0 × 10-5	0.059	0.229	0.181	35.3
Ruminococcaceae NK4A214	Unadj.	3.30×10^{-3}	1.90×10^{-3}	–	0.031	0.073	–	–
	Adj.	-3.00×10^{-4}	6.0 × 10-4	1.2 × 10-4	0.059	0.613	0.0247 *	–
Ruminococcaceae UCG-002	Unadj.	1.25×10^{-2}	7.90×10^{-3}	–	0.052	0.030 *	–	–
	Adj.	2.40×10^{-3}	4.20×10^{-3}	3.3 × 10-4	0.085	0.301	0.0637	46.97
Ruminococcaceae UCG-005	Unadj.	6.40×10^{-3}	3.30×10^{-3}	–	0.002	0.284	–	–
	Adj.	2.50×10^{-3}	1.80×10^{-3}	1.3 × 10-4	–0.0019	0.599	0.404	43.81
Ruminococcaceae UCG-010	Unadj.	5.00×10^{-4}	2.97 × 10-3	–	0.140	<0.001*	–	–
	Adj.	-1.30×10^{-3}	2.3 × 10-3	6.0 × 10-5	0.153	0.018 *	0.1530	22.73

1 Indicates significant correlation * $P < 0.05$ for linear regression analysis.

position, this imbalance needed to be considered when interpreting our findings.

Our findings revealed that Lebanese adults with OB exhibit significantly greater gut microbial diversity compared to their Emirati counterparts. This is supported by multiple alpha-diversity indices, including the Shannon index, observed features, Chao1 richness, and Faith's PD. Greater microbial diversity may indicate a more complex and versatile ecosystem, potentially conferring resilience to metabolic diseases, as various studies have associated increased gut microbiota diversity with improved metabolic profiles in both humans and mice (Astbury *et al.*, 2020; Cotillard *et al.*, 2013; Le Chatelier *et al.*, 2013; Meyer and Bennett, 2016). Additionally, although a meta-analysis found that obesity is linked to alterations in gut microbial composition, including changes in richness and diversity, significant discrepancies were observed across different cohorts (Chanda and De, 2024). For instance, high BMI has been associated with decreased gut microbial diversity, and certain taxa, such as *Christensenellaceae*, have been linked to BMI variations across ethnicities (Balakrishnan *et al.*, 2021).

In terms of beta-diversity, PCoA was used to visualise differences between the Lebanese and Emirati populations, and these were confirmed as statistically significant by pairwise PERMANOVA analyses, indicating marked differentiation in microbial community composition. This suggests that nationality – and by extension, environmental and dietary exposures – may play a critical role in shaping gut microbiota profiles (Parizadeh and Arrieta, 2023; Yasir *et al.*, 2015).

Taxonomic analysis of gut microbiota revealed both shared and distinct features. While both groups exhibited comparable proportions of the dominant phyla *Bacillota* and *Bacteroidota* – consistent with established gut microbiota compositions (Chen *et al.*, 2021; Zhang *et al.*, 2023) – notable differences emerged in less abundant but potentially influential taxa. The Lebanese group displayed significantly higher levels of *Pseudomonadota* (9% vs 3% in Emiratis), *Mycoplasmatota* (q = 0.003), *Cyanobacteriota* (q = 0.009), and *Lentisphaerota* (q = 0.049), whereas the Emirati group exhibited a greater abundance of *Bacteroidota* (q = 0.009). Elevated levels of *Mycoplasmatota* in the

Lebanese group may reflect the influence of Western dietary components, such as high fat and sugar intake, which have been associated with increased obesity risk (Konstantinidis *et al.*, 2020; Napoli *et al.*, 2024). Although the *Bacillota*/*Bacteroidota* ratio has historically been linked to obesity-related microbiota changes (Boulange *et al.*, 2016; Compare *et al.*, 2016; John *et al.*, 2018; Turnbaugh *et al.*, 2008), our results underscore the limitations of using this ratio as a universal marker of obesity. In our study, Lebanese individuals with OB exhibited a higher, but not significant, *Bacillota*/*Bacteroidota* ratio than obese Emiratis, despite the latter presenting with higher overall obesity levels. This discrepancy aligns with recent research questioning the reliability of the *Bacillota*/*Bacteroidota* ratio across ethnically and geographically diverse populations (Magne *et al.*, 2020). While some studies have observed elevated *Bacillota*/*Bacteroidota* ratios in obese individuals (Koliada *et al.*, 2017), others report inconsistent or population-specific patterns (Kim *et al.*, 2019). These findings highlight the need to move beyond broad phylum-level comparisons and instead investigate specific microbial genera and their functional contributions to host metabolism (Bauer *et al.*, 2016).

Geographic, ethnic, and cultural factors are well-documented determinants of gut microbiota composition (Yatsunenko *et al.*, 2012). As previous studies show, Americans, Japanese, Koreans, and Chinese individuals each harbour distinct microbial profiles, with varying proportions of *Bacillota*, *Actinomycetota*, and *Bacteroidota*, respectively (Brooks *et al.*, 2018). At the genus level, variations are similarly pronounced, with *Bacteroides* enriched in Chinese populations, *Prevotella* in Indians, and *Ruminococcus* in the Dutch (Brooks *et al.*, 2018). Our findings reflect these ethnically stratified patterns. Emiratis – characterised by higher BMI – had increased levels of *Bacteroides* and *Parabacteroides*, which are associated with high-fat, high-sugar diets and enhanced energy harvest. Conversely, Lebanese participants had higher abundances of *Alloprevotella* and *Paraprevotella*, linked to high-fibre intake and improved metabolic profiles (Christensen *et al.*, 2018). These results bolster the existing evidence linking *Bacteroides*-dominant microbiota to increased adiposity, while leaner individuals often harbour *Prevotella*-rich communities (Lee *et al.*, 2024). Supporting this, studies comparing French and Saudi populations (Yasir *et al.*, 2015), as well as investigations among Emiratis (Ahmad *et al.*, 2023) and Lebanese (Abou-Samra *et al.*, 2025) have highlighted gut microbiota differences shaped by diet, lifestyle, and cultural practices.

LEfSe analysis further identified taxa that discriminate between the two populations. Emirati individuals showed enrichment in *Bacteroides*, while Lebanese participants had higher levels of *Lachnospiraceae*. Both genera have been previously implicated in metabolic functions related to energy harvest, lipid metabolism, and fat storage (Wu *et al.*, 2024; Yang *et al.*, 2022). However, interpretation of these differences must consider the significant age gap between the groups. Spearman correlation analysis confirmed that age significantly correlated with several taxa, and linear regression models showed that some between-group differences – particularly at the genus level – were attenuated or lost after adjusting for age. This underscores the role of age as a confounding factor in microbiota studies, as also reported in previous research (Chen *et al.*, 2021; De la Cuesta-Zuluaga *et al.*, 2019; Odamaki *et al.*, 2016).

Age-related changes in the gut microbiome have been extensively documented across the human lifespan. Research spanning from infancy to old age has identified key transitions in microbial composition – particularly during early development and later life stages (Odamaki *et al.*, 2016). Some studies report minimal age-related differences (Takagi *et al.*, 2019), while others identify significant associations between age and microbial composition (De la Cuesta-Zuluaga *et al.*, 2019). These inconsistencies indicate that age can act as a confounder in microbiome studies and must be carefully considered. In our cohort, although age explained part of the between-group variation, several taxa – including *Prevotellaceae D_5*, *Clostridiales vadinBB60*, and *Ruminococcaceae UCG-010* – remained significantly associated with Lebanese nationality after adjustment. This suggests that nationality-related dietary and environmental factors continue to influence gut microbiota composition independently of age, consistent with evidence that distinct microbial signatures persist across populations even when controlling for demographic variables (Brooks *et al.*, 2018; Yatsunenko *et al.*, 2012).

Each of these taxa has known links to health-promoting microbial functions. *Prevotellaceae* D_5 is associated with fibre-rich diets and improved glycaemic control (Kovatcheva-Datchary *et al.*, 2015); *Clostridiales vadinBB60* has been found in metabolically healthy individuals and centenarians and is implicated in lipid metabolism and anti-inflammatory effects (Zhang *et al.*, 2019). *Ruminococcaceae UCG-010* plays a role in fibre degradation and short-chain fatty acid production, which support gut health and are linked to GLP-1 release, satiety, and protection against type 2 diabetes (Gryaznova *et al.*, 2022; Mancabelli *et al.*, 2017; Tims

et al., 2013; Tsai *et al.*, 2020; Wei *et al.*, 2018). The persistence of these associations despite age adjustment highlights the key role of cultural and environmental influences tied to nationality in shaping the gut microbiota.

Although ethnicity was not found to have a significant correlation with microbiota composition in a Middle Eastern population, lifestyle and environmental influences exhibited a greater degree of homogeneity compared to the ethnic, sociocultural, economic, and dietary diversity observed within the United States (Brooks *et al.*, 2018). Importantly, our study controlled for methodological consistency – using identical DNA extraction and sequencing protocols – yet still observed significant differences between groups. This reinforces the notion that factors such as diet (Asnicar *et al.*, 2021), genetics (Goodrich *et al.*, 2014), physical activity, and medication use (Heiman and Greenway, 2016) contribute meaningfully to microbiota variation.

Strengths and limitations

This study provides novel comparative insights into how regional and ethnic factors may shape gut microbiota composition in the context of obesity, focusing on two Arab populations living in the MENA region. The use of standardised microbiota sequencing protocols across sites minimised methodological variability, while comprehensive data collection – including anthropometric, biochemical, and selected dietary variables – facilitated robust analysis. The application of linear regression models adjusted for age, along with rigorous participant selection and harmonised methodologies, further strengthened the reliability and interpretability of the findings. Nonetheless, several limitations should be considered. The cross-sectional design limits the ability to infer causality, suggesting that there must be longitudinal research to examine microbiota dynamics over time. The relatively small sample size may constrain the generalisability of the results. This study also focused exclusively on obese participants from a larger cross-sectional dataset that also included normal-weight adults. As such, comparisons with normal-weight controls were beyond the scope of the current analysis but will be explored in a separate study using the same parent cohort. Another notable limitation is the significant age difference between the Lebanese and Emirati participants, which could independently influence gut microbiota composition. While we addressed this through correlation and regression analyses, which confirmed age as a confounding factor, residual confounding cannot be fully excluded. Although age differences between the 2 samples were accounted for, other relevant factors – such as physical activity, medication use, psychosocial stress, socioeconomic status, and genetic background – were not assessed and may have influenced gut microbiota composition. Additionally, dietary assessment was limited to fibre and probiotic intake, omitting other potentially significant dietary components (e.g. fat and protein intake). Variability in laboratory assays between countries may have introduced inconsistencies in biochemical measurements, and the lack of functional microbiota profiling restricted insights into microbial metabolic potential. Additionally, the use of different bioelectric impedance analysis devices across study sites (Tanita in the UAE and InBody in Lebanon) may introduce inter-device variability and measurement bias, which could affect the comparability of body composition data between the two populations.

5 Conclusions

This study highlights significant gut microbiota differences between Lebanese and Emirati adults with OB, shaped by cultural, dietary, and geographic factors. Emiratis exhibited a higher abundance of *Bacteroides* and *Parabacteroides*, bacteria commonly linked to high-fat, low-fibre diets and greater energy harvest. In contrast, Lebanese individuals showed greater microbial diversity and elevated levels of *Alloprevotella*, *Paraprevotella*, and *Mycoplasmatota*, reflecting higher fibre intake. Furthermore, this study reveals that dietary patterns rooted in cultural and geographic context strongly influence the composition of gut microbiota. The study also identified age as key confounder, which significantly influenced the associations between nationality and microbial profiles. These findings highlight the importance of incorporating both age – and ethnicity-specific microbiome signatures when designing targeted obesity interventions. Notably, microbial differences such as higher abundances of *Prevotellaceae D_5*, *Clostridiales vadinBB60*, and *Ruminococcaceae UCG-010* in Lebanese individuals remained significant after adjusting for age, emphasising the potential for culturally driven, microbiota-informed strategies. Ultimately, the gut microbiota may serve as both a biomarker of lifestyle and a modifiable factor in the management of obesity and its metabolic consequences within Arab populations living in the MENA region. Future research should adopt longitudinal designs to elucidate the causal mechanisms linking gut microbiota to obesity and metabolic health, particularly in response to dietary

and lifestyle interventions. Including non-obese control groups and diverse Arab populations will enhance generalisability and provide insights into ethnicity-specific microbial variations. Integrating functional metagenomics, metabolomic profiling, and detailed dietary, lifestyle, and genetic data will deepen our understanding of microbial activity and its metabolic impact. Additionally, culturally tailored dietary interventions and investigations into age-related microbial shifts across life stages are warranted to inform effective, personalised strategies for weight management in the MENA region.

Supplementary materials

Data is available on https://doi.org/10.1163/18762891-bja00111 under Supplementary Materials.

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Authors' contribution

Conceptualization, M.A.S., M.A.A., M.K. and K.V.; methodology, M.A.S., M.A.A., M.K. and K.V.; software, M.A.S., M.A.A., and K.V.; validation, M.K. and K.V.; formal analysis, M.A.S. and M.A.A.; investigation, M.A.S. and M.A.A.; resources, M.K., K.V. and C.A.M.; data curation, M.A.S., M.A.A., M.K. and K.V.; writing – original draft preparation, M.A.S. and M.A.A.; writing – review and editing, M.K., K.V., E.B and C.A.M.; visualization, M.A.S., M.A.A., M.K. and K.V.; supervision, M.K., K.V., and E.B.; project administration, M.K. and K.V.; funding acquisition, C.A.M. and K.V. All authors have read and agreed to the published version of the manuscript.

Conflict of interest

KV is editor in chief of Beneficial Microbes, but has not been involved in the review and decision process of this article. The authors declare no conflict of interest. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

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