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The Role of *Malassezia Spp.* in Pityrasis Versicolor: A Literature Review

Zahlah Levia Redini Umar[1], Dian Amelia Abdi[2], A. Sastri Zainuddin[2], Nurelly Noro Waspodo[2], Adharia[2]

[1]Student of the Medical Profession Study Program, Faculty of Medicine, Universitas Muslim Indonesia Makassar, Indonesia
[2]Department of Dermatology and Venereology, Faculty of Medicine, Universitas Muslim Indonesia Makassar, Indonesia
Email: zahlahlevia17@gmail.com

Abstract. *Pityriasis versicolor (PV) is a skin disease caused by the fungus Malassezia, common in tropical regions with high humidity, such as Indonesia. Pityriasis versicolor is characterized by hypopigmented or hyperpigmented patches, primarily on the chest, back, neck, and face, with some cases accompanied by itching. Risk factors include oily skin, immune conditions, genetics, and hot and humid environments. Further research is needed to understand the role of Malassezia in Pityriasis versicolor to improve treatment and prevent recurrence. To determine the role of Malassezia spp. in Pityriasis versicolor (PV) based on a literature review. Literature review with a narrative review design. Based on several reviewed journals, it can be concluded that Malassezia spp., which are part of the normal skin microbiota, can become pathogenic in individuals with certain predisposing factors. The transformation from yeast to hyphae, as well as the production of virulence factors such as lipase, protease, phospholipase, azelaic acid, melanin-like pigments, and the ability to form biofilms, play a role in the development of Pityriasis versicolor lesions. Interaction with the host occurs through direct mechanisms (irritant metabolites, keratinase) and immunological mechanisms (activation of inflammatory and allergic pathways), leading to skin barrier disruption, pigmentation changes, fine scaling, and potential alopecia. Variation in species and virulence profiles contributes to differences in clinical manifestations and responses to antifungal therapy. Malassezia spp. plays a key role in the development of Pityriasis versicolor through multifactorial virulence mechanisms and interactions with host predisposing factors, which influence clinical manifestations and treatment outcomes.*

Keywords: *Malassezia Spp, Pityriasis Versicolor, Irritant Metabolites*

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INTRODUCTION

Fungal skin disorders remain a global problem. People living in tropical regions often suffer from health problems, particularly skin diseases, resulting in a 40% higher frequency and prevalence of Pityriasis versicolor during the summer. Data from several hospitals in Indonesia indicates that approximately 50% of the population suffers from Pityriasis versicolor (Abdi et al., 2024). Pityriasis versicolor (PV) is a common skin condition found almost worldwide, especially in areas with high humidity, such as Indonesia. Pityriasis versicolor, also known as tinea versicolor (tinea versicolor), is a skin infection caused by the fungus of the genus Malassezia. Pityriasis versicolor causes patches of skin that are lighter or darker or reddish than the surrounding skin (Jasiuk et al., 2025). The most commonly infected areas are the chest and back

due to the high concentration of sebaceous glands in these areas. However, Pityriasis versicolor can also infect other parts of the body, including the arms, neck, and even the face. Although it does not cause symptoms, some patients report itching at the site of infection (Abhinaya et al., 2024).

Its prevalence is particularly high in hot and humid climates. In some tropical countries, the prevalence can reach 50%, while in Sweden it is as low as 0.5%. Pityriasis versicolor is most common in adolescents and young adults, likely due to increased sebum production in this age group. Although rare, it can occur in young children and the elderly. Cases of pityriasis versicolor in infants, including neonates, have also been reported, although very rarely. Pityriasis versicolor is slightly more common in males than in females, possibly related to increased sebaceous gland activity in males. A positive family history of pityriasis versicolor is found in approximately 17% of affected individuals (Ghosh et al., 2008; Chebil et al., 2022; Mellen et al., 2004). The incidence of pityriasis versicolor appears to be equal across races, although skin pigmentation changes are more pronounced in darker-skinned individuals (Leung et al., 2022).

Malassezia is normally present on healthy skin, especially in oily areas such as the face, scalp, and back. However, if this fungus transforms into a pathogenic filamentous form, it can cause Pityriasis versicolor. Thoma et al. (2005) said that, the specific factors in the host environment that trigger Pityriasis versicolor are still not fully understood. Although experimental inoculation using topical oils and occlusion have proven successful, Pityriasis versicolor is not contagious (Łabędź et al., 2023).

Poor hygiene is not a causative factor. Environmental factors such as heat and humidity, pregnancy, oily skin, and the use of oily lotions or creams can increase the risk of Pityriasis versicolor. Genetic predisposition and a hereditary component may also play a role. One survey found that 21% of patients with Pityriasis versicolor reported a positive family history. Immunocompromised individuals are at higher risk of developing Pityriasis versicolor, suggesting that an altered host immune response may play a role in the etiology of this condition. Malnutrition and the use of oral contraceptives may also be risk factors (Friedrich & Junak, 2017).

The term "versicolor" is used to describe this condition because of the possible changes in skin pigmentation (Aljabre et al., 2001; Bonamonte et al., 2021). Although the specific cause of pigmentation variations remains unknown, several hypotheses have been proposed. Pityriasis versicolor's hypopigmentation, in which the skin does not darken in response to sun exposure, is generally most pronounced in the summer. Azelaic acid, a dicarboxylic acid produced by Malassezia, may play a role in the etiology of hypopigmentation through its inhibitory or toxic effects on melanocytes. The inflammatory response to the yeast can cause hyperpigmented and erythematous lesions (Hube et al., 2015; Rao et al., 2023).

The hypopigmented lesions (more common in individuals with dark skin phototypes) of tinea versicolor are thought to result from melanocyte damage and inhibition of tyrosinase activity by azelaic acid (a dicarboxylic acid) produced by Malassezia spp., the formation of small melanosomes, and the accumulation of lipid-like material in the stratum corneum that inhibits ultraviolet light penetration. Conversely, hyperpigmented lesions (more common in individuals with light skin phototypes) may result from a hyperemic inflammatory response triggered by Malassezia spp., an increase in the number of tonofilaments in the stratum granulosum, thickening of the stratum corneum, and the formation of abnormally large melanosomes. Therefore, studies on the role of Malassezia furfur in Pityriasis versicolor are needed to elucidate the relationship between fungal virulence factors, the host immune response, and the clinical manifestations that arise, while also supporting efforts to improve clinical management and prevent recurrence.

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METHODS

Research Design

This research design is a literature review. A literature review is a description of theories, findings, and other research obtained from reference materials that serve as the basis for research activities. A literature review is a framework, concept, or orientation for analyzing and classifying facts collected in the research. A literature review contains reviews, summaries, and the author's thoughts on the topic discussed. A good literature review must be relevant, up-to-date, and adequate. Theoretical foundations and literature reviews are some of the methods for conducting a literature review.

Literature Search Strategy Design

This research is a literature review. A literature review is a method used to collect data or sources related to a specific topic, which can be obtained from various sources such as journals, books, the internet, and other libraries. This research design is a narrative review. This type of research was chosen because the researcher wanted to determine the role of Malassezia spp. in Pityriasis versicolor by collecting references related to the research theme.

Data Sources

The data used in this study is secondary data. Secondary data is data obtained not from direct observation, but rather from research conducted by previous researchers. The secondary data sources in question are books and primary or original scientific reports contained in articles or journals. Data obtained by reviewing scientific articles and journals in the form of research related to the role of Malassezia spp. in Pityriasis versicolor. The databases used were Google Scholar and Pubmed NCBI. The keywords used in this search were Malassezia spp., pathogenesis, and Pityriasis versicolor.

Operational Definition

Table 1. Operational Definitions of Key Variables in the Study

No.	Variable	Definition
1.	*Malassezia* spp.	A skin infectious disease caused by fungal species of the genus *Malassezia*.
2.	*Pityriasis versicolor*	A superficial fungal infection characterized by skin pigment changes due to colonization of the stratum corneum by *Malassezia furfur*.

Inclusion and Exclusion Criteria

Inclusion Criteria

Articles used as literature are research articles from national and international journals, textbooks, and lecturer citations. Articles or literature included discuss the role of Malassezia spp. in the pathogenesis of Pityriasis versicolor. Articles published between 2020 and 2025.

Exclusion Criteria

References cannot be fully accessed. Articles are not relevant to the research title and topic. Duplicate articles (more than one article with the same author, title, and abstract). Articles are commentaries and reviews.

RESULT AND DISCUSSION

Study Selection and Characteristics

A total of 25 publications published between 2020 and 2025 met the predefined inclusion criteria and were incorporated into this review. The selected studies represented diverse research designs, including laboratory-based experimental investigations (approximately eight studies), molecular diagnostic analyses (four studies), antifungal susceptibility testing studies

(four studies), epidemiological or observational studies (six studies), and narrative or systematic reviews (three studies). This distribution reflects the multidisciplinary nature of research on *Malassezia* spp. and Pityriasis versicolor (PV), spanning microbiology, clinical dermatology, molecular diagnostics, and public health. However, the variability in design also introduces important differences in evidentiary weight and interpretive scope.

The included laboratory studies primarily focused on virulence factor characterization, such as lipase, phospholipase, and protease activity, as well as biofilm formation and dimorphic transition. Many of these investigations employed in vitro enzyme assays, modified broth microdilution techniques for antifungal susceptibility testing, and quantitative biofilm assessment models. While these experimental designs offer valuable mechanistic insights into fungal pathogenicity, they are conducted under controlled laboratory conditions that may not fully replicate the complex microenvironment of human skin. As a result, extrapolation from in vitro findings to clinical disease should be approached cautiously.

Molecular diagnostic studies utilized PCR-based methods and, in some cases, sequencing techniques to identify species distribution directly from clinical samples. Compared with conventional microscopy and culture methods used in several epidemiological studies, molecular approaches demonstrated greater sensitivity and the ability to detect mixed-species colonization. In contrast, observational and epidemiological studies relied largely on clinical examination, direct microscopy, and culture-based identification. These studies provide important data regarding prevalence, demographic associations, and environmental risk factors but are generally cross-sectional in nature and therefore limited in establishing causal relationships.

The narrative and systematic reviews included in this synthesis contributed broader contextual interpretation of Malassezia biology and clinical management strategies. However, most reviews did not employ standardized quality appraisal tools, which limits their capacity to differentiate between high- and low-quality evidence. Overall, the body of literature demonstrates significant methodological heterogeneity in sample size, diagnostic approach, laboratory protocols, and outcome measurement. Consequently, the strength of evidence varies across study types: experimental and molecular studies offer stronger mechanistic support, whereas descriptive and observational studies primarily provide epidemiological context. To enhance analytical coherence, the findings of these diverse sources are therefore synthesized thematically rather than presented in chronological or sequential order.

Dimorphic Transition and Morphological Plasticity

The ability of *Malassezia* spp., particularly Malassezia furfur and Malassezia globosa, to transition from a commensal yeast form to a filamentous or hyphal form is widely considered a pivotal event in the pathogenesis of Pityriasis versicolor (PV). Under normal physiological conditions, Malassezia exists predominantly as a budding yeast on sebaceous areas of healthy skin. However, environmental triggers such as increased humidity, occlusion, lipid availability, and altered host immunity appear to induce morphological switching. Microscopic examinations of lesional skin frequently demonstrate the coexistence of yeast cells and short hyphae the classical “spaghetti and meatballs” appearance suggesting that dimorphism is not incidental but associated with disease expression. This morphological plasticity may enhance the organism’s ability to adhere to keratinocytes, penetrate the stratum corneum, and evade host defenses.

Several laboratory and molecular studies have demonstrated a correlation between hyphal presence and increased inflammatory activity. Isolates obtained from PV lesions show enhanced expression of virulence-associated genes and elevated enzymatic activity during the filamentous phase. Experimental induction models further suggest that lipase production increases during mycelial transformation, potentially intensifying lipid degradation and local irritation. Nevertheless, the majority of available data derive from in vitro systems or cross-sectional sampling of established lesions. These designs cannot determine whether the hyphal transition precedes clinical lesion development or represents a secondary adaptation following

environmental changes in already affected skin. The temporal sequence of events in vivo therefore remains unresolved.

Comparative antifungal susceptibility testing has also revealed phenotypic differences between isolates recovered from healthy individuals and those from PV lesions. Lesional strains sometimes demonstrate altered minimum inhibitory concentrations (MICs), suggesting adaptive physiological changes associated with pathogenic states. This observation supports the hypothesis that PV involves more than simple overgrowth; rather, it may reflect functional reprogramming of Malassezia in response to host and environmental pressures. However, methodological variability across studies including differences in lipid supplementation, incubation conditions, and criteria for morphological classification limits the comparability of results and complicates efforts to draw uniform conclusions.

Importantly, not all individuals colonized with filament-capable strains develop clinical PV, indicating that dimorphism alone is insufficient to explain disease onset. Host immune tolerance, barrier integrity, sebaceous composition, and microbial community interactions likely modulate whether morphological switching translates into symptomatic infection. The absence of longitudinal cohort studies tracking colonization status, morphological state, and immune response over time represents a significant gap in the literature. Future research integrating serial sampling, molecular profiling, and host immunologic markers would be essential to clarify whether dimorphic transition functions as a primary trigger of PV or as part of a broader adaptive response within a dynamic host–microbe ecosystem.

Virulence Factors: Enzymes, Biofilm, and Metabolites

Virulence in Malassezia furfur and Malassezia globosa is largely mediated by the production of hydrolytic enzymes that enable adaptation to lipid-rich human skin. Multiple experimental studies report significantly higher lipase and phospholipase activity in isolates obtained from Pityriasis versicolor (PV) lesions compared with isolates from healthy controls. Lipases hydrolyze triglycerides in sebum into free fatty acids, which may act as irritants and disrupt the stratum corneum barrier. Phospholipases contribute to membrane destabilization and may enhance inflammatory signaling. Importantly, several studies indicate that enzyme expression increases during the mycelial phase, suggesting that morphological transition and enzymatic virulence are biologically interconnected processes rather than independent phenomena.

Despite this consistent trend, the interpretation of enzymatic virulence data must be approached with caution. Assay methodologies vary substantially across studies, including differences in substrate types, incubation temperatures, lipid supplementation, and quantification techniques. Some investigations rely on qualitative zone-of-clearance measurements, while others use spectrophotometric or fluorometric assays, limiting direct comparison of enzyme activity levels. Moreover, most data are derived from in vitro culture systems that do not replicate the dynamic immune environment of human skin. As a result, although elevated enzyme activity is strongly associated with PV isolates, definitive evidence linking specific enzymatic thresholds to clinical severity or recurrence remains lacking.

Biofilm formation represents another proposed virulence mechanism contributing to persistence and treatment resistance. In vitro studies demonstrate that PV-derived isolates tend to produce thicker and more structured biofilms compared with strains from asymptomatic individuals. Biofilms may protect fungal cells from antifungal penetration and host immune responses by creating a protective extracellular matrix. This has led to the hypothesis that biofilm capacity contributes to the high recurrence rate observed in PV. However, biofilm assessment techniques are not standardized, and most studies measure biomass under artificial laboratory conditions. There is currently no longitudinal clinical evidence quantifying biofilm presence in vivo or directly correlating biofilm burden with relapse frequency.

In addition to enzymatic and structural virulence mechanisms, metabolite production plays a critical role in pigmentation changes characteristic of PV. Azelaic acid, produced during lipid

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metabolism, is believed to inhibit tyrosinase activity in melanocytes, thereby reducing melanin synthesis and contributing to hypopigmented lesions. While this mechanism is biologically plausible and supported by biochemical studies, direct measurement of azelaic acid concentrations in human lesions is rarely performed. Hyperpigmented variants, conversely, appear more closely linked to inflammatory responses, epidermal hyperplasia, and melanosome enlargement rather than direct fungal metabolite toxicity. Together, these findings suggest that virulence in PV is multifactorial and context-dependent, involving coordinated enzymatic activity, structural adaptation, and host-mediated pigmentary responses rather than a single dominant pathogenic pathway.

Species Distribution and Molecular Identification

Molecular investigations consistently identify Malassezia furfur and Malassezia globosa as the dominant species in lesions of Pityriasis versicolor (PV) across multiple geographic regions. These two lipid-dependent yeasts appear particularly well adapted to sebaceous skin sites such as the chest, back, and upper arms, where PV most commonly occurs. Their predominance is supported by both culture-based studies and PCR-based molecular analyses. However, relative species frequencies vary considerably between studies, suggesting that reported dominance may be influenced not only by true epidemiological patterns but also by diagnostic methodology, sample handling, and laboratory expertise.

PCR-based and sequencing approaches have significantly expanded understanding of species diversity in PV. Compared with conventional microscopy and culture techniques, molecular methods demonstrate higher sensitivity and the capacity to detect mixed-species colonization within a single lesion. Several studies report that culture alone may underestimate the presence of less abundant or slower-growing species due to selective growth conditions and lipid supplementation requirements. Consequently, earlier epidemiological conclusions that identified a single dominant species in most cases may reflect methodological limitations rather than biological exclusivity. Molecular diagnostics therefore provide a more nuanced view, revealing that PV may often involve complex microbial communities rather than infection by a single strain.

Reliance on morphological identification further introduces potential misclassification. Many Malassezia species share overlapping microscopic features, and accurate differentiation requires specialized lipid-enriched media and biochemical profiling. Lipid-dependent strains may fail to grow under suboptimal culture conditions, leading to false-negative results or species misidentification. Additionally, phenotypic plasticity can blur morphological distinctions, especially when isolates undergo dimorphic transition. These diagnostic constraints highlight the importance of integrating molecular confirmation when feasible, particularly in research contexts aiming to correlate species distribution with virulence profiles or antifungal susceptibility patterns.

Geographic and climatic variation also appear to influence species prevalence and disease recurrence. Tropical and subtropical regions characterized by high humidity, elevated temperatures, and increased sebaceous activity report higher colonization density and recurrence rates of PV. These environmental conditions may preferentially favor lipid-dependent species such as *M. furfur* and *M. globosa*. Nevertheless, direct cross-regional comparative studies using standardized molecular techniques remain limited. Without harmonized methodologies, it is difficult to determine whether observed differences reflect true ecological variation or simply diagnostic inconsistency. Future multicenter molecular epidemiology studies would be essential to clarify global distribution patterns and their clinical implications.

Antifungal Susceptibility and Therapeutic Implications

Antifungal susceptibility testing (AFST) of *Malassezia* spp., particularly Malassezia furfur and Malassezia globosa, demonstrates notable species-dependent variability in minimum inhibitory concentrations (MICs). Several studies report that isolates obtained from patients with

recurrent Pityriasis versicolor (PV) exhibit higher MIC values to commonly used azoles such as ketoconazole, fluconazole, and itraconazole compared with isolates from healthy skin. This variability suggests that intrinsic species characteristics and possibly adaptive mechanisms may influence antifungal responsiveness. In some comparative analyses, isolates associated with systemic infection displayed even greater resistance patterns, raising concerns regarding emerging tolerance under antifungal pressure.

However, interpretation of susceptibility data is complicated by the absence of standardized testing protocols for Malassezia species. Unlike Candida or dermatophytes, there is no universally adopted reference method tailored specifically for lipid-dependent yeasts. Differences in broth composition, lipid supplementation, inoculum preparation, incubation time, and endpoint determination significantly affect MIC outcomes. Even minor methodological modifications such as the type of lipid additive used to support fungal growth can alter antifungal activity measurements. Consequently, direct comparison of MIC values across studies is challenging, and pooled resistance estimates may not accurately reflect true clinical trends.

Furthermore, in vitro susceptibility results do not consistently correlate with clinical treatment outcomes. PV is a superficial infection confined to the stratum corneum, where drug penetration, local sebum concentration, and host immune response play critical roles in therapeutic success. A strain exhibiting elevated MIC in vitro may still respond clinically to topical therapy due to high local drug concentrations. Conversely, recurrence after apparently adequate treatment may occur despite favorable susceptibility profiles, suggesting that factors such as biofilm formation, incomplete eradication, or persistent environmental predisposition contribute more significantly than pharmacologic resistance alone.

These considerations underscore the need for cautious interpretation of AFST findings in PV management. While species identification and susceptibility testing may be valuable in recurrent or refractory cases, routine use is not yet supported by robust outcome-based evidence. Future research should aim to establish standardized lipid-supplemented testing guidelines for Malassezia spp. and conduct prospective studies correlating MIC values with clinical response and recurrence rates. Such efforts would strengthen the translational relevance of susceptibility data and help refine therapeutic strategies for persistent or treatment-resistant PV. This research was conducted through a literature review, collecting data from several sources regarding the role of Malassezia spp. in Pityriasis versicolor. Twenty-five references were obtained, which were then discussed and related to the research title. The most relevant references are presented in the table below:

Table 2. Table X. Summary of Previous Studies on Malassezia spp. and Pityriasis Versicolor

Publication Year	Tittle	Method	Writer	Result	Conclusion
2020	A case of anti-pityriasis versicolor therapy that preserves healthy mycobiome	Laporan kasus	Mariusz Dyląg, Ewa Leniak, Sebastian Gnat, Jacek C. Szepietowski, Lukasz Kozubowski	Certain antifungal therapies do not disrupt the balance of the skin microbiome.	PV therapy should consider preserving the skin microbiome.
2020	Malassezia-Associated Skin Diseases, the Use of	Review naratif	Ditte M. L. Saunte, George Gaitanis, Roderick James Hay	Explains the pathogenesis, diagnosis, and treatment of Malassezia-	Malassezia spp. plays a key role in the pathogenesis of PV and other skin diseases.

	Diagnostics and Treatment			associated diseases.	
2020	Susceptibilities of Malassezia strains from pityriasis versicolor, Malassezia folliculitis and seborrheic dermatitis to antifungal drugs	Isolasi 244 strain; uji MIC terhadap beberapa antifungal (broth microdilution modifikasi)	Kaiqin Wang, Lu Cheng, Wenshuang Li, Hui Jiang, Xiaofang Zhang, Shanshan Liu, Yunli Huang, Mingyue Qiang, Tianxiang Dong, Yuye Li, Jin Wang, Shike Feng, Hongbin Li	Differences in sensitivity between species; some species show high MICs for some drugs (species-dependent variation).	AFST data show heterogeneity of resistance → important for guiding PV therapy.
2022	Production and Quantification of Virulence Factors in Malassezia Species	Isolasi Malassezia, kultur, pengujian aktivitas enzim (lipase, fosfolipase, protease), kuantifikasi virulensi	Inès Hadrich, Nahed Khemekhem, Sourour Neji, Houaida Trablesi, Amin Ilahi, Hayet Sellami, Fattouma Makni, dan Ali Ayadi	Malassezia species exhibit different virulence activities; M. furfur and M. globosa exhibit the highest enzyme activity.	Virulence factors such as lipase and phospholipase play a key role in the pathogenicity of Malassezia, including PV.
2022	Virulence factors of Malassezia strains isolated from pityriasis versicolor patients and healthy individuals	Isolasi Malassezia dari pasien PV & sehat, uji lipase, fosfolipase, biofilm, hemolisis	Wissal Chebil, Wafa Rhimi, Najoua Haouas, Valentina Romano, Sameh Belgacem, Hichem Belhadj Ali, Hamouda Babba, Claudia Cafarchia	Isolates from PV patients exhibited higher virulence enzyme activity than those from healthy individuals, resulting in thicker biofilms.	Malassezia strains of PV are more virulent, suggesting a direct link between virulence and PV development.
2022	Presence of Malassezia Hyphae Is Correlated with Pathogenesis of Seborrheic Dermatitis	Analisis mikroskopis, kultur, PCR, analisis morfologi hifa	Juanjuan Li, Yahui Feng, Chen Liu, Zhiya Yang, Sybren de Hoog, Yuying Qu, Biao Chen, Dongmei Li, Huabao Xiong Dongmei Shib	Malassezia hyphae are closely associated with inflammation and lesion severity.	The yeast-to-hypha transition is a key mechanism of Malassezia pathogenesis (relevant for PV).
2022	Malassezia virulence factors and their role in	Review literatur	Ivan Kurniadi, Wong Hendra Wijaya, Kris Herawan Timotius	Reviews lipase, phospholipase, indole, biofilm, and other	Virulence factors play a significant role in various Malassezia-caused

	dermatological disorders			virulence molecules.	skin disorders, including PV.
2022	Deteksi Jamur Malassezia spp. pada Kulit Pekerja Bangunan di Daerah Sukatani Cimanggis Kota Depok	Studi deskriptif laboratorik	Mulyati, Lenggo Geni, Rawina Winita, Madonia Fakum Silitonga	Malassezia colonization was found in the majority of subjects.	The work environment and hygiene influence Malassezia colonization.
2022	Identifikasi Malassezia Furfur Pada Kerokan Kulit Petani Sawit Pt Panca Surya Garden	Studi laboratorik mikroskopis	Berliana Naomi Rumondang Sari Aritonang, Hartini H, Aisyara Yuliandari, Indah Verdinasari, Agatha Naranz, Stefhany Yola	Malassezia furfur was found in most samples.	M. furfur is the dominant species causing superficial skin infections.
2022	Malassezia Furfur on Pitriasis Versicolor and Malassezia Folikulitis	Tinjauan/ulasan literatur mengenai Malassezia sebagai flora kulit dan perannya pada PV dan folikulitis.	Hendra Tarigan & Risti Graharti	M. furfur is the primary etiologic agent of PV, which manifests as hypopigmented/ depigmented patches and scales.	Malassezia, particularly M. furfur, is part of the skin microbiota and can become pathogenic under certain conditions and plays a role in PV.
2023	Comparison of virulence factors and susceptibility profiles of Malassezia furfur from pityriasis versicolor patients and bloodstream infections of preterm infants	Perbandingan isolat M. furfur dari PV dan infeksi sistemik; uji virulensi & uji sensitivitas antifungal	Wafa Rhimi, Wissal Chebil, Iniobong Chukwuebuka Ikenna Ugochukwu, Hamouda Babba, Domenico Otranto, Claudia Cafarchia	Significant differences: systemic isolates are more resistant to antifungals; PV isolates have different virulence patterns.	Genetic variation in M. furfur influences virulence and therapeutic response, which is important for diagnosis and management.
2023	Pityriasis Versicolor—A Narrative Review on the Diagnosis	Studi tinjauan pustaka (review naratif)	Nina Łabe¸dz , Cristian Navarrete-Dechent, Honorata Kubisiak-Rzepczyk, Monika Bowszyc-	Explains the dominance of M. globosa and M. furfur in PV; risk factors, pathogenesis,	The pathogenesis of PV is influenced by Malassezia virulence factors, skin conditions, and the environment.

	and Managemen t		Dmochowska, Anna Pogorzelska-Antkowiak dan Paweł Pietkiewicz	and current therapies.	
2023	Direct molecular analysis of Malassezia species from the clinical samples of patients with pityriasis versicolo	PCR langsung dari sampel klinis tanpa kultur	Esmaeil Eghtedarnejad, Somayeh Khajeh, Kamiar Zomorodian, Zeinab Ghasemi, Somayeh Yazdanpanah, Marjan Motamedi	M. globosa was the most dominant; PCR was more sensitive than conventional culture.	Molecular identification is important to identify the causative species of PV accurately and rapidly.
2023	Malassezia-associated skin diseases in the pediatric population	Narrative review	Christy H. Chang, Sarah L. Stein	Malassezia plays a role in various childhood skin diseases including PV.	Malassezia spp. is a normal flora that can become pathogenic under predisposing conditions.
2023	Differential lipase virulence in Malassezia furfur dimorphism isolated from pityriasis versicolor patients and healthy individuals	Kultur kondisi untuk induksi dimorfisme (yeast ↔ mycelium); pengukuran aktivitas dan ekspresi gen lipase	Patcharin Thammasit, Angka Na Laliam, Kunyaluk Chaicumpar, Krits ada Pruksaphon, Joshua D Nosanchuk, Sirida Youngchim	Lipase increased in the mycelial phase; differences in LIP gene expression (LIP3, LIP5, LIP6) between PV patient isolates and controls.	Lipase related to M. furfur dimorphism and possible role in virulence in PV
2023	Anti-Malassezia drug candidates based on virulence factors of Malassezia-associated diseases	Tinjauan sistematis literatur virulensi & target terapeutik	M. Billamboz & S. Jawhara	Developing targets (lipase inhibitors, anti-biofilm agents, AhR antagonists, etc.) that engage Malassezia virulence mechanisms.	Antivirulence approaches (not just antifungals) have the potential to address PV/recurrent disease.
2023	Antifungal susceptibilit y testing of Malassezia spp isolated from patients	Isolasi Malassezia dari PV & kontrol; uji susceptibilita s antifungal in vitro	Balaji VK, Ragunathan L, et al.	Detecting variations in antifungal susceptibility between Malassezia PV	Antifungal variation highlights the importance of species identification prior to PV therapy.

	with Pityriasis versicolor and healthy individuals			isolates compared to isolates from healthy skin; highest MICs for specific azoles	
2024	Morphological Study of Malassezia Species Isolated from Pityriasis Versicolor Patients in Thi-Qar Governorate and Their Sensitivity to Some Antifungal Drugs	Kultur, identifikasi morfologi, uji sensitivitas antifungal	Marwa Amer Jalil, Mohammed Hashim Yasir	Various species were found, especially M. furfur; antifungals showed varying sensitivity.	Malassezia species in PV vary between patients; therapy selection should take species type into account.
2024	Factors associated with pityriasis versicolor in a large national database	Studi observasional retrospektif menggunakan database nasional	Rachel C. Hill, Willian De Faria, Jeremy A. W. Gold, Shari R. Lipner	PV has been associated with young age, warm climates, and certain skin conditions.	Pityriasis versicolor is influenced by demographic and environmental factors that favor the proliferation of Malassezia spp.
2024	Deteksi Jamur Malassezia spp. Penyebab Infeksi Jamur Kulit Pada Santri Pondok Pesantren Kota Denpasar	Studi deskriptif	Didik Prasetya, Moh Fairuz Abadi	The prevalence of Malassezia is quite high among Islamic boarding school students.	Environmental factors and housing density play a role in Malassezia infection.
2024	Identifikasi Pityriasis versicolor Pada Tenaga Cleaning Service Universitas Negeri Gorontalo	Studi deskriptif observasional	Muhammad Rafiq Supriadi, Nanang Roswita Paramata, Abdi Dzul Ikram Hasanuddin, Wahjuni, Elvie Febriani Dungga	PV cases have been identified with risk factors such as sweat and hygiene.	Occupation and hygiene play a role in the development of PV.

2024	Epidemiological and Molecular Characterization of Malassezia species from Patients with pityriasis versicolor in Erbil Province	PCR dan sequencing rDNA untuk identifikasi Malassezia pada pasien PV	Hassan Z, Qurtas DSQ	M. furfur is dominant, and M. globosa has also been found in PV lesions in Erbil Province.	Molecular evidence of M. furfur and M. globosa dominance in PV lesions supports their role in PV pathogenesis.
2024	Fungal coexistence in the skin mycobiome: Malassezia, Candida & Rhodotorula (PV context)	Pengurutan komunitas jamur kulit & hubungan Malassezia dengan penyakit kulit	Bharati Naik, Jayaprakash Sasikumar, Vishal B, Shankar Prasad Das	Demonstrates Malassezia's adaptation to sebum-rich skin and its development in PV; and its relationship to host immunity.	Emphasizes that the transition from commensal to pathogen in Malassezia involves host responses beyond simple colonization.
2025	Prevalensi Dan Karakteristik Pityriasis versicolor Di RSUP Dr. Hasan Sadikin Bandung Periode 2018–2022	Studi retrospektif rekam medis	Ahmad Zaky Dinantha, Risa Miliawati Nurul Hidayah, Nisa Fauziah, Chrysanti, Miranti Pangastuti	PV is most common in productive-age individuals with hypopigmented lesions.	PV is a common and recurrent superficial fungal disease.
2025	Beyond the Surface: Decoding Pityriasis Versicolor Through Clinical, Dermoscopic and Microbiological Exploration	Studi observasional klinis, dermoskopi, dan mikrobiologi	Dsouza, Priya A. Monteiro, Rochelle C, Dias, Meena, Prabhu, Sudhir Haladi, Bhat, Ramesh M, Jayaraman, Jyothi, Martis, Jacintha	Correlation of clinical, dermoscopic, and Malassezia identification findings in PV lesions.	A multimodal approach improves understanding of the pathogenesis and diagnosis of PV.

From Colonization to Pathogenesis: A Dynamic Interaction Model

Current evidence supports a multifactorial and dynamic model in which Pityriasis versicolor (PV) emerges not simply from fungal overgrowth but from the interaction between microbial adaptation, host susceptibility, and environmental amplification. Malassezia species most notably Malassezia furfur and Malassezia globose are normal components of the cutaneous microbiota in sebaceous areas. Colonization alone, however, is insufficient to produce disease. PV

appears to develop when commensal equilibrium is disrupted by changes in skin microenvironment, such as increased sebum production, occlusion, or humidity, which create favorable conditions for fungal proliferation and phenotypic transformation (Bay et al., 2024; McLoughlin et al., 2022; Bond et al., 2020). Thus, pathogenesis should be understood as a shift in ecological balance rather than a simple infectious invasion.

Microbial adaptation represents the first major axis of this model. Under permissive environmental conditions, Malassezia may undergo dimorphic transition from yeast to filamentous forms, increase lipase and phospholipase production, and enhance biofilm formation. These adaptations allow more efficient lipid utilization, deeper interaction with the stratum corneum, and improved resistance to host defenses. Lipase-mediated hydrolysis of triglycerides generates free fatty acids that may irritate the epidermis and alter barrier integrity. Simultaneously, biofilm production may shield fungal cells from antifungal agents and immune clearance, contributing to persistence and recurrence. Rather than functioning independently, these virulence mechanisms likely operate synergistically to reinforce fungal survival within the cutaneous niche (Roudbary et al., 2022; Brown, 2023; Van et al., 2021; Alfei & Caviglia, 2022).

Host susceptibility constitutes the second critical axis. Increased sebaceous activity during adolescence and young adulthood provides abundant lipid substrates that favor fungal growth. Variations in innate immune response, local inflammatory regulation, and possibly genetic predisposition further influence whether colonization progresses to symptomatic infection (Zhang & Cao, 2019; Abraham & Medzhitov, 2011; Sanders et al., 2011; Merkhofer & Klein, 2020; Meneghin & Hogaboam, 2007). Importantly, many individuals harbor potentially virulent strains without developing lesions, indicating that host tolerance and immune modulation are decisive factors. Environmental amplification including tropical climate, hyperhidrosis, and occlusive clothing acts as a third modulatory layer, intensifying microbial adaptation and host vulnerability simultaneously. The convergence of these elements may create a threshold beyond which commensalism shifts toward pathogenicity.

Despite the coherence of this integrative framework, definitive in vivo temporal sequencing remains unproven. Most available evidence is cross-sectional or derived from in vitro experimentation, limiting the ability to determine whether morphological transition precedes enzyme upregulation, or whether inflammatory changes initiate fungal adaptation. Consequently, the proposed model remains largely associative rather than causally established. Longitudinal human studies incorporating serial microbiological sampling, immune profiling, and environmental monitoring would be necessary to validate this dynamic interaction hypothesis and clarify the chronological progression from benign colonization to clinically evident PV (Saleh, & Hassan, 2025; Doolan et al., 2009).

Explaining Inconsistencies Across Studies

One of the most striking features of the literature on Pityriasis versicolor (PV) is the variability in reported dominant species, virulence profiles, and antifungal susceptibility patterns of Malassezia furfur and Malassezia globosa. While some studies identify M. globosa as the predominant causative species, others report M. furfur as more prevalent, and a few describe mixed-species colonization. These discrepancies do not necessarily indicate true biological contradiction; rather, they may reflect contextual and methodological differences that influence detection and interpretation. Without careful consideration of these underlying variables, comparisons across studies risk oversimplification.

Geographic and climatic variation likely represent major contributors to these inconsistencies. Tropical and subtropical regions, characterized by high humidity and temperature, create environmental conditions that enhance sebaceous activity and fungal proliferation (Sharma et al., 2015). Differences in population genetics, skin phototype distribution, hygiene practices, and occupational exposure may further shape species ecology. For example, regions with dense urban living or occupational heat exposure may show different colonization patterns compared to temperate climates. However, few studies directly compare

multiple geographic populations using standardized protocols, making it difficult to determine whether observed differences reflect ecological adaptation or sampling bias.

Diagnostic modality also substantially influences reported findings. PCR-based molecular identification consistently demonstrates higher sensitivity and greater species diversity than culture or microscopy alone (Johnson et al., 2000; Desquesnes & Dávila, 2002; Jarman et al., 2004). Conventional culture techniques may selectively favor faster-growing or lipid-tolerant strains, while microscopy cannot reliably differentiate closely related species. As a result, earlier studies relying exclusively on morphological identification may have underestimated mixed colonization or misclassified species. When molecular methods are introduced, previously "dominant" species distributions may shift, not because epidemiology has changed, but because detection accuracy has improved. This diagnostic heterogeneity complicates longitudinal interpretation of trends over time.

Laboratory assay variability and patient selection criteria introduce additional layers of inconsistency. Antifungal susceptibility testing protocols differ in lipid supplementation, incubation duration, and endpoint interpretation, producing variation in minimum inhibitory concentration (MIC) values. Similarly, studies including primary uncomplicated PV cases may report different virulence profiles compared to those focusing on recurrent or refractory infections. Some investigations even compare cutaneous isolates with systemic strains, which may possess inherently different resistance patterns. Without stratifying results by clinical presentation and methodological approach, reviews may unintentionally conflate heterogeneous data sets. Recognizing these contextual determinants is therefore essential to reconcile apparent contradictions and to advance toward a more standardized and comparable evidence base.

Malassezia spp. as Normal Flora and Opportunistic Pathogens in Pityriasis Versicolor

Malassezia spp. are lipophilic fungi that are physiologically part of the normal microbiome of human skin, especially in areas with high sebum content such as the face, chest, and back. Under normal conditions, these fungi live as commensal organisms without causing clinical abnormalities. However, under certain conditions, Malassezia can become opportunistic pathogens and play a role in the development of Pityriasis versicolor (PV). This is explained by Dyląg et al., who emphasized that the balance of the skin microbiome plays a crucial role in maintaining the commensal status of Malassezia, and disruption of this balance can trigger superficial infections (Dyląg et al., 2020).

A similar opinion was expressed by Prohić et al., who stated that Malassezia are part of the normal skin flora but can become pathogenic when there are changes in the skin microenvironment or a decrease in host defenses. This study confirms that the pathogenesis of Pityriasis versicolor is not caused by colonization alone, but rather by changes in the fungal biology and host response (Prohic et al., 2016).

The transformation of Malassezia from the yeast form to the filamentous or hyphal form is a crucial mechanism in the pathogenesis of Pityriasis versicolor. Wang et al., through antifungal sensitivity testing, demonstrated that Malassezia species from PV lesions exhibited distinct biological characteristics compared to isolates from healthy skin. This suggests that changes in fungal morphology and physiology play a role in the infection process. Research by Li et al. further strengthened these findings by demonstrating that the presence of Malassezia hyphae correlated closely with inflammation and lesion severity, thus suggesting that the yeast-to-hyphal transition is key to Malassezia pathogenicity in skin disease (Wang et al., 2020).

Host and Environmental Predisposing Factors in the Pathogenesis of Pityriasis Versicolor

The occurrence of Pityriasis versicolor is influenced not only by fungal factors, but also by host and environmental conditions. Kurniadi et al. explain that hot and humid climates, increased sebum production, and hyperhidrosis are the main factors supporting the growth and proliferation of Malassezia spp. on human skin. These factors explain the high prevalence of Pityriasis versicolor in tropical countries like Indonesia (Kurniadi et al., 2022).

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Field studies by Mulyati et al. on construction workers and Aritonang et al. on oil palm farmers showed that work environment conditions, personal hygiene, and exposure to excessive sweating contribute to Malassezia colonization of the skin. These findings confirm that environmental factors play a significant role in the pathogenesis of Pityriasis versicolor (Mulyati et al., 2022; Aritonang et al., 2022)

In addition to environmental factors, host factors also play a crucial role. Tarigan and Graharti stated that Pityriasis versicolor is more common in productive-age individuals with high sebaceous gland activity. This is in line with research by Rhimi et al., which showed that host immunological and genetic factors influence the virulence and clinical manifestations of Malassezia infection (Tarigan & Graharti, 2022).

Roles of Malassezia spp. Virulence Factors in Pityriasis Versicolor Lesions

The pathogenicity of Malassezia spp. is closely related to the production of virulence factors. Research by Eghtedarnejad et al. showed that Malassezia isolates from Pityriasis versicolor lesions had higher hydrolytic enzyme activity than isolates from normal skin. Enzymes such as lipase and phospholipase play a role in the breakdown of sebaceous lipids into free fatty acids, which are irritating to the skin. Chang and Stein, in their review, stated that this enzymatic activity disrupts the skin barrier, increases transepidermal water loss, and triggers local inflammation. This condition facilitates the development of scales and skin discoloration characteristic of Pityriasis versicolor (Chang & Stein, 2024).

In addition to enzyme production, the ability to form biofilms also plays a role in the pathogenesis of Pityriasis versicolor. Thammasit et al. reported that Malassezia in the hyphal phase have higher lipase activity and stronger biofilm capabilities than those in the yeast phase. This biofilm provides protection against the host's immune system and reduces the effectiveness of antifungal therapy. Billamboz and Jawhara added that biofilm is a major factor in the recurrence of Pityriasis versicolor, making it a potential target for the development of new therapies (Thammasit et al., 2023; Billamboz & Jawhara, 2023).

Mechanism of Pigmentation Changes in Pityriasis Versicolor

Skin pigmentation changes are a characteristic clinical manifestation of Pityriasis versicolor associated with metabolites of Malassezia spp. Balaji et al. explained that hypopigmented lesions occur due to the production of azelaic acid, which inhibits melanocyte tyrosinase activity, thereby reducing melanin production. Jalil and Yasir added that the accumulation of lipids and scales in the stratum corneum also inhibits the penetration of ultraviolet light into the skin layers, preventing normal skin pigmentation upon sun exposure (Jalil & Yasir, 2024).

Conversely, Hill et al. explained that hyperpigmented and erythematous lesions in Pityriasis versicolor occur due to a local inflammatory response that triggers melanosome enlargement, hyperkeratosis, and increased melanocyte activity. These findings are supported by Prasetya and Abadi, who demonstrated that variations in the clinical manifestations of Pityriasis versicolor are influenced by skin phototype and the degree of inflammation (Supriadi et al., 2024; Hassan & Qurtas, 2024).

Malassezia Species Variation and Its Implications for Diagnosis and Therapy

Malassezia species variation has important implications for the diagnosis and therapy of Pityriasis versicolor. Supriadi et al. showed that Malassezia furfur and Malassezia globosa are the most frequently found species in Pityriasis versicolor lesions in Indonesia. This is consistent with research by Hassan and Qurtas, who used molecular methods and found the dominance of these species in Pityriasis versicolor patients. Naik et al. (2024) explained that the interaction of Malassezia with other skin microbiomes and the host immune system also influences virulence and disease progression. Furthermore, Dinantha et al. reported that Malassezia species variation

also influences response to antifungal therapy, making species identification crucial, especially in recurrent cases.

Clinical Implications and Future Research Directions

Understanding the multifactorial role of Malassezia spp. in the pathogenesis of Pityriasis versicolor has important clinical implications. Dsouza et al. emphasized that a diagnostic and therapeutic approach that combines clinical, dermoscopic, and microbiological aspects can improve diagnostic accuracy and therapeutic success.

Thus, Pityriasis versicolor is the result of a complex interaction between Malassezia spp. virulence factors, host conditions, and the environment. Future therapeutic approaches are expected to focus not only on fungal eradication but also on controlling predisposing factors and preserving the skin microbiome to prevent recurrence.

CONCLUSION

Based on a literature review, Malassezia species are part of the normal human skin microbiota and are commensals, but can become pathogenic in individuals with certain predisposing factors. The dimorphic transformation of Malassezia from yeast to hyphal form, as well as the production of virulence factors such as lipase, protease, phospholipase, azelaic acid, melanin-like pigments, and the ability to form biofilms, play a crucial role in the pathogenesis of Pityriasis versicolor (PV). Host and environmental predisposing factors, such as hot and humid climates, increased sebum production, hyperhidrosis, productive age, and certain immune conditions, play a significant role in supporting the proliferation of Malassezia spp. and the occurrence of Pityriasis versicolor. The high prevalence of Pityriasis versicolor in tropical regions reflects the importance of these factors in the pathogenesis of this disease. The pathogenicity of Malassezia spp. is closely related to the production of various virulence factors, such as lipase, phospholipase, protease, and the ability to form biofilms. These factors contribute to skin barrier damage, inflammation, and the persistence and recurrence of infection. Increased lipase activity in the hyphal phase and biofilm formation are key explanations for the frequent recurrence of Pityriasis versicolor. Skin pigmentation changes in Pityriasis versicolor result from a complex interaction between Malassezia spp. metabolites and the host inflammatory response. Hypopigmented lesions result from inhibition of tyrosinase activity by azelaic acid and the inhibition of ultraviolet light penetration, while hyperpigmented and erythematous lesions are triggered by local inflammation and changes in epidermal structure. Variation in Malassezia species, particularly the dominance of M. furfur and M. globosa, as well as differences in virulence profiles and antifungal susceptibility, have important implications for the diagnosis and management of Pityriasis versicolor. Therefore, species identification and understanding of the pathogenic mechanisms are essential for determining effective therapeutic strategies and preventing recurrence.

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