

**Minutes of the 2nd meeting of
“*Candida tropicalis* Study Group in Asia”**

Date: March 5, 2026

Time: 14:00–15:30 (GMT+8)

Video conference: Meeting Link:

<https://teams.microsoft.com/meet/42461618375251?p=MHtOWnqtKc32GOrGM2>

Presence:

Country	Name	Affiliation
Taiwan	Hsiu-Jung Lo	National Health Research Institutes
Taiwan	Kuo-Yun Tseng	National Health Research Institutes
Taiwan	Yin-Zhi Chen	National Health Research Institutes
Indonesia	Farida Nur Oktoviani	Universitas Gadjah Mada, Micorbiology
Indonesia	Setyaning Pawestri	University of Mataram
Singapore	Clement Kin-Ming Tsui	National Centre for Infectious Diseases in Singapore
Singapore	Li Ning	A*STAR Infectious Diseases Labs (A*IDL)

Absence

Country	Name	Affiliation
China	Meng Xiao	Peking Union Medical College Hospital (PUMCH), Chinese Academy of Medical Sciences (CAMS)
China	Xin Fan	Beijing Institute of Respiratory Medicine and Beijing Chao-Yang Hospital, Capital Medical University
China	Zili Zhou	Shanghai Institute of Materia Medica, Chinese
Indonesia	Eggi Arguni	Universitas Gadjah Mada
Indonesia	Rima	Universitas Gadjah Mada
Indonesia	Tri Wibawa	Universitas Gadjah Mada
Japan	Hiroko Kawasaki	Shizuoka University; NBRCBCRC NITE
Japan	YuKa Nagatsuka	
Korea	In Young Yoo	Seoul St. Mary's Hospital
Korea	Yeon-Joon Park	Seoul St. Mary's Hospital
Philippines	Raul V. Destura	University of the Philippines-Manila National Institutes of Health
Singapore	Dan Zhang	Temasek Life Sciences Laboratory
Thailand	Arkom Chaiwongkot	Chulalongkorn University
Thailand	Jidapa Cherry Szekely	Prince of Songkla University
Vietnam	Thi Thu Hoai Nguyen	International University

Agenda:

New members self-Introduction: 5 minutes/person

Introduction of genotype analysis and rapidly identify clade 4 *Candida tropicalis* by Kuo-Yun . (See Appendix 1).

Introduction of the distribution of yeast species causing infections in hospitals associated with Universitas Gadjah Mada by Farida.

Introduction of the preliminary data of distribution of genotype of azole-resistant *C. tropicalis* causing candidemia in Singapore by Clement.

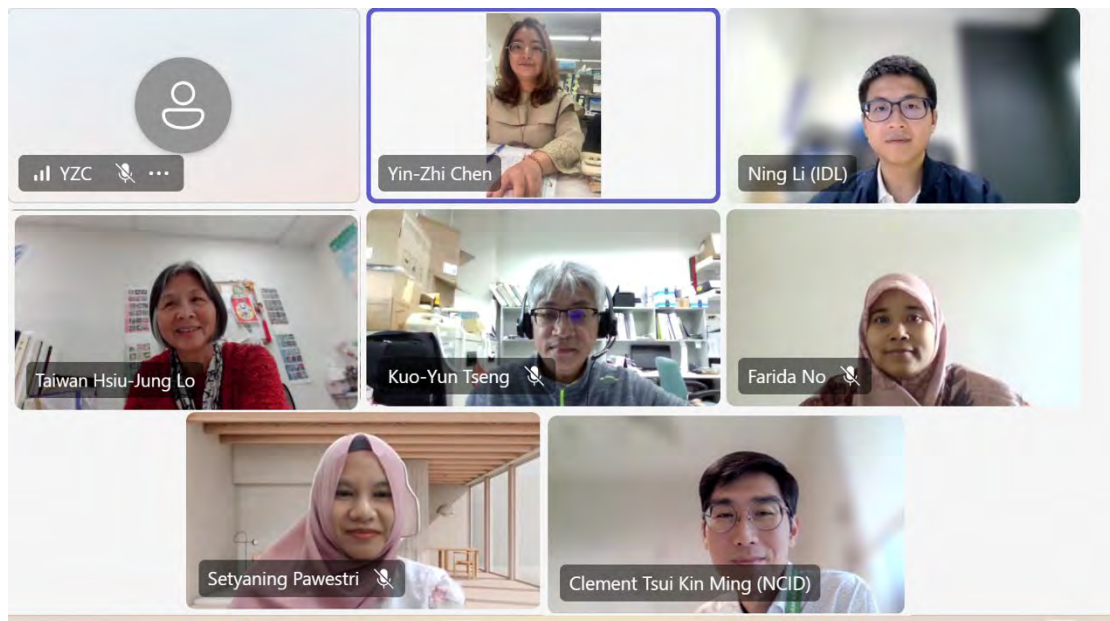
Briefly data about potential antifungal agent development by Li

Notes:

Thanks Setyaning from University of Mataram for helping to invite researchers who are interested in this study group.

We may hold a video meeting bimonthly.

Photos



Appendix 1: Introduction of genotype analysis and rapidly identify clade 4 *Candida tropicalis*



Dual Strategies for Tracking the Predominant Azole-Resistant *Candida tropicalis*: Rapid Marker Detection and High-Throughput Nanopore Genotyping

Kuo-Yun Tseng (曾國鏊), Yin-Zhi Chen, Min-Nan Tseng, Jyh-Nong Tsai, Hsing-Lung Liu, Yu-Chieh Liao, Chih-Chao Lin, De-Jiun Tsai, Feng-Jui Chen, Li-Yun Hsieh, Chiao-Mei Lin, Hsiu-Jung Lo

Dr. Hsiu-Jung Lo Lab
Taiwan Mycology Reference Center
National Institute of Infectious Diseases and Vaccinology
National Health Research Institutes

A small, square, grayscale microscopic image showing several rounded, budding cells, likely representing fungal spores or hyphae, is positioned in the top left corner.

Outline:

➤ **The Burden of Fungal Infections**

- Global threats & WHO priority pathogens.
- Epidemiology in Taiwan (TSARY surveillance data).

➤ **The Emergence of Azole-Resistant *Candida tropicalis***

- Dominance of the clade 4 genotype in clinical and environmental settings.

➤ **Strategy I: High-Throughput Surveillance**

➤ **Strategy II: Rapid Diagnostic Markers**

➤ **Conclusion & Future Perspectives**



Fungal Infections: Emerging Threats to Human Health

- 6,500,000 invasive fungal infection
- 3,800,000 deaths associated with fungal infections
- **2,500,000 deaths directly caused by fungal infections**

Denning DW et al., *Lancet Infect Dis.* 2024 Jul;24(7):e428-e438.

WHO response

2022: fungal priority pathogens list (FPPL)

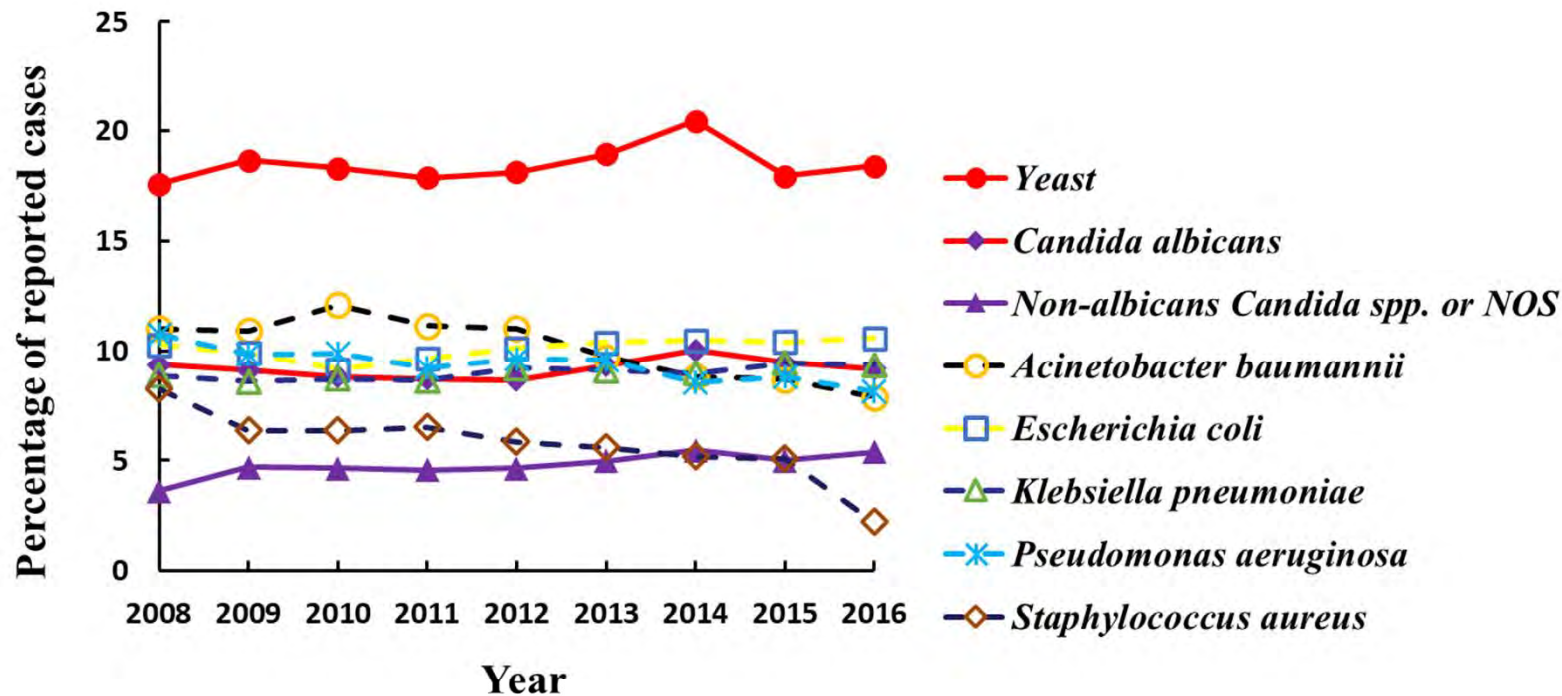
2024: Recommendations for the treatment of *Trichomonas vaginalis*, *Mycoplasma genitalium*, *Candida albicans*, bacterial vaginosis and human papillomavirus (anogenital warts)

2025: First-ever reports on fungal tests and treatments.

- Addressed the critical lack of medicines and **diagnostic tools** for invasive fungal disease.



Yeast Is Leading Cause of Nosocomial Infections in Taiwan



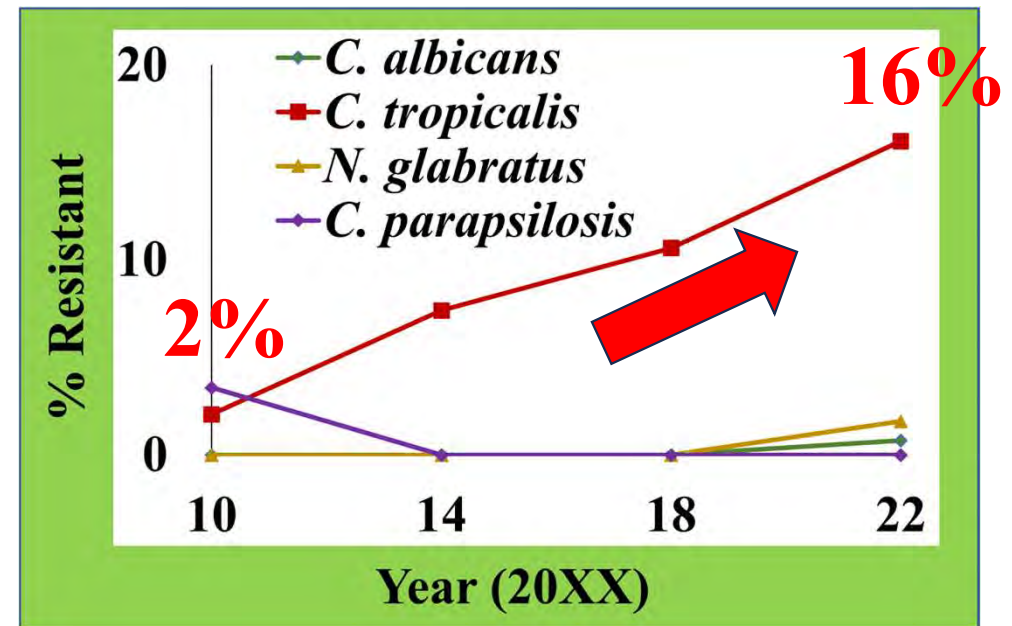
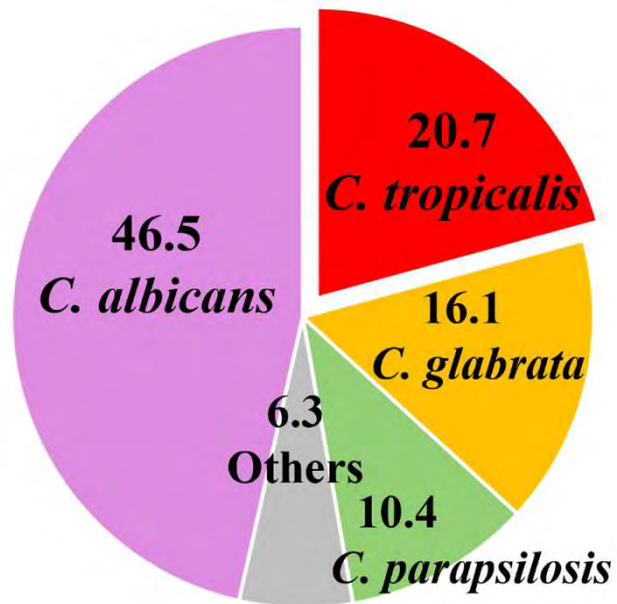
**Taiwan CDC:
Taiwan Nosocomial
Infection
Surveillance (TNIS)
inpatients in
intensive care units
(ICU)**

To monitor the trends in species distribution and drug susceptibility of yeast pathogens in Taiwan, we conduct Taiwan Surveillance of Antimicrobial Resistance of Yeasts (TSARY) every 4 years since 1999.



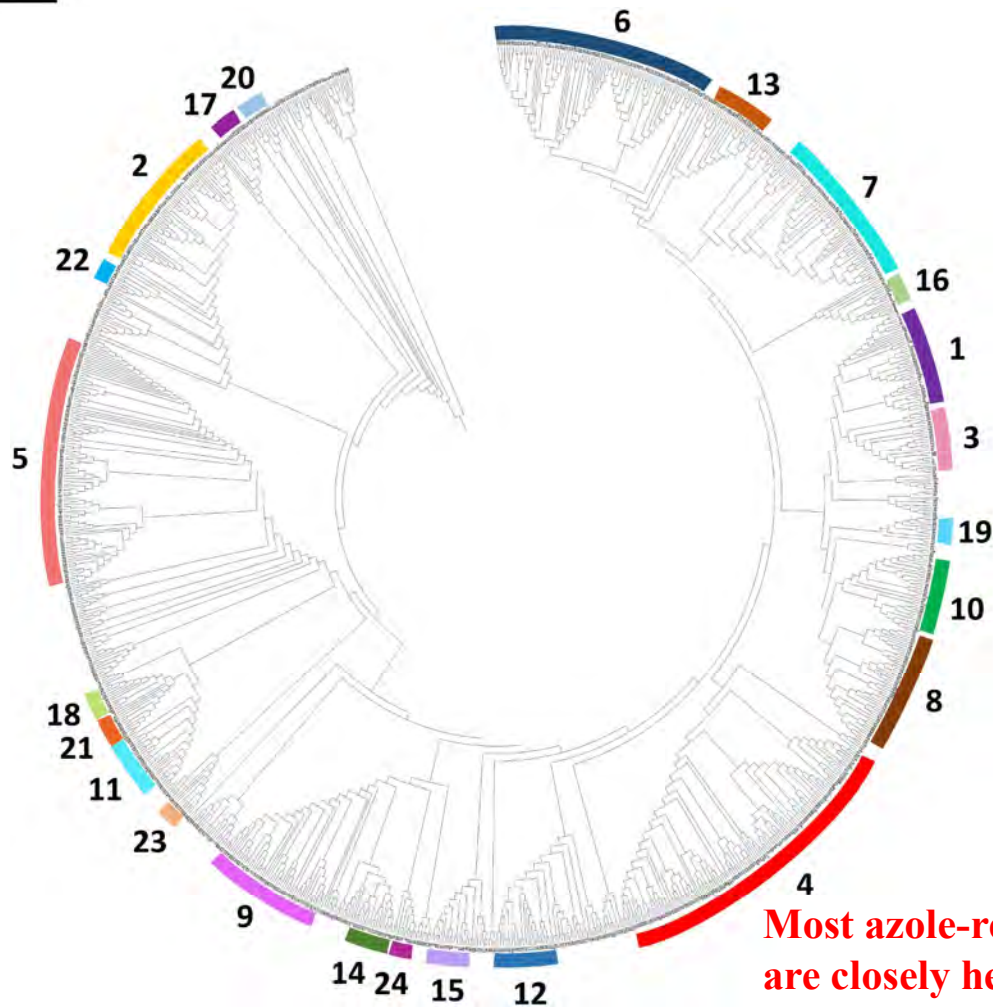
Candida tropicalis in TSARYs

Candida Species from Sterilize Sites in TSARY 2010-2022



- **The most common non-albicans *Candida* species.**
- **Higher fluconazole-resistant rate compared to other *Candida* spp.**
- **Are the drug-resistant *C. tropicalis* isolates genetically closely related?**

MLST Phylogenetic Tree



- The multilocus sequence typing (MLST) method has been developed to define population structures within a species and can reveal differences in geographical origins through online databases.
- The *C. tropicalis* MLST system is based on the sequences of six selected genes (*ICL1*, *MDR1*, *SAPT2*, *SAPT4*, *XYR1*, and *ZWF1a*).



A Predominant Azole-Resistant *Candida tropicalis* Clade 4 Genotype



Clinical settings: Patients

Taiwan: 94.5% (86/91)(TSARY 2014 to 2022)

China: 73.1% (133/172)

Singapore: yes

Thailand: yes

Australia: yes

Fan X, et al. *Nat Commun.* 2023;14(1):8369 (2023)

Environment

Taiwan:

Fruit surfaces, soil, and water (95.1%, 98/103)(2012, 2018, 2023)

Hospital ICU environment (100%, 2/2)

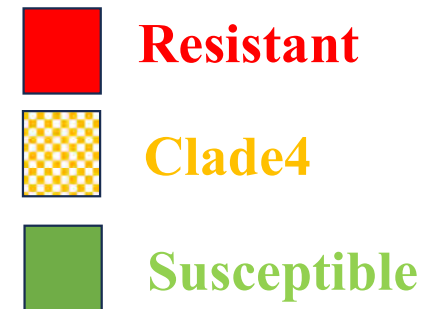
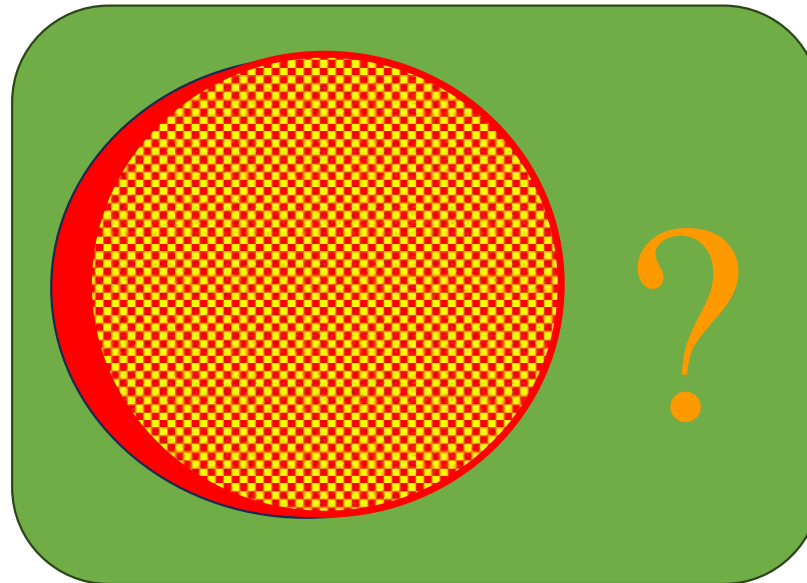
Tsai DJ, et al. *J Microbiol Immunol Infect.* 2024;57(6):947-956.

Can we use MLST to identify azole-resistant *C. tropicalis*?

Can MLST Serve as a Method for Diagnosis?



- Most of azole resistant *C. tropicalis* belonged to clade 4 genotype.
- How about in susceptible isolation?



What is the proportion of clade 4 among susceptible isolates?

We need a high-throughput method to facilitate large-scale surveillance.

Multiplex PCR and MinION Sequencing



Multiplex PCR



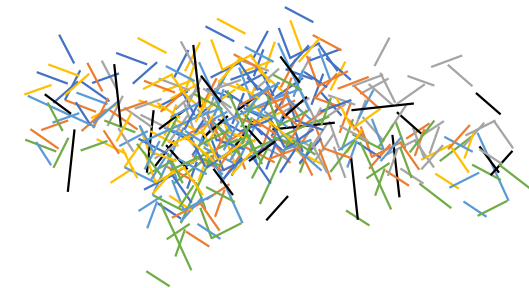
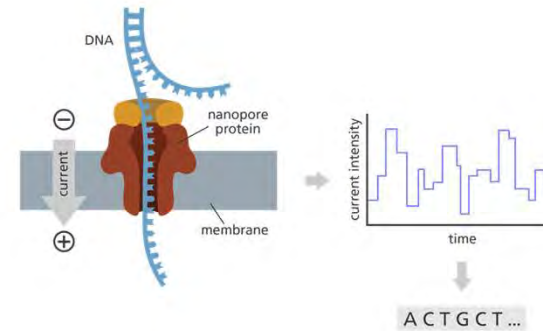
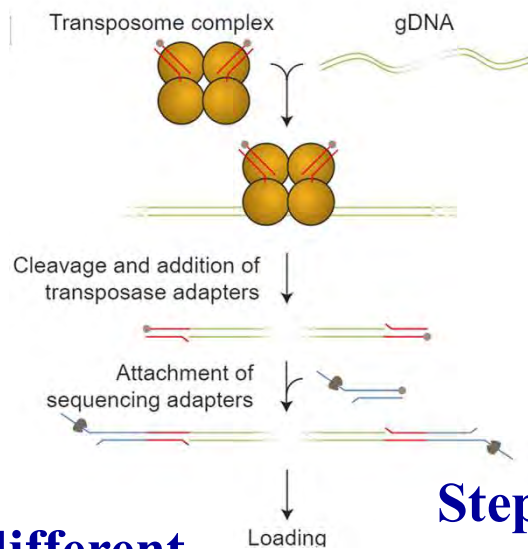
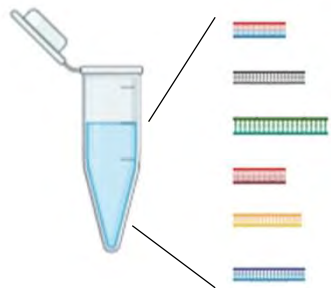
The library preparation



MinION sequencing

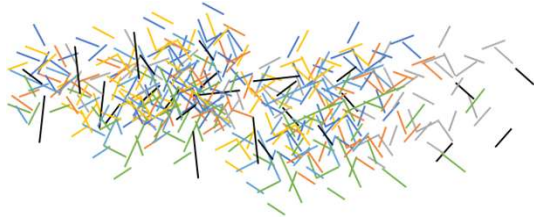


How to analyse big data?



Step 1:
Amplified several different DNA sequences simultaneously

Step 2-3:
Oxford Nanopore system
High-throughput



Nanopore raw data

Guppy

Nanopore reads



Minimap2

Target genes grouping

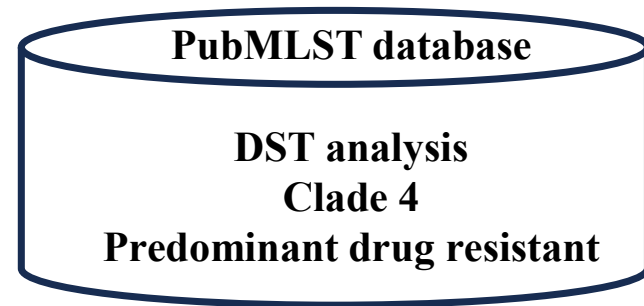
BCFtools/Medaka

IUPAC consensus sequence



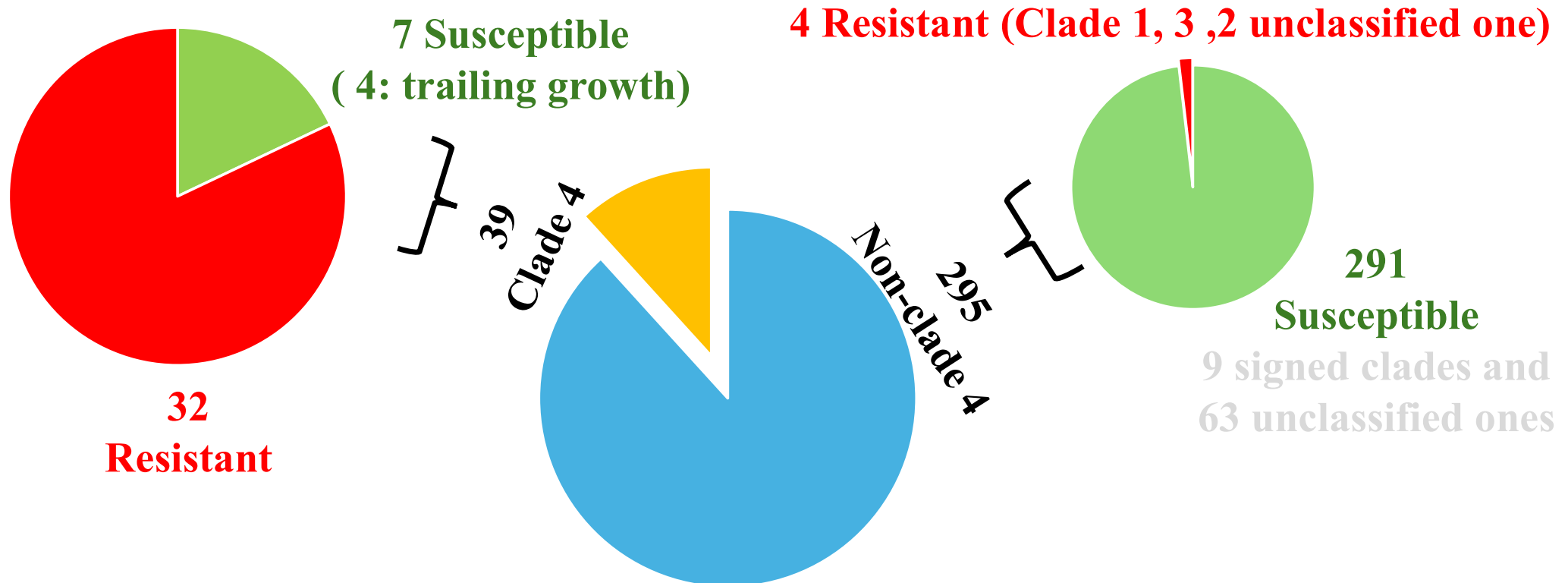
Bioinformatics Pipeline:

- **Tools:** Python script integrating Minimap2 & Medaka.
- **Process:** Automated assembly of 6 MLST gene fragments.
- **Outcome:** Identification of Clade 4 genotype. Prediction of azole resistance.





Comprehensively Investigation (334 Samples from TSARY 2022)



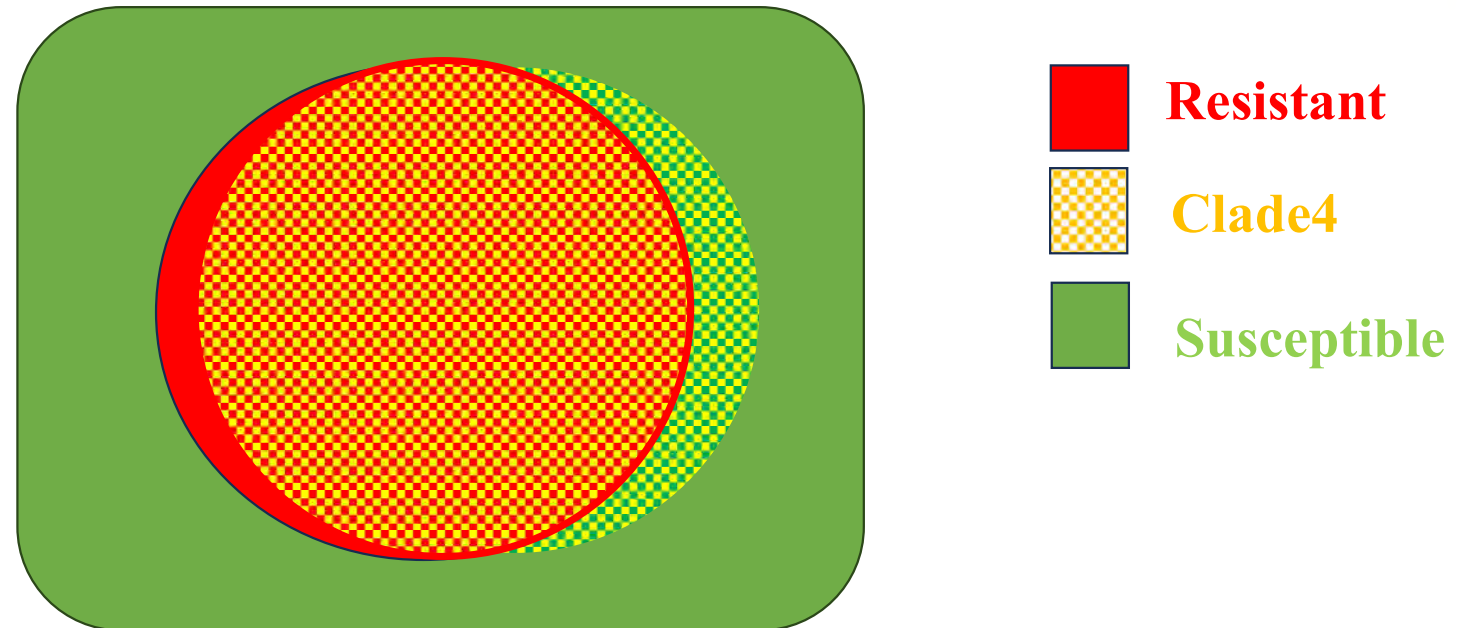
82% (32/39) of clade 4 *C. tropicalis* are resistant to fluconazole.

57% (4/7) of susceptible clade 4 isolates have fluconazole-trailing growth, which is one step toward resistance.

92.3% (36/39) of clade 4 isolates warrant closer attention



Clade 4 Genotype \approx Azole resistance



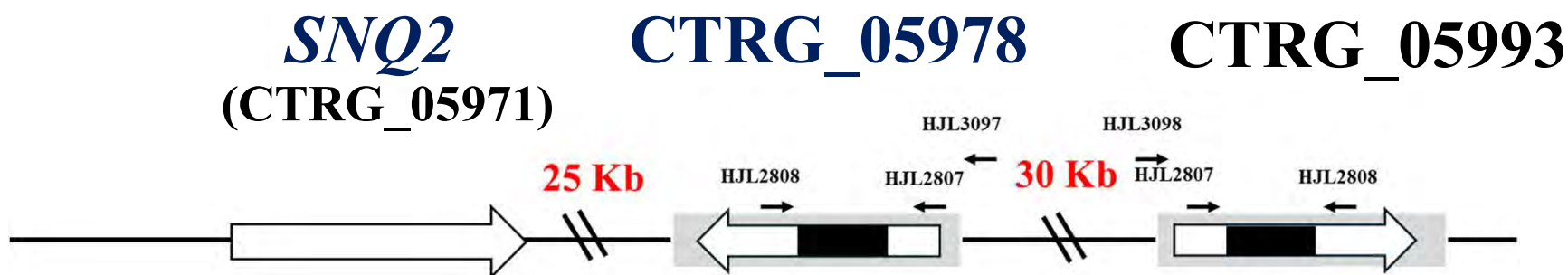
- Most resistant *C. tropicalis* isolates are clade 4 genotype
- Most clade 4 genotypes are resistant.

Can we take this idea and make it practical for point-of-care testing?

SNQ2 and *CTRG_05978* Genotypes Are Associated with the Clade 4 Genotype



Hitchhiking

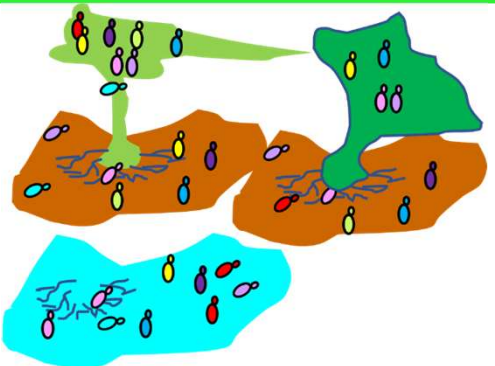


Tseng et al." *FEMS yeast research* vol. 24 (2024)

	<i>CTRG_05978</i> only	<i>SNQ2</i> only	Combined <i>CTRG_05978</i> and <i>SNQ2</i>
Sensitivity	0.821	0.788	0.982
Specificity	0.891	0.931	0.898

(From 165 Taiwan isolates & 161 Global isolates)

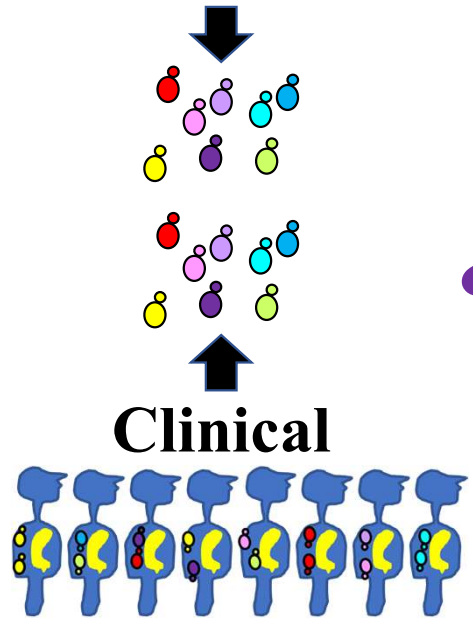
How to Diagnose?



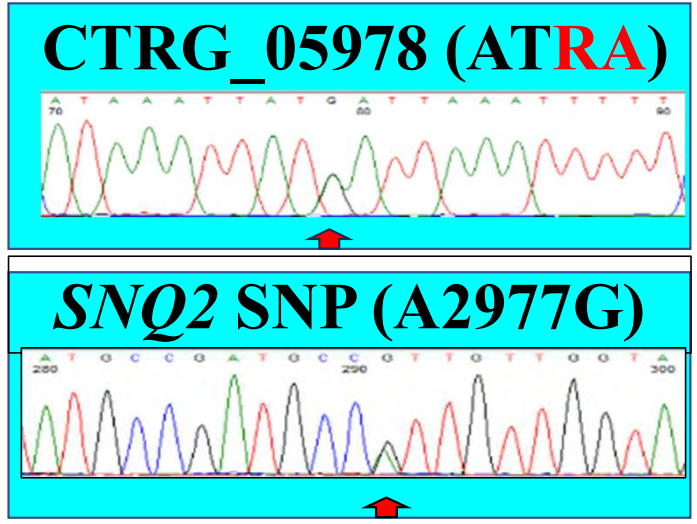
Environment

Markers for rapidly identifying drug-resistant *C. tropicalis*

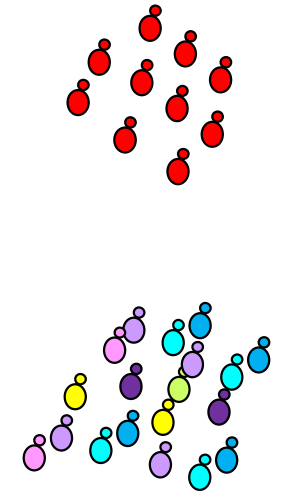
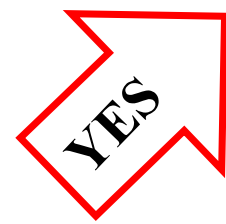
Clade 4: predominant drug-resistant genotype



Clinical



&



Non-Clade 4

Clinical Application: Upgrading Current Diagnostics



<https://www.t2biosystems.com/>



<https://www.alphachrom.hr/>

Setting up the FilmArray is Easy – Sample in, Results out



<https://www.biofire.com/>

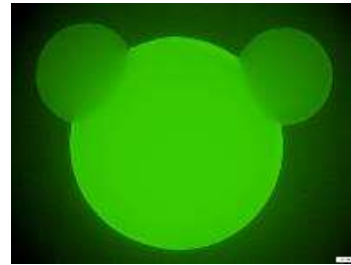
- **Current Limitation:** Commercial kits identify *C. tropicalis* only, not resistance.
- **Our Solution:** Add *SNQ2* & *CTRG_05978* markers.
- **The Upgrade:**
Detects: *C. tropicalis* infection.
Identifies: Predominant azole-resistant Clade 4.
- **Benefit:** Rapid, targeted antifungal therapy without culture delays.

Take Home Message

- **The clade 4 azole-resistant *C. tropicalis* genotype is persistent in both clinical settings and environment.**
- **Multiplex PCR combined with MinION sequencing offers a method for comprehensive surveillance.**
- **The genotypes of CTRG_05978 and *SNQ2* serves as potential markers for rapid diagnosis of clade 4 *C. tropicalis*.**



Thanks for your attention!



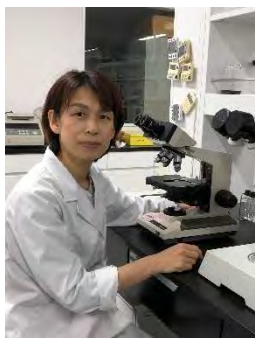
Appendix 2: personal information



Dr. Hsiu-Jung Lo

Investigator and Deputy Director
Taiwan Mycology Reference Laboratory
National Institute of Infectious Diseases and Vaccinology
National Health Research Institutes
Taiwan
Email: hjlo@nhri.edu.tw
Phone: +886 37206166 ext. 35516

Dr. Hsiu-Jung Lo is a Taiwanese Medical Mycologist currently serving as the General Secretary of Mycological Society of the Republic of China, Taiwan Mycology Reference Laboratory, and National Infectious Diseases Bank. She obtained her bachelor's degree from the Department of Plant Pathology at National Chung-Hsing University and her Ph.D. degree from the Department of Biology at Indiana University at Bloomington, US. Then, she was a postdoctoral fellow at Whitehead Institute for Biomedical Research, US, devoted to revealing the regulation of morphological switch of the most common fungal pathogen, *Candida albicans*. She moved back to Taiwan and joined National Health Research Institutes in 1999. Her researches focus on epidemiology of yeast infections by conducting Taiwan Surveillance of Antimicrobial Resistance of Yeasts (TSARY) and mechanisms of antifungal drug resistance, especially on *Candida tropicalis*. Her recently findings that a predominant genotype of azole-resistant *C. tropicalis* not only causes infections in human but also spreads in the environment reemphasize the importance of the concept of "One Health".



Dr. Yuka Nagatsuka

Lecturer

Laboratory of Clinical Pharmacodynamics

Faculty of Pharmacy, Fukuyama University

Hiroshima, Japan

Email: yhanda@fukuyama-u.ac.jp

Phone: +81-84-936-2112 (ex.5136)

Dr. Yuka Nagatsuka is a pharmaceutical microbiologist and medical mycologist at Fukuyama University, Japan. Her research focuses on antifungal susceptibility testing and molecular phylogenetic analysis of yeasts, including both pathogenic and environmental species. She has extensive experience in CLSI M27 broth microdilution testing across multiple antifungal classes, including azoles, echinocandins, amphotericin B, and 5-flucytosine.

Her work examines the relationship between phylogenetic clades and MIC distributions. She has identified clades showing reduced susceptibility across multiple antifungal classes, suggesting that certain evolutionary lineages may exhibit multidrug tolerance patterns. By integrating phenotypic susceptibility data with sequence-based phylogenetic analysis, she aims to clarify the evolutionary context of antifungal resistance. This perspective may complement studies focusing on acquired resistance driven by environmental or agricultural selection pressure.

She also has access to citrus orchards in Japan and can collect environmental yeast isolates, with direct information on fungicide usage to enable accurate linkage under a One Health framework.

For this study group, she hopes to contribute standardized antifungal susceptibility data and to collaborate in integrating MIC profiles with phylogenetic or genomic data across Asia. She is particularly interested in learning from genomic perspectives while contributing from her phenotypic expertise.



Fig. Citrus orchard in Japan (family-owned), potential site for environmental sampling.



Dr. In Young Yoo, MD, PhD

Assistant Professor of Department of Laboratory Medicine
(Clinical Microbiology)

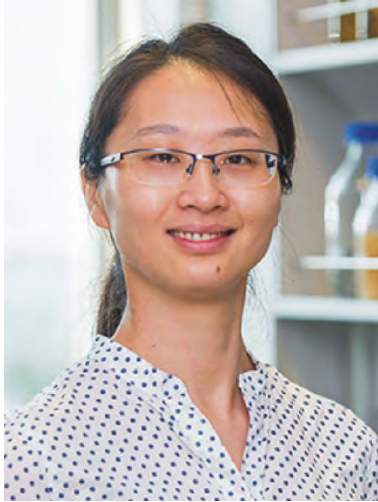
Seoul St. Mary's Hospital

Email: yy00@naver.com

Phone: 82)2-2258-1698

Dr. In Young Yoo is an assistant professor of clinical microbiology at Seoul St. Mary's Hospital, The Catholic University of Korea. She received her MD from Kyungpook National University School of Medicine and completed her PhD in Laboratory Medicine at Sungkyunkwan University. She completed residency and fellowship training at Samsung Medical Center and a short-term observership at Memorial Sloan Kettering Cancer Center.

Her research focuses on clinical microbiology diagnostics, including molecular pathogen detection, mycobacterial drug resistance, automated susceptibility testing, MALDI-TOF MS identification, and direct testing from positive blood cultures. She has served as the principal investigator of a research project focused on the detection of antifungal-resistant *Candida* using MALDI-TOF mass spectrometry and is currently involved in funded projects related to *Aspergillus* diagnostics and invasive fungal infections.



Dr. Dan Zhang

Principal Investigator and Adjunct Assistant Professor

Temasek life sciences laboratory (TLL)

Department of Biological Sciences

National University of Singapore (NUS)

Singapore

Email: zhangdan@tll.org.sg; dbszdan@nus.edu.sg

Phone: +65 68727490

Dr. Dan Zhang received her bachelor's degree in bioengineering from Shanghai Jiao Tong University, China, in 2006, and her Ph.D. in cell biology from the NUS in 2013. After brief postdoctoral training, she established her lab as a Young Investigator at TLL in 2014 and was promoted to Principal Investigator in 2019. Her research focuses on elucidating the mechanisms that regulate membrane contact sites (MCSs) using the model fission yeast *Schizosaccharomyces pombe*. MCSs serve as critical hubs for coordinating lipid distribution, signalling, and inter-organelle communication, and her recent work has demonstrated their roles in cellular homeostasis and cell polarity. More recently, her lab has expanded to investigate whether similar mechanisms operate in human pathogenic fungi, including *Candida albicans* and *Candida auris*, with particular emphasis on stress responses, adaptation, and the evolution of antimicrobial resistance (AMR). One major goal of her study is to bridge fundamental cell biology with clinically relevant questions in fungal pathogenesis and AMR, and to develop strategies for disease surveillance and prevention.

Hiroko Kawasaki, Shizuoka University / NITE-NBRC

My Background,

- My specialty is the taxonomy of microorganisms, including yeast, and I have used that knowledge to support research as my life's work.
- I have experience implementing the SATREPS project (a Japanese JICA/JST fund) and serving as a project officer for the Japanese Human Biomaterials Biobank Network Project.

Current work;

- a. Coordinator for promoting innovation promotion and social collaboration at Shizuoka University, and also the ABS (Access and Benefit Sharing) Coordination Desk at Shizuoka University.
- b. Advisor on NBRC's BRC management, the research of rapid identification of microorganisms, and other international cooperation at National Institute of Technology Evaluation (NITE).
- c. World Federation of Culture Collection (WFCC) Executive Board member and the WFCC Secretariat.
- d. ISO/TC276 biotechnology Expert



Therefore, I do not currently have a laboratory where I can conduct own experiments. However, through the BRC network, it is possible to provide research support for the collection of strains needed and the identification of species and subspecies levels. In addition, it may be possible to help with the integration of the microbial data platform DBRP provided by NITE/NBRC and the database provided by WDCM.

1. Isolation of *Candida tropicalis* in nature

Through microbial diversity studies, *Candida tropicalis* was isolated in joint research with Thailand and Indonesia.

When isolating yeast in Japan, I don't have the impression that it is well separated.

2. Public Culture Collections

Candida tropicalis preserved in the NBRC collection in Japan (to which I belong)
They are also preserved in microorganism collections at IMF, MMRC, and Chiba University, which focus on medical fungi.

3. Rapid identification of microorganisms using MALDI-TOF MS

In EU teams, they provided the database for yeast and fungi identification

In Japan, we have developed new method for yeast identification system using MALDI-TOF MS data. There is a possibility of joint research?

No.	NBRC No.	Scientific Name	Source of Isolation	Locality of Source	Country/region of Origin
1	0006	Candida tropicalis			
2	0199	Candida tropicalis	sakura-miso		Japan
3	0587	Candida tropicalis			
4	0618	Candida tropicalis			
5	1400T	Candida tropicalis	Bronchitic patient		
6	1401	Candida tropicalis	Iranian dates		Japan
7	1402	Candida tropicalis			
8	1403	Candida tropicalis	lung		Austria
9	1404	Candida tropicalis	infected hand		Hungary
10	1647	Candida tropicalis			
11	10241	Candida tropicalis	human blood		USA
12	105112	Candida tropicalis	Moss	Huai Nam Khao mangrove forest, Trad Province, Thailand	Thailand
13	105113	Candida tropicalis	Insect frass	Bangkhen, Bangkok Province, Thailand	Thailand
14	105114	Candida tropicalis	insect frass	Bangkhen, Bangkok Province, Thailand	Thailand
15	110296	Candida tropicalis	woodchip	Batusanger, Tanah Datar, West Sumatra, Indonesia	Indonesia
16	110303	Candida tropicalis	decayed leaf of palm	Batusanger, Tanah Datar, West Sumatra, Indonesia	Indonesia
17	110305	Candida tropicalis	decayed wood	Anai valley, Padang Panjang, West Sumatra, Indonesia	Indonesia
18	110306	Candida tropicalis	decayed wood	near waterfall, Anai river, Padang Panjang, West Sumatra, Indonesia	Indonesia
19	110309	Candida tropicalis	decayed wood	Bung Hatta Botanical Garden, Padang, West Sumatra, Indonesia	Indonesia
20	110313	Candida tropicalis	woodchip	Batusanger, Tanah Datar, West Sumatra, Indonesia	Indonesia
21	110319	Candida tropicalis	decayed wood	Anai valley, Padang Panjang, West Sumatra, Indonesia	Indonesia
22	110320	Candida tropicalis	decayed wood	near waterfall, Anai river, Padang Panjang, West Sumatra, Indonesia	Indonesia
23	110323	Candida tropicalis	decayed wood	Bung Hatta Botanical Garden, Padang, West Sumatra, Indonesia	Indonesia
24	110325	Candida tropicalis	decayed wood (Albasia)	Bung Hatta Botanical Garden, Padang, West Sumatra, Indonesia	Indonesia
25	110337	Candida tropicalis	decayed wood	Anai valley, Padang Panjang, West Sumatra, Indonesia	Indonesia
26	111289	Candida tropicalis	Soil	Kakaban Is., Berau, East Kalimantan (2.14000000,118.50972222)	Indonesia
27	111302	Candida tropicalis	Soil	Mahakam river, East Kalimantan (-0.80138888,117.22916666)	Indonesia
28	RD055364	Candida sp.	Flower: Japanese quince		Japan
29	RD012205	Candida sp.	Soil		Japan
30	RD055032	Candida sp.	Flower: Hibiscus rosa-sinensis		Japan
31	RD055057	Candida sp.	Soil		Japan
32	RD055059	Candida sp.	Soil		Japan

IFM Culture Collection

at Medical Mycology Research Center (MMRC*), Chiba University

Candida tropicalis

69654(D) 69548(D) 69489(D) 69454(D) 69441(D) 69439(D) 68816 68322(D) 68201(D/M) 65846(D) 65457(D)
65456(D) 65231(D) 64556(D) 64458(D) 64457(D) 63840(D) 63625(D) 63520(D) 63517(D) 63268(D) 63267(D)
62625(D) 61949(D) 61749(D) 61742(D) 61575(D) 61204(D) 61189(D) 61181(D) 61175(D) 61011(D) 61007(D)
61005(D) 60905(D) 60903(D) 60802(D) 60801(D) 60667(D) 60090(D) 59937(D) 59934(D) 59930(D) 59927(D)
59926(D) 59925(D) 59623(D) 59285(D) 59267(D) 59266(D) 59254(D) 59252(D) 59175(D) 59106(D) 59019(D)
59004(D) 59003(D) 59002(D) 58987(D) 58852(D) 58280(D) 57742(D) 57734(D) 57733(D) 57401(D) 57204(D)
56879(D) 56869(D) 56167(D) 56165(D) 56155(D) 56153(D) 55865 55380(D) 55379(D/R) 55318(D) 55301(D)
55270(D) 55269(D) 54903(D) 54899(D) 54896(D) 54895(D) 54893(D) 54674(D) 53912(D) 53910(D) 53904(D)
53901(D) 53819(D) 53750(D) 53749(D) 53747(D) 53690 53481(D) 53468(D) 53457(D) 53382(D) 53341(D)
53337(D) 52360(D) 52358(D) 52282(D) 52280(D) 51591(D) 51587(D) 51585(D) 51583(D) 51581(D) 51580(D)
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48028(D) 48020(D) 48017(D) 48015(D) 47821(D) 47580(D) 47100(D) 46822(D) 46820(D/R) 46818(D) 46817(D)
40011(D) 5654(D/R) 5496(D) 5439(D)

*MMRC: as a joint Usage/Research Center, MMRC has been actively engaged in promoting joint research of medical mycology and its related educational activities by cooperating with universities, public institutions, medical institutions, and Chiba University.