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**IDENTIFICATION OF NON-DERMATOPHYTE FUNGI CAUSING
ONYCHOMYCOSIS IN THE TOENAILS OF RICE FARMERS IN GAMPONG
RUMAH PANJANG, SOUTHWEST ACEH REGENCY**

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ABSTRACT

Onychomycosis is a fungal nail infection most commonly caused by dermatophyte fungi; however, non-dermatophyte fungi such as *Aspergillus* sp. and the yeast *Candida albicans* are now increasingly recognized as important etiological agents, particularly among individuals with continuous exposure to damp and unclean environments, such as rice farmers. This study aimed to identify the non-dermatophyte fungi causing onychomycosis in the toenails of rice farmers in Gampong Rumah Panjang, Southwest Aceh Regency. This descriptive study was conducted in July 2024, with sample examination performed at the Microbiology Laboratory of the Department of Medical Laboratory Technology, Poltekkes Kemenkes Aceh. The study population comprised 40 rice farmers, from whom 20 were selected as samples through a purposive sampling technique based on nail abnormality criteria (brittleness and/or discoloration). Nail scraping samples were examined directly using 10% KOH and cultured on Sabouraud Dextrose Agar (SDA) medium, followed by macroscopic and microscopic identification. Of the 20 samples examined, non-dermatophyte fungi were identified in 6 samples (30%), comprising *Aspergillus niger* (4 samples) and *Candida albicans* (2 samples), the latter confirmed by the germ tube test. It can be concluded that non-dermatophyte fungi contribute to the etiology of onychomycosis in the toenails of rice farmers in Gampong Rumah Panjang, with a positive rate of 30% and a negative rate of 70%. These findings add to the epidemiological data on non-dermatophyte onychomycosis among farmer populations in Aceh Province, which have previously been scarcely reported.

Keywords: Non-Dermatophyte Fungi, Onychomycosis, Rice Farmers

INTRODUCTION

Onychomycosis is a chronic fungal infection of the nail plate that represents the most common nail disorder in the adult population, accounting for approximately half of all nail disease

cases (Gupta et al., 2024b). The condition has historically been closely associated with dermatophyte infections such as *Microsporum*, *Trichophyton*, and *Epidermophyton*, leading to the widespread use of the term *tinea unguium*; however, this term technically refers only to onychomycosis caused by dermatophytes. A systematic review and meta-analysis of 219 studies conducted between 2013 and 2023 reported an onychomycosis prevalence of 24.19% in clinic/hospital-based populations and 8.57% in community-based populations, with the highest prevalence observed in Southeast Asia (Wongyikul et al., 2026).

Besides dermatophytes, non-dermatophyte fungi comprising non-dermatophyte moulds (NDM) such as *Aspergillus* sp., *Fusarium* sp., and *Scopulariopsis* sp., as well as yeasts such as *Candida albicans*, have been reported as causative agents of onychomycosis, with a global prevalence of approximately 6.9% among culture-confirmed cases, *Aspergillus* being the most frequently identified NDM genus (Gupta et al., 2024a). A large-scale molecular epidemiological study of more than 700,000 nail specimens in the United States found *Aspergillus* in 7.0% and *Candida* in approximately 3.5–4% of mycologically confirmed onychomycosis cases, with women and older adults showing a higher risk of NDM and yeast infection compared with men and younger adults (Gupta et al., 2024b). Non-dermatophyte fungi were previously often regarded as laboratory contaminants or secondary pathogens; however, recent studies have confirmed their role as emerging primary pathogens, particularly among individuals with continuous exposure to damp, unclean environments and repeated nail trauma (Husain et al., 2025; Bitew et al., 2022). Failure to differentiate between dermatophyte and non-dermatophyte infections may result in inappropriate antifungal therapy selection, given that the susceptibility profiles of NDM to terbinafine and itraconazole differ from those of dermatophytes (Gupta et al., 2024a). Globally, the prevalence of onychomycosis in special populations with high-risk environmental exposure has also been reported to differ from that of the general population (Gupta et al., 2024c), reinforcing the importance of research on at-risk groups such as rice farmers.

In Indonesia, several studies among farming populations have reported relatively high rates of onychomycosis, including 40% among farmers in South Bengkulu Regency (Hayati & Marselina, 2021), 47.5% among farmers in Palembang (Nurfadilah et al., 2021), 66.67% among farmers in Ciamis (Mufliha, 2018), 66.7% among rice farmers in Serijabo Village, Ogan Ilir (Oktari, 2022), and 63% dermatophyte infections versus 37% non-dermatophyte infections among farmers in Sukoharjo (Prabandari et al., 2024). In contrast, a study among farmers in Kelurahan Handil Bakti Palaran, East Kalimantan, found *Aspergillus* sp. (60%) to be the most dominant non-dermatophyte group compared with *Trichophyton* sp. (10%) among dermatophytes, with a significant association observed between infection and the habit of not wearing footwear while working ($p=0.026$) (Nita et al., 2025), consistent with findings among rice farmers in Rajeg Village, Tangerang, which likewise reported the involvement of non-dermatophyte mould fungi (Aisy et al., 2024).

Nevertheless, most of these studies have limited identification to the group level (dermatophyte versus non-dermatophyte) without yeast confirmation via the germ tube test, and the majority were conducted outside Aceh Province. Within Aceh itself, publications on non-

dermatophyte fungi as a cause of onychomycosis remain very limited and generally focus on trader populations rather than farmers, as in a study of fish traders at Pasar Pusong, Lhokseumawe (Kesha, 2024), while other publications on *tinea unguium* in Aceh have largely taken the form of health education activities, such as nail fungus education for the elderly in Banda Aceh City, without accompanying laboratory identification (Rahmayanti et al., 2024a). To date, no specific data on non-dermatophyte fungi causing onychomycosis among rice farmers in Southwest Aceh Regency have been reported.

This gap in the literature forms the basis of the novelty of the present study, namely: (1) this study represents the first identification of non-dermatophyte fungi, encompassing both mould and yeast groups, as a cause of onychomycosis among the rice farmer population in Gampong Rumah Panjang, Southwest Aceh Regency; (2) the yeast *Candida albicans* was specifically confirmed through the germ tube test, thereby clearly distinguishing between the mould and yeast groups, which in many similar studies are merely combined into a single ‘non-dermatophyte’ category without further confirmation; and (3) this study aligns its terminology with current clinical mycological understanding by using the term onychomycosis rather than *tinea unguium*, which technically refers only to dermatophyte infection, thereby more accurately reflecting the non-dermatophyte etiological spectrum that is the focus of this study (Gupta et al., 2024a).

Farmers in Gampong Rumah Panjang, Southwest Aceh Regency, work in rice fields with prolonged direct contact with soil, water, and mud without the use of personal protective equipment, resulting in feet that are frequently in a damp condition—an environment that favors the growth of non-dermatophyte fungi. Preliminary observation revealed yellowish to blackish discoloration, brittleness, and malodor of the farmers' toenails. Based on these observations, the authors were prompted to conduct a study to identify the non-dermatophyte fungi causing onychomycosis in the toenails of rice farmers in Gampong Rumah Panjang, Southwest Aceh Regency.

METHODS

This study employed a descriptive design aimed at describing the presence or absence of non-dermatophyte fungi causing onychomycosis in the toenails of farmers (Adiputra et al., 2021). The study was conducted at the Microbiology Laboratory of the Department of Medical Laboratory Technology, Poltekkes Kemenkes Aceh, in July 2024. The study population consisted of 40 rice farmers from Gampong Rumah Panjang, Southwest Aceh Regency. Samples were determined using a purposive sampling technique based on the criteria of nail brittleness and/or discoloration (yellowish/blackish), yielding a sample of 20 individuals.

Examination Procedure

1. Pre-Analytical. The instruments used included an oven, autoclave, stove, microscope, Erlenmeyer flask, beaker glass, object glass, cover glass, incubator, petri dish, stirring rod, spoon, inoculation loop, spirit lamp, and analytical balance, together with materials comprising Sabouraud Dextrose Agar (SDA) medium, distilled water, 10% KOH, and chloramphenicol

antibiotic. Glassware was sterilized using an oven at 140°C for 1–4 hours (Hidayat & Isnawati, 2021).

2. Analytical. SDA medium was prepared by weighing 26 g of medium into an Erlenmeyer flask, adding 400 mL of distilled water, homogenizing the mixture over a stove, adding 1 g of chloramphenicol once the mixture had cooled slightly, and then dispensing 15–20 mL into petri dishes to solidify (Naim, 2016). Nail scraping samples were collected using a sterile scalpel after cleaning the nail with an alcohol swab, placed into sealed plastic sample bags, and transported to the laboratory (Khatimah, 2018). Direct examination was performed by applying 10% KOH to an object glass containing the sample and observing it under a microscope at 10×–40× magnification. Samples were also cultured on SDA medium and incubated for 7 days at 37°C, with daily observation. Macroscopic identification covered colony shape, color, and surface texture, while microscopic identification was performed using 10% KOH at 10×10 and 40×10 magnification. Colonies suspected to be yeasts were confirmed using the germ tube test (addition of 1 mL serum, incubation, and observation for pseudohyphae) (Rahmayanti et al., 2022; Rahmayanti et al., 2024b).

3. Post-Analytical. Data were analyzed by calculating the percentage of positive and negative non-dermatophyte fungal findings using the relative frequency formula: Frequency = (number of positive/negative samples ÷ total samples) × 100% (Latifah et al., 2019).

RESULTS AND DISCUSSION

The results of the identification of non-dermatophyte fungi causing onychomycosis in the toenails of rice farmers in Gampong Rumah Panjang, Southwest Aceh Regency, are presented in Table 1 below.

Table 1. Results of Non-Dermatophyte Fungal Culture Examination Causing Onychomycosis on SDA Medium

Sample on SDA Medium	Result	Fungal Species
Sample 1	Negative (-)	No fungal growth
Sample 2	Positive (+)	<i>Aspergillus niger</i>
Sample 3	Positive (+)	<i>Aspergillus niger</i>
Sample 4	Negative (-)	No fungal growth
Sample 5	Negative (-)	No fungal growth
Sample 6	Negative (-)	No fungal growth
Sample 7	Negative (-)	No fungal growth
Sample 8	Negative (-)	No fungal growth
Sample 9	Negative (-)	No fungal growth
Sample 10	Negative (-)	No fungal growth
Sample 11	Negative (-)	No fungal growth
Sample 12	Negative (-)	No fungal growth
Sample 13	Positive (+)	<i>Aspergillus niger</i>

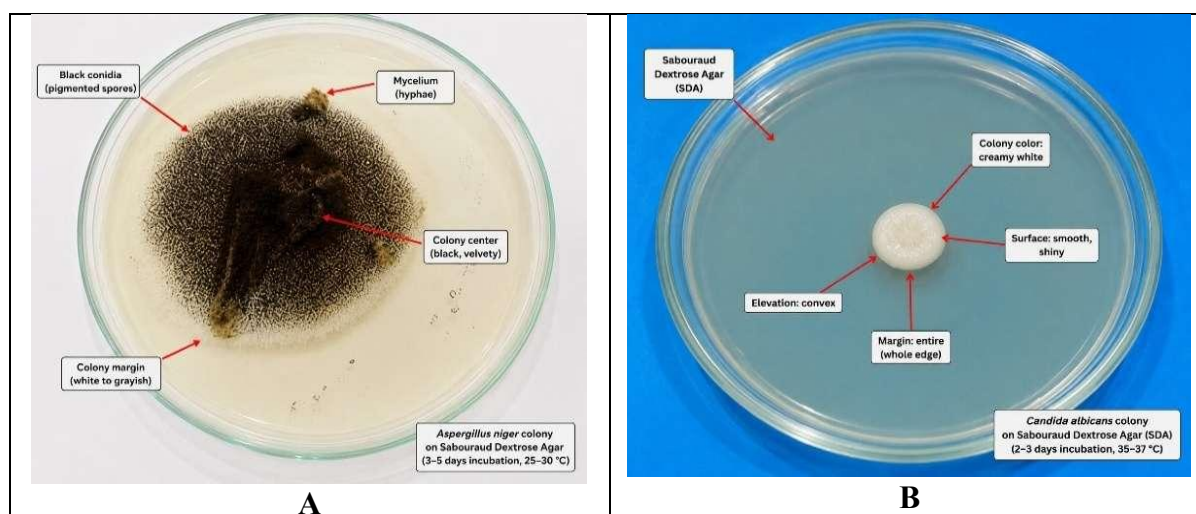
Sample on SDA Medium	Result	Fungal Species
Sample 14	Positive (+)	<i>Candida albicans</i>
Sample 15	Negative (-)	No fungal growth
Sample 16	Positive (+)	<i>Aspergillus niger</i>
Sample 17	Negative (-)	No fungal growth
Sample 18	Positive (+)	<i>Candida albicans</i>
Sample 19	Negative (-)	No fungal growth
Sample 20	Negative (-)	No fungal growth

As shown in Table 1, culture examination on SDA medium revealed non-dermatophyte fungal growth in samples 2, 3, 13, 14, 16, and 18, consisting of *Aspergillus niger* and *Candida albicans*, whereas the remaining samples showed no fungal colony growth.

Table 2. Percentage of Non-Dermatophyte Fungal Culture Results Causing Onychomycosis Among Rice Farmers in Gampong Rumah Panjang, Southwest Aceh Regency

No.	Inoculation Result	Frequency	Percentage (%)
1.	Positive for non-dermatophyte fungi	6	30
2.	Negative for non-dermatophyte fungi	14	70
	Total	20	100

As shown in Table 2, the percentage of non-dermatophyte fungal culture results causing onychomycosis among rice farmers in Gampong Rumah Panjang, Southwest Aceh Regency, was 30% positive and 70% negative. To confirm *Candida albicans*, a germ tube test was performed by adding 1 mL of serum followed by incubation, revealing pseudohyphae, or elongated septate germ tubes, in samples 14 and 18, confirming the identity of *Candida albicans* as a yeast-group non-dermatophyte fungus (Figure 1.B and D).



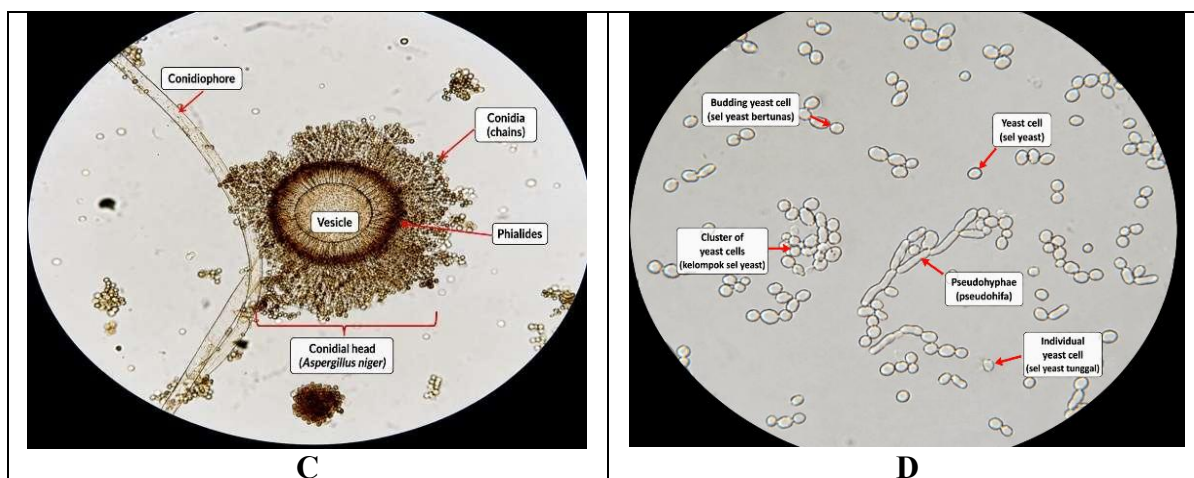


Figure 1. (A) Macroscopic colony of *Aspergillus niger*; (B) Macroscopic colony of *Candida albicans*; (C) Microscopic view of *Aspergillus niger* (400× magnification); (D) Microscopic view of *Candida albicans* (400× magnification), showing pseudohyphae resulting from the germ tube test.

Discussion

This study aimed to identify the presence or absence of non-dermatophyte fungi causing onychomycosis in the toenails of rice farmers in Gampong Rumah Panjang. Direct examination using 10% KOH revealed no fungal elements (hyphae or yeast cells) in most samples, whereas samples subsequently confirmed positive by culture showed fungal elements consistent with non-dermatophyte morphology. Culture examination revealed growth of the non-dermatophyte fungi *Aspergillus niger* and *Candida albicans*. It should be emphasized that *Candida albicans* is a yeast belonging to the non-dermatophyte group, as it differs morphologically and biologically from the true keratinolytic fungi. Accordingly, all positive findings (30%) in this study represent non-dermatophyte fungi causing onychomycosis in the toenails of the farmers examined.

These findings are consistent with the comprehensive review by Gupta et al. (2024a), which confirmed *Aspergillus* as one of the most common non-dermatophyte mould (NDM) genera causing onychomycosis globally, alongside *Scopulariopsis* and *Fusarium*. These moulds are ubiquitous in soil, water, and organic matter, allowing them to contaminate nails in spore form during direct contact with the agricultural environment. Historically, NDM were often considered contaminants that opportunistically colonized keratin previously damaged by mechanical trauma; however, recent studies by Husain et al. (2025) and Bitew et al. (2022) have shown that under conditions of continuous exposure to damp, unclean environments, such as those experienced by rice farmers, NDM, including *Aspergillus*, may also act as primary causative agents of onychomycosis rather than merely as secondary contaminants.

The dominance of *Aspergillus niger* observed in this study is consistent with findings among farmers in Kelurahan Handil Bakti Palaran, East Kalimantan, which likewise reported *Aspergillus* sp. as the most frequently isolated non-dermatophyte group (60%), significantly associated with the habit of not wearing footwear while working ($p=0.026$) (Nita et al., 2025). Meanwhile, the confirmation of *Candida albicans* through the germ tube test in this study reinforces the large-

scale molecular epidemiological data reported by Gupta et al. (2024b), which showed that yeasts, including *C. albicans*, consistently contribute to onychomycosis and are more frequently found in individuals with prolonged exposure to water and moisture—conditions closely resembling the activities of rice farmers who work submerged in paddy field mud for extended periods.

The 70% negative sample rate observed may be attributable to an inadequate quantity of fungal elements in the samples, cross-contamination by other microorganisms during sample collection or inoculation, or the possibility that the duration of farmers' contact with soil is not always directly proportional to the degree of fungal nail infection (Widiati et al., 2016). The ubiquitous presence of airborne *Aspergillus* spores also poses a risk of media contamination during the inoculation process, highlighting the need for repeated culture to confirm the pathogenic role of NDM, as recommended by Gupta et al (2024a).

Overall, these findings reinforce that non-dermatophyte fungi, encompassing both the mould group (*Aspergillus niger*) and the yeast group (*Candida albicans*), play an important role as causative agents of onychomycosis in the toenails of rice farmers continuously exposed to soil, water, and mud without adequate personal protective equipment. This study helps to fill the existing gap in epidemiological data on non-dermatophyte onychomycosis among farming populations in Aceh Province, which have previously been scarcely reported.

CONCLUSION

Based on the identification of non-dermatophyte fungi causing onychomycosis in the toenails of rice farmers in Gampong Rumah Panjang, Southwest Aceh Regency, non-dermatophyte fungi were found in 6 of 20 samples (30%), comprising *Aspergillus niger* (4 samples) and *Candida albicans* (2 samples confirmed by the germ tube test), while 14 samples (70%) showed no fungal colony growth. *Aspergillus niger* was the most frequently identified non-dermatophyte species. This study constitutes the first report on the identification of non-dermatophyte fungi among the rice farmer population in Southwest Aceh Regency, thereby contributing to the epidemiological mapping of non-dermatophyte onychomycosis in Aceh Province. The use of personal protective equipment during farming activities is recommended, along with consideration of non-dermatophyte etiology in the diagnosis of onychomycosis among at-risk populations.

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