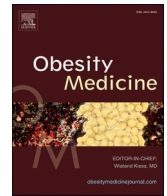




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## Gut microbiota-derived metabolites as early biomarkers for childhood obesity: A policy commentary from urban African populations

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## ABSTRACT

Obesity among children is rapidly increasing in urban African settings due to the Westernisation of diets and decreased physical exercise, as well as socioeconomic inequality. Changes in the composition of gut microbiota, especially depletion of short-chain fatty acids (SCFAs), increase in branched-chain amino acids (BCAAs), and alterations in the bile acid metabolism, are becoming early, non-invasive predictors of metabolic risk. Though comparable microbiome-based early-detection models have been designed regarding Latin American and Asian paediatric populations, the commentary aims at the African urban setting, where a combination of undernutrition and obesity, the use of street foods and the rapid urban-rural migration generate unique microbial profiles. We synthesise data in Nairobi, Kampala, and Lagos, including region-specific taxa such as *Succinivibrio*, *Treponema*, and *Methanobrevibacter*. Our suggestions are specific, low-cost interventions, such as the incorporation of fiber-rich foods into national school feeding programs and the use of Ghana-developed lateral-flow SCFA assays that cost less than US\$2 per test. This is a policy-orientated narrative with no collection of primary data. The search of literature in PubMed, Scopus, and African health research repositories (2015–2025) was carried out with the use of the terms associated with gut microbiota, childhood obesity, microbial metabolites, and Africa. Our focus is to transform microbiome science into scalable, culturally appropriate, and cost-effective public health interventions.

### 1. Methods

This policy commentary synthesises peer-reviewed literature and public health survey data (2015–2025) relevant to gut microbiota, microbial metabolites, and childhood obesity in African urban populations. Sources were identified via PubMed, Scopus, and African health research libraries using combinations of: *gut microbiota*, *childhood obesity*, *SCFAs*, *BCAAs*, *microbial metabolites*, *Africa*, and *urban diet*.

**Inclusion criteria:** (i) human paediatric studies, (ii) African urban settings, (iii) data on microbial metabolites.

**Exclusion criteria:** animal-only studies or microbiome research without metabolite measures.

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**Table 1** prevalence estimates were drawn from national or municipal health surveys and WHO regional datasets, with year, sample size, and age range (5–19 years) provided in footnotes.

**Ethics statement:** No new human data were collected; ethical approval was not applicable.

## 2. Introduction

There are well over 150 million children and adolescents worldwide with childhood obesity three times more prevalent than it was in 1990, with urban African regions registering some of the most rapid growth, as **Table 1** indicates. In Nairobi, Kampala, and Lagos, the prevalence of obesity has increased dramatically in the last decade as a result of the transition to ultra-processed foods over traditional diets rich in fibre, along with decreasing physical activity and growing socioeconomic disparities (Al-Jawaldeh and Abbass, 2022). The urban African populations are under a dual burden of under-nutrition in certain subpopulations and obesity in others, which means that standard risk assessment using the BMI is inadequate.

The gut microbiome is a key component of energy balance, immune regulation, and metabolic signalling. Recently, there is evidence that microbiome-derived metabolites like SCFAs, BCAAs, and bile acids may be biomarkers of metabolic dysfunction prior to the development of overt obesity (Mburu et al., 2025). However, the majority of the data is related to high-income and non-African settings, which is why there is an urgent necessity to obtain African-specific knowledge that would reflect the peculiarities of dietary and environmental habits and patterns of microbial colonisation (Wilson et al., 2020).

Although Latin American and Asian frameworks have been developed that connect the gut microbiota to early diagnosis of obesity, the urban environment of Africa is unique: the prevalence of street foods, the fast rural-urban migration that changes the microbial ecology, and the microbial taxa distributions, i.e., the abundance of *Succinivibrio*, *Treponema*, and *Methanobrevibacter* with possible effects on metabolism (Lappé et al., 2019). This commentary places microbiome science within the policy context of Africa in the hope that the discovery of biomarkers is harmonised with the action of public health.

## 3. Gut microbiota-derived metabolites and obesity risk

### 3.1. Evidence strength and causality limitations

The association between gut microbiota composition and obesity is well-documented; however, causality remains incompletely established (Magalhães et al., 2025). In African paediatric populations, reduced butyrate-producing bacteria, elevated isobutyrate, high circulating BCAAs, and altered secondary bile acid profiles have been reported in obesity-prone groups (Stephens et al., 2018). While these metabolites are plausible early biomarkers, their predictive validity requires longitudinal African cohorts to confirm whether they precede or simply accompany obesity onset (Lazar et al., 2019).

### 3.2. Mechanistic links

- SCFA imbalance:** The overabundance of acetate, propionate and butyrate can influence the production of satiety hormones and adipogenesis (Yang et al., 2018).
- An increased level of BCAAs:** Branched-chain amino acids (BCAAs) in the plasma are associated with insulin resistance and early metabolic syndrome in obese children (De Marco et al., 2021).
- Bile acid imbalance:** Bile acids are secondary, and they regulate the uptake and burning of lipids via FXR/TGR5 signalling (De Marco et al., 2021).
- Endotoxemia and inflammation:** chronic low-grade inflammation is facilitated by increased translocation of lipopolysaccharide (LPS) (Yang et al., 2018).

**Table 1**

Childhood obesity, gut microbiota biomarkers, and public health challenges in urban African Cities (2025).

City	Estimated Childhood Obesity Rate (2025)	Change Since 2010	Key Drivers	Observed Microbial Biomarkers	Public Health Challenges
Nairobi	18 % (95 % CI 16.3–19.7) <sup>a</sup>	+10 %	Westernised diets, sedentary lifestyles, processed school meals	Low SCFAs, altered Firmicutes/Bacteroidetes ratio	Double burden of malnutrition, limited nutrition surveillance
Kampala	15 % (95 % CI 13.5–16.5) <sup>b</sup>	+8 %	Urbanisation, ultra-processed foods, reduced activity	Reduced microbial diversity, elevated bile acids	Coexistence of undernutrition and obesity, weak research infrastructure
Lagos	22 % (95 % CI 20.1–23.9) <sup>c</sup>	+12 %	High fried/street food intake, sugary beverages, inactivity	Elevated BCAAs, microbial dysbiosis	Socioeconomic inequality, rising NCD burden in children

**Key:** SCFAs = short-chain fatty acids; BCAAs = branched-chain amino acids.

<sup>a</sup> Kenya National Adolescent Nutrition Survey 2023 (ages 5–19, N = 1950).

<sup>b</sup> Uganda Ministry of Health Child Health Survey (2023) (ages 5–19, N = 2010).

<sup>c</sup> Lagos State Ministry of Health Nutrition Surveillance (2023) (ages 5–19, N = 2130).

#### 4. Urban diets and microbiome disruption

Urbanisation has led to the replacement of paediatric diets with whole grains, legumes and fermented foods with refined carbohydrates, fried snacks and sugar-sweetened beverages (Catalkaya et al., 2020). Low -fibre consumption leads to a decrease in the production of SCFA and microbial diversity, and the loss of traditional fermented foods reduces beneficial taxa even more. All analyses in Nairobi, Kampala, and Lagos connect these dietary habits with dysbiosis, lower SCFA levels, and metabolic risk (Ramaboli et al., 2024).

#### 5. Targeted nutritional interventions and specificity challenges

Microbiota–nutrient responses vary considerably by enterotype, genetic predisposition, and immune status.

- **Prevotella-dominant** children may respond best to high-fibre interventions.
- **Bacteroides-dominant** children may benefit more from low-glycaemic dietary approaches. African paediatric intervention studies rarely stratify participants before treatment. We recommend baseline gut profiling via low-cost portable qPCR kits to match interventions to microbial profiles and improve specificity (Lazaros et al., 2025).

#### 6. Mitigating microbiota dynamism

The structure of gut microbiota is dynamic; profiles can change in days with short-term dietary changes, which may complicate monitoring using biomarkers. To overcome this, longitudinal sampling is required in African paediatric cohorts at baseline, 3 months, and 6–12 months so as to differentiate between stable changes and transient swings. The introduction of repeated measures in school-based screening would allow tracking the biomarkers more reliably.

#### 7. Comparative advantage over conventional diagnostics

BMI and waist circumference are inexpensive and widely used but can underestimate metabolic risk in children with normal weight but abnormal metabolic profiles. SCFA and LPS assays provide functional insight into gut–host interactions, enabling earlier detection. For example, Ghana’s lateral-flow SCFA test (<US\$2, <30 min turnaround) can be used alongside anthropometry in school health programmes. While initial costs are higher, modelling suggests that earlier intervention could reduce long-term NCD care costs by preventing progression.

#### 8. Policy recommendations

1. **Integrate microbiome goals into school-feeding programmes** – e.g., Ghana’s School Feeding Programme and Nigeria’s Home Grown School Feeding can incorporate millet, beans, and fermented maize to boost SCFA production.
2. **Expand access to affordable diagnostics** – Deploy SCFA test strips in urban clinics for early screening.
3. **Establish regional metabolomic databases** – Coordinate through the African Academy of Sciences to standardise biomarker validation.
4. **Cultural adaptation** – Engage community stakeholders to align interventions with local food traditions.

#### 9. Conclusion

The current dietary and lifestyle changes pose distinctive metabolic risks to urban African children. Metabolites of the gut microbiota, SCFAs, BCAAs, and bile acids, provide early biomarkers that can predict at-risk individuals even before clinical obesity has taken place. However, we need to confirm the causality, biomarker specificity, and targeting of the intervention in African longitudinal cohorts. Making diagnostics affordable, increasing fibre access by providing school meals, dampening microbiota dynamics through repeated sampling, and constructing regional metabolomic databases can turn microbiome science into a viable long-term population health policy. Synergistic investment in research, diagnostics, and culturally informed policy will be critical to the successful implementation of microbiome-based early detection as a fair and effective strategy for preventing childhood obesity in Africa.

#### CRedit authorship contribution statement

**Okechukwu Paul-Chima Ugwu:** Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Data curation, Conceptualization. **Fabian C. Ogenyi:** Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Software, Methodology, Conceptualization. **Chinyere N. Ugwu:** Writing – review & editing, Writing – original draft, Validation, Methodology, Data curation. **Melvin Nnaemeka Ugwu:** Writing – review & editing, Writing – original draft, Visualization, Supervision, Conceptualization.

**Consent to participate**

Not applicable.

**Consent to publish declaration**

Not applicable.

**Ethics approval**

Not applicable.

**Clinical trial date of registration**

Not applicable.

**Clinical trial registration number**

Not applicable.

**Clinical trial registry**

Not applicable.

**Availability of data and material**

All used data is fully presented in the manuscript.

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**Declaration of competing interest**

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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