Background: Biologic disease modifying anti-rheumatic drugs (bDMARDs) have significantly improved the prognosis for patients with rheumatoid arthritis (RA). However, due to their immunosuppressive nature, concerns remain about the potential for infection in patients receiving these medications. Aims: To evaluate the incidence of serious infections (SI) in a Western Australian cohort of patients with RA who are receiving bDMARDs. The role of confounders including age, gender, comorbidities and use of glucocorticoids was also evaluated. The incidence of SI was defined as any infection necessitating admission to the hospital and the use of antibiotics. Methods: A 10-year retrospective review was conducted of all patients with RA who were receiving bDMARDs at three tertiary hospitals in Western Australia. Discharge summaries and all available clinic letters were reviewed and patient demographics and clinical data were collected. Pearson Chi-squared test and Student’s t-test were used for comparing demographic factors and clinical variables between the groups with SI and those without. Results: One hundred and two patients met the inclusion criteria for the period 2006–2016, 25 of whom had been admitted with SI, accounting for a total of 46 admissions. Skin and soft tissue infections were the most common (28%) followed by respiratory infections (26%) and urinary tract infections (20%). The incidence rate of SI was 8.98 per 100 person years. The rate was lowest with adalimumab (5.27 per 100 person years) and highest with infliximab (34.5 per 100 person years). Those with SI were older (68 years vs 60 years; P = 0.02) and had been on bDMARDs for longer period of time (6.05 years vs 4.68 years; P = 0.04). There was no significant increase in length of stay due to co-administration of glucocorticoids. The presence of comorbidities did not play a significant role in increasing the risk of SI. Conclusion: Age and duration of bDMARD use were statistically significant factors associated with an increased risk of SI. Comorbidities did not play a significant role in increasing the incidence of SI. Patients who were on both glucocorticoids and bDMARDs did not have a significant increase in length of stay when compared with patients who were just on bDMARDs. More research is needed in this area with larger numbers to draw statistically significant conclusions regarding the role of comorbidities in SI risk and the individual infection risk associated with each bDMARD.

The aim of this study was to describe the burden and organism antibiotic resistance patterns of skin and soft tissue infections (SSTI) due to Staphylococcus aureus presenting in a remote Australian Northern Territory community in the Barkly region. We collated reported antibiograms of all skin and superficial soft tissue swab specimens obtained from the town's Indigenous medical clinic from 12 of the 13 months between November 2016 and December 2017. Clinician's notes for the consultation associated with each test request were examined to determine the nature of the clinical problem and to access other relevant data. Amongst 309 tissue swab specimens, S. aureus was cultured in 215 (70%), of which 202 isolations were from Indigenous Australians. Of the 215 S. aureus, 98 [46%, 95% confidence interval (CI) 31–52] were methicillin resistant S. aureus (MRSA) and 117 (54%, 95% CI 48–61) sensitive (MSSA). Significant numbers were also resistant to other frequently used oral antibiotics, with resistance to erythromycin in 52 (24%), clindamycin in 51 (24%), trimethoprim in 22 (10%) and fusidic acid in eight (4%). In the Barkly region of Australia's NT in 2017, community-acquired staphylococcal SSTI needing professional care is equally likely to be caused by MRSA as by MSSA

To estimate prevalence and persistence of 19 common paediatric conditions from infancy to 14-15 years. Design: Population-based prospective cohort study. Setting: Australia. Participants: Parallel cohorts assessed biennially from 2004 to 2014 from ages 0-1 and 4-5 years to 10-11 and 14-15 years, respectively, in the Longitudinal Study of Australian Children. Main outcome measures: 19 health conditions: 17 parent-reported, 2 (overweight/obesity, obesity) directly assessed. Two general measures: health status, special health care needs. Analysis: (1) prevalence estimated in 2-year age-bands and (2) persistence rates calculated at each subsequent time point for each condition among affected children. Results: 10 090 children participated in Wave 1 and 6717 in all waves. From age 2, more than 60% of children were experiencing at least one health condition at any age. Distinct prevalence patterns by age-bands comprised eight conditions that steadily rose (overweight/obesity, obesity, injury, anxiety/depression, frequent headaches, abdominal pain, autism spectrum disorder, attention-deficit hyperactivity disorder). Six conditions fell with age (eczema, sleep problems, day-wetting, soiling, constipation, recurrent tonsillitis), three remained stable (asthma, diabetes, epilepsy) and two peaked in mid-childhood (dental decay, recurrent ear infections). Conditions were more likely to persist if present for 2 years; persistence was especially high for obesity beyond 6-7 (91.3%-95.1% persisting at 14-15). Conclusions: Beyond infancy, most Australian children are experiencing at least one ongoing health condition at any given time. This study's age-specific estimates of prevalence and persistence should assist families and clinicians to plan care. Conditions showing little resolution (obesity, asthma, attention-deficit hyperactivity disorder) require long-term planning and management.

The Central Australian Indigenous population has a high incidence of Staphylococcus aureus bacteremia (SAB) but little is known about the local molecular epidemiology. Methods: Prospective observational study of bacteremic and nasal colonizing S.aureus isolates between June 2006 to June 2010. All isolates underwent single nucleotide polymorphism (SNP) genotyping and testing for the presence of the Panton-Valentine Leucocidin (pvl) gene. Results: Invasive isolates (n=97) were predominantly ST93 (26.6%) and pvl positive (54.3%), which was associated with skin and soft tissue infections (OR 4.35, 95% CI 1.16, 16.31). Non-multiresistant MRSA accounted for 31.9% of bacteremic samples and showed a trend to being healthcare associated (OR 2.16, 95% CI 0.86, 5.40). Non-invasive isolates (n=54) were rarely ST93 (1.9%) or pvl positive (7.4%). Conclusions: In Central Australia, ST93 was the dominant S.aureus clone, and was frequently pvl positive and associated with an aggressive clinical phenotype. Whether non-nasal carriage is more important with invasive clones or whether colonization occurs only transiently remains to be elucidated.

Two meticillin-resistant Staphylococcus aureus (MRSA) clones, sequence type (ST) 22 and ST239, have successfully spread globally. Across Australia, ST22 has supplanted ST239 as the main healthcare-associated MRSA. To understand the reasons underlying this shift, the epidemiology and clinical features of infections due to ST22 and ST239 MRSA isolates from a tertiary hospital in Melbourne, Australia were compared. Methods: Over six months, consecutive MRSA isolates with clinical data were collected from specimens referred to Alfred Health Pathology (AHP). Isolates were genotyped by a multi-locus-sequence-typing-based high-resolution melting method. Findings: Three hundred and twenty-eight of 1079 (30%) S. aureus isolated by AHP were MRSA. Of these, 313 were genotyped; 78 (25%) were clonal complex (CC) 22 (representing ST22) and 142 (45%) were CC239 (representing ST239). Common clinical syndromes included skin or soft tissue, respiratory tract and osteo-articular infections. On multi-variate logistic regression, compared with CC239, CC22 was associated with older patients [adjusted odds ratio (aOR) 1.04 for each year increase, 95% confidence interval (CI) 1.02-1.07)], and patients from subacute hospitals (aOR 2.7, 95% CI 1.2-5.8) or long-term care facilities (LTCFs; aOR 5.5, 95% CI 2.0-14.5). Median time from patient admission to MRSA isolation was nine days for CC239 and one day for CC22 (< 0.01). MRSA strain epidemiology varied according to hospital unit. Conclusions: CC22 and CC239 MRSA have differing ecological niches. CC22 is associated with elderly patients in LTCFs, and CC239 is associated with nosocomial acquisition. Infection control strategies involving LTCFs and their residents will likely be required to achieve continued MRSA control.

There are limited data on the epidemiology, diagnosis and optimal management of nontuberculous mycobacterial (NTM) disease in children. Methods: Retrospective cohort study of NTM cases over a 10-year-period at a tertiary referral hospital in Australia. Results: A total of 140 children with NTM disease, including 107 with lymphadenitis and 25 with skin and soft tissue infections (SSTIs), were identified. The estimated incidence of NTM disease was 0.6-1.6 cases / 100,000 children / year; no increasing trend was observed over the study period. Temporal analyses revealed a seasonal incidence cycle around 12 months, with peaks in late winter/spring and troughs in autumn. Mycobacterium-avium-complex accounted for most cases (77.8%), followed by Mycobacterium ulcerans (14.4%) and Mycobacterium marinum (3.3%). Polymerase chain reaction testing had higher sensitivity than culture and microscopy for acid-fast bacilli (92.0%, 67.2% and 35.7%, respectively). The majority of lymphadenitis cases underwent surgical excision (97.2%); multiple recurrences in this group were less common in cases treated with clarithromycin and rifampicin compared with clarithromycin alone or no anti-mycobacterial drugs (0% versus 7.1%; OR:0.73). SSTI recurrences were also less common in cases treated with two anti-mycobacterial drugs compared with one or none (10.5% versus 33.3%; OR:0.23). Conclusions: There was seasonal variation in the incidence of NTM disease, analogous to recently published observations in tuberculosis, which have been linked to seasonal variation in vitamin D. Our finding that anti-mycobacterial combination therapy was associated with a reduced risk of recurrences in patients with NTM lymphadenitis or SSTI requires further confirmation in prospective trials. © 2016 Tebruegge et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Scabies is a skin disease that, through secondary bacterial skin infection (impetigo), can lead to serious complications such as septicaemia, renal disease, and rheumatic heart disease. Yet the worldwide prevalence of scabies is uncertain. We undertook a systematic review, searching several databases and the grey literature, for population-based studies that reported on the prevalence of scabies and impetigo in a community setting. All included studies were assessed for quality. 2409 articles were identified and 48 studies were included. Data were available for all regions except North America. The prevalence of scabies ranged from 0·2% to 71·4%. All regions except for Europe and the Middle East included populations with a prevalence greater than 10%. Overall, scabies prevalence was highest in the Pacific and Latin American regions, and was substantially higher in children than in adolescents and adults. Impetigo was common, particularly in children, with the highest prevalence in Australian Aboriginal communities (49·0%). Comprehensive scabies control strategies are urgently needed, such as a community-based mass drug administration approach, along with a more systematic approach to the monitoring of disease burden.

The clinical and molecular epidemiology of Staphylococcus aureus disease has changed considerably over the past two decades, particularly with the emergence and spread of community-associated methicillin-resistant S. aureus (CA-MRSA) clones. Indeed, some of the first global descriptions of CA-MRSA were from remote indigenous communities in Western Australia, and from Pacific Peoples in New Zealand. The epidemiology of S. aureus infections in the South West Pacific has several unique features, largely because of the relative geographical isolation and unique indigenous communities residing in this region. In particular, a number of distinct CA-MRSA clones circulate in Australia and New Zealand, such as sequence type (ST) 93 methicillin-resistant S. aureus (MRSA) (Queensland clone) and clonal complex 75 S. aureus (Staphylococcus argenteus) in Australia, and ST30 MRSA (Southwest Pacific clone) in New Zealand. In addition, there is a disproportionate burden of S. aureus disease in indigenous paediatric populations, particularly in remote Aboriginal communities in Australia, and in Pacific Peoples and Maori in New Zealand. In this review, we provide a contemporary overview of the clinical and molecular epidemiology of S. aureus disease in the South West Pacific region, with a particular focus on features distinct to this region.

We used a national survey of 7578 randomly selected respondents in 2008-2009 to identify the period prevalence of acute respiratory infection (ARI) by season and state, and to estimate the incidence of ARI in the Australian community. A case was defined as any episode of cold or flu with at least one of the following symptoms: fever, chills, sore throat, running nose, or cough in the past 4 weeks. Frequency data were weighted to the Australian population. The response rate to the survey was 49%, and 19·9% (1505/7578) of respondents reported an ARI in the previous 4 weeks, which extrapolated to 68·9 million cases [95% confidence interval (CI) 65·1-72·7] of ARI in Australia annually. The incidence was 3·2 (95% CI 3·0-3·4) cases of ARI/person per year, and was highest in young children and lowest in older people. ARI imposes a significant burden on Australian society.

Development of a group B streptococcal vaccine (GBS) vaccine is the most promising approach for the prevention of GBS infections in babies, given the potential adverse effects of intrapartum antibiotic prophylaxis as well as the need for effective prevention of both adult and late perinatal disease. There are numerous prevention strategies at this time but none are 100% effective in the eradication of neonatal early onset GBS disease and there are no preventative strategies for late onset disease. The need for a GBS vaccine is therefore, of utmost importance. Efforts applying genomics to GBS vaccine development have led to the identification of novel vaccine candidates. The publication of GBS whole genomes coupled with new technologies including multigenome screening and bioinformatics has also allowed researchers to overcome the serotype limitation of earlier vaccine preparations in the search of a universal effective vaccine against GBS. This review brings together the key arguments concerning the potential need of a GBS vaccine in developed countries and describes the current status with GBS epidemiology and microbiology in these countries.

Following the recent H1N1 influenza pandemic we were able to describe seropositivity in a repre-sentative sample of adults prior to the availability of a specific vaccine. Methods: This cross-sectional serological study is set in the Barwon Statistical Division, Australia. Blood samples were collected from September 2009 through to May 2010, from 1184 individuals (569 men, 615 women; median age 61.7 years), randomly selected from electoral rolls. Serum was analysed for specific H1N1 immunity using a haemagglutination inhibition test. A self-report provided information about symptoms, demographics and healthcare. Associations between H1N1 infection, gender, households and occupation were determined using logistic regression, adjusting for age. Results: Of 1184 individuals, 129 (58 men, 71 women) were seropositive. Gender-adjusted age-specific prevalence was: 8.3% 20-29 years, 13.5% 30-39, 10.4% 40-49, 6.5% 50-59, 9.7% 60-69, 10.3% 70-79, 18.8% 80+. Standardised prevalence was 10.3% (95%CI 9.6-11.0). No associations were detected between seropositivity and gender (OR=0.82, 95%CI 0.57-1.19) or being a healthcare worker (OR=1.43, 95%CI 0.62-3.29). Smokers (OR=1.86, 95%CI 1.09-3.15) and those socioeconomically disadvantaged (OR=2.52, 95%CI 1.24-5.13) were at increased risk. Among 129 seropositive individuals, 31 reported symptoms that were either mild (n = 13) or moderate (time off work, doctor visit, n = 18). For age <60, 39.6% of seropositive individuals reported symptoms, whereas the proportion was 13.2% for age 60+. Conclusions: Following the pandemic, the proportion of seropositive adults was low, but significant subclinical infection was found. Social disadvantage increased the likelihood of infection. The low symptom rate for older ages may relate to pre-existing immunity.

Background Infection control and antibiotic resistant organisms are a community health concern. This article presents findings of a cross sectional study of 100 users of the Thirroul Medical Practice clinical treatment room, in Thirroul, New South Wales. Methods Nasal Staphylococcus aureus colonisation rates and risk factors were investigated. Results Twenty-six percent of participants (n=26) were found to have S. aureus; 11.5% (n=3) of cases were community acquired methicillin resistant S. aureus. Methicillin resistant S. aureus was significantly correlated with older age (p=0.02) and skin infection within the preceding year (p=0.03). Clinical staff (n=15) had low rates of S. aureus at 6.6% (n=1) and no methicillin resistant S. aureus. Discussion Overall, S. aureus rates were unremarkable, but methicillin resistant S. aureus rates were higher than elsewhere with older patients most at risk. General practice staff developing infection control strategies should consider the vulnerable nature and cross-contamination risks in this group of patients. Encouragingly, clinical staff showed low levels of S. aureus and no methicillin resistant S. aureus.

Over 20 years, from October 1989, the Darwin prospective melioidosis study has documented 540 cases from tropical Australia, providing new insights into epidemiology and the clinical spectrum. Principal Findings: The principal presentation was pneumonia in 278 (51%), genitourinary infection in 76 (14%), skin infection in 68 (13%), bacteremia without evident focus in 59 (11%), septic arthritis/osteomyelitis in 20 (4%) and neurological melioidosis in 14 (3%). 298 (55%) were bacteremic and 116 (21%) developed septic shock (58 fatal). Internal organ abscesses and secondary foci in lungs and/or joints were common. Prostatic abscesses occurred in 76 (20% of 372 males). 96 (18%) had occupational exposure to Burkholderia pseudomallei. 118 (22%) had a specific recreational or occupational incident considered the likely infecting event. 436 (81%) presented during the monsoonal wet season. The higher proportion with pneumonia in December to February supports the hypothesis of infection by inhalation during severe weather events. Recurrent melioidosis occurred in 29, mostly attributed to poor adherence to therapy. Mortality decreased from 30% in the first 5 years to 9% in the last five years (p<0.001). Risk factors for melioidosis included diabetes (39%), hazardous alcohol use (39%), chronic lung disease (26%) and chronic renal disease (12%). There was no identifiable risk factor in 20%. Of the 77 fatal cases (14%), 75 had at least one risk factor; the other 2 were elderly. On multivariate analysis of risk factors, age, location and season, the only independent predictors of mortality were the presence of at least one risk factor (OR 9.4; 95% CI 2.3-39) and age ≥ 50 years (OR 2.0; 95% CI 1.2-2.3). Conclusions: Melioidosis should be seen as an opportunistic infection that is unlikely to kill a healthy person, provided infection is diagnosed early and resources are available to provide appropriate antibiotics and critical care.

Methicillin-resistant Staphylococcus aureus (MRSA) PFGE strain type USA300 (multilocus sequence type 8, clonal complex 8, staphylococcal cassette chromosome mec type IV) was first reported in the USA as a cause of skin and soft issue infection among college football players in Pennsylvania and among prisoners in Missouri in 2000. Over the next 5 years, USA300 became the predominant community-associated MRSA strain in the USA. It was the most common PFGE type recovered from skin and soft tissue infections in persons presenting to 11 emergency departments across the USA, and caused outbreaks in Native American populations, children in daycare centres, military recruits, prison inmates and among men who have sex with men. Although predominantly a cause of skin and soft issue infection, USA300 isolates also have been recovered from cases of invasive disease including bacteraemia, endocarditis, severe necrotizing pneumonia and osteomyelitis. Isolates of USA300 usually carry the genes encoding the Panton-Valentine leucocidin and the arginine catabolic mobile element, but rarely carry staphylococcal enterotoxin genes. USA300 isolates are becoming more resistant to antimicrobial agents, including erythromycin, levofloxacin, mupirocin and tetracycline, and have spread to Europe, South America and Australia. The emergence of the MRSA USA300 strain type represents a unique biological success story.

To determine the prevalence, incidence and risk factors for pharyngeal Chlamydia trachomatis in the community based Health in Men (HIM) cohort of HIV negative homosexual men in Sydney, Australia. Methods: From January 2003, all HIM participants were offered annual screening for pharyngeal chlamydia using BD ProbeTec nucleic acid amplification testing (NAAT). Detailed sexual behavioural data were collected every 6 months, and risk factors for infection and hazard ratios were calculated using Cox regression. Results: Among 1427 participants enrolled, the prevalence of pharyngeal chlamydia on initial testing was 1.06% and the incidence rate was 0.58 per 100 person-years. More than 50% of all infections were identified on baseline testing and 68% of men with pharyngeal infection had no evidence of concurrent anogenital chlamydia. There was no association of pharyngeal chlamydia with sore throat. Infection was significantly associated with increasing frequency of receptive penile-oral sex with ejaculation with casual partners (p = 0.009), although approximately half of infections occurred in participants not reporting this risk behaviour. Neither kissing nor oro-anal practices were associated with infection. Conclusion: The incidence of pharyngeal chlamydia infection in the HIM study was relatively low; however, the relatively high prevalence on baseline testing compared to incidence suggests a long duration of infection. Occasional screening for pharyngeal chlamydia in homosexual men who frequently practise receptive oral sex with ejaculation may be warranted.

Streptococcus dysgalactiae subsp. equisimilis (groups C and G streptococci [GCS/GGS]) is an increasingly recognized human pathogen, although it may follow indirect pathways. Prospective surveillance of selected households in 3 remote Aboriginal communities in Australia provided 337 GCS/GGS isolates that were emm sequence-typed. Lancefield group C isolates (GCS) were localized to specific households and group G isolates (GGS) were more evenly distributed. GCS/GGS was more frequently recovered from the throat than group A streptococci (GAS [S. pyogenes]) but rarely recovered from skin sores, and then only with Staphylococcus aureus or GAS. Symptomatic GGS/GGC pharyngitis was also rare. Specific emm sequence types of GCS/GGS did not appear to cycle through the communities (sequential strain replacement) in a manner suggesting acquisition of type-specific immunity. These communities already have high levels of streptococcal and poststreptococcal disease. GCS/GGS may increase in importance as it acquires key virulence factors from GAS by lateral gene transfer.