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Gut Microbiota Types between Well-Grown and Stunted Children: A Systematic Review

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Abstract

Stunting, is one of the malnutrition in the prepartum period up to the first two years of life and often exacerbated by recurrent gastrointestinal infections after birth. This study explores from various databases including Science Direct, Pubmed, Scopus, Springer Link, Sage Journal,, with keywords: "stunting, gut microbiota, toddler". In this study, 8 open access articles published dddonebetween 2016 and 2024 were used as sources of information according to the PRISMA 2020 guideline, with criteria based on the PICOTS framework (Population, Intervention, Comparator, Outcomes, Timing, and Setting). The main stages of the PRISMA process included identification, screening, and eligibility. It was found that the presence of gut microbiota plays a role in stunting. Gastrointestinal infections have specific mechanisms that can lead to impaired growth and postnatal growth. Deficiency of non-pathogenic gut microbiota is considered to be the main cause. Changes in gut bacterial composition in children under five are associated with increased gastrointestinal frequency, which in turn leads to chronic growth disorders.

Keywords: *Gut Microbiota; Stunting; Toddler*

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INTRODUCTION

One of the most important unresolved global health problems is stunting, where children experience growth failure caused by chronic undernutrition, which can impact development and growth (Perin et al., 2020). According to a 2020 WHO report, stunting affects more than 149 million children under 5 years old worldwide. The prevalence of stunting in Indonesia was found to be 21.5% in 2023 (Ministry of Health of the Republic of Indonesia, 2023), which translates to around 4 million people, exceeding the WHO guideline standard of 20%. According to The Global Nutrition

Report (2020) Indonesia actually ranks third with the highest frequency of stunting in children under 5 years old.

Stunting is thought to be be caused by combination of many factors such as poor nutrition in the uterus, poor nutrition intake in early childhood and infectious disease (UNICEF, 2023). Infectious diseases are direct causes that can lead to stunting and respiratory tract infections, diarrhea is also listed as the most common disease in developing countries and mostly occurs in Asia (Aridiyah et al., 2015).

One of the organs that develops after a toddler is born is the digestive system (Rafiuddin & Purwanty, 2020). Starting from birth, the growth of bacteria in the digestive system occurs gradually. Throughout childhood and adulthood, the environment and food consumed also have an impact. Many pathogenic and non-pathogenic bacteria that are essential for the growth of the human body lives in the digestive tract (Hossain et al., 2019). Low immunity and disease lead to an overgrowth of pathogenic bacteria in the digestive tract, which can consequently reduce the amount of probiotics in the digestive system and cause malabsorption of nutrients, which hinders the growth of children under the age of five (Shinsugi et al., 2015).

A collection of microorganisms called the microbiota lives inside the host organism and includes bacteria, viruses and other creatures. The microbiota in the gastrointestinal tract plays an important role in immunity or nutrient absorption. Stunting is more often due to the gut microbiota (Sinharoy et al., 2021). Toddlers with stunted growth have a different gut microbiota composition than those with adequate nutritional status. Furthermore, it affects proliferation and maturation of intestinal epithelial cells, absorption of nutrition and the mucosal defense against pathogen, which is essential for optimal growth (Vaivada et al., 2020). Even though food consumption is enough, dysbiosis or the absence of one of the beneficial microbiota can disrupt the mechanism of food digestion and the formation of different vitamins, leading to growth problems. Stunted children do not get the nutrients their bodies need, which makes them vulnerable to infectious infections. Stunted children also experience changes in microbiota composition and quantity between probiotic and pathogenic bacteria as a result of this scenario. In stunted toddlers, *Escherichia coli/Shigella* sp. and *Compylobacter* sp. were more common, while non-pathogenic microbiota were less common (Thahir et al., 2020). Increased energy loss through fecal excretion in stunted children and ingestion of pathogens were thought to be the cause of these changes (Hardjo & Selene, 2018; Rinanda et al., 2023). In this article, we will review the bacterial profile of the gut microbiota in stunted and normally developing toddlers.

METHOD

A systematic search was conducted in February 2024 in PubMed, Science Direct, Sage Journals, Scopus, and Springer links. The search terms were "gut microbiota AND stunting AND toddlers" resulting in the discovery of 1274 articles published from 2016 to 2024. The time frame from 2016 to 2024 was chosen to ensure that the study incorporated the most recent and relevant findings, reflecting the latest advancements and understanding in the field of gut microbiota and its impact on stunting in toddlers.Then the articles were selected based on duplication (duplicate

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article titles) to 226, based on the title and corresponding abstract to 30 articles, then 20 full paper/text articles were taken. The articles were then briefly reviewed to ensure that the articles were taken according to the participants, intervention, comparator, outcome, timeframe, and setting (PICOTS) elements (Table 1) (Frandsen et al., 2020). After passing the inclusion screening, articles were selected based on eligibility tests, assessments carried out on the retrieved articles, and then analyzed according to the inclusion data. The inclusion criteria for articles were English, information on microbiota and stunting, full paper/text and open access. Exclusion criteria were duplication and not fully accessible (Figure 1).

Table 1. Inclusion Criteria Based on PICOTS Elements

PICOTS	**Inclusion Criteria**
Participant	Stunting and normal growth toddlers
Intervention	Gut microbiota
Comparator	Composition type between microbiota in stunted and normally developing toddlers
Outcome	Identify the type of microbiota composition between the two groups, including microbial diversity, dominant bacterial types, and the presence of pathogenic bacteria
Timeframe	Publication year 2016-2024
Setting	All countries

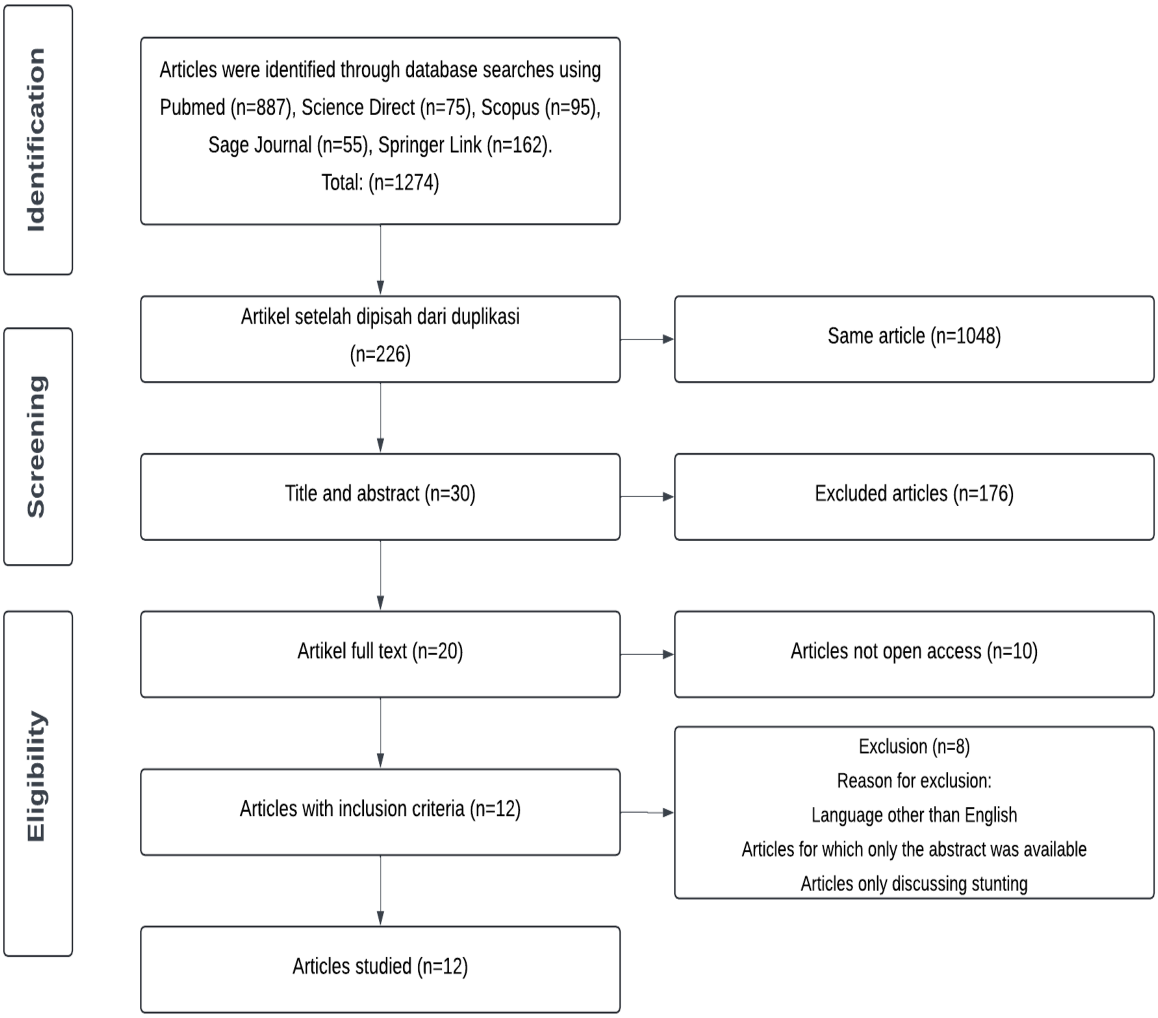

Figure 1. Diagram PRISMA (author's design)

RESULT AND DISCUSSION

Table 2. Literature Study Findings

No	Author	Title	Location	Subject and Method	Result
1	(Rinanda et al., 2023)	Correlation between gut microbiota composition, enteric infections and linear growth impairment: a case–control study in childhood stunting in Pidie, Aceh, Indonesia	Indonesia	Case control study. Involved 42 subjects aged 24-59 months, consisting of 21 stunted children and 21 normal children. Gut microbiome profiling was performed using 16S rDNA amplicons sequencing.	*Firmucutes* population (50%) was exceptionally higher than *Bacteroidetes* (34%) in stunted children.
2	(Surono et al., 2021)	Differences in immune status and fecal SCFA between Indonesian stunted childreen and children with normal nutritional status	Indonesia	Cross sectional research design. Micriobial metabolites valerate and acetate were analyzed with LBP ELISA kit protocol while SCFA was measured with GC-MS	In stunted children's feces, valerate, acetate and SCFA was significantly higher These metabolites was correlated with *Providencia*, *Ruminiclostidrium*, *Eschericia Shigella*, *Eubacterium*
3	(Surono et al., 2021)	Gut Microbiota profile of Indonesian stunted children ans children with normal nutrition status	Indonesia	Subjects were toddlers 3-5 years old. 78 children wisurnoth stunting aged 3-5 years old. 53 children with normal nutrition status. Fecal analysis using 16S rRNA sequencing.	Healthy children had higher *Prevotella* than stunted children
4	(Masrul et al., 2020)	Microbiota Profile with Stunting Children in West Sumatera Province, Indonesia	Indonesia	48 stunted children in West Sumatra Province, Indonesia. Fecal analysis using 16S rRNA sequencing	Stunted children predominantly had high *Firmicutes* (47.52%), *Proteobacteria* (21.12%), and *Bacteroidetes* (16.15%). In stunted children, the GI microbiota is rich in inflammatory bacteria such as the genus *Desulfovibrio*

					and the order *Campylobacterales*.
5	Perin et al., 2020	A Retrospective Case–Control Study of the Relationship between the Gut Microbiota, Enteropathy, and Child Growth	Bangladesh	Cross sectional reserach design. Subjects were 68 children aged 6-31 months in Mirzapur. Fecal analysis using 16S rRNA sequencing	In stunted children, it was found that pathogenic *Eschericia* and *Shigella* population was increased. In the other hand, beneficial *Proteobacteria* and *Prevotella* was decreased
6	Zambruni et al., 2019	Stunting Is Preceded by Intestinal Mucosal Damage and Microbiome Changes and Is Associated with Systemic Inflammation in a Cohort of Peruvian Infants	Peru	Subjects were 78 infants aged 5-12 months living in rural Peru for 6 months. Biomarker serum analysis of intestinal damage (I-FABP and zonulin). Biomarker serum analysis of inflammation (TNF, IL-1B, IL-6, CD14). Fecal sample analysis	Stunted children had higher I-FABP and CD14 in their blood. These was correlated with worse nutritional status. Stunted children had higher level of *Colinsella*, *Clostridium sensu stricto* and *Ruminococcus* 1 and 2. Stunted children had lower level of *Pridencia*
7	Vonaesch et al., 2018	Stunted chilhood growth is associated with decompartmentalization of the gastrointestinal tract and overgrowth of oropharyngeal taxa	Central Africa	Subjects were children aged 2-5 years months totaling 404 children. Fecal analysis using 16S rRNA sequencing	Stunted children stool were highly populated with pathogenic *Escherichia coli*, *Shigella sp*, and *Compylobacter sp*. Non-stunted children stool were dominated by non-pathogenic bacteria such as *Lactobacili*, *H.pylori*, *Streptobacili*, *Bifidobacteriaceae*
8	(Dinh et al., 2016)	Longitudinal Analysis of the Intestinal Microbiota in Persistenly Stunted Young Children in South India	South India	Cross sectional reserach design. Children aged 2 monhts up to 3 years old. 10 children with low birth weight and	Higher level of *Bacteroidetes*, *Desulfovibrio* and *Campylobacteral* was observed in stunted children. These were

persistent stunting and 10 children with normal birth weight and no stunting (control) Fecal analysis using 16S rRNA sequencing	associated with inflammation. Higher level of *Bifidobacterium longum* and *Lactobacillus mucosae* was observed in non stunted children

Pathogenic and non-pathogenic bacteria

Various factors contribute to stunting in children, including inadequate nutritional intake, gut microbiota imbalance, and socioeconomic status and history of respiratory infections (De Sanctis et al., 2021). The presence of pathogenic and non-pathogenic bacteria in the gut can play a role in stunting (Nagao-Kitamoto et al., 2016). Environmental factors, energy intake, and sanitation also influence stunting.

The study of Vonaesch et al., (2018) confirmed that there was an increase in enteropathogenic bacteria in the intestines and excessive bacteria in the oropharynx in stunted children’s stool samples. The findings of this study showed the presence of bacteria such as *Compylobacter sp, Shigella sp, Escherichia coli*, , and in stunted children’s stool, while in children who were not stunted, non-pathogenic bacteria such as *Lactobacillus*, *H.pylori*, *Streptobacili*, *Bifidobacteriaceae* in the stomach, duodenum were dominant. The increase of beneficial microorganisms in the digestive tract may contribute to the prevention of growth disorders.

The results found in Dinh et al., (2016) study showed that in toddlers with normal nutritional status, a higher number of *Bifidobacterium longum* and *Lactobacillus* were found in the feces, while in stunted toddlers, *Campylobacterales* and *Desulfovibrio* were found which are known to cause inflammation. On the other hand, a study conducted by Kamil et al., (2021) in Yogyakarta found that the population *Proteobacteria* in stunted children are 2.34 times higher compared to normal children. In healthy children, bacterial composition tends to be dominated by *Bacteroidetes* and *Bifidobacterium*. *Bifidobacterium* has a role in protecting the digestive tract from pathogenic microbes and is usually more abundant in toddlers with normal nutritional status.

Differences in the microbiota of stunted and normal children

The microbiota has an important role in various bodily processes of the body, such as nutrition metabolism, as well as in immune system modulation, immune system regulation, and protection against pathogenic bacteria. The microbiota is located in various parts of the human body, such as in the respiratory system, the skin, urogenital tract and gastrointestinal system (Helmyati et al., 2017). Based on the research reviewed, there are differences in the types of bacteria found in children who are stunted and children with normal growth and development. Surono et al., (2021) showed that gut microbiota plays a role in fermenting dietary fiber as a source of energy for children. The presence of Prevotella microbiota species, which are non-pathogenic microbes, contributes by producing additional energy from food in the form of SCFA (Short-Chain Fatty Acid), which is beneficial for children with growth disorders. Shivakumar et al., (2021) confirmed this finding by analyzing the stool of healthy children aged 1-6 years. The microbiota found predominantly was Prevotella.

In the same study, Shivakumar et al., (2021), found that the number of beneficial microbiota such as Bifidobacterium longum had a positive correlation with the nutritional status parameter body weight per age (BB/U). This is confirmed by Dinh et al., (2016) inform that healthy children with normal nutritional status had higher beneficial bacteria such as *Bifidobacterium longum*. On the other hand, children with pathogenic bacteria infection such as Shigella had a higher chance of being stunted. Children who were not stunted had gut microbiota with higher *Bifidobacterium longum* than children who were stunted. Children with enterotoxigenic *Escherichia coli* infection had higher fecal Calprotectin concentrations and children with Shigella infection had a higher chance of being stunted.

Research by Zambruni et al., (2019) found that in stunted children, there was an increase of *Clostridium sensu stricto*, *Collinsella* and *Ruminococcus* population, while *Providencia* population decreased. Likewise, it is supported by research from Rinanda et al., (2023) which says that the population of *Firmicutes* (50%) is higher than *Bacteroidetes* (34%) in stunted children. Aziz et al., (2023) confirmed the *Eschericia coli* pathogen in the microbiota of gastrointestinal tract in stunted children.

From these studies, it was concluded that pathogenic microbiota played an important role in stunting. *Eschericia* and *Shigella*, can damage the intestine, leading to chronic inflammation, abnormalities in nutritional absorption and competition against healthy population of beneficial microbiota such as *Bifidobacterium longum* and *Prevotella*. Furthermore, these pathogenic microbiota can cause diarrhea which in turn excrete more nutrients which the host is already lacking (Aziz et al., 2023; Bagamian et al., 2023).

CONCLUSION

The gut microbiota profiles that dominate in stunted children are *Proteobacteria*, *Escherichia coli*, *Shigella sp*, *Compylobacter sp*, *Desulfovibrio*, *Firmicutes*, *Proteobacteria*, *Bacteroidetes*, *Ruminococcus*, *Actinobacteria*, and *Verrucomicrobia*. While in the gut microbiota of non-stunted children, the dominating microbiota are *Prevotelli*, *Lactobacili*, *H. pylory*, *Streptobacili*, and *Bidifobacteriaceae*.

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