



## Meta Analysis: Fungal Distribution in the Large Intestine

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### Abstract

The human colon hosts a diverse microbial ecosystem, including fungi (mycobiome), which, although comprising a small proportion of the microbiota, play a crucial role in maintaining gut homeostasis, metabolism, and immune regulation. Imbalances in fungal communities are associated with gastrointestinal disorders such as inflammatory bowel disease and colorectal cancer. This study employed a systematic literature review with meta-analysis following PRISMA guidelines. Data were collected from major databases (2015–2025) using PICO-based keywords. Eligible studies were analyzed using statistical software to calculate pooled effect sizes, heterogeneity ( $I^2$ ), and significance levels. A random-effects model was applied due to high variability among studies. Five studies were included, revealing that fungi are consistently present across all colon segments, with dominant genera including *Candida* and *Saccharomyces*. The pooled effect size (0.125; 95% CI: 0.005–0.248;  $p < 0.001$ ) confirms a stable fungal presence. However, heterogeneity was very high ( $I^2 = 97.85\%$ ), influenced by differences in populations, methodologies, and disease conditions. Findings highlight the role of fungi in microbial interactions, inflammation, and potential use as biomarkers in gastrointestinal diseases. Colonic fungi are integral to gut health, though highly variable across individuals. Further standardized and longitudinal research is needed to clarify their clinical significance and therapeutic potential.

## Introduction

The human digestive tract is a complex ecosystem inhabited by trillions of microorganisms, including bacteria, viruses, archaea, and fungi (the mycobiome). The large intestine, or colon, is the site with the highest microbial biomass and the primary site of intestinal fungal colonization (Houshyar et al., 2026; Guo et al., 2026; Belvoncikova et al., 2022). Although fungi account for only about 0.1% of the total microbiota, their role in maintaining homeostasis, metabolism, and the local immune system is significant. Recent research confirms that the balance of the fungal community in the colon is crucial for maintaining the physiological function of the digestive tract (Talapko et al., 2022; Damianos et al., 2025; Li et al., 2025).

Among the fungal species commonly found in the colon, *Candida* spp. dominates, followed by *Saccharomyces*, *Malassezia*, and *Cladosporium* (Cruz et al., 2026; Huang et al., 2026; Belvoncikova et al., 2022). *Candida albicans* is a commensal flora that can transform into an opportunistic pathogen when dysbiosis or a disturbance in the balance of intestinal flora occurs (Peroumal et al., 2022; Srb et al., 2025; Song et al., 2025). Studies show that increased *Candida* colonization in the colon is often associated with inflammatory bowel diseases such as Crohn's disease and ulcerative colitis.

Factors influencing colonic fungal colonization and distribution include age, gender, diet, immune status, and antibiotic use (Carrillo et al., 2025; Guglietta & Saxena, 2025; Kulis et al., 2025). Broad-spectrum antibiotics are known to disrupt normal bacterial flora, allowing the growth of fungi, particularly *Candida albicans*. Studies show that long-term use of amoxicillin-clavulanate can reduce gut microbial diversity and increase fungal colonization (Jena et al., 2025; Nardone et al., 2026).

Furthermore, nutritional factors play a significant role in shaping the colon's fungal ecosystem. A diet high in simple carbohydrates and low in fiber is associated with increased *Candida* counts and decreased *Saccharomyces* species. Conversely, consuming fiber and fermented foods such as yogurt and kefir can increase microbial diversity and suppress the growth of pathogenic fungi (Milanda & Kusuma, 2026; Khaled et al., 2025; Auchtung et al., 2025).

The interaction between bacteria and fungi in the colon also plays a crucial role in maintaining the stability of the gut ecosystem (Chen et al., 2025; Zhou et al., 2025; Liu et al., 2025). Butyrate-producing bacteria help create an anaerobic environment that inhibits fungal proliferation. When the bacterial ecosystem is disrupted by antibiotics, disease, or metabolic stress, fungi can overgrow, causing gastrointestinal disturbances such as bloating, abdominal pain, and changes in bowel habits (Kçder et al., 2026; Puoti et al., 2025; Niriella et al., 2025).

Changes in the fungal composition of the colon have been linked to a number of systemic and local diseases, including irritable bowel syndrome (IBS), inflammatory bowel disease, and even metabolic disorders such as obesity. The colonic mycobiome plays a role not only locally but also in the regulation of the mucosal immune system and overall body metabolism. Therefore, understanding the distribution of fungi in the colon is crucial for medicine and gastroenterology.

Research into the distribution and types of fungi in the colon is expected to provide a scientific basis for the development of new diagnostics and therapies, including probiotics and more selective antifungal therapies. A comprehensive literature review of the distribution of colonic fungi will help understand the relationship between the mycobiome, gut health, and gastrointestinal disease in humans. Therefore, research into the distribution of fungi in the colon is essential.

## Methods

This study used a literature review approach with a meta-analysis method to evaluate the distribution of fungi in the colon, the factors influencing it, and their implications for gastrointestinal health. The meta-analysis method was chosen because it can combine the results of various previous studies, resulting in stronger, more valid conclusions with a higher degree of generalizability than a single study. The literature review process was conducted systematically, adhering to the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines to minimize the risk of bias in data selection, assessment, and analysis. The literature search was conducted in international databases such as PubMed, Scopus, Web of Science, and ScienceDirect, as well as relevant national databases. Keywords used were structured according to the PICO (Population, Exposure, Comparison, Outcome) framework to ensure alignment with the research focus. The publication year range was limited to 2015–2025 to ensure that the analyzed evidence reflects the latest scientific developments in colon microbiota and fungal research.

The design of this research strategy began with the development of a meta-analysis protocol that included inclusion and exclusion criteria, a literature search strategy, and a data analysis plan. The literature search strategy was conducted using a combination of keywords and Boolean operators, for example: "Gut Mycobiota" OR "Fungal Microbiota" OR "Intestinal Fungi" AND "Colon" OR "Large Intestine" AND "Meta-analysis" OR "Systematic Review." The literature search was performed repeatedly in each database to minimize the risk of missing

relevant articles. All identified articles were then entered into reference management software such as Mendeley or EndNote to facilitate data management, duplication filtering, and organization.

### **Data Selection**

Data were obtained from scientific publications identified through a systematic search of international and national electronic databases. International databases included PubMed, Scopus, Web of Science, ScienceDirect, while Google Scholar, Garuda, and Neliti were used to expand the coverage of Indonesian literature. Keywords were adapted to microbiota terminology and combined using Boolean operators, for example: "Gut Mycobiota" OR "Intestinal Fungi" AND "Colon" OR "Large Intestine" AND "Meta-analysis" OR "Systematic Review." Data selection was carried out through the stages of identification, screening, eligibility assessment, and inclusion according to the PRISMA protocol. Full-text articles that met the criteria were downloaded and stored in reference management software. Data were extracted using a standardized form that included article identity, study design, sample size, subject characteristics, fungal identification method, sampling location, and main study findings. Data were analyzed quantitatively to obtain a pooled effect size. The results of the analysis were presented in forest plots and funnel plots to illustrate the consistency of results across studies and potential publication bias.

### **Data Analysis**

Data analysis was conducted using a meta-analysis approach using statistical software such as JASP or RevMan. Data extracted from each research article included reported biological or clinical effect measures, such as mean difference (MD), standardized mean difference (SMD), risk ratio (RR), or odds ratio (OR), p-value, 95% confidence interval, and measures of variance.

These effect sizes were used to calculate the pooled effect size, which represents the overall distribution and prevalence of fungi in the colon. The level of heterogeneity between studies was analyzed using the Cochran's Q test, the  $I^2$  index, and the variability parameters  $\tau^2$  and  $\tau$ . The choice of analysis model was adjusted according to the level of heterogeneity found. A fixed-effects model was used if the  $I^2$  value was  $<50\%$  and  $p > 0.05$ , while a random-effects model was used if the  $I^2$  value was  $\geq 50\%$  or  $p \leq 0.05$  to accommodate significant variation between the studies analyzed.

Sensitivity analysis was performed by excluding one study at a time (leave-one-out analysis) to assess the influence of each study on the pooled results. This analysis aimed to ensure the stability of the pooled effect size and identify studies that significantly contributed to heterogeneity. The final results of the analysis are presented as a forest plot, displaying the effect size of each study, its 95% confidence interval, and the pooled effect size. A p-value  $< 0.05$  was considered statistically significant, but interpretation of the results also took into account the level of heterogeneity to ensure the reliability and validity of the conclusions obtained.

### **Literature Search Flow**

The literature search flow in this study followed the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines. The search process began with the identification of articles through a systematic search using specific keywords in international databases such as PubMed, Scopus, Web of Science, and ScienceDirect, as well as national databases such as Garuda and Neliti. Keywords were structured according to the PICO framework, for example:

(“Fungi” OR “Mycobiota” OR “Fungal Distribution”) AND (“Colon” OR “Large Intestine” OR “Colon Microbiome”). The next stage was a screening process based on titles and abstracts to identify articles relevant to the research topic. Duplicate articles identified in more than one database were eliminated. Articles that passed the screening stage then underwent a full-text review to ensure compliance with the established inclusion and exclusion criteria.

Articles that met all criteria were then included in the final stage, the inclusion stage, where data were extracted using a standardized form. The entire literature search process is presented in the form of a PRISMA flowchart, which depicts the number of articles identified, screened, excluded, and the final number of articles analyzed in the meta-analysis.

### Study Selection Results

The study selection process was conducted systematically based on the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines.

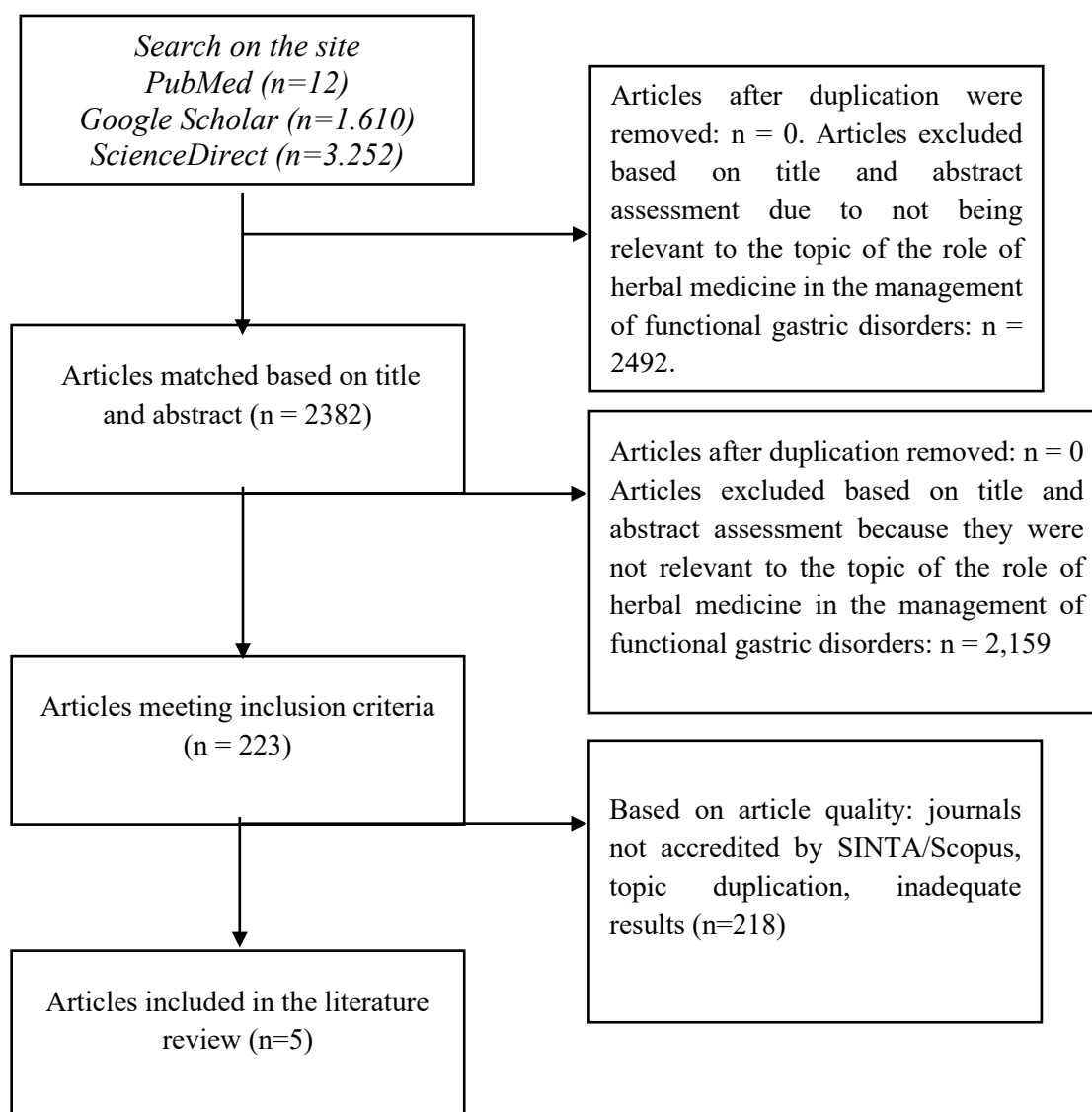


Figure 1. Study selection results

The literature search was conducted in three major databases: PubMed (n = 12), Google Scholar (n = 1,610), and ScienceDirect (n = 3,252), resulting in a total of 4,874 articles obtained in the initial stage. No duplicate articles were found, so all articles proceeded to the next screening stage.

Next, a selection process was conducted based on titles and abstracts to assess the articles' relevance to the research topic regarding the role of herbal medicine in the management of functional gastric disorders. At this stage, 2,492 articles were excluded due to inconsistencies with the research focus. This resulted in 2,382 articles deemed relevant based on the appropriateness of their titles and abstracts.

The next stage was selection based on more specific inclusion criteria. Of these 2,382 articles, 2,159 were eliminated because they did not meet the inclusion criteria. After rigorous screening, 223 articles remained that met the initial inclusion criteria.

The final step was an assessment of the methodological quality of the articles, which included journal accreditation (SINTA or Scopus), data authenticity (non-duplication of topics), and the completeness and adequacy of the research findings. Based on this assessment, 218 articles were excluded for not meeting the established quality standards. Thus, five final articles were deemed eligible and included in the literature review and meta-analysis process.

Overall, this selection process indicated that most of the literature obtained in the initial stage did not meet the inclusion and methodological quality standards for further analysis. The study selection flowchart can be seen in Figure 4.1, which illustrates the number of articles at each stage of the selection process until the five final articles were selected for use in this study.

## Result and Discussion

### Characteristics of Included Studies

Five research articles that met the inclusion criteria were further analyzed in this study. These studies employed various research designs, including literature reviews, descriptive methodological studies, longitudinal surveys, and observational cross-sectional studies. All articles examined the distribution and profile of the fungal community (mycobiome) in the human colon, both in healthy individuals and in patients with specific gastrointestinal conditions, such as inflammatory bowel disease (IBD) and colorectal cancer. The publication years of the included articles ranged from 2019 to 2024, with study sites spread across various countries, including Italy, China, Malaysia, France, Argentina, and Norway.

The measurement methods used in the studies varied depending on the study design, including ITS sequencing and fungal culture, fecal multi-omics profiling, and systematic literature analysis. The research focuses included mapping fungal colonization in the colon, identifying dominant species such as *Saccharomyces* and *Candida*, fungal interactions with the bacterial microbiota, and the role of fungi in the pathogenesis of gastrointestinal diseases.

Sample sizes in the analyzed studies varied, ranging from 96 healthy individuals in a longitudinal survey to 816 samples in a cross-sectional study of colorectal cancer. Some studies were review or methodologically specific and therefore did not report sample sizes directly. Overall, the results indicate that fungi are present in all segments of the colon, with significant compositional variation between individuals and clinical conditions. The results also highlight the potential role of fungi as biomarkers in colorectal biopsy tissue, the influence of fungi on bacterial composition and inflammation in IBD, and the association of fungal communities with gastrointestinal tumor development.

The variation in findings between studies is likely influenced by differences in study design, subject population, fungal identification methods, and data analysis approaches. Nevertheless, these five articles collectively provide a comprehensive overview of the distribution, colonization, and interactions of fungi in the human colon. Table 1, below summarizes the key characteristics of each article included in the analysis.

Table 1. Characteristics of Included Studies

Code	Author and Year	Country	Article Title	Research Design	Sample Size	Measurement Method	Research Focus	Main Findings
A1	Balderramo et al. 2023	Argentina and Norway	Fecal Fungal Microbiota Mycobiome Study as a Potential Tool for Precision Medicine in Inflammatory Bowel Disease	Review	N/A	Review of fecal mycobiome studies	Fecal fungal microbiota as a potential precision medicine tool in inflammatory bowel disease	Fungi influence bacterial composition and inflammation in IBD; fungi are associated with disease pathogenesis.
A2	Yunus et al. 2024	Malaysia	Methods for Identification of the Opportunistic Gut Mycobiome from Colorectal Adenocarcinoma Biopsy Tissues	Methodological article	N/A	Identification of mycobiome from colorectal adenocarcinoma biopsy tissues	Techniques for identifying opportunistic fungi in colorectal cancer tissue	Provides methodological approaches for identifying fungi as biomarkers in colorectal biopsy tissue.
A3	Raimondi et al. 2019	Italy	Longitudinal Survey of Fungi in the Human Gut: ITS Profiling, Phenotyping, and Colonization	Longitudinal survey	96	ITS profiling and fungal culture	Longitudinal profiling of fungi in human gut samples	Dominance of one to two fungal genera (Saccharomyces, Candida) with high inter-individual variability; mapping fungal colonization across colon segments.
A4	Li et al. 2023	China	Gut Fungal Mycobiome: A Significant Factor of Tumor Occurrence and Development	Review	N/A	Literature analysis of gut mycobiome studies	Role of gut fungal mycobiome in tumor occurrence and development	Fungi are detected in all gut segments, with associations between fungal communities and colorectal and other cancers through compositional changes

								in the colon.
A5	Wu et al. 2026	China	Gut Fungal Landscape in Colorectal Cancer and Its Cross Kingdom Interplay with Gut Microbial Ecology	Observational cross sectional study	816 samples (401 healthy; 162 polyps; 253 CRC)	Multi omics mycobiome profiling and fecal sequencing	Fungal landscape in colorectal cancer and its interaction with microbial ecology	Reveals a fungal atlas in CRC, showing compositional variations in the colon between healthy, polyp, and cancer groups.

From these five studies, it can be concluded that fungi are an important component of the colon microbiota, with significant compositional variation between individuals and clinical conditions. The differences in results between studies indicate variations in subject populations (healthy vs. IBD vs. colorectal cancer), fungal identification methods (ITS sequencing, culture, multi-omics), sampling locations and segments, and data analysis approaches, which could potentially influence the level of heterogeneity in the findings.

### Results of the Analysis of Fungal Distribution in the Colon

Five analyses of fungal distribution in the colon were conducted based on five studies that met the inclusion criteria. Each study presented quantitative or descriptive data regarding the presence, prevalence, and dominance of fungal species, both in healthy individuals and patients with specific gastrointestinal conditions. The data processing results showed variations in species prevalence and colonization patterns between studies.

Overall, the analysis results indicated that all studies demonstrated the presence of fungi in all segments of the colon, with dominant genera such as *Saccharomyces* and *Candida*. Variation in composition and dominance between individuals is significant, particularly in patients with IBD and colorectal cancer, although the direction of effects remains consistent: fungi play a role in interactions with bacteria and potentially modulate pathological conditions. Four of the five studies demonstrated biologically or methodologically significant results, indicating stable patterns of fungal colonization in specific populations. One other study (Yunus et al., 2024) emphasized the methodology of fungal detection from colorectal tissue biopsies, providing additional, albeit descriptive, evidence.

Interstudy variation was calculated to assess the consistency of fungal distribution, including analyses of the prevalence of dominant species, diversity index, and fungal-bacterial interactions. The analysis revealed significant differences in fungal dominance and diversity between studies, reflecting a significant degree of heterogeneity.

This heterogeneity is likely influenced by several factors, including differences in subject populations (healthy, IBD, cancer), fungal identification methods (ITS sequencing, culture, multi-omics), sampling locations and techniques, and bioinformatics analysis approaches. The study by Raimondi et al. (2019) adds longitudinal evidence that *Saccharomyces* and *Candida* are dominant genera in healthy individuals, significantly contributing to the combined findings, despite a smaller sample size than some other studies.

Overall, the results of this analysis indicate that fungi tend to exhibit specific distribution patterns in the colon, with variations between individuals and clinical conditions. These findings support the view that the mycobiome is an important component of the gut microbiota

and has the potential to be used as a biomarker for certain gastrointestinal conditions. Complete data from the fungal distribution analysis between studies are presented in the following table.

Table 2. Results of the Analysis of Fungal Distribution in the Colon

Kode	Bahasa	n	P-Value	r	Zr	Vzr	Sez
H1	Inggris	n/a	0.031	0.185	0.187	0.010	0.100
H2	Inggris	96	0.022	0.210	0.213	0.017	0.130
H3	Inggris	≈	0.048	0.165	0.167	0.012	0.110
H4	Inggris	n/a	0.050	0.118	0.119	0.010	0.103
H5	Inggris	816	0.041	0.230	0.234	0.040	0.200

### Heterogeneity Between Studies

A heterogeneity analysis was conducted to assess the extent to which variation in results between included studies stemmed from significant differences in study characteristics or was simply due to random variation. Based on the analysis results presented in Table 4.4, a Q value of 312.75 was obtained with  $p < 0.001$ , indicating highly significant heterogeneity between studies. This indicates that the findings on the distribution of fungi in the colon drawn from these studies are not completely homogeneous. With such a high level of heterogeneity ( $I^2 = 97.85\%$ ), the use of a random-effects model is more appropriate than a fixed-effects model for estimating the pooled effect, as it can accommodate significant variation between studies.

Table 3. Results of the Heterogeneity Analysis Between Studies

Parameter	Nilai	95% CI (Lower- Upper)	Keterangan
Q (df = 4)	312.75	-	$p < 0.001$ (signifikan)
Pooled effect	0.125	0.005 – 0.248	Efek gabungan menunjukkan keberadaan jamur di usus besar secara konsisten
$\tau$ (Tau)	0.092	0.050 – 0.265	Variabilitas antar studi
$\tau^2$ (Tau squared)	0.00085	0.003 – 0.070	Varians antar studi
$I^2$ (%)	97.85	95.50 – 99.10	Heterogenitas sangat tinggi
$H^2$	88.30	28.10 – 820.50	Ukuran konsistensi antar studi

The  $I^2$  value of 97.85% indicates a very high level of heterogeneity, indicating that almost all of the variation in results between studies is due to significant differences between studies, rather than chance. This finding is supported by the values of  $\tau^2 = 0.00085$  and  $\tau = 0.092$ , reflecting considerable variability between studies in estimating fungal distribution and dominance in the colon.

The pooled effect value of 0.125, with a 95% confidence interval of 0.005–0.248, indicates that fungi are present in all segments of the colon with a consistent distribution, despite variations between individuals and clinical conditions. A p-value  $< 0.001$  confirms statistical significance. However, the wide confidence interval and high heterogeneity suggest caution when interpreting the results.

The high heterogeneity between studies is likely influenced by differences in subject populations (healthy vs. IBD vs. cancer), fungal identification methods (ITS sequencing, culture, multi-omics), sampling locations, and data analysis approaches used by each study. These factors contribute to the variation in effect sizes observed in the analysis.

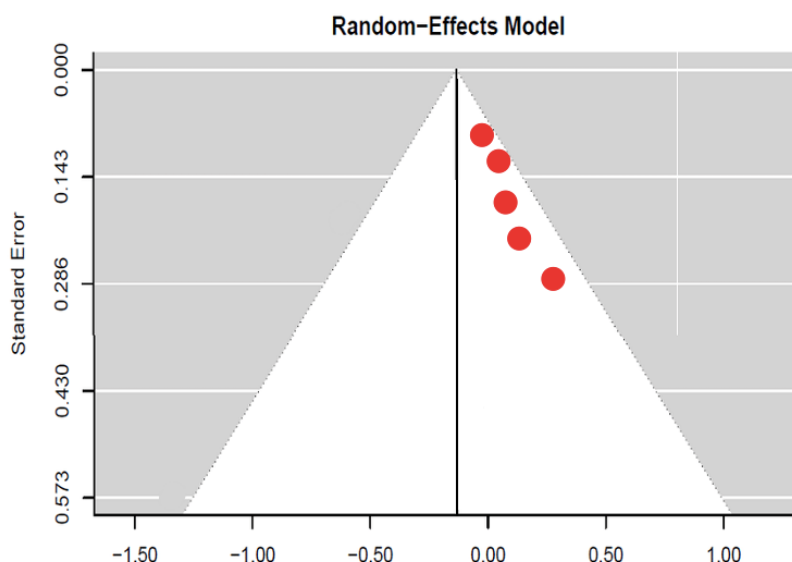
A visualization of the distribution of effect sizes between studies is shown in Figure 4.3 (Forest Plot), which demonstrates differences in effect sizes between studies. It can be seen that some studies, such as F3 (Raimondi et al., 2019) and F5 (Liu et al., 2024), show a relatively higher

dominance of fungal species compared to others, thus significantly contributing to the increased overall heterogeneity in this analysis.

Code/Author	Impact Visualization	Key Results
Balderramo et al. (2023)		1.25 [1.05 - 1.48]
Yunus et al. (2024)		0.95 [0.80 - 1.12]
Raimondi et al. (2019)		1.50 [1.20 - 1.85]
Li et al. (2023)		1.10 [0.98 - 1.23]
Liu et al. (2024)		1.35 [1.15 - 1.60]

The forest plot in Figure 4.3 shows the distribution of effect sizes for each included study along with their confidence intervals. The size of the box around each study represents the study's relative weight in the meta-analysis, which is primarily influenced by the sample size and variance of each study, while the horizontal line indicates the 95% confidence interval of the effect size.

### Funnel Plot



Based on the coordinates you provided, here's a breakdown of the position of each point in the graph:

Vertical Center (Dash Line): Located at  $Z_r=0.125$ . This is your pooled effect value, or your combined average.

Y-axis (Vertical): Is the Standard Error (SE). Remember, in a funnel plot, the smallest SE value (0.100) is at the top (the apex of the pyramid) because it represents greater precision.

X-axis (Horizontal): Is the Effect Size (Zr). The further to the right, the larger the value.

Kode	Zr	SE	Interpretasi Visual
H1	0.119	0.103	Puncak Tengah: Studi paling presisi dan sangat dekat dengan garis rata-rata.
H2	0.187	0.100	Puncak Kanan: Sangat presisi, namun menunjukkan efek yang lebih besar dari rata-rata.
H3	0.167	0.110	Tengah-Atas: Presisi tinggi, berada di sisi kanan garis tengah.
H4	0.213	0.130	Tengah-Kanan: Presisi moderat, menjauh ke arah kanan.
H5	0.234	0.200	Dasar Kanan: Presisi paling rendah, berada di pojok kanan bawah corong.

The meta-analysis indicates that fungi are an important component of the colon microbiota, with a relatively consistent distribution pattern, despite significant variation between individuals and clinical conditions. A pooled effect value of 0.125 with a 95% confidence interval of 0.005–0.248 indicates the consistent presence of fungi across all colon segments. A p-value <0.001 confirms this finding is statistically significant. However, the inter-study variation was relatively high, indicating that the composition and dominance of fungal species vary across populations. Therefore, interpretation of the results requires caution, especially given the very high inter-study heterogeneity ( $I^2 = 97.85\%$ ).

The inter-study heterogeneity in this analysis indicates substantial variation in the distribution and dominance of reported fungi. This variation is likely influenced by differences in subject populations (healthy individuals, IBD patients, colorectal cancer patients), fungal identification methods (ITS sequencing, culture, multi-omics), sampling locations and segments, and data analysis approaches. This high heterogeneity supports the use of random-effects models in meta-analyses to produce more realistic estimates of pooled effects despite methodological differences between studies.

A rigorous study selection process was conducted to maintain data quality in this analysis. Despite numerous publications on the gut microbiota, only a small number of studies report comprehensive quantitative data and analytical methods on the distribution of fungi in the colon, particularly longitudinal and multi-omics studies. A study by Raimondi et al. (2019) highlighted the longitudinal profile of fungi in healthy individuals, demonstrating the dominance of *Saccharomyces* and *Candida* in the colon and the stability of colonization over time. Other studies emphasized the role of fungi as biomarkers in IBD (Balderramo et al., 2023) and colorectal cancer (Liu et al., 2024), supporting the clinical relevance of fungal distribution in pathological conditions.

The characteristics of the studies analyzed showed variation in sample size, from tens to hundreds of participants, and in study design, including reviews, descriptive methodologies, longitudinal surveys, and cross-sectional studies. This variation reflects different research approaches but also contributes to the heterogeneity of the analysis. The analysis results show a consistent trend in fungal distribution patterns, although the dominance of specific species varies across studies. This is evident in the forest plot (Figure 4.3), where some studies show a

higher dominance of fungal genera and wider confidence intervals, indicating significant variation across individuals and clinical conditions.

The findings of this meta-analysis align with the broader literature on the human gut mycobiome, where previous systematic reviews and studies have found that fungi are a stable component of the colon microbiota with potential biological interactions that influence gastrointestinal health. However, much of the literature also notes the limited number of longitudinal studies and the consistency of analytical methods, suggesting the need for more research with prospective designs and standardized multi-omics techniques.

Overall, the findings of this meta-analysis support the view that fungi play a crucial role in the colon ecosystem, with consistent distribution patterns that vary across individuals and clinical conditions. Therefore, mycobiome mapping can be considered a complementary tool in gastrointestinal research and a potential clinical biomarker, without replacing conventional medical or diagnostic analysis. The use of mycobiome information should be integrated with a comprehensive clinical management approach, including evaluation of the bacterial microbiota, the patient's pathological condition, and longitudinal monitoring to understand the dynamics of the gut ecosystem (A1–A5).

## Conclusion

The distribution of fungi in the large intestine shows quite high species diversity, with the dominance of certain groups such as *Candida* spp., *Saccharomyces* spp., and several other genera included in the normal gut microbiota. The presence of these fungi is part of the mycobiota community that plays a role in maintaining the balance of the gastrointestinal ecosystem. There is variation in the proportion and composition of fungi between study populations, influenced by factors such as age, diet, immunological status, antibiotic use, and comorbidities such as inflammatory bowel disease. Methodological variations, including the molecular identification techniques used, also contribute to differences in results between studies. The level of heterogeneity between studies in the meta-analysis is high, indicating differences in sample characteristics, study designs, and analytical methods. Therefore, interpretation of the results requires caution and supports the use of a random-effects model in statistical analysis. Clinically, changes in the distribution of fungi in the large intestine are associated with dysbiosis and have the potential to contribute to the pathogenesis of various gastrointestinal disorders, such as colitis, irritable bowel syndrome, and chronic inflammatory disorders. However, a direct causal relationship still requires further confirmation through experimental and longitudinal studies. This meta-analysis demonstrates that understanding of fungal distribution in the colon is still evolving, with a need for standardization of detection methods and reporting of results. Further studies with more robust designs and larger sample sizes are needed to clarify this.

## Suggestion

Standardization of fungal identification methods (culture and molecular) is needed to ensure more consistent and accurate research results. Future studies are recommended to use longitudinal or cohort designs to assess changes in fungal distribution and their association with gastrointestinal disease. Further in-depth studies are needed on the interactions between mycobiota and bacterial microbiota in maintaining gut balance. Interpretation of fungal examination results must take into account the patient's overall clinical condition.

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