

Supplementary Materials

This document contains seven supplementary tables providing the full, unabridged data underlying the analyses presented in the main manuscript; and four supplementary figures. Tables S1–S6 describe the complete cross-sectional dataset ($n = 1,000$ records). Table S7 provides full anonymised trajectory summaries for the ten multi-sample patients with the most clinically notable serial culture courses (longitudinal cohort, $n = 91$). All patient identifiers have been replaced with sequential anonymous codes (PT-01 through PT-10 for Table S8; PT-01 through PT-05 for Table S5 in the main manuscript) in full compliance with the study ethics approval.

S1. Monthly isolate counts by year — raw data

Table S2 provides the complete monthly isolate counts for each of the three study years. The combined total column sums across all years. Cells marked '0*' in 2024 reflect months for which no data were available in the electronic record system at the time of extraction; these most likely represent months not yet processed rather than true zero incidence, given that 2024 was a partial-year extraction. The annual total row shows 999 rather than 1,000 because one record lacked year information and could not be assigned to a calendar year.

Table S1. Monthly raw isolate counts by year. '0*' in 2024 = months with no recorded data (partial-year extraction); true zero incidence cannot be assumed. Combined total = sum across all three years. †One record lacks year data and is excluded from the annual subtotals but included in the main $n=1,000$ cohort.

Month	2022	2023	2024	Combined total
January	0	18	8	26
February	35	38	28	101
March	45	37	41	123
April	61	15	55	131
May	16	30	46	92
June	40	19	48	107
July	44	29	12	85
August	31	26	0*	57
September	26	47	0*	73
October	40	50	0*	90
November	44	20	0*	64
December	31	19	0*	50
Annual total	413	348	238	999†

†Total across all monthly data = 999; one record (0.1%) lacked a year designation and is excluded from year-stratified analyses but included in all cross-sectional analyses in the main manuscript.

S2. Complete species frequency table with 95% confidence intervals

Table S2 lists all 21 distinct fungal taxa identified in the study cohort, including rare organisms (≤ 2 isolates) not individually described in the main text. Proportions and 95% confidence intervals are calculated among the 795 records with a named fungal isolate, using the Wilson score interval method. Note that the denominators for the main manuscript ($n = 1,000$) and this table ($n = 795$) differ: 205 records had no yeast species recorded in the primary field (predominantly records where only filamentous fungi were detected, or where the specimen yielded mixed microbiota not individually speciated).

Supplementary Table S2. Fungal species/organism distribution ($n = 1,000$).

Percentages sum to more than 100% because 18 specimens (1.8%) showed co-isolation of a *Candida* species together with filamentous fungi in the same specimen (see Section 3.4 and Figure 5). 95% confidence intervals calculated using the Wilson score method.

<i>Candida albicans</i>	451	45.1	42.0	48.2	Albicans — generally azole-susceptible
Filamentous fungi	258	25.8	23.2	28.6	Non-Candida mould (<i>Aspergillus</i> -predominant)
<i>Candida</i> spp. (unspeciated)	122	12.2	10.3	14.4	Unspeciated — ID incomplete
<i>Candida krusei</i>	66	6.6	5.2	8.3	Non-albicans — intrinsic fluconazole resistance
<i>Candida glabrata</i>	31	3.1	2.2	4.4	Non-albicans — dose-dependent azole susceptibility
<i>Candida parapsilosis</i>	17	1.7	1.1	2.7	Non-albicans — biofilm/catheter-associated
<i>Candida tropicalis</i>	9	0.9	0.5	1.7	Non-albicans — high virulence in neutropenia
<i>Cryptococcus laurentii</i>	6	0.6	0.3	1.3	Non-Candida yeast — assess immunosuppression
<i>Candida dubliniensis</i>	4	0.4	0.2	1.0	Non-albicans — may mimic <i>C. albicans</i>
<i>Candida lusitanae</i>	4	0.4	0.2	1.0	Non-albicans — possible amphotericin B resistance
Other rare species	52	5.2	4.0	6.8	Mixed/rare — see Section 3.4

"*Candida* spp. (unspecified)" refers to isolates for which no species-level identification was attempted or achieved (see Section 2.4/Limitations regarding reagent availability); this differs from cases in which *C. albicans* was specifically excluded but the non-albicans species was not further specified, which are included in the "Other rare species" category.

S3. Complete diagnostic list with normalisation key

The original database contained 83 distinct diagnostic entries in Romanian, many representing the same clinical condition under different abbreviations, spelling variants, or terminologies. Table S3 presents all diagnoses normalised to standardised English

categories, with the complete list of original Romanian terms that were mapped to each category. This normalisation was applied consistently throughout all analyses in the main manuscript.

Table S3. Complete diagnostic categories (standardised English) with mapping from original Romanian database entries. n = total records assigned to each category after normalisation. The most frequent single-term variants are listed; minor variants (n=1) not listed individually are aggregated in 'Other/unspecified'.

Diagnosis (standardised EN)	n	%	Original Romanian terms / variants
Acute respiratory failure (ARF / IRA)	417	41.7	<i>Includes all entries: IRA, insuficienta respiratorie acuta, Insuficienta respiratorie acuta, IR, insuficienta respiiratorie acuta</i>
General medical examination	158	15.8	<i>EMG, ex.medical, examen medical general, examinare medicala generala, ex.general, examen medial general</i>
Haemoptysis	30	3.0	<i>hemoptizii, hemoptizii</i>
Fever / febrile illness	30	3.0	<i>febra, febra persistenta</i>
Bronchiectasis	26	2.6	<i>bronsiectazie, bronsiectazii, Bronsiectazii</i>
Tracheal tumour	22	2.2	<i>tumora trahee, tumora traheii, tumora traheei, afectiuni ale traheei, afectiune a traheei, trahee</i>
Pleural effusion / pleurisy	17	1.7	<i>revarsare pleurala, pleurezie, pleurezii, afectiune pleurala</i>
COPD	18	1.8	<i>BPOC, bpoc, Bpoc</i>
Pulmonary malignancy / tumour	25	2.5	<i>tumora, tumora maligna, tumoare, tumoare maligna, tumora maligna bronhii, tumora cu alte localizari, tumora pleurei, tumora maligna lob superior, Tumoare</i>
Pneumonia	16	1.6	<i>pneumonie, bronhopneumonie, pneumonie bacteriana, pneumonie lobara, pneumonii, pneumopatii</i>
Tuberculosis	21	2.1	<i>tbc, TBC, tuberculoza, tuberkulosa pulmonara, tuberculoza pulmonara</i>
Cough / bronchitis	8	0.8	<i>tuse, bronsita, bronsita cronica</i>
Interstitial lung disease	3	0.3	<i>boala pulmonara interstitiala, BPI, bpi</i>
Asthma	4	0.4	<i>astm, astm cu predominanta alergica</i>
Pulmonary abscess	2	0.2	<i>abces pulmonar</i>
Pneumothorax	2	0.2	<i>pneumotorax, pneumotorax nespecificat</i>
Subglottic stenosis	2	0.2	<i>stenoza subglotica</i>
Sarcoidosis	1	0.1	<i>sarcoidoza</i>
Pyothorax / empyema	1	0.1	<i>piotorax</i>
Other / unspecified	97	9.7	<i>alerte boli pulmonare, boala pulmonara, durere, durere acuta, IACRS, alte afectiuni, and unlisted entries</i>

Normalisation was performed by two independent reviewers with resolution of disagreements by consensus. The 'Other/unspecified' category includes 14 entries coded as '-' in the original database, single-occurrence entries not fitting established categories, and entries that could not be reliably interpreted (e.g., 'gromulom' — presumed 'granulom').

S4. Specimen type distribution

Table S4 confirms that the vast majority of records (99.7%) are from bronchial aspirate specimens, validating the characterisation of this as a bronchial aspirate cohort throughout the main manuscript. The two slightly different database labels ('aspirat' vs 'aspirat bronsic') refer to the same procedure.

Table S4. Distribution of specimen types in the 1,000-record cohort. Bronchial aspirate (aspirat / aspirat bronsic) accounts for 99.7% of all specimens.

Specimen type	n	%	Note
Bronchial aspirate (aspirat)	989	98.9	Endobronchial secretions via bronchoscope or endotracheal/tracheostomy tube
Bronchial aspirate (aspirat bronsic)	8	0.8	As above, alternative labelling in database
Pulmonary abscess fluid	1	0.1	Direct aspiration or drainage
Other secretions	1	0.1	Unspecified respiratory secretion
Unlabelled (produs patologic)	1	0.1	Specimen type not specified in record
Total	1,000	100.0	

'Produs patologic' = generic term for 'pathological product/specimen'; used in early 2022 records before standardised specimen labelling was implemented.

S5. Semi-quantitative colony counts stratified by year

Table S5 presents the full colony load distribution broken down by year. The sharp increase in the 'not quantified' proportion in 2024 (50.0% vs 26.9% in 2022) is consistent with the partial-year data extraction hypothesis — records from later months of 2024 may have been captured with incomplete laboratory results. The high-load (>100 CFU/mL) proportion decreased from 23.0% in 2022 to 13.0% in 2024, which should be interpreted in the context of this methodological limitation rather than as a genuine clinical improvement trend.

Table S5. Semi-quantitative colony load distribution by year. Values shown as n (% of annual total). The sharp increase in 'not quantified' records in 2024 most likely reflects partial-year data capture. †One record lacks year data.

Year	>100 CFU/mL (high)	30–100 CFU/mL (moderate)	10–30 CFU/mL (low-mod)	<10 CFU/mL (low)	Not quantified	Annual total
2022	95 (23.0)	120 (29.0)	50 (12.1)	37 (9.0)	111 (26.9)	413
2023	64 (18.4)	100 (28.7)	37 (10.6)	63 (18.1)	84 (24.1)	348
2024	31 (13.0)	29 (12.2)	12 (5.0)	47 (19.7)	119 (50.0)	238
Total	190 (19.0)	249 (24.9)	99 (9.9)	147 (14.7)	314 (31.4)	999†

Colony load tiers: high >100 CFU/mL; moderate 30–100 CFU/mL (including >20, >30, >50 tier entries); low-moderate 10–30 CFU/mL (including >5, >10, >15 tier entries); low <10 CFU/mL (including exact counts of 1–10). 'Not quantified' includes records where the colonies field was empty or contained only a non-numeric value. †One record lacks year data and is excluded from year-stratified subtotals.

S6. Filamentous fungal co-isolation rates by ward

Table S6 presents co-isolation rates of filamentous fungi (alongside yeast species) for each ward/section. The highest rates are in Pulmonary Surgery (SZ: 48.7%, pooling both SZ and sz coding variants) and selected general wards (Wards 2, 4, 5: 23–25%). The ICU rate (12.8%) is comparatively low despite its high absolute isolate volume, which may reflect the different diagnostic context — acute illness rather than chronic structural lung disease. The overall hospital co-isolation rate of 22.3% substantially exceeds that reported in many published series and likely reflects the structural lung damage prevalent in this patient population.

Table S6. Filamentous fungal co-isolation rates by ward/section (n = 1,000). 'Co-isolation' = at least one filamentous fungus detected in the same specimen record alongside a yeast species. 'Outpatient/Other' aggregates ambulatory, surgical block, oncology, and unspecified entries.

Ward/section	Co-isolation (n)	Total isolates	Co-isolation rate (%)	Notes
ICU	33	258	12.8	Most isolates from mechanically ventilated patients; mixed flora consistent with structural lung compromise
Ward 1	19	109	17.4	General pneumology; elevated co-isolation suggests structural lung disease substrate
Ward 2	9	36	25.0	
Ward 3	20	97	20.6	
Ward 4	23	100	23.0	
Ward 5	11	47	23.4	
Ward 6	7	33	21.2	
Ward 7	13	93	14.0	
Pulm. Surgery	56	115	48.7	Highest co-isolation rate — post-surgical airways prone to mixed fungal flora; pooled SZ/sz entries
Outpatient/Other	20	88	22.7	Includes ambulatory, surgical block, and unspecified records
Total	223	1,000	22.3	Hospital-wide co-isolation rate

Filamentous fungi identified in this cohort include predominantly *Aspergillus* spp. (species not consistently documented in the database), and occasional entries labelled 'fungi filamentosi' without species designation.

S7. Anonymised trajectory summaries for a representative subset of ten of the 91 multi-sample patients (illustrative selection; full cohort statistics are reported in Section 3.11).

Table S7 provides the complete trajectory summaries for the ten patients in the longitudinal cohort ($n = 91$ total) with the most clinically notable serial culture courses — defined as the patients with the highest number of serial cultures and/or the most clinically significant species changes. All patient identifiers have been anonymised using sequential codes (PT-01 through PT-10). No date, ward, or clinical information that could enable re-identification has been included beyond what is stated. The full anonymised multi-sample dataset (91 patients, 207 records) is available on request from the corresponding author, subject to ethics committee approval.

Table S7. Anonymised trajectory summaries for the ten most clinically notable multi-sample patients (selected by number of serial cultures and/or significance of species shift). Patient codes PT-01 to PT-10 do not correspond to chronological admission order. All patients are from the 2022–2024 cohort, Romanian tertiary pulmonology hospital. Age and sex are provided as demographic context only. ICU = Intensive Care Unit; NAC = non-albicans Candida; CFU = colony-forming units per mL.

Patient code	Age (yr)	Sex	Cultures (n)	Summary trajectory and key observation
PT-01	80	M	8	ICU — <i>C. albicans</i> ×5 → <i>C. glabrata</i> ×2, Oct–Dec 2022; max load >100 CFU/mL; longest mycological trajectory in cohort
PT-02	74	M	4	ICU — <i>C. krusei</i> → <i>C. glabrata</i> → <i>C. krusei</i> ×2, Aug–Sep 2022; oscillating NAC dominance; dual colonisation suspected
PT-03	67	M	3	ICU — <i>C. albicans</i> ×2 → <i>Cryptococcus laurentii</i> >100 CFU, Oct 2023; unexplained; immunodeficiency suspected
PT-04	69	M	3	ICU — <i>C. albicans</i> ×2 (>100 CFU) → <i>C. krusei</i> , Nov 2022; probable fluconazole-pressure selection
PT-05	70	M	2	Ward 4 → ATI transfer — <i>C. albicans</i> on ward, <i>C. glabrata</i> in ICU; severity-linked species shift
PT-06	68	M	3	ICU — <i>Cryptococcus laurentii</i> (Nov 2023) → <i>C. albicans</i> ×2 (Dec 2023); <i>Cryptococcus</i> as first isolate
PT-07	71	M	2	Ward 4 — <i>C. glabrata</i> → <i>C. krusei</i> , Nov 2022; mixed NAC colonisation; both at significant load
PT-08	55	F	3	Ward 2 — <i>C. albicans</i> >100 CFU (Mar) → <i>C. tropicalis</i> 10 CFU (May) → negative (Jun); probable treatment response or spontaneous resolution

PT-09	77	M	3	ICU — <i>C. albicans</i> load escalation: 50→30→100 CFU across 3 months; same species, increasing burden
PT-10	79	M	5	ICU — <i>C. albicans</i> sustained at >100 CFU/mL across 2 months; classic persistent high-load ICU colonisation

Patient codes are not persistent identifiers and differ from codes used in other supplementary tables or figures. 'Ward 4 → ATI transfer' (PT-05) indicates that the two cultures were obtained from different wards during the same or closely consecutive admissions. Species trajectories use '→' to indicate temporal succession; '×n' indicates the number of consecutive cultures yielding the same organism. Colony loads: >100 = >100 CFU/mL; 50 = >50 CFU/mL; 30 = >30 CFU/mL; 10 = >10 CFU/mL; all semi-quantitative estimates. The full anonymised longitudinal dataset is available on request from the corresponding author.

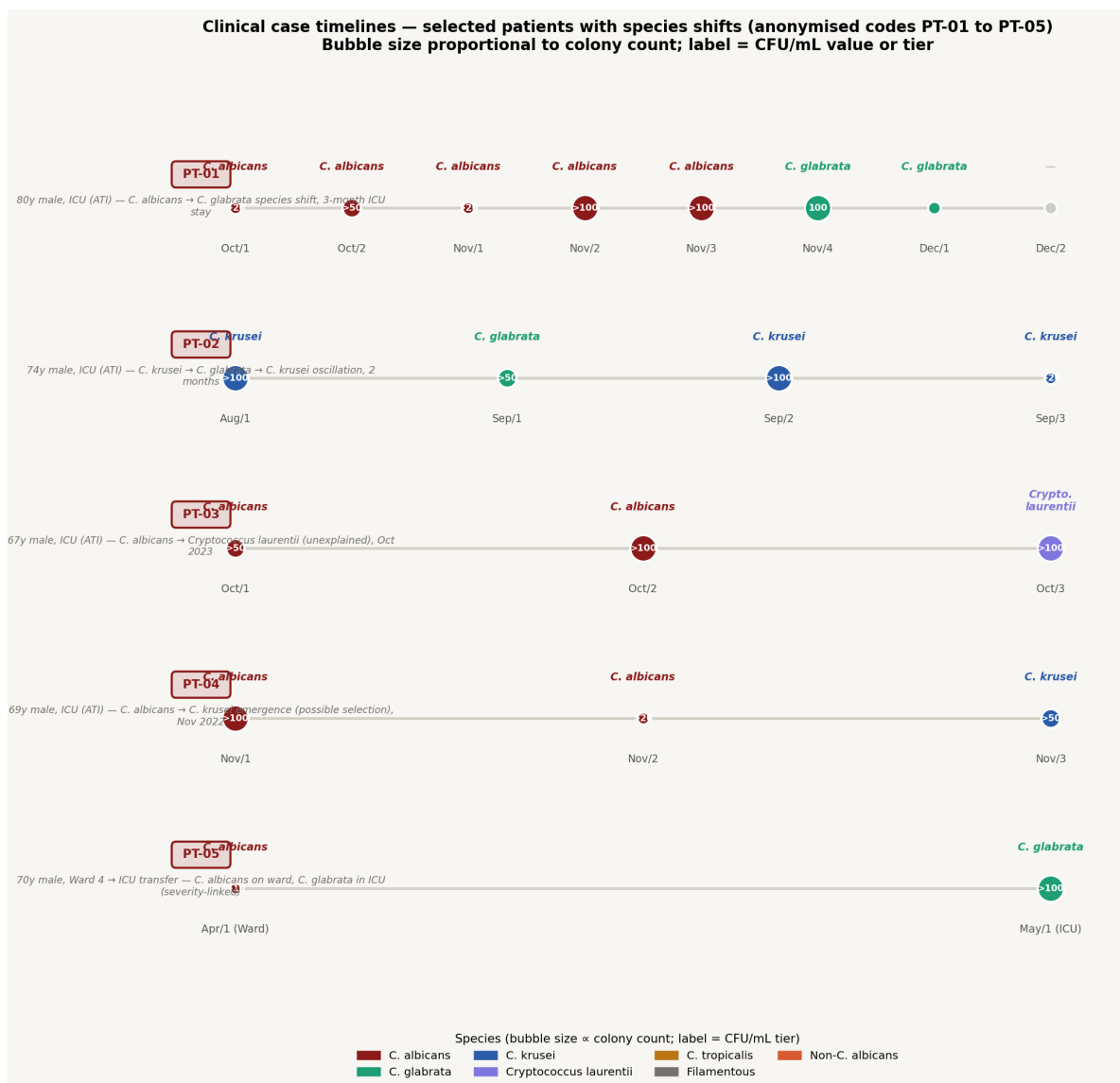


Figure S1. Individual patient timelines for five key cases (bubble size ∝ approximate colony count; label = CFU/mL). **PT-01:** 8 cultures Oct–Dec 2022; *C. albicans* escalating to >100 CFU before *C. glabrata* emergence. **PT-02:** oscillating *C. krusei*/*C. glabrata* — dual colonisation with alternating dominance. **PT-03:** *Cryptococcus laurentii* at >100 CFU following two *C. albicans* cultures — unexplained; immunosuppression suspected. **PT-04:** *C. krusei* emergence after two high-load *C. albicans* samples — possible selection. **PT-05:** *C. albicans* on ward → *C. glabrata* in ICU after transfer — severity-linked species shift.

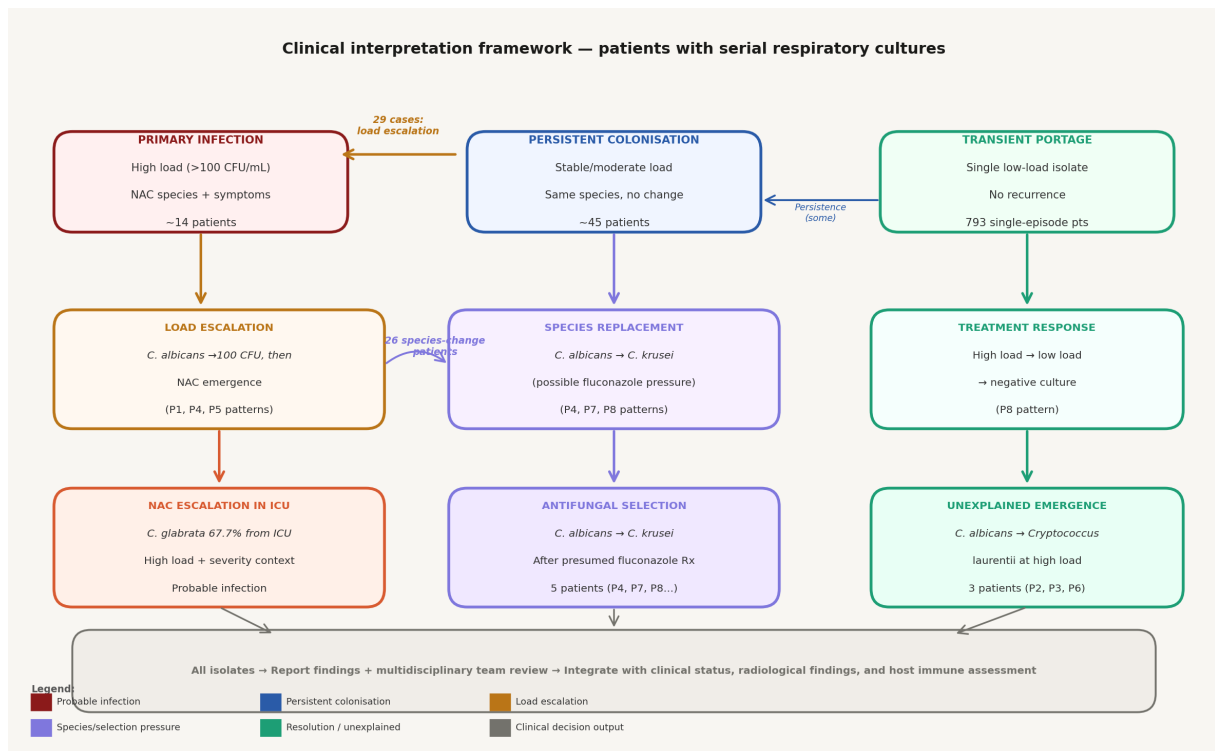


Figure S2. Clinical interpretation framework for multi-sample patients. Three categories (top row): primary infection (~14 patients), colonisation (~45 patients), and transient portage (the 793 single-episode patients). Arrows indicate documented transition pathways: load escalation toward infection (n=29); species replacement under pressure (n=26); unexplained *Cryptococcus laurentii* emergence (n=3, with suspected immunosuppression). This is a conceptual interpretation tool, not a validated diagnostic algorithm.

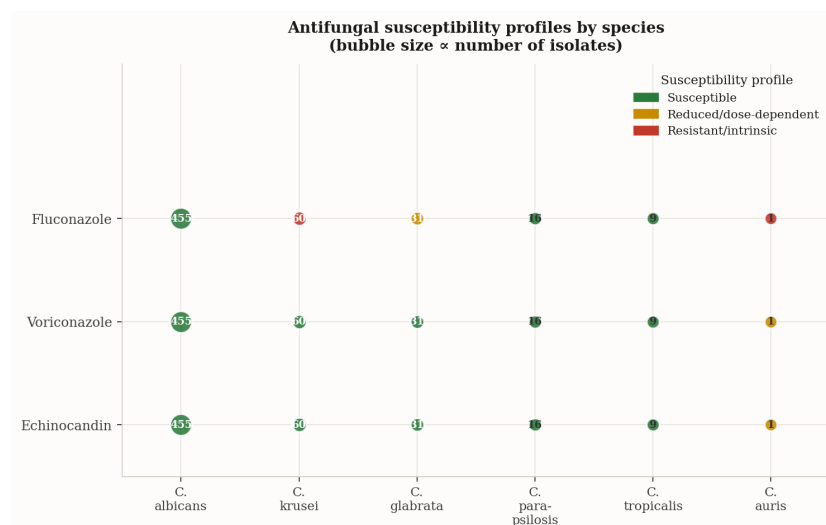


Figure S3. Antifungal susceptibility profiles by species (bubble chart). Bubble size $\propto$ isolate count; colour: green = susceptible, amber = dose-dependent/reduced susceptibility, red = intrinsically resistant or multidrug-resistant. Three antifungal classes across the y-axis: fluconazole (top), voriconazole (middle), echinocandin (bottom). *C. krusei* (n=60) is red for fluconazole, green for voriconazole and echinocandin. *C. glabrata* (n=31) is amber for fluconazole. *C. auris* (n=1) is red for all three classes. *C. albicans* and *C. parapsilosis* remain susceptible across all classes. Designations based on EUCAST/CLSI intrinsic resistance criteria; individual isolate susceptibility testing was not performed.

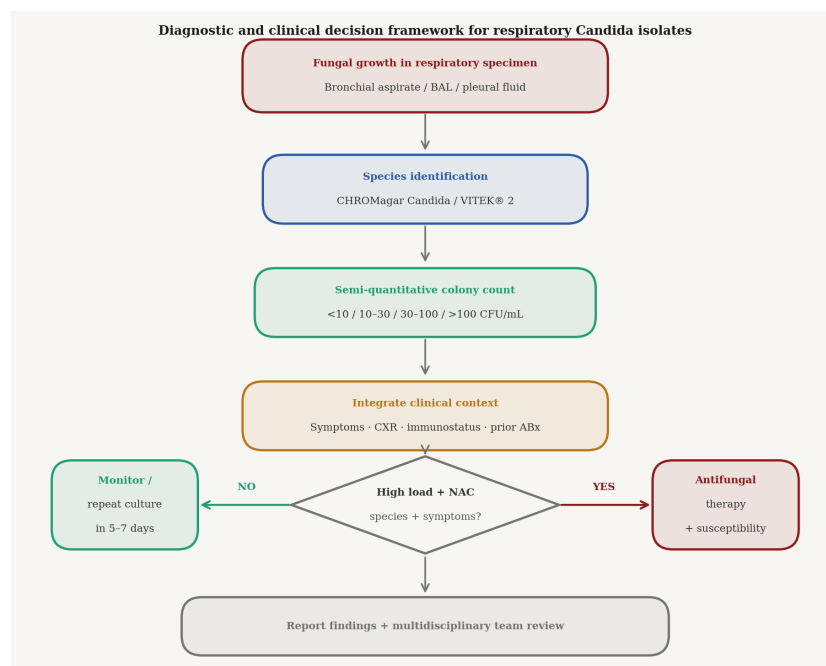


Figure S4. Proposed clinical decision framework for *Candida* respiratory isolates in a pulmonology setting. The algorithm proceeds from fungal growth detection through species identification, colony count assessment, and clinical integration to a binary decision node. The node weights three factors: high colony load (>100 CFU/mL), NAC species (especially fluconazole-resistant), and clinical symptoms. High load + NAC + symptoms → antifungal therapy with susceptibility testing; absence of this combination → monitor and repeat culture in 5–7 days. All results feed into multidisciplinary review. NAC = non-albicans *Candida*; CXR = chest X-ray.