INTERNAL MEDICINE JOURNAL

RACP Specialists. Together

Check for updates

doi:10.1111/imj.70020

ORIGINAL ARTICLE

Sputum microbiology data and related clinical outcomes among adult Aboriginal Australians with bronchiectasis

Claire Gibbs,[1,2] Timothy Howarth [3,4] Sudharsan Venkatesan,[2,5] Sanjana S. Heraganahally [6] Asanga Abeyaratne[7,8] and Subash S. Heraganahally [1,2,3,9]

Departments of [1]Respiratory and Sleep Medicine, [5]Infectious Diseases, and [8]Medicine, Royal Darwin Hospital, [2]Flinders University, College of Medicine and Public Health, [3]Darwin Respiratory and Sleep Health, Darwin Private Hospital, [7]Menzies School of Health Research, and [9]School of Medicine, Charles Darwin University, Darwin, Northern Territory, [6]Division of Medicine, The Prince Charles Hospital, Brisbane, Queensland, Australia, and [4]Department of Technical Physics, University of Eastern Finland, Kuopio, Finland

Key words
bacterial infections, clinical outcomes, exacerbations, fungal infections, microorganism, pulmonary.

Correspondence
Subash S. Heraganahally, Department of Respiratory and Sleep Medicine, Royal Darwin Hospital, Darwin, NT 0810, Australia.
Email: subash.heraganahally@nt.gov.au

Received 24 January 2024; accepted 28 January 2025.

ABSTRACT

Background: Sputum microbiology is an integral aspect of managing patients with bronchiectasis. Adult Aboriginal Australians have a high bronchiectasis disease burden; however, as yet there is sparce literature detailing the sputum microbiology profile in this population.

Aims: To assess the sputum microbiology profile among Aboriginal patients aged ≥18 years with chest computed tomography-confirmed bronchiectasis in the Top End Northern Territory of Australia.

Method: All available sputum samples processed in a single laboratory service with established protocols for examining and reporting sputum microbiology results between 2011 through 2020 were assessed in relation to demographics, lung function parameters, chest radiology, inhaled pharmacotherapy, hospital admissions restricted to respiratory conditions and all-cause mortality.

Results: Four hundred twenty-eight patients (median age 47 years, 56% female) had sputum cultures available to assess. *Haemophilus spp.* was the most common (64%), followed by yeast/*Candida spp.* (53%) and *Pseudomonas spp.* (36%). Polymicrobial cultures were noted in 92% of patients. There were significant geographic differences on a region-wise and community-wise basis. Patients with yeast/*Candida spp.* and *Pseudomonas spp.* recorded more hospitalisations (median 7 (interquartile range (IQR) 3–14) and 8 (IQR 4–16)). In multivariate models, both yeast/*Candida spp.* (odds ratio (OR) 2.63 (95% confidence interval (CI) 1.68–4.14)) and *Pseudomonas spp.* (OR 1.95 (95% CI 1.25–3.04)) were associated with increased odds for mortality. Other than higher *Pseudomonas spp.* isolated with the use of inhaled corticosteroids, no significant association was observed either with lung function or chest radiology.

Conclusion: Adult Aboriginal Australians with bronchiectasis harbour a significant microorganism load that may play a role in overall morbidity and mortality.

Abbreviations: CI, confidence interval; COPD, chronic obstructive pulmonary disease; CT, computed tomography; DR, Darwin rural; DU, Darwin urban; EA, Arnhem land; FEV_1, forced expiratory volume in 1 s; FVC, forced vital capacity; ICS, inhaled corticosteroids; ICU, intensive care unit; IQR, interquartile range; KR, Katherine region; LABA, long-acting beta agonist; LAMA, long-acting muscarinic agent; NT, northern territory; OR, odds ratio; RDH, royal Darwin hospital; SABA, short-acting beta agonist; SAMA, short-acting muscarinic agent; TEHS, Top End Health Service

Funding: This research received the Thoracic Society of Australia and New Zealand (TSANZ) - Robert Pierce Grant-In-Aid for Indigenous Lung Health. The TSANZ did not have any role in the study design, data collection, analysis or interpretation.
Conflict of interest: None.

© 2025 The Author(s). *Internal Medicine Journal* published by John Wiley & Sons Australia, Ltd on behalf of Royal Australasian College of Physicians.
This is an open access article under the terms of the Creative Commons Attribution-NonCommercial-NoDerivs License, which permits use and distribution in any medium, provided the original work is properly cited, the use is non-commercial and no modifications or adaptations are made.

Introduction

Bronchiectasis is a chronic progressive respiratory disease, with the clinical hallmarks of cough, sputum production and respiratory infections associated with bronchial dilatation.[1] It is often the final common pathway of multiple aetiologies (infectious and non-infectious) and concurrent pathophysiological processes resulting in a spectrum of clinical presentations.[2] Chronic respiratory tract infections play a pivotal role in the pathogenesis and pathophysiology of bronchiectasis.[3] There are significant geographical variations, with a substantial burden of bronchiectasis in countries and populations with a high incidence of respiratory infections.[4,5]

The northern territory (NT) is a sparsely populated territory of the Australian mainland, with a population of 233 000 in 2021, of which 26.3% self-identify as Aboriginal and/or Torres Strait islander (the highest proportion in Australia).[6] The age-standardised burden of respiratory disease among adult Aboriginal Australians in the NT is 2.7 times higher compared to non-Aboriginal Australians.[7,8] Although the true incidence of bronchiectasis in Aboriginal Australian adults is unknown, especially in rural/remote communities,[9] it has been shown to be higher than non-Aboriginal Australians.[10]

Lower respiratory tract infections and associated hospital admissions are substantially higher for Aboriginal Australians, including patients with bronchiectasis.[11,12] Commensal organisms may become pathogenic in individuals with bronchiectasis due to mucous thickening, impaired mucociliary clearance and dysregulated immunity.[2] The initial stimulation and persistent inflammation associated with bronchiectasis (including exacerbations) could be due to bacteria, mycobacteria, viruses and/or fungi.[2] Common bacterial organisms associated with bronchiectasis include *Haemophilus influenzae*, *Pseudomonas aeruginosa*, *Moraxella catarrhalis*, *Streptococcus pneumoniae* and *Staphylococcus aureus*.[1,3,13,14] Infections are often polymicrobial, especially in children.[4] Exacerbations and hospitalisation are associated with higher airway bacterial loads, with organisms undergoing adaptations to facilitate immune evasion.[15]

Among adult Aboriginal Australians with bronchiectasis, the limited available data indicate that the most common pathogens isolated from sputum cultures are *H. influenzae*, *S. pneumoniae* and *M. catarrhalis*.[10] Studies from Central Australia have also shown strong associations between bronchiectasis and human T-cell leukaemia virus-1 infection.[16] Bronchiectasis-related outcomes are significantly worse for Aboriginal Australians than their non-Aboriginal counterparts, with death at a significantly younger age (almost 20 years earlier).[17,18]

Despite ample evidence to suggest that adult Aboriginal Australians have a higher burden of bronchiectasis, knowledge surrounding the significance of sputum microbiology to outcomes among adult Aboriginal Australian patients is lacking. This study aims to assess the relationship between sputum microbiology and relevant clinical parameters, hospital admissions and mortality among an adult Aboriginal Australian cohort diagnosed to have bronchiectasis over a 10-year period (2011–2020) from the Top End Health Service (TEHS) region of the NT of Australia.

Methods

Setting and study participants

This study was conducted at the respiratory and sleep division based at the Royal Darwin Hospital (RDH), and Darwin Private Hospital, within the TEHS. Participants were Australian Aboriginal patients aged ≥18 years identified to have bronchiectasis via International Statistical Classification of Diseases (ICD) 10th Revision code J47, coded at separation from an in-patient admission across the three hospitals in the TEHS region and confirmed with chest computed tomography (CT) scan between 2011 and 2020.[17]

Ethics

This study is a part of a larger project examining various aspects of bronchiectasis disease profiles among the adult Aboriginal Australian population residing in the TEHS health districts and was approved by the human research ethics governance/committee of the TEHS, NT and Menzies school of health research (Reference: HREC; 2019–3547).

Sputum microbiology data

All available sputum microbiology results between 2011 through 2020 were retrieved via patients' electronic medical records, irrespective of ambulatory out-patients' settings or during hospital admissions. Sputum cultures were undertaken as per the discretion of treating medical practitioners. All sputum samples were processed in a single microbiology/pathology service based in the TEHS region: "Territory Pathology Service" with standard established protocols. All sputum culture reports were scrutinised for the quality of the sample and excluded if indicative of poor quality/contaminated samples. Patient sputum microbiology data were analysed in two ways for this study: (i) on the patient level, if patients were observed to have multiple sputum examinations, any cultured microorganisms were counted only once, irrespective of whether it was cultured

© 2025 The Author(s). *Internal Medicine Journal* published by John Wiley & Sons Australia, Ltd on behalf of Royal Australasian College of Physicians.

14455994, 2025, 5, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/imj.70020 by Edith Cowan University, Wiley Online Library on [18/05/2025]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Table 1 Sputum microbiology data by sex

Sputum microbiology	Total ($N = 428$)	Female ($n = 238$)	Male ($n = 190$)
Haemophilus spp.	272 (63.6%)	145 (60.9%)	127 (66.8%)
Yeast/*Candida spp.*	227 (53%)	117 (49.2%)	110 (57.9%)
Streptococcus spp.	160 (37.4%)	88 (37%)	72 (37.9%)
Pseudomonas spp.	155 (36.2%)	81 (34%)	74 (38.9%)
Moraxella spp.	130 (30.4%)	78 (32.8%)	52 (27.4%)
Staphylococcus spp.	84 (19.6%)	44 (18.5%)	40 (21.1%)
Mycobacterium	53 (12.4%)	20 (8.4%)	33 (17.4%)*
Aspergillus spp.	45 (10.5%)	26 (10.9%)	19 (10%)
Non-*Aspergillus* fungi	39 (9.1%)	20 (8.4%)	19 (10%)
Klebsiella spp.	31 (7.2%)	14 (5.9%)	17 (8.9%)
Burkholderia spp.	22 (5.1%)	12 (5%)	10 (5.3%)
Others	424 (99.1%)	236 (99.2%)	188 (98.9%)

Differences between females and males tested via univariate logistic regression.
*Indicates significant difference with Romano-Wolf *P*-value <0.05. *spp.*, species.

multiple times; and (ii) on the hospital admission level, all available sputum culture results within respiratory-related hospital admissions (ICD code J) were assessed individually, irrespective of whether they were from the same patient across multiple admissions. Information pertaining to viral pathogens were not examined.

Sputum microbiology and clinical data assessment

Sputum results were pragmatically categorised into 11 distinct categories as per common microorganisms encountered in day-to-day clinical practice (Table S1). Sputum microbiology results were assessed against demographics, residence location (by TEHS region and community), smoking status, body mass index, lung function parameters (LFPs; spirometry), comorbidities, inhaled pharmacotherapy use, immunoglobulin levels, chest CT findings, hospital admission rates (restricted to ICD J presentations), need for intensive care unit (ICU) admission and overall all-cause mortality (followed until April 2023). A subgroup analysis was undertaken to assess the sputum microbiology data during acute hospitalisation during exacerbation of respiratory airway disease (ICD code J) during the study window.

Statistical analysis

Differences in demographic and clinical variables between females and males with sputum cultures were tested via univariate quantile regression (continuous parameters) or logistic regression (categorical parameters), with Romano-Wolf (RW) adjustment for multiple hypothesis testing. Pairwise correlations between sputum culture categories and lobar involvement were tested via Pearson pairwise correlation coefficient (R^2), with *P*-values adjusted via Bonferroni correction. Univariate and multivariate quantile regression models were utilised to explore the effect of sputum categories on the number of hospitalisations for patients across the study period, with the multivariate models adjusted for age, sex, urban residence, chronic obstructive pulmonary disease (COPD) and hypertension, inhaled pharmacotherapy prescription (short-acting beta agonist (SABA), short-acting muscarinic agent (SAMA), long-acting beta agonist (LABA), long-acting muscarinic agent (LAMA), inhaled corticosteroids (ICSs)) and bilateral radiological extent with models reported as beta coefficients (95% confidence intervals (CIs)). Univariate and multivariate logistic regression models were utilised to explore the association between sputum categories and mortality, adjusting for the same factors as the quantile regression models, and reported as odds ratios (ORs) and 95% CIs. All regression models were adjusted for multiple hypothesis testing via RW correction with 250 bootstrap replications. All analyses were conducted in STATA IC 15 (College Station, Texas) and alpha was set to $P < 0.05$ throughout.

Results

Demographics and clinical data

Of the 459 patients identified to have bronchiectasis, 428 had either outpatient or during respiratory-related hospital admission sputum culture available to be included for analysis (Table S2). The median age was 47 years (interquartile range (IQR) 40–56 years), with 56% female, and 7% residing in urban areas. Of the 428 patients, 387 had at least one hospital admission (median five admissions, IQR 2–10) for a total of 3474 hospital admissions. Of the 387 patients with a hospital admission, 315 had a sputum culture recorded within at least one hospital admission, with 3157 admissions recording a sputum culture in total.

Sputum microbiology results

Haemophilus species (*spp.*) were the most commonly cultured (64%), followed by yeast/*Candida spp.* (53%), *Streptococcus spp.* (37%), *Pseudomonas spp.* (36%) and *Moraxella spp.* (30%) (Table 1). Mycobacteria were more common among males than females (17.4 vs 8.4%, $P = 0.04$). Most patients (92.3%) had two or more micro-organism species cultured. *Haemophilus spp.* with *Streptococcus spp.* were

© 2025 The Author(s). *Internal Medicine Journal* published by John Wiley & Sons Australia, Ltd on behalf of Royal Australasian College of Physicians.

14455994, 2025, 5, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/imj.70020 by Edith Cowan University, Wiley Online Library on [18/05/2025]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

cultured together in 134 patients (31.3%; $R^2 = 0.324$, $P < 0.001$) and *Moraxella spp*. with *Streptococcus spp*. in 80 (18.7%; $R^2 = 0.330$, $P < 0.001$), with both pairings showing the strongest Pearson pairwise correlations (Fig. S1). *Haemophilus spp*. and yeast *spp*. were the most common co-cultures identified (153 patients, 35.8%; $R^2 = 0.085$, $P = 1.000$); however, Pearson pairwise correlation was not significant (Table S3).

Relationship of sputum microbiology by patients' geographic location

Haemophilus spp. prevalence was stable across the four health districts (range 61.3%–63.8%) (Fig. 1). However, *Streptococcus spp*. prevalence ranged from 22.5% (Darwin Urban) to 46.2% (Katherine). *Pseudomonas spp*. was more common in the Darwin urban region (48.4%), with little variation between other regions (range 30.1%–38.6%).

On a community-by-community basis (including only those with >10 bronchiectasis cases), *Haemophilus spp*. was the most cultured organism in 11 of 13 communities (range 43%–87%), with yeast/*Candida spp*. being the most cultured in the remaining two of 13 (58% and 59%) (Fig. 2). Yeast/*Candida spp*. were the second most common in nine of 13 communities (range 36%–67%), with *Streptococcus spp*. the second most common in three of 13 (36%, 42% and 57%).

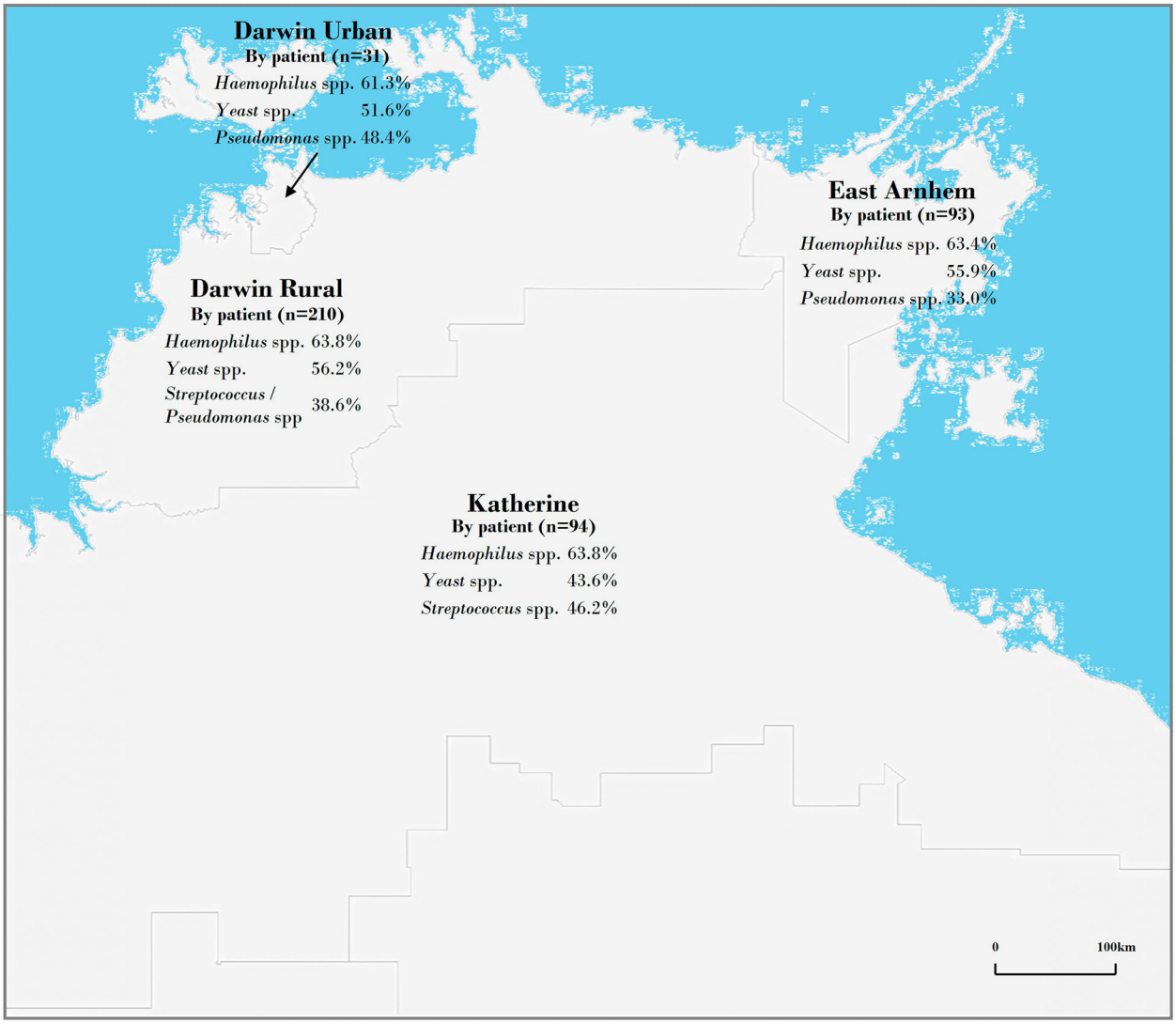

Figure 1 Relationship of sputum microbiology by patients' geographic location in the Top End Health Service districts showing the three most frequently cultured micro-organisms. *spp*., species.

© 2025 The Author(s). *Internal Medicine Journal* published by John Wiley & Sons Australia, Ltd on behalf of Royal Australasian College of Physicians.

14455994, 2025, 5, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/imj.70020 by Edith Cowan University, Wiley Online Library on [18/05/2025]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

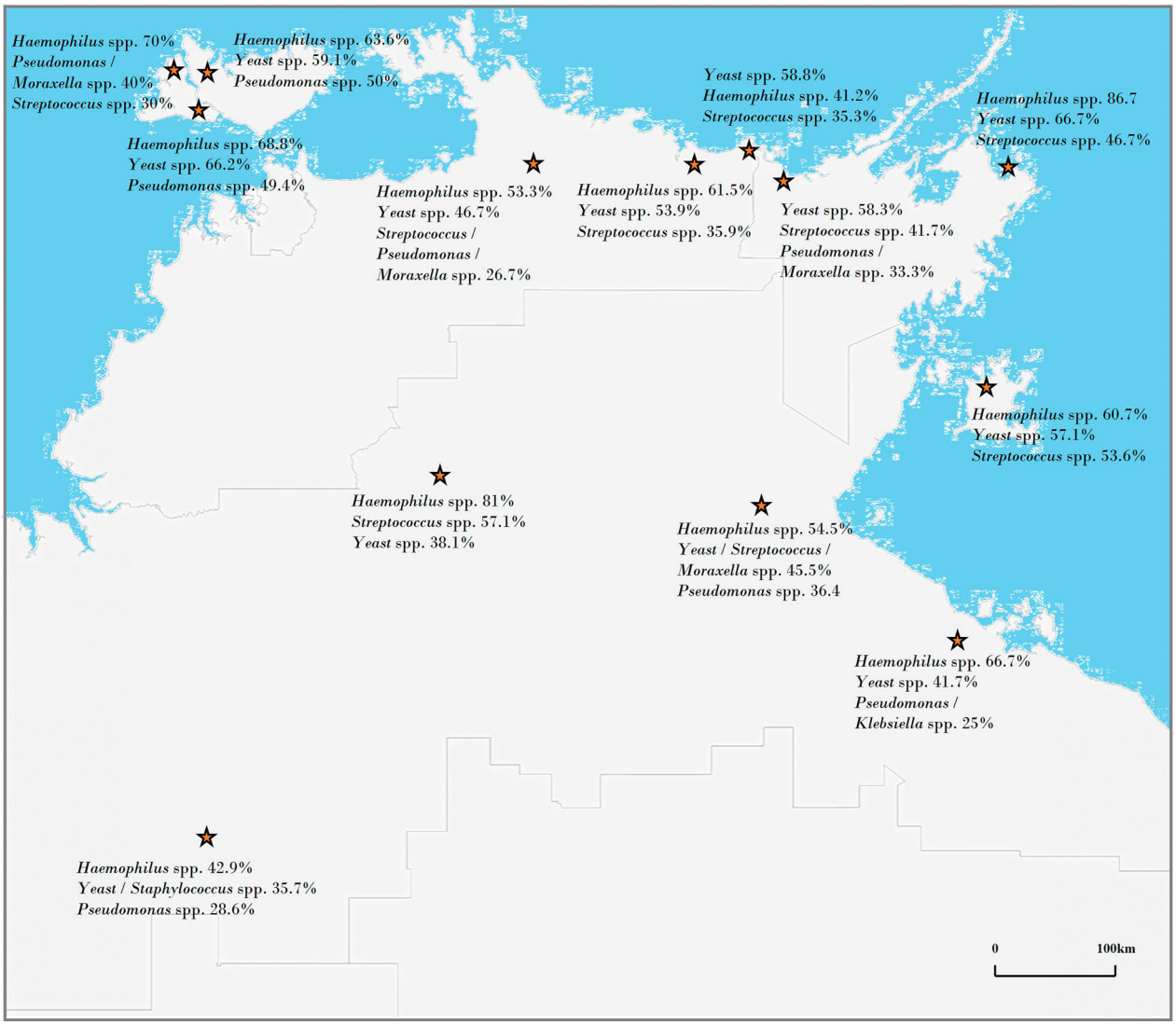

Figure 2 Relationship of sputum microbiology by patients' geographic location in the Top End Health Service districts showing approximate community locations with >10 cases and the three most frequently cultured micro-organisms. *spp.*, species.

Sputum microbiology data during exacerbation and hospital admissions

A total of 3157 sputum samples were recorded during acute hospital admissions (Mycobacterium data were not captured for each hospital admission) with females having a fewer number of admissions with sputum recorded than males (median 5 (IQR 2–10) vs 6 (IQR 23)). *Haemophilus spp*. were the most common (6.7%), followed by yeast/*Candida spp*. (6.1%) and *Pseudomonas spp*. (6%) (Table 2). Males recorded more *Pseudomonas spp*. (7.1% vs 4.6%, RW $P = 0.015$), while females recorded more *Staphylococcus spp*. (2.1% vs 1.2%). Differences in sputum microbiology by geographic region were noted, but failed to reach statistical significance (Fig. S2).

Sputum microbiology relationship to hospital admission and mortality data — regression analysis

Pseudomonas spp. (4.88 (95% CI 3.20–6.56)), *Moraxella spp*. (4.07 (95% CI 2.39–5.76)), yeast/*Candida spp*. (3.67 (95% CI 2.14–5.2)), *Staphylococcus spp*. (3.6 (95% CI 1.91–5.30)), *Streptococcus spp*. (3.46 (95% CI 1.82–5.09)), *Aspergillus spp*. (3.05 (95% CI 0.26–5.85)) or *Haemophilus spp*. (2.76 (95% CI 1.09–4.44)) were associated with significantly increased hospitalisations. The increase in hospitalisations with *Pseudomonas spp*. was significantly larger than that associated with *Haemophilus spp*. ($P = 0.023$), yeast *spp*. ($P = 0.013$) and *Staphylococcus spp*. ($P = 0.038$). After RW adjustment, the significance of

© 2025 The Author(s). *Internal Medicine Journal* published by John Wiley & Sons Australia, Ltd on behalf of Royal Australasian College of Physicians.

14455994, 2025, 5, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/imj.70020 by Edith Cowan University, Wiley Online Library on [18/05/2025]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Table 2 Sputum cultures within hospital admissions by sex

Sputum microbiology	Recorded during hospital admissions ($n = 3157$)	Female ($n = 1450$)	Male ($n = 1707$)	RW *P*-value
Haemophilus spp.	212 (6.7%)	96 (6.6%)	116 (6.8%)	0.968
Yeast/*Candida spp.*	192 (6.1%)	98 (6.8%)	94 (5.5%)	0.659
Pseudomonas spp.	188 (6%)	66 (4.6%)	122 (7.1%)	0.015*
Streptococcus spp.	108 (3.4%)	48 (3.3%)	60 (3.5%)	0.968
Moraxella spp.	88 (2.8%)	43 (3%)	45 (2.6%)	0.968
Staphylococcus spp.	51 (1.6%)	31 (2.1%)	20 (1.2%)	0.214
Non-*Aspergillus* fungi	20 (0.6%)	8 (0.6%)	12 (0.7%)	0.968
Aspergillus spp.	19 (0.6%)	9 (0.6%)	10 (0.6%)	0.968
Klebsiella spp.	12 (0.4%)	4 (0.3%)	8 (0.5%)	0.960
Burkholderia spp.	3 (0.1%)	2 (0.1%)	1 (0.1%)	0.659

*Indicates significance at Romano-Wolf (RW) $P < 0.05$ via univariate logistic regression. *spp.*, species.

all associations were fully attenuated. In multivariate logistic models, yeast/*Candida spp.* (OR 2.63 (95% CI 1.68–4.14)), *Pseudomonas spp.* (OR 1.95 (95% CI 1.25–3.04)) and *Staphylococcus spp.* (OR 1.72 (95% CI 1–2.95)) were associated with increased odds of mortality (Fig. 3). The association with yeast/*Candida spp.* remained significant (RW *P*-value = 0.006) and *Pseudomonas spp.* was borderline significant (RW *P*-value = 0.062) after RW adjustment.

Clinical outcomes in relation to sputum microbiology

Patients with yeast/*Candida spp.* or *Pseudomonas spp.* displayed increased prevalence of COPD (yeast/*Candida spp.* 91.6 vs no yeast/*Candida spp.* 77.1%, $P = 0.055$ and *Pseudomonas spp.* 93.5 vs no *pseudomonas spp.* 79.9%, $P = 0.121$) (Table S4). A greater proportion of patients with yeast/*Candida spp.* or *pseudomonas spp.* recorded at least one hospitalisation (yeast/*Candida spp.* 96.9 vs no yeast/*Candida spp.* 83.1%, $P = 0.048$ and *Pseudomonas spp.* 97.4 vs 86.4%, $P = 0.163$). Among those who recorded one or more hospitalisation, patients with yeast/*Candida spp.* or *Pseudomonas spp.* recorded more hospitalisations than patients without (yeast/*Candida spp.* 7 (IQR 3–14) vs 3 (IQR 2–6), $P = 0.055$ and *Pseudomonas spp.* 8 (IQR 4–16) vs 3 (IQR 2–7), $P = 0.028$). Those with yeast/*Candida spp.* also recorded a greater proportion with an ICU visit (42.3 vs 13.2%, $P = 0.014$).

Relationship of sputum microbiology data to chest CT findings, spirometry, immunoglobulin levels and inhaled pharmacotherapy use

Most patients had lower lobe and bilateral involvement; however, Pearson pairwise correlation was weak between all micro-organisms and CT findings.

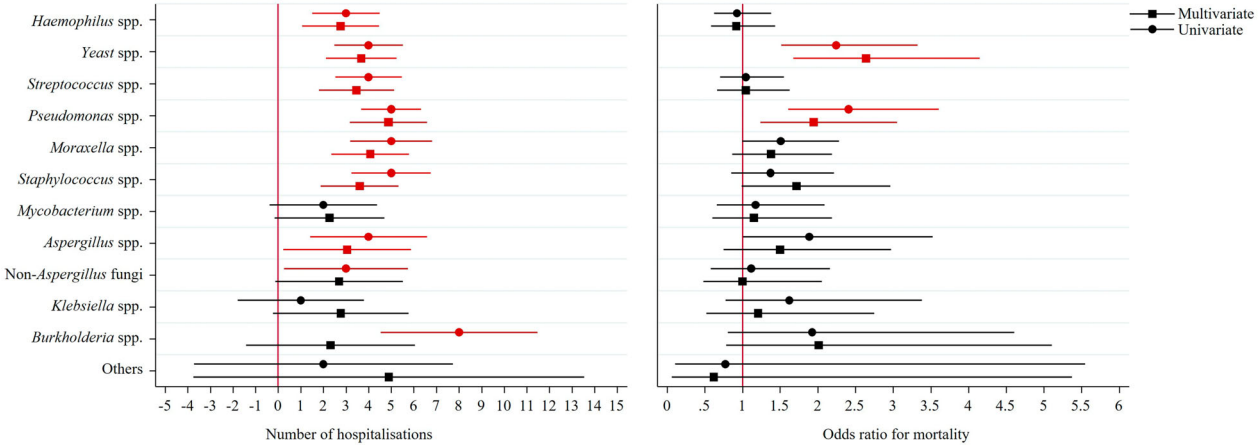

Figure 3 Coefficients plot for univariate and multivariate effects of sputum cultures upon hospitalisations, and mortality. Coloured lines indicate those which retained significance following Romano-Wolff multiple hypothesis testing adjustment at $P < 0.05$. *spp.*, species.

© 2025 The Author(s). *Internal Medicine Journal* published by John Wiley & Sons Australia, Ltd on behalf of Royal Australasian College of Physicians.

14455994, 2025, 5, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/imj.70020 by Edith Cowan University, Wiley Online Library on [18/05/2025]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Though LFPs were low in this sample, there were no differences between any specific micro-organism. Most patients recorded high IgA and IgG values (77% and 78% respectively), but there were no significant differences in immunoglobulin absolute values by presence of any micro-organism. SABA (62.6%) and LABA (61.9%) were the most common inhaled medications, followed by ICS (55.6%), LAMA (47.4%) and SAMA (7.5%). More patients using SABA or ICS recorded *Pseudomonas spp*. compared to patients not using SABA or ICS (SABA 42.2 vs 26.3% ($P = 0.037$) and ICS 43.3 vs 27.4% ($P = 0.037$)) (Table 3).

Discussion

To the best of the authors' knowledge, this is the first study to demonstrate sputum microbiology data in an adult Aboriginal Australian population with bronchiectasis, and has illustrated the following:

1 *Haemophilus spp*. is the most common organism.
2 Polymicrobial cultures are frequent, with *Haemophilus spp*. and yeast/*Candida spp*. commonly co-cultured.
3 Geographical variations in the sputum microbiology exist.
4 *Pseudomonas spp*. or yeast/*Candida spp*. increase hospitalisation rates and all-cause mortality.

One of the major clinical manifestations of bronchiectasis is a vicious cycle of recurrent lower airway infections and worsening airway function due to ongoing chronic airway inflammation, leading to lower quality of life, higher hospitalisation rates and mortality.[19,20] Extensive research has been undertaken to study the sputum microbiology profiles and related clinical outcomes among patients with bronchiectasis across various ethnic populations globally.[21,22] However, among adult Indigenous patients, despite evidence to suggest a higher burden of respiratory disorders, including higher health care utilisation rates, hospital admission rates and mortality,[12,23] data pertaining to respiratory microbiology/microbiome are sparse and mostly restricted to children and young adults.[24,25]

Our results show sputum microbiology profiles similar to what has been reported from geographical regions such as Africa, the Indian-subcontinent and low-income countries.[26–28] We also observed polymicrobial isolates were frequent, especially with concurrent isolation of *Haemophilus spp*. and *Streptococcus spp*., *Moraxella spp*. and *Streptococcus spp*., and *Haemophilus spp*. and yeast/*Candida spp*. The implications of polymicrobial isolates in the study cohort are not exactly known, as this study was retrospective in nature and acute hospital admission details against sputum microbiology data were not examined prospectively. However, it is reasonable to speculate that this will have substantial implications in the management of patients with acute exacerbations and in the choice of empirical anti-microbial therapy among Aboriginal Australian patients.[29] Moreover, there were regional and community-wise differences in the micro-organism isolated. Knowledge of the most prevalent micro-organisms in a given community/region can guide early interventions with appropriate antibiotics during exacerbations, thereby reducing the need for hospitalisation and associated health care cost. However, the significance of some of the isolates is not entirely clear, as the isolated organisms may be mere commensal. In the recent past there has been significant interest in the research communities assessing the respiratory microbiome among patients with bronchiectasis.[30,31]

In this study, a significant proportion of participants had fungi cultured, including *Aspergillus spp*., yeast/

Table 3 Pharmacotherapy recorded for patients by micro-organism finding

Sputum microbiology	SABA ($n = 268$)	*P*-value	SAMA ($n = 32$)	*P*-value	LABA ($n = 265$)	*P*-value	LAMA ($n = 203$)	*P*-value	ICS ($n = 238$)	*P*-value
Haemophilus spp.	177 (66%)	0.963	19 (59.4%)	1.000	165 (62.3%)	1.000	133 (65.5%)	1.000	145 (60.9%)	1.000
Yeast/*Candida spp*.	152 (56.7%)	0.805	20 (62.5%)	1.000	156 (58.9%)	0.171	118 (58.1%)	0.805	138 (58%)	0.549
Streptococcus spp.	108 (40.3%)	0.927	14 (43.8%)	1.000	107 (40.4%)	0.927	85 (41.9%)	0.902	95 (39.9%)	1.000
Pseudomonas spp.	113 (42.2%)	0.037*	11 (34.4%)	1.000	110 (41.5%)	0.220	88 (43.3%)	0.220	103 (43.3%)	0.037*
Moraxella spp.	92 (34.3%)	0.549	11 (34.4%)	1.000	89 (33.6%)	0.902	65 (32%)	1.000	78 (32.8%)	1.000
Staphylococcus spp.	64 (23.9%)	0.244	10 (31.3%)	0.915	59 (22.3%)	0.915	47 (23.2%)	0.915	53 (22.3%)	0.951
Aspergillus spp.	32 (11.9%)	1.000	6 (18.8%)	0.951	34 (12.8%)	0.805	21 (10.3%)	1.000	30 (12.6%)	0.951
Mycobacteria	30 (11.2%)	1.000	3 (9.4%)	1.000	36 (13.6%)	1.000	22 (10.8%)	1.000	31 (13%)	1.000
Non-*Aspergillus* fungi	27 (10.1%)	1.000	2 (6.3%)	1.000	26 (9.8%)	1.000	21 (10.3%)	1.000	22 (9.2%)	1.000
Klebsiella spp.	19 (7.1%)	1.000	1 (3.1%)	1.000	17 (6.4%)	1.000	12 (5.9%)	1.000	17 (7.1%)	1.000

*Indicates *P*-value <0.05.
Values are displayed as median (interquartile range). *P*-value obtained via multivariate quantile regression, following Romano-Wolf adjustment.
ICS, inhaled corticosteroid; LABA, long-acting beta agonist; LAMA, long-acting muscarinic agent; SABA, short-acting beta agonist; SAMA, short-acting muscarinic agent; *spp*., species.

© 2025 The Author(s). *Internal Medicine Journal* published by John Wiley & Sons Australia, Ltd on behalf of Royal Australasian College of Physicians.

14455994, 2025, 5, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/imj.70020 by Edith Cowan University, Wiley Online Library on [18/05/2025]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Candida and non-*Aspergillus* fungi. Moreover, isolation of yeast/Candia *spp*. was associated with higher hospital admission rates and all-cause mortality. Again, the clinical relevance of this remains unclear, as the fungal load may be related to prior exposure to broad-spectrum antimicrobials. Moreover, we observed the concurrent presence of other microorganisms alongside yeast/*Candida spp*. (192 patients with yeast/*Candida*, during the same hospital admission also had concurrent sputum cultures positive for *Haemophilus*: seven (3.7%); *Pseudomonas*: six (3.1%); *Staphylococcus*: six (3.1%); and *Streptococcus*: three (1.6%)). Similarly, in a previous prospective, observational study, *Candida spp*. was attributed as the causative agent in community-acquired pneumonia and these patients were noted to demonstrate the concurrent presence of *S. pneumoniae*, *S. aureus*, or *Pseudomonas*.[32]

The significance of fungal isolates among patients with bronchiectasis has generally received little attention in the past, although this is gaining interest.[33,34] Studies have illustrated that differing social determinants and environmental exposures between populations may place non-Caucasian populations at higher risk of fungal infections than Caucasian populations.[35] Furthermore, indigenous peoples globally typically experience disadvantage with several social determinants, such as inadequate housing, household overcrowding, indoor air pollution, childhood chronic infections and poor access to health care and so forth.[36,37] Hence, growth of fungal species from sputum samples in Aboriginal Australian patients with bronchiectasis may require greater scrutiny.

Our study mirrored what has been demonstrated in previous reports, with the presence of *Pseudomonas spp*. being associated with poor outcomes.[38] A previous study from this region[10] had demonstrated a higher prevalence of *Pseudomonas spp*. cultured in non-Aboriginal patients in comparison to Aboriginal Australian patients with bronchiectasis; however, we did not have data to directly compare the outcomes between Aboriginal Australian and non-Aboriginal patients. Although isolation of *Staphylococcus spp*. was not associated with higher hospital admission rates as compared to patients demonstrating *Pseudomonas spp*. or yeast/*Candida spp*., the presence of *Staphylococcus spp*. showed a borderline significant association with all-cause mortality. Aboriginal Australians are reported to have higher rates of *Staphylococcus spp*. bacteraemia than non-Aboriginal Australians, including community-associated methicillin-resistant *Staphylococcus aureus*.[39] It is plausible that *Staphylococcus spp*. may have contributed to severe lower respiratory tract infection/pneumonia in our study cohort in the backdrop of having bronchiectasis.[40] Our study also showed that bronchiectasis is higher in females compared to males.[41] This may be attributed to a higher prevalence of underlying connective tissue diseases and influence of hormones in females.[42,43] In our study, we observed a marginally higher number of males with cultured Mycobacteria, in contrast to previous studies that have demonstrated an association between non-tuberculous mycobacteria and a female preponderance.[44]

Although we did not observe any correlation between inhaled pharmacotherapy and any studied outcomes, including hospitalisation rates and mortality, the use of ICSs was observed to be higher among patients with cultured *Pseudomonas spp*. It is difficult to conclude whether the use of ICSs influenced higher *Pseudomonas spp*. infection rates, including higher hospitalisation rates and mortality.

Immunoglobulin deficiencies are well established to be associated with bronchiectasis and to perpetrate ongoing respiratory tract infections.[19] However, rather than deficiency, we noticed higher immunoglobulin levels, especially for IgA and IgG. This finding may be reflective of continued chronic inflammatory responses to infections among our patients,[45] hence indirectly reflecting a persistent and chronic respiratory inflammatory process secondary to bronchiectasis.

Sputum microbiology profiles and related clinical outcomes in adult Aboriginal Australian patients with bronchiectasis diverge, at least in some respects, from what is conventionally known in other non-Indigenous populations. This is likely related to social determinants of health for Indigenous persons, as well as other complex health determinants, including differing aetiological factors and co-morbidities. There is also heterogeneity of bronchiectasis disease manifestations within the population and geographic regions. Hence, future prospective studies are needed to better understand sputum microbiology characteristics, including respiratory microbiome profiles not only among Aboriginal Australians but also Indigenous peoples globally.

Limitation

This study's outcomes pertain to Aboriginal Australian people residing in the TEHS region of Australia and the results cannot be generalised to the wider Aboriginal Australian population or to Indigenous people globally. All available sputum microbiology data were collected during the study window between 2011 and 2020 across various time points. Hence, we were not able to correlate accurately the sputum data with the related clinical outcomes, rather it was represented as overall outcomes. We did not collect treatment details during hospital admissions or during exacerbations. Nor did we examine

© 2025 The Author(s). *Internal Medicine Journal* published by John Wiley & Sons Australia, Ltd on behalf of Royal Australasian College of Physicians.

14455994, 2025, 5, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/imj.70020 by Edith Cowan University, Wiley Online Library on [18/05/2025]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

data on viruses (such as detection via polymerase chain reaction) and acknowledge their potential significance in bronchiectasis exacerbations. Moreover, we did not have lung function data or immunoglobulin data for all patients, which may have induced bias in these sections. Furthermore, the mortality data presented are all-cause related and as such we do not know whether the mortality was directly related to sputum microbiology results. Nevertheless, this is the first study to represent sputum microbiology data in an adult Aboriginal population with bronchiectasis from the top end NT making pathways for prospective studies for the future.

Conclusion

This study demonstrated heterogeneity in the sputum microbiology profile among adult Aboriginal Australian patients within the TEHS region. *Haemophilus spp*. was the most common microorganism and polymicrobial cultures were also common. *Pseudomonas spp*. and yeast/*Candida spp*. significantly increased hospitalisation rates and all-cause mortality. Immunoglobulin levels are high, potentially indicating persistent chronic respiratory inflammatory processes. Further prospective studies are warranted to better understand the respiratory microbiome among indigenous patients with bronchiectasis.

Acknowledgements

We thank the Thoracic Society of Australia and New Zealand (TSANZ) research grant assessment committee members for providing support through the Robert Pierce Grant-In-Aid for Indigenous Lung Health. We thank Associate Professor Linda Ford - indigenous Australian woman, a Mak Mak Marranunggu descendent from the Delissaville, Wagait Larrakia Aboriginal Land Trust and the Gurudju Aboriginal Land Trust in the TEHS region of NT in facilitating Mrs. Adriana Ticoalu from the Northern Institute, Charles Darwin University, Darwin, NT, Australia, in helping with gathering population data for this study. We extend our sincere apparition to all the health workers at the TEHS, in particular at the RDH, in providing care for our patients and to our current and former respiratory physicians. We also extend our sincere apparition to all the RDH medical services, in particular the Territory Pathology service. We also thank Dr. Shiidheshwar Ravichandran, Dr. Davaadorj Erdenebayar, Dr. Eleanor Bulford from the Division of Medicine, RDH and Flinders University medical students Haiping Zhou, George Kypreos and Bilal Mir for their help during this study. Open access publishing facilitated by Charles Darwin University, as part of the Wiley - Charles Darwin University agreement via the Council of Australian University Librarians.

References

1 Polverino E, Goeminne PC, McDonnell MJ, Aliberti S, Marshall SE, Loebinger MR *et al*. European respiratory society guidelines for the management of adult bronchiectasis. *Eur Respir J* 2017; **50**: 1700629.
2 Chalmers JD, Chang AB, Chotirmall SH, Dhar R, McShane PJ. Bronchiectasis. *Nat Rev Dis Primers* 2018; **4**: 45.
3 Solarat B, Perea L, Faner R, de La Rosa D, Martínez-García MÁ, Sibila O. Pathophysiology of chronic bronchial infection in bronchiectasis. *Arch Bronconeumol* 2023; **59**: 101–8.
4 Chandrasekaran R, Aogáin MM, Chalmers JD, Elborn SJ, Chotirmall SH. Geographic variation in the aetiology, epidemiology and microbiology of bronchiectasis. *BMC Pulm Med* 2018; **18**: 83.
5 Choi H, Lee H, Ra SW, Kim HK, Lee JS, Um SJ *et al*. On behalf of the KMBARC. Clinical characteristics of patients with post-tuberculosis bronchiectasis: findings from the KMBARC registry. *J Clin Med* 2021; **10**: 4542.
6 Statistics ABo. Snapshot of Northern Territory 2021 [Cited 2022 Jun 28]. Available from URL: https://www.abs.gov.au/articles/snapshot-nt-2021.
7 Howarth TP, Jersmann HPA, Majoni SW, Mo L, Ben Saad H, Ford LP *et al*. The 'ABC' of respiratory disorders among adult indigenous people: asthma, bronchiectasis and COPD among aboriginal Australians - a systematic review. *BMJ Open Respir Res* 2023; **10**: e001738.
8 AIo H, Welfare. *Australian burden of disease study: Impact and Causes of Illness and Death in Aboriginal and Torres Strait Islander People 2018*. Canberra: AIHW; 2022.
9 Howarth T, Heraganahally SS, Heraganahally SS. Bronchiectasis among adult first nations indigenous people – a scoping review. *Curr Respir Med Rev* 2023; **19**: 36–51.
10 Mehra S, Chang AB, Lam CK, Campbell S, Mingi JJ, Thomas I *et al*. Bronchiectasis among Australian aboriginal and non-aboriginal patients in the regional and remote population of the Northern Territory of Australia. *Rural Remote Health* 2021; **21**: 6390.
11 Pak A, Adegboye OA, Eisen DP, McBryde ES. Hospitalisations related to lower respiratory tract infections in northern Queensland. *Aust N Z J Public Health* 2021; **45**: 430–6.
12 Heraganahally SS, Ghimire RH, Howarth T, Kankanamalage OM, Palmer D, Falhammar H. Comparison and outcomes of emergency department presentations with respiratory disorders among Australian indigenous and non-indigenous patients. *BMC Emerg Med* 2022; **22**: 11.
13 Chalmers JD, Smith MP, McHugh BJ, Doherty C, Govan JR, Hill AT. Short- and long-term antibiotic treatment reduces airway and systemic inflammation in non-cystic fibrosis bronchiectasis. *Am J Respir Crit Care Med* 2012; **186**: 657–65.
14 Metersky ML, Aksamit TR, Barker A, Choate R, Daley CL, Daniels LA *et al*. The prevalence and significance of staphylococcus aureus in patients with non-cystic fibrosis bronchiectasis. *Ann Am Thorac Soc* 2018; **15**: 365–70.
15 Chalmers JD, Hill AT. Mechanisms of immune dysfunction and bacterial

© 2025 The Author(s). *Internal Medicine Journal* published by John Wiley & Sons Australia, Ltd on behalf of Royal Australasian College of Physicians.

14455994, 2025, 5, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/imj.70020 by Edith Cowan University, Wiley Online Library on [18/05/2025]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

persistence in non-cystic fibrosis bronchiectasis. *Mol Immunol* 2013; **55**: 27–34.
16 Einsiedel L, Fernandes L, Spelman T, Steinfort D, Gotuzzo E. Bronchiectasis is associated with human T-lymphotropic virus 1 infection in an indigenous Australian population. *Clin Infect Dis* 2012; **54**: 43–50.
17 Gibbs C, Howarth T, Ticoalu A, Chen W, Abeyaratne A, Ford LP *et al*. Bronchiectasis among indigenous adults in the top end of the Northern Territory, 2011–2020: a retrospective cohort study. *Med J Aust* 2024; **220**: 188–95.
18 Blackall SR, Hong JB, King P, Wong C, Einsiedel L, Rémond MGW *et al*. Bronchiectasis in indigenous and non-indigenous residents of Australia and New Zealand. *Respirology* 2018; **23**: 743–9.
19 Boyton RJ, Altmann DM. Bronchiectasis: current concepts in pathogenesis, immunology, and microbiology. *Ann Rev Pathol: Mech Dis* 2016; **11**: 523–54.
20 Biatobock DR, da SM PM, Olmedo DWV, Barlem ELD, Ramos DF. Bronchiectasis: morbidity and mortality in Brazil and its impact on hospitalization rates. *Rev Soc cient Parag* 2022; **27**: 61–73.
21 McShane PJ, Naureckas ET, Strek ME. Bronchiectasis in a diverse US population: effects of ethnicity on etiology and sputum culture. *Chest* 2012; **142**: 159–67.
22 Borekci S, Halis AN, Aygun G, Musellim B. Bacterial colonization and associated factors in patients with bronchiectasis. *Ann Thorac Med* 2016; **11**: 55–9.
23 Vigneault LP, Diendere E, Sohier-Poirier C, Hanna MA, Poirier A, St-Onge M. Acute health care among indigenous patients in Canada: a scoping review. *Int J Circumpolar Health* 2021; **80**: 1.
24 Cleary DW, Morris DE, Anderson RA, Jones J, Alattraqchi AG, Rahman NIA *et al*. The upper respiratory tract microbiome of indigenous orang Asli in north-eastern peninsular Malaysia. *Biofilms Microbiomes* 2021; **7**: 1.
25 Coleman A, Zaugg J, Wood A, Cottrell K, Håkansson EG, Adams J *et al*. Upper respiratory tract microbiome of Australian aboriginal and Torres Strait islander children in ear and nose health and disease. *Microbiol Spectr* 2021; **9**: e0036721.
26 Bopaka RG, El Khattabi W, Janah H, Jabri H, Afif H. Bronchiectasis: a bacteriological profile. *Pan Afr Med J* 2015; **22**: 378.
27 Sunny S, Ninan M. Clinical, radiological and microbiological profile of patients with bronchiectasis in a tertiary care center in South Kerala. *Ind J Immunol Respir Med* 2023; **8**: 79–86.
28 Shahid S, Jabbar ABA, Wagley A, Musharraf MD, Zahid H, Zubair SM *et al*. Non-cystic fibrosis bronchiectasis: a retrospective review of clinical, radiological, microbiological and lung function profile at a tertiary care center of low-middle income country. *Monaldi Arch Chest Dis* 2023; **94**. https://doi.org/10.4081/monaldi.2023.2718.
29 Polverino E, Rosales-Mayor E, Torres A. Exacerbation of Bronchiectasis Bronchiectasis 2017:205–22. https://doi.org/10.1007/978-3-319-61452-6_15.
30 Richardson H, Dicker AJ, Barclay H, Chalmers JD. The microbiome in bronchiectasis. *Eur Respir Rev* 2019; **28**: 190048.
31 Purcell P, Jary H, Perry A, Perry JD, Stewart CJ, Nelson A *et al*. Polymicrobial airway bacterial communities in adult bronchiectasis patients. *BMC Microbiol* 2014; **14**: 130.
32 Moss BJ, Musher DM. Candida species in community-acquired pneumonia in patients with chronic aspiration. *Pneumonia (Nathan)* 2021; **13**: 12.
33 Máiz L, Nieto R, Cantón R, de la Pedrosa EGG, Martinez-García MÁ. Fungi in bronchiectasis: a concise review. *Int J Mol Sci* 2018; **19**: 142.
34 Cuthbertson L, Felton I, James P, Cox MJ, Bilton D, Schelenz S *et al*. The fungal airway microbiome in cystic fibrosis and non-cystic fibrosis bronchiectasis. *J Cyst Fibros* 2021; **20**: 295–302.
35 Jenks JD, Aneke CI, Al-Obaidi MM, Egger M, Garcia L, Gaines T *et al*. Race and ethnicity: risk factors for fungal infections? *PLoS Pathog* 2023; **19**: e1011025.
36 Bailie RS, Wayte KJ. Housing and health in indigenous communities: key issues for housing and health improvement in remote aboriginal and Torres Strait islander communities. *Aust J Rural Health* 2006; **14**: 178–83.
37 Kovesi T, Gilbert NL, Stocco C, Fugler D, Dales RE, Guay M *et al*. Indoor air quality and the risk of lower respiratory tract infections in young Canadian inuit children. *CMAJ* 2007; **177**: 155–60.
38 Evans SA, Turner SM, Bosch BJ, Hardy CC, Woodhead MA. Lung function in bronchiectasis: the influence of Pseudomonas aeruginosa. *Eur Respir J* 1996; **9**: 1601–4.
39 Tong SY, van Hal SJ, Einsiedel L, Currie BJ, Turnidge JD. Australian New Zealand cooperative on outcomes in staphylococcal sepsis. Impact of ethnicity and socio-economic status on Staphylococcus aureus bacteremia incidence and mortality: a heavy burden in indigenous Australians. *BMC Infect Dis* 2012; **12**: 249.
40 Clemente MG, Olveira C, Girón R, Máiz L, Sibila O, Golpe R *et al*. Impact of chronic bronchial infection by staphylococcus aureus on bronchiectasis. *J Clin Med* 2022; **11**: 3960.
41 Venning V, Bartlett J, Jayaram L. Patients hospitalized with an infective exacerbation of bronchiectasis unrelated to cystic fibrosis: clinical, physiological and sputum characteristics. *Respirology* 2017; **22**: 922–7.
42 Zhou YY, Wang YH, He SQ, Wang WY, Wang XY, Li DS *et al*. Gender differences in clinical characteristics of patients with non-cystic fibrosis bronchiectasis in different age groups in northern China. *Clin Respir J* 2023; **17**: 311–9.
43 Vidaillac C, Yong VFL, Jaggi TK, Soh MM, Chotirmall SH. Gender differences in bronchiectasis: a real issue? *Breathe (Sheff)* 2018; **14**: 108–21.
44 Mirsaeidi M, Sadikot RT. Gender susceptibility to mycobacterial infections in patients with non-CF bronchiectasis. *Int J Mycobacteriol* 2015; **4**: 92–6.
45 Stead A, Douglas JG, Broadfoot CJ, Kaminski ER, Herriot R. Humoral immunity and bronchiectasis. *Clin Exp Immunol* 2002; **130**: 325–30.

© 2025 The Author(s). *Internal Medicine Journal* published by John Wiley & Sons Australia, Ltd on behalf of Royal Australasian College of Physicians.

14455994, 2025, 5, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/imj.70020 by Edith Cowan University, Wiley Online Library on [18/05/2025]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Supporting Information

Additional supporting information may be found in the online version of this article at the publisher's web-site:

Supplementary Figure 1 Pearson pairwise correlations for sputum microbiology results.
Supplementary Figure 2 Differences in sputum microbiology by geographic region.
Supplementary Table 1 Categorisation of sputum cultures in the study participants.
Supplementary Table 2. Demographic and clinical profile of included patients by gender.
Supplementary Table 3. Co-occurrence of sputum cultures within patients with bronchiectasis.
Supplementary Table 4. Demographic and clinical details for patients who recorded either non-*Aspergillus* fungi or *Pseudomonas spp*. culture, compared with those who did not.

© 2025 The Author(s). *Internal Medicine Journal* published by John Wiley & Sons Australia, Ltd on behalf of Royal Australasian College of Physicians.

14455994, 2025, 5, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/imj.70020 by Edith Cowan University, Wiley Online Library on [18/05/2025]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License