determinants. CF patients are infected with not unique sequence types of *S. aureus*, but with sequence types that are widely prevalent among the population of Russia. Regarding Russian CF patients, *MRSA* ST8 with SCCmec type IV can be considered epidemic.

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The role of horizontal Gene transfer in the development of resistance in *Achromobacter ruhlandii*

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Objective: To study the molecular basis of resistance in the predominant genotype of *Achromobacter ruhlandii* ST36, which has been prevalent for 10 years (2008-2018) among cystic fibrosis patients in Russia.
Methods: For five strains of *A. ruhlandii* ST36 isolated in 2008 (1 strain), 2013 (1 strain), and 2016 (3 strains), Next Generation Sequencing was performed, and bioinformatic analysis was conducted. Computer programs and web resources used included Blast, NCBI, ResFinder, and PubMLST.
Results: In the *A. ruhlandii* strains, resistance was attributed to the presence of the genes *OXA258* (class D β-lactamase), *strB* (aminoglycoside-6-phosphotransferase), and *catB* (chloramphenicol acetyltransferase), which facilitate the degradation of β-lactam antibiotics, streptomycin, and chloramphenicol, respectively. Additionally, efflux pumps (AxyABM, AxyXY-OprZ, MdtABC-TolC, MexHI-OpmD, EmrAB-OMF, YdhE/NorM, MexPQ-OpmE) were identified, which expel antibiotics of various groups and toxic substances for bacteria, such as copper, zinc, cobalt, magnesium, cadmium, arsenic, and chromium. In the *A. ruhlandii* ST36 strain from 2016, unlike other isolates of *A. ruhlandii* ST36, the genes *aadA* and *strA*, which encode aminoglycoside-modifying enzymes, were found. These genes were located on the same contig as the gene *sul1*, which confers resistance to sulfonamides and is part of a class 1 integron. These genes were acquired as part of an integron with a mobile genetic element through horizontal gene transfer. The nucleotide sequence of this contig exhibited regions that were 99% identical to segments from various plasmids isolated from different bacteria, such as the plasmid pKLC102 from *Pseudomonas aeruginosa* strain C.
Conclusion: The analysis of the complete genomes of five clonal strains of *A. ruhlandii* ST36 revealed the presence of a strain with an acquired plasmid, further demonstrating the role of horizontal gene transfer in the formation of multidrug-resistant strains.

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Promoting uniformity in microbiological sample collection in Italian cystic fibrosis centers: investigating practices and introducing a standardization poster

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Objectives: This study examines the variability in biological specimen collection practices in Italian CF Centers (CFCs), highlighting the need for standardized procedures and adherence to microbiological guidelines. The aim was to develop an accessible tool to reduce inconsistencies in specimen collection and storage across all CFCs in Italy.
Methods: In spring 2021, an unvalidated interview tool was created by the authors and administered by phone to nursing staff from 23 CFCs. The interviews focused on five key questions regarding sample collection methods for sputum, nasal lavage, throat swab, nasal swab, hypopharyngeal aspirate, and bronchoalveolar lavage. These questions explored the collection method, whether the sample was taken at the center, if the patient was fasting, the type of collector used, who performed the procedure, the storage conditions (temperature, time, and home collection). Additional questions were asked for sputum, induced sputum collection and for nasal lavage on the pre-collection technique. The data collected was compared to the 2018 microbiological recommendations for CF patients.
Results: The results revealed significant variation in sample collection practices across the centers. While sputum collection, the gold standard in CF microbiology, was consistently performed, other practices varied widely. The findings highlighted inconsistencies in both sample collection and storage, indicating the need for improved standardization in these processes.
Conclusions: To facilitate knowledge sharing and improve practices, an educational poster was developed. It provides clear guidance on proper specimen collection techniques, required materials and storage guidelines. The poster aims to ensure that all CFC staff can easily access and refer to the information, promoting the standardization of specimen collection and storage practices across the centers. It will be distributed to all CFCs to support consistent, high-quality care for CF patients.

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Clinical impact of chronic multidrug resistant *Pseudomonas aeruginosa* infection in children with cystic fibrosis

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Objectives: Multidrug-resistant (MDR) *Pseudomonas aeruginosa* is an important issue for physicians who take care of patients with cystic fibrosis(CF).
Methods: We performed a single-center, retrospective,observational study at a tertiary referral centre. The primary endpoint was the comparison of FEV_1 % predicted levels at acquisition,1.5 year prior and 1.5 year after periods between children with CF (CwCF) who had chronic MDR *P. aeruginosa* and non-MDR but *P. aeruginosa* infection. Secondary endpoint included change in FEV_1% predicted from acquisition and after 1.5 year. Chronic colonization was defined according to the modified Leeds criteria. Patients aged ≥5 years who have regular 3-month clinical follow-up were included in the study.
Results: 48 CwCF had chronic *P. aeruginosa* infection and 19 of them were MDR *P. aeruginosa*(39.5%).No statistically significant difference was observed between two groups in terms of age, gender and follow-up duration. MDR *P. aeruginosa* positive group had a higher proportion of children with diabetes and celiac disease compared to non-MDR *P. aeruginosa* group (p=0.04,p=0.04; respectively).
FEV_1% predicted of MDR *P. aeruginosa* group were significantly lower; prior (77[IQR,55-96] vs 94[IQR,84-106]), at acquisition (76[QR,49-95] vs 91[IQR 79-109]) and after (68 [IQR,47-92] vs 97 [IQR,88-108]) from that obtained in non-MDR *P. aeruginosa* group (p=0.02, p=0.01, p<0.001). However, change in FEV_1% predicted between acquisition and after period was (-4[IQR,-12- 1] vs 1[IQR,-5- 10]; p=0.04). Number of pulmonary exacerbations in MDR *P. aeruginosa* group were higher both in prior and after acquisition period(p=0.011, p=0.04).
Conclusion: The presence of chronic MDR *P. aeruginosa* infection causes a significant decrease in FEV_1 % predicted in CwCF even when compared with the presence of chronic non-MDR but *P. aeruginosa* infection. There is a need for increased awareness and multi-center clinical studies in MDR *P. aeruginosa* in developing countries.

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Impact of modulator therapy on the chronic colonization of lower respiratory tract pathogens in children: data from the cystic fibrosis registry of Turkey

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