The social network in cystic fibrosis centre care and the risk of shared \textit{Pseudomonas aeruginosa} strain infection

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\textbf{Background:} During a recent national prevalence study of 983 Australian cystic fibrosis (CF) patients two predominant \textit{Pseudomonas aeruginosa} genotypes, AUST-01 and AUST-02, were identified in 22\% and 18\% patients, respectively. It is unclear whether patient movement plays a role in the distribution and prevalence of these strains.

\textbf{Objectives:} To explore prior patient movement between Australian CF centres and to describe and visualise the network characteristics of AUST-01 and AUST-02 infection.

\textbf{Methods:} Patient movements were analysed using social network analysis, using a 2-mode network and two 1-mode networks (patients linked to other patients via a common centre and a network of centres linked to other centres via a common patient). Network connectivity included estimations of degree centrality, k-core membership and betweenness.

\textbf{Results:} A total of 515 (52\%) patients established prior contact with at least one other centre, 126 (13\%) with at least two centres, and 20 (2\%) with at least three other centres. The proportion of AUST-01 and AUST-02 infections in patients highly connected to other centres (contact with at least 1, 2 or 3 centres) was significantly higher (mean: 24\%) than patients with no prior centre contact (mean: 12\%).

\textbf{Conclusion:} The association of patients with a limited set of centres may support \textit{P. aeruginosa} transmission. Capturing patient-centre network connectivity improves our ability to explain the potential transmission of dominant shared \textit{P. aeruginosa} strains.

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\textbf{445} The prevalence and significance of methicillin resistant \textit{Staphylococcus aureus} infection in patients with cystic fibrosis in a Macedonian CF center

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\textbf{Objectives:} Pulmonary infection with MRSA is an increasing problem for patients with CF over the past decade. The objectives of this study were to determine the prevalence of MRSA infection in a Macedonian CF center and the impact of chronic MRSA colonization on lung function and nutritional status. The efficacy of our eradication strategy was also assessed.

\textbf{Methods:} A retrospective review of all MRSA-positive patients from 2007 to 2012 was undertaken. Chronic infection was defined as persistently or ≥3 consecutive MRSA-positive respiratory cultures during at least 6 months follow-up period. Data collected included FVC, FEV\textsubscript{1}, and standard deviation score for weight for height (z/W/H), prior and two years after MRSA diagnosis. MRSA eradication was attempted with two oral antibiotics for 4 weeks and nebulised Vancomycin for 2 weeks.

\textbf{Results:} Of 110 CF patients (aged 1−31 years), 37 (33.6\%) were identified as having respiratory cultures positive for MRSA at some point in time. Mean age at first acquisition of MRSA was 8.6±5.9 years. 14 have developed chronic infection, thus, successful eradication was achieved in 62\% of patients. The prevalence of chronic MRSA colonization in our CF population amounted to 12.7\%. Mean FVC, FEV\textsubscript{1}, and z/W/H values, prior and two years after MRSA colonization, in this group were: 91.9±21.1 vs 92.3±20.6, 89.7±24.2 vs 82.8±23.2, −0.09±0.8 vs −0.02±0.7, respectively. The differences were not significant.

\textbf{Conclusions:} Chronic MRSA infection has neutral or deleterious effects in patients with more severe lung disease. High prevalence of MRSA infection in our center indicate the needs for enhanced segregation, infection control policy and eradication treatment.

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\textbf{446} A multiple-locus variable-number tandem repeat analysis (MLVA) typing scheme developed for genetic fingerprinting of \textit{Burkholderia cenocepacia} and applied to nation-wide epidemiological analysis

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\textbf{Objectives:} \textit{Burkholderia cenocepacia} complex organisms are recognized to be transmitted among patients, requiring epidemiological surveillance. We describe a MLVA typing scheme for \textit{B. cenocepacia} and applied to nation-wide population analysis. The development of a MLVA scheme for \textit{B. multicroarum} accounts for most infections.

\textbf{Methods:} Potential VNTR loci were identified upon analysis of the annotated genome sequences of strain AU1054, J2315 and MCO-3, and 10 of them were selected on the basis of polymorphism and repeat size. A collection of 100 \textit{B. cenocepacia} isolates (49 IIA, 41 IIB, 8 IIIC and 2 IIID), including 75 clinical isolates from the Observatoire cepacia collection, and 25 reference strains, was used to evaluate typeability, epidemiological concordance and discriminatory power of MLVA, compared with PCR-rhibotyping, PFGE, and, if discordant, with MLST. Stability was assessed by testing 39 successive isolates from 13 patients.

\textbf{Results:} Typeability ranged from 91 to 100\%, except for 1 marker, which was not amplified in 53\% of IIA isolates. Allelic variation was more important in IIIB than within IIA isolates. The analysis of 39 epidemiologically related strains demonstrated complete epidemiological concordance. Discriminatory power was assessed comparing 59 epidemiologically unrelated isolates, which were distributed in 28 unique MLVA types and 10 shared types, among which 4 belonged to globally distributed lineages (ST32, ST122, ST234, ST241). MLVA types were shown to be stable in 11 patients, whereas a single locus variation was observed in 2 patients.

\textbf{Conclusion:} MLVA appears to be a promising cost-effective method for \textit{B. cenocepacia} population analysis. The development of a MLVA scheme for \textit{B. multicroarum} is in progress.

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\textbf{447} Trombones – A potential source of recurrent \textit{Burkholderia cepacia} complex infection?

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\textbf{Objectives:} \textit{Burkholderia cepacia} complex (Bcc) is a significant cause of morbidity and mortality in people with cystic fibrosis (CF). Infection with some members of the Bcc (e.g. \textit{Burkholderia cenocepacia}) can also be a contra-indication to transplantation. We report a case of recurrent \textit{Burkholderia cepacia} IIIB (BC IIIB) infection in which a trombone was implicated as a potential source of recurrence.

\textbf{Methods:} In February 2009 a routine sputum sample from 48 year old male with CF grew BC IIIB. The identity was confirmed by recA sequencing. Eradication therapy was commenced immediately and he received two weeks of intravenous amikacin, meropenem and cefazidime in combination, all three of which the isolate was susceptible to. This was followed by a further three months of aerosolised amikacin which stopped in June 2009. Over the next year the patient submitted 11 sputum samples, all of which were negative for Bcc. However, in July 2010 a sputum sample again grew BC IIIB. Despite further attempts to eradicate the organism it persisted and he was still sputum-positive for BC IIIB in October 2012. The subject was noted to be a keen trombone player. In August 2010 the instrument was sampled. Although samples from the mouthpiece and bell failed to yield BC IIIB, the organism was isolated from the spit value.

\textbf{Conclusion:} Musical instruments could be a potential source of recurrent Bcc infection in people with CF. Consideration should be given to the proper cleaning and maintenance of musical instruments, particularly in those undergoing eradication therapy for CF-associated pathogens.