The primary outcome was microbiological eradication of *Mycobacteria abscessus* measured by conversion to negative sputum cultures. Secondary endpoints were sputum conversion to smear negative MABSC, radiographic improvements on HRCT, and safety and tolerability of the treatment regimen.
Results: For the 8 patients with positive MABSC culture the baseline forced expiratory volume in 1 second (FEV_1) ranged between moderate to severe disease (FEV_1 Range 45%-70% predicted). Majority of the patients (n = 7 (88%)) had non-cavitary changes in HRCT. One patient had multiple apical lung cavities. The average time to initiate treatment from the first MABSC culture was 24 months. The average intensive phase of IV treatment period was 8.5 weeks. The main antibiotics used were: Amikacin, Imipenem, Tigecycline and Azithromycin. The average continuation phase period was 13.4 months. The most commonly used therapies in the continuation phase were Meropenem nebulised, Azithromycin, Minocycline, Linezolid and Clofazimine. Of the 8 patients, 50% of patients are smear and culture negative to date. The HRCT changes were stable in 43% (n = 3), one patient showed progressive disease on HRCT and one patient showed improvement in cavitary disease.
Conclusion: Management and treatment of MABSC is difficult, although eradication can be successful. The main challenges are treatment toxicity and lengthy duration of therapy.

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Monitoring the distribution and genotypic diversity of Burkholderiales bacteria in Russian cystic fibrosis patients in the year of the COVID-19 pandemic

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B. cenocepacia ST709 and *A. ruhlandii* ST36 and 261 are epidemic and the most dangerous for Russian CF patients. Strict infection control helped to preclude further spread of epidemic strains. However, during the 2020 SARS-CoV-2 pandemic it was vital to monitor Burkholderiales in the lung microbiome of CF patients.
The samples (sputum/aspirate/BAL/culture) of 66 patients (28 children, 38 adult) of 9 months - 34 years old were collected and analysed by MLST protocols.
Burkholderiales were identified in the samples of 23 patients (26.3% of children and 46.4% of adults). Among adult patients, *Achromobacter* (*A. xylosoxidans*, *A. ruhlandii*, *A. pulmonis)* was the most abundant in the lung microbiome in 7 cases. In the other 4 patients, the *A. xylosoxidans* was an additional bacterium with the prevalence of *P. aeruginosa.* The lung microbiome of the youngest patient from this group was the most diverse and included *Streptococcus* sp., *A. xylosoxidans, P. aeruginosa*, *M. abscessus.* Another adult patient had a co-infection with *Achromobacter* (genogroup 3) and *B. multivorans* (ST891). A co-infection (*A. xylosoxidans* ST127/*B. cenocepacia* ST1772) was revealed in CF infant on the first year of life, too. Timely therapy helped to normalise the lung microbiome. Only one child was infected with epidemic *A. ruhlandii* ST261 dominated in the microbiome. Other children had *A. ruhlandii* ST263 or *A. xylosoxidans* as additional bacteria against the background of *Prevotella* sp., *Granulicatella* sp. or *E. coli. B. cenocepacia* was detected in the samples of 6 children. Epidemic ST709 was diagnosed in one child. Children from the Far East and the Volga Federal District demonstrated ST which are endemic and epidemic for these regions (ST241 and 208, respectively).
Burkholderiales are detected in the samples of both children and adult CF patients. The lung microbiome monitoring is important for timely identification and eradication of Burkholderiales to prevent the chronisation of the lung infection.

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Fungal airway colonisation in cystic fibrosis patients in the Institute for Respiratory Diseases in Children - Skopje, Republic of North Macedonia

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Objectives: Respiratory tract of cystic fibrosis (CF) patients has polymicrobial colonisation. Clinical impact of the fungal colonisation in CF patients is still much less understood. Here, we provide epidemiological data of fungal airway colonisation in CF patients in CF department in the Institute for Respiratory Diseases in Children in Skopje, Republic of North Macedonia.
Methods: We reviewed data of 41 CF patients (mean age 19 years), 21 male (51.2%) and 20 female (48.8%) who were followed in our Institute over a 1-year period. A total of 277 sputum samples were collected, with a mean of 6.7 per patient. Standard microbiological procedures were used for isolation and identification of the bacteria and fungi. The fungal isolates were identified as *Candida species* or *Candida albicans*; *Aspergillus species* or *Aspergillus fumigatus*.
Results: The total number of positive fungal culture was 70.28 patients; (68.3%) had at least one positive fungal culture, 11 of them (39.3%) had 2 or more identical fungal isolates during the follow-up period. Almost the same distribution was observed between male and female, 15/13 respectively. According to the place of living, fungal colonisation is more associated with urban life 19/28 (67.9%) than rural life 9/28 (32.1%). The prevalence of the isolated fungal species was *Aspergillus spp.* 11/70 (15.7%), *Aspergillus fumigatus* 8/70 (11.4%), *Candida spp.* 12/70 (17.1%) and *Candida albicans* 39/70 (55.7%).
Conclusion: Fungal airway colonisation is frequent in CF patients, especially in those who live in the cities. The most prevalent fungal isolate in sputum of CF patients in our Institute was *Candida albicans*.

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Relationship between clinical and environmental strains of emerging opportunistic pathogens in cystic fibrosis and diversity in the home environment

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The sources of acquisition of opportunistic pathogens are poorly known, particularly for waterborne species such as *Pseudomonas aeruginosa* (Pa), emerging pathogens *Stenotrophomonas maltophilia* (Sm), *Achromobacter* sp. (Ac) and non-tuberculous mycobacteria (NTM). Study objective (PatHome project) is to gain a better knowledge of the domestic reservoirs of these bacteria and to describe the epidemiological links between clinical and domestic environmental strains of patients.
Domestic (water points, drains, moist areas) and sputum samples of Sm- or Ac-colonised patients were seeded on different selective agar media for bacteria of interest. Species were identified by mass spectrometry. *nrdA* and *guaA* gene sequencing was used for Ac and Sm strains genotyping. Clinical and environmental strains of identical genotypes were compared by pulsed-field gel electrophoresis.
9 sampling campaigns were carried out in 6 patients' houses. Sm and NTM were identified for 100% of the campaigns, Ac for 89% (8/9) and Pa for 67% (6/9). Sm and Ac were mostly isolated from kitchen and bathroom drains, and Pa from drains and washing machines. A wide distribution of NTM has been observed. For 3 patients (50%), identical genotypes were observed between sputum and home environment. Environmental strains came from: (1) Ac and NTM strains isolated from the sink drain, suggesting aerosol transmission;, (2) Sm strains isolated from the kitchen drain, suggesting contamination through fomites such as baby bottles (infant