biomass of pre-formed static biofilms, in a dose dependent manner. CLSM measurements showed within 10 minutes, 200 µg/ml PAAG removed greater than 60% of the bacteria and more than 90% of the bacteria within the biofilm within 1 hour of treatment. PAAG also works in a synergistic manner with antibiotics such as tobramycin and meropenem to reduce their MIC.

Conclusion: PAAG, a polycationic glycopolymer, effectively disrupts recalcitrant biofilms formed by clinically relevant Bcc. Further, this molecule synergizes commonly used antibiotics, thereby increasing the effective arsenal for Bcc treatment. Together with its mucolytic capacity, PAAG's anti-biofilm and antibiotic potentiation activities hold great promise for clinically-translatable Bcc therapy.

P150

Achromobacter prevalence, species distribution and infection status results from a large UK adult cystic fibrosis centre

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Objectives: *Achromobacter* currently comprises 26 named species and its prevalence in CF is increasing but much remains unknown. This study aimed to determine prevalence, species distribution and tendency of chronic infection of *Achromobacter* at a large adult UK centre.

Methods: All isolations of *Achromobacter* spp from 2008 to 2018 were identified. Species identification was confirmed using *nrdA* sequencing. Leeds criteria were used to classify infection status of all patients with >12 months since first *Achromobacter* spp isolation and for each species, the proportion of patients that developed chronic infection was calculated.

Results: Between 2013 to 2018 patient numbers rose from 423 to 435 and prevalence of *Achromobacter* spp increased from 3.7% to 6.9%. 53 out of 60 patients with *Achromobacter* infection between 2008 and 2018 had >12 months of follow up. Of these, 28 (52.8%) developed chronic infection. *Achromobacter xylosoxidans* accounted for 35 (58.3%) of infections, but 7 other named species were isolated from our patients. Of 31 patients with *A. xylosoxidans* infection and >12 months of follow up 20 (64.5%) developed chronic infection.

Achromobacter Species	Species distribution, % (number of patients)	Chronic infection in patients with >12 months follow up, % (number of patients)
Achromobacter xylosoxidans	58.3 (35)	64.5 (20)
Achromobacter insuavis	11.7 (7)	0 (1)
Achromobacter undesignated species	8.3 (5)	25 (1)
Achromobacter dolens	6.6 (4)	100 (3)
Achromobacter mucicolens	5 (3)	0 (2)
Achromobacter spanius	3.3 (2)	0 (0)
Achromobacter ruhlandii	3.3 (2)	50 (1)
Achromobacter marplatensis	1.7 (1)	0 (0)
Achromobacter deleyi	1.7 (1)	0 (0)

[Achromobacter species distribution and proportion of patients with >12 months of follow up who have developed chronic infection]

Conclusion: Prevalence of *Achromobacter* is increasing. *A. xyloxidans* is the most prevalent species at our centre but several other species are also encountered. Approximately half of our patients develop chronic infection following first isolation of *Achromobacter,* with *A. xylosoxidans* and *A. dolens* being likely to lead to chronic infection.

P151

Diversity of *Staphylococcus aureus* clones among cystic fibrosis patients in the Russian Federation

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Objectives: *Staphylococcus aureus is the predominant microorganism in patient with* cystic fibrosis (CF). According to Russian CF Register the prevalence of *S. aureus* among CF patients is 58,0%. The aim of this study was to assess antimicrobial resistance and genotypic diversity of *S. aureus* isolates colonizing CF patients in Russia.

Methods: A total of 556 isolates from the airways of 400 patients with CF were subjected to antibiotic susceptibility analysis and 240 strains were genotyped using restriction fragment length polymorphism (RFLP) of coagulase gene (coa), RAPD-PCR, MLST and SCCmec typing.

Results: 189 (34%) multidrug-resistant isolates and 48 (8,6%) methicillin-resistant *S. aureus* (*MRSA*) isolates were identified. All strains were susceptible to vancomycin, teicoplanin and daptomycin. 31 of the *MRSA* isolates carried *SCCmec* type IV and 9 isolates *SCCmec* types III. *SCCmec* types of 8 strains were not identified. 240 isolates by *coa* gene RFLP typing and RAPD-PCR were clustered into 20 clusters and 41 were of individual genotypes. Simpson coefficient for *S. aureus* was 0,9, and for *MRSA* — 0,84. This showed high genetic diversity of isolates. They belonged to ST1, ST5, ST8, ST45, ST30, ST97 and others. 29,4% of patients with *MRSA* were colonized with *MRSA* ST8 harboring SCCmec type IVc and 9,8% - with *MRSA* ST1 spa type t127 with SCCmec type IVa. Among ST8 we found *MRSA* of spa types t008 and t024. These spa types include international epidemic clones and are the most common types circulating in Russian hospitals. Thus we suppose their intra-hospital acquisition.

Conclusion: This study revealed high *genetic diversity* of *S. aureus* isolates from CF patients in Russia. CF patients are not colonized with any unique ST or *spa* type but rather colonized with the STs being currently spread in a Russian population. Individuals with CF *can* become colonized with *MRSA* both in hospital and outside the hospital.

P152

Comparative *in vitro* activities of ceragenins and various antibiotics against *Achromobacter* species isolated from cystic fibrosis patients

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Objectives: *Achromobacter* species are Gram negative bacilli that are widely distributed in the environment. Since the ability of these species exhibits innate resistance to many antibiotics,effective treatment can be challenging. The ceragenins-cationic steroid antibiotics-(CSA) are a new class of antimicrobial agent and designed to mimic the activities of antimicrobial peptides. This study was aimed to investigate the antimicrobial activities of first/second generations CSAs and various antibiotics against 30 *Achromobacter* species isolated from patients with cystic fibrosis.

Methods: The antimicrobial activities of first generation CSAs (CSA-13, CSA-44), second generation CSAs (CSA-131,CSA-138,CSA-142) and various antibiotics (meropenem, colistin, tobramycin and t*rimethoprim/sulfamethoxazole*) were studied against 30 *Achromobacter* species. MICs were determined following microdilution method according to CLSI.

Results: MIC_{50} and MIC_{90} values of CSAs differ from 4 to 16 µg/ml and 8 to 32 µg/ml. CSA-13 and CSA-131 showed the lowest MIC_{50} and MIC_{90} values. Furthermore CSA-13 and CSA-44 as first generation CSAs; CSA-138 and CSA-142 as second generation CSAs have meaningful activities. The antimicrobial effects of CSAs were similar or lower than tested antibiotics.

Meropenem	MIC50 (μg/ml):0.125	MIC90 (μg/ml):2
Colistin	MIC50 (μg/ml):2	MIC90 (μg/ml):16
Tobramycin	MIC50 (μg/ml):32	MIC90 (μg/ml):128
Trimethoprim/sulfamethoxazole	MIC50 (μg/ml):1	MIC90 (μg/ml):8
CSA-13	MIC50 (μg/ml):4	MIC90 (μg/ml):8
CSA-44	MIC50 (μg/ml):8	MIC90 (μg/ml):32
CSA-131	MIC50 (μg/ml):4	MIC90 (μg/ml):8
CSA-138	MIC50 (μg/ml):16	MIC90 (μg/ml):32
CSA-142	MIC50 (μg/ml):16	MIC90 (μg/ml):32
CSA-192	MIC50 (μg/ml):8	MIC90 (μg/ml):32

[In vitro antimicrobial activities of ceragenins and various antibiotics against 30 strains of Achromobacter species]

Conclusions: CSAs have significant antimicrobial effects on *Achromobacter* species. To our knowledge, this is the first study to investigate the *in vitro* activities of ceragenins.

P153

Impact of *Achromobacter xylosoxidans* on the respiratory function of adult patients with cystic fibrosis

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Objectives: The prevalence of Achromobacter xylosoxidans (Ax) lung colonization in cystic fibrosis (CF) patients has increased, but its impact on lung function is controversial. The aim of this study was to evaluate the long-term effects of Ax colonization on respiratory function of adult patients with CF in the first 3 years after identification of Ax colonization.
Methods: This was a case-control retrospective study performed at a single CF center in Lille, France. Data for 72 CF patients were evaluated, 36 of whom had at least one sputum culture positive for Ax. Patients were matched for age, sex, and Pseudomonas aeruginosa (Pa) colonization with control patients who were uninfected by Ax. Respiratory function and exacerbation frequency were evaluated between 1 year prior to and 3 years after Ax isolation.
Results: Compared with the control (Ax−) group, the Ax+ group had a lower FEV1 at baseline (median [interquartile range]: 55.2% [50.6–59.8%] vs 73.8% [67.2–80.4%], p = 0.005), a greater decline in FEV1 in the first year after Ax identification (mean [standard error]: −153.6 [16.1] mL/year vs −63.8 [18.5] mL/year, p = 0.0003), and more exacerbations in the first 3 years after Ax identification (median [interquartile range]: 9 [7–12] vs 7 [5–10], p = 0.03). Subgroup analysis indicated that Ax+ patients co-colonized with Pa (n = 27; 75%) had a greater decline in FEV1 (p = 0.003) and more pulmonary exacerbations in the first year after Ax identification (p = 0.037) than the Ax+ Pa− patients. Patients with chronic Ax colonization (n = 23, 64%) had more exacerbations than intermittently colonized patients in the third year after Ax identification (p = 0.012), but the decline in FEV1 was not significantly different (p = 0.17).
Conclusion: Ax colonization exacerbates the decline in respiratory function of CF patients. Chronic Ax colonization and Pa co-colonization may be markers of more severe respiratory disease in Ax+ patients.

P154

Investigation of the microbial community associated with *Mycobacterium abscessus* infection

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Objectives: Cystic fibrosis (CF) is characterised by frequent pulmonary exacerbations, typically linked to pathogens such as *Pseudomonas aeruginosa* (*PA*), a known accelerator of lung function decline. Previous studies investigating the community structure of *PA* demonstrate that it is a dominant community member and highly resilient to antibiotics. In comparison, limited knowledge exists for pathogens such as *Mycobacterium abscessus (MAB)* which is also linked to accelerated lung function decline. We aimed to describe the bacterial community of people with CF (PWCF) chronically colonised with *MAB* and retrospectively analyse the impact of *MAB* on lung function over a 3-year study period.
Methods: Sputum samples were collected from 44 PWCF: 23 *MAB* cases and 21 matched *PA* controls. Clinical and demographic data was collated, and lung function analysis was conducted comparing FEV1 decline. This was also analysed by sub-dividing cases based on the presence of nontuberculous *mycobacterium* pulmonary disease (NTM-PD) following ATS guidelines. 16S rRNA sampling was utilised to sequence 60 DNA extracts, and an operational taxonomic unit table was generated allowing for compositional analysis.
Results: Infection with *MAB* led to a significant decline in FEV1 in the cases (−7.88%) compared to controls (+1.00%), (p = 0.002) and a significant decrease was seen with NTM-PD (p = 0.006). ANOSIM analysis revealed significant compositional differences in core and satellite taxa (p = 0.0113, R = 0.08015) with no significant difference seen in taxa diversity or richness.
Conclusion: The presence of *MAB* leads to a unique bacterial community structure in the CF lung. The accelerated lung function decline demonstrated highlights the clinical significance of this bacteria and this is the first study to find a significant association between rates of lung function decline and NTM-PD. The presence of compositional differences may indicate a need to re-evaluate current treatments strategies.

P155

Sample decontamination - how does treatment really affect the recovery of nontuberculous mycobacteria

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Objectives: Nontuberculous mycobacteria (NTM), primarily members of the Mycobacterium abscessus complex (MABSC) and Mycobacterium avium complex (MAC) represent significant respiratory pathogens. Current guidelines recommend the detection of NTM through culture, following sample decontamination. Unfortunately decontamination may reduce NTM viability. We aimed to utilise RGM medium (a selective culture medium for NTM) to assess the impact of several decontamination methods on NTM recovery.
Methods: Samples from 26 patients know to be colonised with MABSC or MAC were homogenised and eight equal aliquots taken. Each aliquot was subjected to one of eight treatments: saline (control); direct inoculation, 4% NaOH (Petroff method); N-acetyl L-cysteine NALC and sodium hydroxide (NALC-NaOH); 5% oxalic acid; NALC-NaOH + oxalic acid dual treatment; N/2 H2SO4; and 1% chlorhexidine. Following treatment, samples were inoculated across three RGM plates and incubated at 30°. Colony counts were taken after 4, 7 and 14 days.
Results: From 22 samples containing MABSC, average colony counts were reduced following treatment in the order: direct inoculation (100% recovered), saline (100%); oxalic acid (73.5%); H2SO4 (68.2%); chlorhexidine (36.5%); NaOH-NALC (15.9%); NaOH-NALC + oxalic acid dual treatment (9.2%); NaOH (1.8%). From 4 samples containing MAC, recovery reduced in the order: direct inoculation (100%), saline (100%); oxalic acid (95.9%); NaOH-NALC (93.5%); NaOH (82.5%); chlorhexidine (80.6%); H2SO4 (79.9%); NaOH-NALC + oxalic acid dual treatment (35.9%).
Conclusion: Excluding saline controls and direct inoculation onto RGM medium, all decontamination methods were detrimental to NTM recovery. MABSC were more susceptible to the harsh decontamination treatments than MAC, with methods containing NaOH being most detrimental. Although MAC were less affected by each method, 4.1–21.1% losses were still observed following any single treatment.

P156

Nontuberculous mycobacteria infection in people with cystic fibrosis attending cystic fibrosis treatment clinics in Australia

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