45 Decision making by young adults with CF about risk of patient–patient and environmental acquisition of infection

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Objectives: Our previous study qualitatively explored decision-making about exposure to potential risk of infection in young people with CF, highlighting the role of competing social demands and gaps in knowledge. The current study extended this, exploring judgements about risk in a national sample.
Methods: People with CF were invited to complete an online survey via social media forums hosted by the UK CF Trust. This focused on participants' decisions in 4 hypothetical risk scenarios, beliefs underlying decisions, and perceived importance of different sources of information.
Results: 75 respondents; mean age 24; 65% female. Many were less aware of environmental risks such as cleaning stables (72% saw this as medium-no risk), but better informed about person-person risk (only 13% would meet another person with CF, 3% if they have cepacia), though even here there were gaps in knowledge (32% did not know what cepacia was). Decisions were responsive to available risk information: 45% would not visit a friend on a ward where there was MRSA, and this rose to 73% if the friend had MRSA. Uncertainty about their own infection status was also important. The most trusted sources of advice were verbal and written information from the team, followed by the CF Trust and the internet.
Conclusion: Though this sample was CF Trust forum users and arguably more active than most with CF, knowledge still varied widely. Young people with CF make active decisions about exposure to risk of infection, but these are not always based on reliable knowledge, particularly of environmental risk. This is an ongoing study. Full results and thematic analyses of narrative responses will be presented.

46 Microbiological airway flora in children with cystic fibrosis in the first year of life (To treat or not to treat, that's the question!)

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In children with cystic fibrosis (CF) pulmonary microbial colonization and infection are important prognostic factors. In Germany a national CF newborn screening does not exist by now and only little is known about the microbial respiratory flora of children with CF in the first years of life.
In Dresden a regional newborn screening program for eastern Saxony exists since 1996. Thus, a microbiological monitoring for patients with CF was already performed from diagnosis in the first month of life throughout babyhood and we collected data from 1997 on.
In the following, we want to demonstrate the microbial colonization of 55 patients in our center in their first year of life. In all patients we found bacteria other than normal flora of mouth and throat. Most commonly we detected *Staphylococcus aureus*, *Haemophilus influenzae* and *Escherichia coli*, but also a variety of many other such as *Klebsiella*, *Serratia*, *Streptococcus*, *Enterobacter*, *Enterococcus* and *Acinetobacter* species, *Bacillus cereus*, *Branhamella catarrhalis*, and more. We also detected *Pseudomonas aeruginosa* and other *Pseudomonas* species already in patients at this young age. In several patients we found fungi in the throat swab, such as *Aspergillus*, *Candida* and *Saccharomyces* species.
Most of the patients needed antibiotic therapy in their first year of life due to pulmonary exacerbation, but the clinical symptoms in many cases did not correlate with the microbiological findings by throat swab.
With the introduction of a national newborn screening program for CF hopefully end of this year, we will have to discuss the influence of these bacterial findings in the first year of life on the prognosis and the need for treatment.

47 Diagnostic dilemmas for CF microbiology labs using MALDI-TOF

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Objectives: The identification of certain bacterial species from the sputum of patients with CF carries prognostic significance so accurate identification is essential. MALDI-TOF technology promises rapid and accurate identification of the sometimes difficult bacteria *Pseudomonas aeruginosa*, members of the *Burkholderia cepacia* and other non fermenting organisms. We have compared results from bioMérieux MALDI-TOF and Bruker MALDI-TOF for the *Burkholderia cepacia* complex (Bcc).
Methods: A range of organisms from patients attending a Paediatric CF Centre were identified using 2 MALDI-TOF systems and in-house molecular methodology with referral of isolates to a Reference Laboratory if appropriate.
Results: Five isolates categorised as *P. aeruginosa* on the bioMérieux system were identified by in-house 16s ribosomal DNA sequencing or Reference Laboratory testing as *P. nitroreducens.* On retesting on the Bruker MALDI-TOF all 5 strains were identified as *P. nitroreducens.* Ninety-four PCR-confirmed Bcc strains were tested in parallel and both MALDI-TOF machines categorised them within the *cepacia* complex. At Genomovar level, *B. multivorans* and *B. vietnamiensis* gave concordant results on the 2 systems. All of 28 *B. cepacia* identified on the bioMérieux MALDI-TOF were *B. cenocepacia* according to Bruker.
Conclusion: Misidentification of *P. aeruginosa* and *B. cenocepacia* is unacceptable as incorrect segregation and antibiotic management of patients would ensue. Refinement and compatibility of MALDI-TOF databases is essential before this technology can replace current DNA based identification methods and needs to be supported by relevant and robust EQA schemes.

48 Altered gut microbiota in stable patients with cystic fibrosis (CF) compared to controls and its relationship with intravenous (IV) antibiotic usage and lung function

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Objectives: CF is associated with altered digestive function and thus nutrient availability for gut microbes in addition to altered gut microbiota, compared with healthy controls. Equally intensive antibiotic and nutritional therapy may further compound this. We present results from the largest CF gut microbiota study to date.
Methods: The gut microbiota of 43 stable adults with CF was compared to 69 age-matched controls. DNA was extracted from faecal samples and the V4 region of the 16S rRNA gene was sequenced using 454-pyrosequencing. Results were correlated with baseline $\%FEV_1$ results and to total courses of IVs in the previous 12 months.
Results: The gut microbiota diversity of patients with CF was significantly reduced compared to controls ($p < 0.05$ for all α diversity tests). Significantly increased proportions of Firmicutes ($p = 0.029$) and decreased Bacteroidetes ($p < 0.001$) occurred in those with CF compared to controls. There were significant reductions in proportions of bacteria associated with gut health in those with CF, including decreased *Faecalibacterium*, *Roseburia* and *Bifidobacterium* ($p < 0.001$). A negative correlation between the number of IV courses and gut diversity [Simpson's diversity index: correlation coefficient (r) = –0.383, $p = 0.0111$] and a positive correlation between FEV_1 and gut diversity (Simpson's diversity index: $r = 0.47$, $p = 0.0015$) was found in those with CF.
Conclusion: This study highlights that patients with CF have an altered gut microbiota which correlates with clinical outcomes. Further longitudinal studies will enable us to interrogate the causality of such microbiota alterations and determine the potential role of probiotics in CF therapy.