Phenotypic and Genotypic Characterization of Antimicrobial-Resistant (AMR) Strains from the ATCC® Collection

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Shahin S. Ali, PhD; Briana Benton, BS; Scott V. Nguyen, PhD; Anthony Muhle, MSc; Vicktor Escobar, BS; Linda Holloway, MS; Kendra Grosso, BS; Joseph Petrone, PhD; Jonathan L. Jacobs, PhD; Victoria Knight-Connoni, PhD
ATCC, Manassas, VA 20110

Background

Antimicrobial resistance (AMR) is a global health crisis recognized by the WHO Priority Pathogens List,[1,2] which identifies critical threats such as carbapenem-resistant *Acinetobacter baumannii* and *Candida auris. Trichophyton indotineae* is an emerging fungal pathogen that has recently been isolated in the US. These pathogens pose significant challenges for treatment and infection control.[3] To accelerate the development of diagnostics and therapeutics, researchers need access to standardized, well-characterized strains. ATCC addresses this need by providing a curated collection of bacterial and fungal AMR strains, each extensively characterized both phenotypically and genotypically. Strains include minimum inhibitory concentration (MIC) values, susceptibility profiles, and whole-genome sequencing (WGS) data generated using Illumina and Oxford Nanopore platforms for high accuracy and depth. Annotated genomes and methylation data are available through the ATCC Genome Portal (genomes.atcc.org). By bridging genomic insights with clinical applications, ATCC empowers global efforts to combat AMR and supports innovation in antifungal and antibacterial research.

Methods

To determine MIC profiles, antibiotic susceptibility was assessed primarily using VITEK2 AST cards (bioMérieux), selecting one or two cards per organism to cover a broad range of antibiotics. Interpretations for resistant, intermediate, and susceptible categories followed CLSI standards (27th Edition). For *Neisseria gonorrhoeae*, susceptibility was assessed using Etest strips (bioMérieux) with MIC interpretation per CLSI M100-Ed35. Fungal susceptibility results were based on depositor-provided data and guidelines.

Genomic analysis employed ISO 9001-compliant pipelines for sequencing, assembly, and annotation. High-quality DNA was sequenced using Illumina and Oxford Nanopore Technologies platforms, and data were combined to generate complete *de novo* hybrid assemblies. Assemblies were annotated via NCBI PGAP[4] and curated for antimicrobial resistance genes using NCBI AMRFinderPlus, CARD (RGI), and ResFinder for bacteria.[5] Assembled genomes for *C. auris* and *T. indotineae* strains were analyzed for antifungal resistance mutations with FungAMR[6] through ChroQueTas. Clade determination for *C. auris* was performed by AuriClass (https://github.com/RIVM-bioinformatics/auriclass).

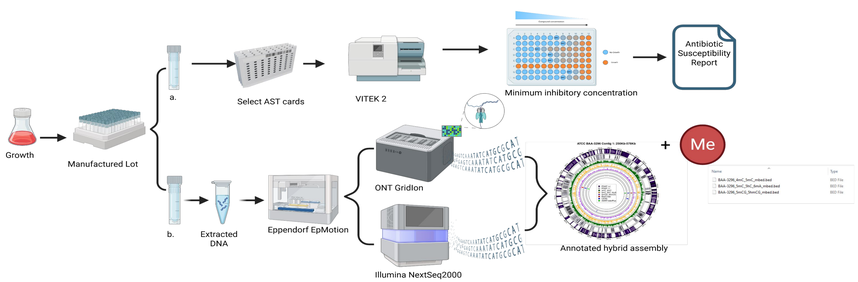

Figure 1: Workflow for phenotypic and genotypic characterization of ATCC AMR strains. (A) The appropriate VITEK 2 AST cards (bioMérieux) are selected and loaded on to the VITEK 2 instrument to produce the MIC profile. (B) DNA is extracted using a method best suited for organism type and next-generation sequencing (NGS) libraries are produced and loaded on the NextSeq 2000 (Illumina) and GridIon (Oxford Nanopore Technologies) instruments. Data from both platforms were quality controlled and a subsequent hybrid genome assembly was produced and annotated. ONT base called data was further analyzed for the presence of methylated nucleotides. Image created using BioRender.com

Results

Table 1: No of ATCC® strains on the WHO priority pathogens list:[1,2] Critical group.

WHO Critical Priority Pathogens	No of ATCC® strains
Carbapenem-resistant *Acinetobacter baumannii*	10
Carbapenem-resistant *Klebsiella pneumoniae*	10
Carbapenem-resistant *Escherichia coli*	6
Third-generation cephalosporin-resistant *Escherichia coli*	12
Third-generation cephalosporin-resistant *Klebsiella pneumoniae*	13
Rifampicin-resistant *Mycobacterium tuberculosis*	3
Aspergillus fumigatus	191
Candida albicans	227
Candida auris	8
Cryptococcus neoformans	134
ATCC® Offerings AMR data are available for 625 strains across 157 species	

Download the complete list and AMR profiles of the bacterial Priority Antimicrobial-Resistant Strains

Access whole-genome sequences of these AMR strains on the ATCC Genome Portal genomes.atcc.org

Explore our complete collection of AMR strains www.atcc.org/superbugs

Table 2: AMR profile of *Candida aurius* strains from the ATCC® collection. Strains are categorized as resistant (red), intermediate (yellow), susceptible (blue), or unspecified (gray) per CLSI/CDC breakpoints (µg/mL).

Antifungal Class	Antifungal Type	MYA-5000™	MYA-5001™	MYA-5002™	MYA-5003™	MYA-5043™	MYA-5044™	MYA-5045™	MYA-5046™
Azoles	Fluconazole	≥ 64	2	≥ 64	≥ 64	64	64	32	64
	Isavuconazole		0.015	0.03	0.5	0.25	0.5	0.03	0.03
	Itraconazole		0.06	0.12	0.5				
	Posaconazole		0.03	0.06	0.06	0.25	0.12	0.06	0.12
	Voriconazole	0.5	0.015	1	2	2	2	0.06	0.5
Echinocandins	Anidulafungin		0.03	0.12	0.25	0.25	0.12	2	2
	Caspofungin	0.12	0.12	0.25	0.25	0.5	0.5	8	0.25
	Micafungin	0.06	0.03	0.12	0.25	0.12	0.12	4	0.5
Polyenes	Amphotericin B		0.125	0.125	0.5	2	2	1	1
Clade		I	II	III	IV	I	I	IV	III
Isolation Information	Country	Pakistan	Japan	South Africa	Venezuela	Kuwait	Germany	Panama	Australia
	Year of isolation	2015	2009	2012	2012	2022	2022	2022	2019
	Source (Human)	Urine	Auditory canal	Blood	Blood	Lymph Nodes	Trachea	Ureter	Skin
Antifungal mutations		Cyp51: Lys143Arg Tac1: Ala640Val	No AMR mutations	Cyp51: Val125Ala, Phe126Leu	Cyp51: Try132Phe	Cyp51: Try132Phe	Cyp51: Try132Phe	Cyp51: Lys143Arg Fks: Arg1354Gly	Cyp51: Val125Ala, Phe126Leu

Table 3: AMR profile of additional 31 *Candida auris* strains coming to the ATCC® collection. Strains are categorized as resistant (red), susceptible (blue), or unspecified (gray) per CLSI/CDC breakpoints.

Antifungal Class	Antifungal Type	No. of strains				
		11	15	3	1	1
Azoles	Fluconazole	R	R	R	R	R
	Isavuconazole	NA	NA	NA	NA	NA
	Itraconazole	NA	NA	NA	NA	NA
	Posaconazole	NA	NA	NA	NA	NA
	Voriconazole	NA	NA	NA	NA	NA
Echinocandins	Anidulafungin	S	S	S	R	R
	Caspofungin	S	S	R	R	R
	Micafungin	S	S	S	S	R
Polyenes	Amphotericin B	S	R	R	R	S
Isolation Information	Country	NY, USA				
	Year of isolation	2021-2024				
	Source	Human				
Clade		I				

Table 4: AMR profile of 15 *Trichophyton indotineae* strains in the ATCC® collection. Strains are categorized as resistant (red), susceptible (blue), or unspecified (gray) per CLSI/CDC breakpoints.

ATCC® id	Antifungal Type		Isolation Information			Mutations in SQLE protein
	Terbinafine	Itraconazole	Country	Year	Source	
MYA-5021™	R	S	Germany	2018	Skin tinea	Phe397Leu Ala448Thr
MYA-5022™	S	R	Germany	2018	Skin tinea	Ala448Thr
MYA-5023™	R	S	Germany	2019	Skin tinea	Phe397Leu
MYA-5024™	R	S	Germany	2019	Skin tinea	Leu393Phe
MYA-5025™	R	S	Germany	2020	Skin tinea	Phe397Leu
MYA-5026™	S	R	Germany	2021	Skin tinea	Ala448Thr
MYA-5027™	R	S	Austria	2021	Skin tinea	Phe397Leu
MYA-5028™	S	S	Austria	2022	Skin tinea	No mutation
MYA-5029™	S	S	Poland	2019	Skin tinea	No mutation
MYA-5030™	S	S	Germany	2023	Skin tinea	Ala448Thr
MYA-5031™			Finland	2020	Skin tinea	His440Tyr
MYA-5032™	R	R	Switzerland	2019	Skin tinea	Phe397Leu
MYA-5033™	R	R	Estonia	2019	Skin tinea	Phe397Leu Ala448Thr
MYA-5034™			India	2018	Skin tinea	Ala448Thr
MYA-5035™			India	2018	Skin tinea	Phe397Leu

Conclusion

Here, we highlight a diverse set of recent clinically relevant isolates of *Candida auris* and *Trichophyton indotineae* added to the ATCC® collection. These strains are extensively characterized antimicrobial-resistant isolates that are available to the research community. Each strain is provided with:

- **Source information** – Geography, collection date, and collection source.
- **Susceptibility data** – MIC values and susceptibility profiles for targeted drugs.
- **Genetic data** – The complete and assembled genome sequence, annotated with antibiotic resistance genes. Identified a novel Fks R1354G mutation that may be linked to echinocandin resistance in *C. auris.*

Overall, this diverse collection of highly characterized AMR strains provides a valuable resource for diagnostics and therapeutic development.

References:
1. WHO bacterial priority pathogens list, 2024. https://www.who.int/publications/i/item/9789240093461
2. WHO fungal priority pathogens, 2022. https://www.who.int/publications/i/item/9789240060241
3. MMWR Morb Mortal Wkly Rep72: 536–537, 2023. http://dx.doi.org/10.15585/mmwr.mm7219a4
4. Nucleic Acids Res 44(14): 6614-6624, 2016.
5. Nucleic Acids Res 53(W1): W20–W31, 2025.
6. Nat Microbiol 10(9): 2338-2352, 2025.

ATCC 10801 University Boulevard, Manassas, Virginia 20110-2209 **Phone:** 800.638.6597 **Email:** sales@atcc.org **Web:** www.atcc.org