Prevalence and spa genotype characterization of Staphylococcus aureus isolated from patients attending Gothenburg CF centre

E.A. Johansson1,2, M. Oshaim3, A. Lindblad4, P. Ericson1,5, C. Welinder-Olsson1,2, 1Sahlgrenska University Hospital, Clinical Microbiology, Gothenburg, Sweden; 2Gothenburg University, Inot of Biomedicine, Gothenburg, Sweden; 3Sahlgrenska University Hospital, CF Centre, Gothenburg, Sweden; 4Sahlgrenska University Hospital/East, Queen Silvia Childrens Hospital, Gothenburg, Sweden; 5Sahlgrenska University Hospital, Dept of Respiratory Medicine and Allergology, Gothenburg, Sweden

Objectives: Staphylococcus aureus (S.a) is a major cause of pulmonary infection in CF patients. In order to survey the status at the CF centre in Gothenburg concerning the prevalence, persistence and the incidence of patient transmission of S.a we have for the first time performed genotyping of S.a isolates.

Methods: S.a isolated from 82 CF patients, aged 3–56 years, were collected between 2011 until 2012. All isolates were determined as MSSA. Of the CF patients included, 34 patients had provided ≥2 isolates with at least 6 months in-between during the study period. The chosen 68 S.a isolates were genotyped using the spa-method. Briefly, the variable region of protein A was sequenced and the spa-types were determined with Ridom StaphType software and type codes were assigned.

Results: We identified 39 different spa-types in the analysed collection. The most common spa-type was t021 (n = 3), which is described as a widespread clone. Strain pairs from 14 patients (41%) showed identical spa-types over time and 13 patients (38%) showed different spa-types which however not exclude the co-existence of the first identified type. From 6 patients only one S.a isolate was able to be genotyped, and for the isolates from one CF patient we were not able to get a spa-type at all. These isolates could be new strains of S.a with different molecular properties.

Conclusion: The population structure of S.a isolates recovered from Gothenburg CF centre patients was investigated by spa typing and showed high genotypic diversity. The results indicate a variable persistence of S.a clones and that patient-to-patient transmission at the centre is rare.

NTM: lessons from the UK CF registry

S.J. MacNeill1, G. Vamvakas1, M. Rosenthal2, 1Imperial College London, Occupational and Environmental Medicine, London, United Kingdom; 2Royal Brompton Hospital, Paediatric Respiratory, London, United Kingdom

Objectives: Non tuberculous mycobacteria (NTM) is becoming an increasingly common, serious problem in CF care and risk factors remain uncertain. We interrogated the UK CF Registry to investigate predictors.

Methods: All patients in England born after 1980 with a first report of NTM between 2008 and 2012 (cases) were matched with 2 controls without reported NTM isolation (CF diabetes, oral/inhaled steroid use, ABPA diagnosis, long term ventilation quintile at isolation together with factors reported from the year BEFORE isolation). For each NTM isolate at least one sample/year collected for culture and always when they do not respond our standard antibiotic therapy but for the latter proved statistically significant (OR=1.89, 95% CI 1.24–2.90). A preliminary conditional logistic model to half the dataset was developed. The model considered age, centre of care and the English Index of Multiple Deprivation quintile at isolation together with factors reported from the year BEFORE NTM isolation (CF diabetes, oral/inhaled steroid use, ABPA diagnosis, long term macrolide/azithromycin use and IV antibiotic use > or ≤14 days). The final model included ABPA diagnosis, inhaled corticosteroid use and IV antibiotic use, but only the latter proved statistically significant (OR=1.89, 95% CI 1.24–2.90). Conclusion: In our modelling dataset, only IV antibiotic use >14 days the previous year was significantly associated with new reporting of NTM and the origins of NTM remain unclear. We now aim to explore the ability of this model to predict NTM in the other half of the cohort – our testing dataset.

Low prevalence of non-tuberculous mycobacteria (NTM) in a referral CF center in Brazil: methodological limitation or reality?

T.B. Aiello1, R.M. Mauch1, P.D. Salles2, E.P. Bensi1, I.A. Paschoa1, M.C. Pereira2, A.D. Tora3, A.F. Ribeiro3, J.D. Ribeiro3, C.E. Levy1, 1UNICAMP/Faculty of Medical Sciences, Clinical Pathology, Campinas, Brazil; 2UNICAMP/Faculty of Medical Sciences, Clinical Medicine, Campinas, Brazil; 3UNICAMP/Faculty of Medical Sciences, Pediatric, Campinas, Brazil

Objectives: Investigate the presence of opportunistic mycobacteria in CF patients attended by a referral center in Brazil.

Methods: A review of the microbiological cultures from respiratory tract samples from 212 confirmed CF patients has been made from the 2009–2013 MGIT Beckton & Dickson’s database. The samples were processed in a University Reference Regional Mycobacteria’s laboratory which includes in the routine automation and molecular resources.

Results: In the period of 5 years, only 3 patients (5 samples) have presented a positive sputum culture for mycobacteria, at average age 47.3 years (range 33–72). One case of each of the following NTM species was identified: M. avium, M. abscessus and M. fortuitum.

Conclusion: Since two years ago we started an intensive follow up of adolescent and adults patients looking for NTM with at least one sample/year collected for culture and always when they do not respond our standard antibiotic therapy but our rate of isolation is still very low. We have introduced changes in the processing and culture but without success and If these results persist, the epidemiological conditions or early routine BCG vaccination could explain our findings.

Common clone of Mycobacterium abscessus identified among adults and children in a large UK CF Centre

M. Denton1, T. Lee2, C. Etherington1, D. Peckham1, 1Leeds General Infirmary, Microbiology, Leeds, United Kingdom; 2Paediatric Cystic Fibrosis Unit, Leeds, United Kingdom; 3Adult Cystic Fibrosis Unit, Leeds, United Kingdom

Background: The occurrence of common clones of M. abscessus (MA) has been identified among our CF patients. MA has been identified from a large UK CF Centre. As the prevalence of MA in our own Adult and Paediatric Units has increased we arranged for all our isolates to be typed.

Methods: All current attendees to the Leeds Adult and Paediatric Units who had grown MA on at least one occasion were identified. MA was cultured using a commercial liquid culture system and was confirmed by molecular methods at a Mycobacteriology Reference Laboratory. All confirmed isolates were typed at the Central Public Health Laboratory (Colindale, London) using Variable Number Tandem Repeat (VNTR).

Results: MA was identified from 37 patients with CF (25 adults, 12 children). Fifteen patients (eight adults, seven children) shared the same VNTR profile (referred to as Cluster I, ST26 lineage); four patients (all adults) shared another VNTR profile (referred to as Cluster II, ST1 lineage); two adults shared a very similar VNTR profile and the remaining 16 patients (11 adults, 5 children) each had their own unique VNTR profile. Extensive epidemiological investigations were unable to identify clear links between those patients sharing the same VNTR profile. Water testing conducted in the Paediatric CF Unit was negative. Although both units had already adopted strict segregation policies before the emergence of this problem, further measures have been introduced in line with recent UK CF Trust guidance.

Conclusion: This report provides further evidence of the clonal dissemination of MA among CF patients. The mechanism is unclear. CF units should undertake typing of MA and review infection prevention measures as a matter of urgency.