Going overboard with microbiology – women and children first

The Autumn Symposium of the British Society for Microbial Technology took place at the Merseyside Maritime Museum in Liverpool last October. On behalf of the BSMT, Mark Wilks reports on a comprehensive and stimulating programme.

Over 100 microbiologists, mainly biomedical scientists, clinical scientists and medical microbiologists, attended the Autumn Symposium of the British Society for Microbial Technology (BSMT), the focus of this one-day event being on the role of microbiology in paediatric and women's healthcare.

Paediatric overview: keynote lecture

Professor Eric Bolton (BSMT President) chaired the morning session, and introduced the first speaker, Dr Andrew Riordan (Consultant in Paediatric Infectious Diseases and Immunology, Alder Hey Hospital, Liverpool), who gave an overview of paediatric microbiology and what he called the three golden rules of paediatrics (Table 1).

Children are particularly susceptible to infections such as group B *Streptococcus*, *Kingella kingae* and parechovirus, which are often only seen in small children. *K. kingae* is a β-haemolytic Gram-negative aerobic coccobacillus and a common cause of paediatric bacteraemia, and the leading cause of osteomyelitis and septic arthritis in children aged six to 36 months. It is not nearly so important in adults. Hospital-acquired infections in paediatric wards are usually lower respiratory tract viral infections (eg respiratory syncytial virus) or gastrointestinal (eg rotavirus) as opposed to bacterial infections such as methicillin-resistant *Staphylococcus aureus* (MRSA) in an adult ward.

Infections may present with different severity. For example, chicken pox is less severe in children than in adults, and asymptomatic carriage of *Clostridium difficile* is common. Children grow and develop: a child's immune system is not fully functional until eight years of age, and peaks at around 14 years. Most severe infections are seen in toddlers, particularly children less than two months of age. Public Health England (PHE) data on invasive bacterial infection episodes in infants from 2011/12 to 2016/17 demonstrate that very young children, particularly in the first two months of life, are at the greatest risk of infection.

Infections affecting a child almost always affect the family who care for that child, particularly in the case of the common cold. Children may also be infected by a family member with infections such as tuberculosis (TB) and

Table 1. Three golden rules of paediatrics.

■ Children are not little adults, they have different infections
■ Infections may present with different severity
■ When treating children, treat the family

The Merseyside Maritime Museum played host to the symposium delegates, speakers and sponsors, many of whom had travelled significant distances.

human immunodeficiency virus (HIV), and children may infect other family members with infections such as chickenpox and pertussis

There is clear evidence of decreasing admissions for meningitis and some of which is due to the availability of vaccination (eg HIB meningitis introduced in 1992). However, significant evidence demonstrates that emergency hospital admissions of less than a day are increasing. The rates of culture-confirmed invasive bacterial infections in children vary and may be of the order of 1, representing a lot of testing to identify a small number of cases.

Commercial support proves crucial in the continued success of BSMT conferences and symposia.

Contaminated blood cultures

Taking blood cultures in an aseptic manner can be especially challenging in infants and children, and evidence suggests contamination by skin organisms is higher in this population than in adults – up to 40% in some series. This can lead to unnecessary further laboratory testing, hospitalisation and antibiotic administration. There are several molecular tests that can be used to help in deciding what to do with a positive blood culture result.

Dr Riordan described his evaluation of the BIOFIRE instrument and FILMARRAY blood culture identification panel (FA-BCIP) for rapid identification of bacteria, *Candida* and antibiotic resistance. This identifies eight Gram-positive bacteria, 11 Gram-negative bacteria, five *Candida* spp, and three antimicrobial resistance genes (*mecA*, *vanA/B*, KPC). The hands-on time is only two minutes and the turnaround time an hour.

The test was performed on 117 positive blood cultures, with 74 (63%) growing clinically significant organisms, and 43 (37%) growing contaminants. FA-BCIP results were judged to alter clinical management in 63 of the 117 episodes (54%). Antimicrobials were started/altered in 23 (19%) episodes and de-escalated/withheld/stopped in 29 (25%) episodes. Ten children were discharged from hospital earlier, which saved a cumulative total of 14 bed days. The problem, as so often is the case with new technology, is the cost. The capital outlay is approximately $36,500, and each test costs $129.

Microbiology of cystic fibrosis

For the past 40 years the approach to studying infections in the airways of patients with cystic fibrosis (CF) has largely paralleled that taken in the study of other human infectious diseases. Typically, a microorganism recovered in culture from an infected site is studied in isolation using various *in vitro* and *in vivo* models intended to approximate some facet of the human infection. This has yielded a wealth of information regarding microbial virulence factors and pathogenic mechanisms. However, its limitations when applied to a chronic polymicrobial infection like CF have become increasingly apparent. Given this new understanding of infection in CF, there has been a move away from thinking of the individual pathogen to considering the airway microbial community as a pathogenic unit.

Professor Chris van der Gast (Manchester Metropolitan University) was previously more used to studying the interaction of many different types of bacteria in soil and water in the environment, and is now applying methods developed from studying the microbial ecology of those sites to the CF lung.

Translating microbiomics to CF management

Classical methods have provided a wealth of information on the epidemiology of emblematic CF pathogens – by age and over years, and emergent pathogens of concern such as non-tuberculosis mycobacteria (NTMs) and *Aspergillus* are now being added. Of course this approach cannot provide retrospective examination of emergent pathogens (eg *Pandoreara* spp.) or enigmatic anaerobes (eg *Prevotella* spp, V*eillonella* spp. and *Rothia*). Professor van der Gast described an ambitious long-term project and a global first to characterise the microbiome of the CF lung, starting with the Manchester paediatric and adult CF patients. The idea being to sample patients annually and capture all bacterial and fungal taxa.

Antibiotic susceptibility in a microbiome context

Beyond characterising the flora, the aim is also to improve the relevance of antibiotic susceptibility testing, where susceptibility profiles from the last visit to clinic are used to inform treatment for a current exacerbation, but this last visit could have been from months previously. The newer approach is to consider the patient's lung microbiome as the 'pathogenic unit'. Patient's sputum containing the intact microbiome would be applied to a CF lung epithelial cell line, allowing replication of the pathogen-host environment. Testing with and without antibiotics using quantitative-PCR detection of all bacteria (16S rRNA gene) and all fungi (internal transcribed spacer [ITS]) to measure growth, then indicates susceptibility or resistance. The approach should be more rapid, accurate and cost-effective than existing methods and can also be targeted at pathogens of concern (eg *Pseudomonas aeruginosa*, NTM species).

Personalised models of infection

The most exciting development was the possibility to generate personalised models of infection. The team at MMU was able to generate CF patient-specific induced pluripotent stem cells (iPSCs) that can be directed to become lung epithelium cells, which crucially can incorporate the patient's own *CFTR* mutation and their underlying genetic factors. Critically, they can then recreate host-pathogen interactions by directly introducing the patient's own sputum or strains of their pathogens to the cell lines.

Group B streptococci and other neonatal infections – a massive burden of disease

It is sobering to reflect on just how great the burden of neonatal bacterial disease remains. The World Health Organization (WHO) estimates that 600,000 deaths occur globally due to neonatal infections. Group B streptococci (GBS) cause 300,000 cases of disease and 90,000 deaths annually, on top of which it causes moderate or severe disability and 10,000 survivors, and may cause 57,000 stillbirths and 3.5 million premature births annually.

In addition, but often omitted, there are at least 33,000 deaths per annum due to maternal invasive GBS disease.

Dr Jim Gray (Consultant Microbiologist, Birmingham Women's and Children's NHS Foundation Trust) described the types of neonatal infections in terms of congenital, partum and post-partum (hospital-acquired and acquired at home) and the most common microbial species that cause very early-, early- and late-onset infections in the neonatal intensive care unit (NICU). Neonatal GBS infection can be classified by early-onset (EOGBS) and late-onset (LOGBS). The former are cases with onset in the first seven days, while the latter present between seven days and three months. With LOGBS, immunisation is the only feasible preventative strategy. In the USA, cases of early-onset GBS were reduced by 80% after the introduction from about 1996 of a national prevention policy, involving universal screening, which meant that up to 30% of pregnant women received antibiotics. This reduction has now plateaued and there is increasing concern regarding the unnecessary prescription of antibiotics both from the point of view of developing resistance and of side-effects.

Intrapartum antibiotic prophylaxis reduces early-onset disease but does not prevent late-onset disease. The use of intrapartum antibiotic prophylaxis (IAP) was discussed as a means of preventing EOGBS, stressing that antibiotics active against GBS should be given as soon as possible after the onset of labour. How the need for IAP is determined was discussed, with the UK currently using a risk factor-based approach, but in the USA and other European countries a screening-based approach as late as possible in pregnancy has been adopted. Stakeholders in the UK continue to lobby to change UK policy.

Detection strategies for GBS were discussed comparing enrichment culture, with up to three days to reach a result, with PCR which reports results in less than one hour. In the current era of antibiotic stewardship serious consideration must be given to the number of women and babies exposed to antibiotics that are of no benefit. With this in mind, it was suggested that the adoption of a testing in labour screening programme could lead to 45,000 fewer women receiving antibiotics.

Pressure for a national programme for GBS screening should be considered in the light of evidence, and we must be careful to resist pressure to change without that evidence. If we do change practice without evidence we may be doing more harm than good.

A national screening programme will have little effect on LOGBS infections but a maternal GBS vaccine would have a higher impact than IAP both on EOGBS and LOGBS infections. Higher coverage could be achieved especially in under-resourced settings and could be added relatively easily to existing programmes of antenatal care. It would also have the benefit of reducing antibiotic exposure (22 million women per annum). Several promising candidate vaccines are in phase II and III trials.

Urinary tract infection diagnosis and the urinary microbiome

Urine is the most common specimen in all microbiology laboratories and arguably the worst handled. Dr Robin Howe (Consultant Microbiologist, Public Health Wales Microbiology Cardiff, University Hospital of Wales, Cardiff) gave a fascinating presentation which looked at the sometimes conflicting guidance and evidence available to clinicians when treating urinary tract infection (UTI), and considered how the application of new technology using metagenomics analysis might help in the future.

There are increasing numbers of children presenting as acute admissions, and UTI is the most common cause of fever of unknown origin in paediatric patients, affecting 4% of boys and 11% of girls by the age of 16. The disease can present significant long-term impacts including impaired renal function, recurrent pyelonephritis and hypertension. Diagnosis is of course difficult, with patients often being preverbal and lacking obvious symptoms, and the acquisition of uncontaminated specimens particularly difficult.

Dr Howe raised concern about the reliability of a microbiological diagnosis of UTI. It is difficult to distinguish between contamination and colonisation bacteriologically, and the reliability of the identification of pyuria and diagnosis. The current UK SMI, like many other guidelines, refers to the original work of Kass in adult women in 1957. The SMI refers to the significance of repeat isolates from two specimens, with colony counts $\geq 10^6$ colony-forming units (cfu)/L ($\geq 10^3$ cfu/mL) of a species being significant in paediatrics in a voided urine, and pure growths of 10^7–10^8 cfu/L (10^4–10^5 cfu/mL) being indicative in carefully taken specimens.

Dr Howe then drew the audience's attention to the plethora of conflicting guidance available. In the USA a 'clean' specimen may be collected by catheterisation or suprapubic aspiration, making interpretation of the significance of any growth much easier. This approach is very rare in the UK. The DUTY (Diagnosis of Urinary Tract infection in Young children) Study (on which Dr Howe was a co-investigator) attempted to develop algorithms based on signs and symptoms, to identify children accurately in whom a urine specimen should be obtained, assess whether dipstick analysis provides additional diagnostic information, model the cost-effectiveness of algorithms and compare contamination rates between clean catch urines and pad specimens. The objective being to design an algorithm for primary care that would lead to optimal selection of patients who would have a urine submitted for microbiology. The study demonstrated depressingly poor correlation between laboratories in reporting UTI and the relevant clinical data, and between microscopy and flow cytometry.

Dr Howe raised concerns that newer laboratory methods have not been validated against clinical diagnosis. In particular, the increasing use of small inocula covering only a fraction of a plate

Professor Brian Duerden CBE and speakers on the afternoon programme field questions at the end of the session.

makes it very difficult to define mixtures and may lead to the undercounting of colonies due to colony crowding – in consequence, the 'factory' approach of the modern high-volume microbiology laboratory to new methods may lead to reduced reliability.

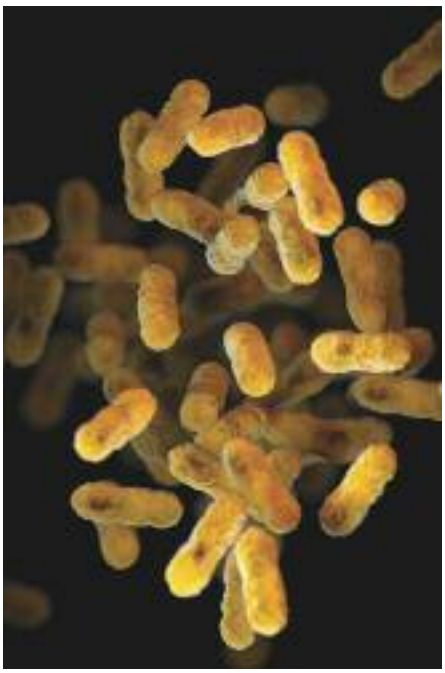
Metagenomics to the rescue?

However, Dr Howe raised the possibility that the use of metagenomics analysis of 16S rRNA may help. Studies have revealed the presence of complex microbiomes that include unculturable bacteria, which may suggest an association between the microbiome and urological disease. The yet to be published Eurica study looked at 128 children, predominantly those acutely ill children presenting without microbiologically confirmed UTI. DNA was extracted from samples with 16S rRNA gene sequence data converted into bacterial species distribution and load. Eleven culture-negative samples in the study (23.9%) were shown to have greater than 10^7 reads/mL of predominant organisms, five of which were *Enterococcus faecalis*. Eight samples (26.7 %) that were culture-positive were identified as false positives. Twelve samples (48.8%) with reported mixed culture showed greater than 10^7 reads/mL of a predominant organism suggestive of UTI. It may be that molecular methods will provide answers in those cases that culture has not been able to resolve.

The rise and fall of pertussis: evaluation of the Pertussis Immunisation Programme for pregnant women

Professor Brian Duerden CBE chaired the afternoon session and introduced Helen Campbell (Senior Clinical Scientist, Immunisation and Countermeasures, National Infection Service, PHE Colindale), who gave an overview of whooping cough disease. It is caused by *Bordetella pertussis*, a pathogen which is almost exclusively human and transmitted by close contact. Severity varies with age and complications in infants, the most vulnerable group, can include respiratory pneumonia, collapsed lungs, apnoea, brain damage, weight loss, dehydration and occasionally death. She showed a short but harrowing video of a child with whooping cough so delegates could hear the characteristic 'whoop' sound as the child drew in breath between coughing fits.

Vaccination is the most effective strategy to prevent transmission. Despite good uptake of the vaccine in children and infants, at the time there was a very large increase of laboratory confirmed



CDC/Sarah Bailey Cutchin

A group of aerobic, Gram-negative, *Bordetella pertussis* bacteria (based on scanning electron microscopic [SEM] image).

cases of whooping cough in England and Wales in 2011 and 2012 resulting in 14 deaths, all in infants under nine weeks of age. A similar pattern occurred in the USA. The reasons for this are still unclear but may be because the newer vaccine, while having fewer side-effects, is not quite as effective, or due to natural population turnover and incomplete vaccination coverage. Whatever the reason, this increase was the largest outbreak of the disease for 20 years and 70–75% of infant cases occurred before the first vaccine dose was administered at age two months or above. The normal regime is three doses, each one month apart, followed by a booster dose six months later.

As a response to the outbreak and in an attempt to protect infants from birth, the Department of Heath introduced in October 2012 a temporary vaccination programme for pregnant women using Repevax (dT5aP/IPV). The initial target was to administer this single dose between 28 and 32 weeks' gestation and it was offered in every pregnancy. From July 2014 the vaccine was changed to Boostix – IPV (dt3a P/IPV). Later in 2016 guidance was updated to advise women that they should be vaccinated from 16 weeks, ideally between 20 and 28 weeks (usually after the 20-week scan). Similar programmes with vaccine administered at varying gestation ages have also been introduced in a number of other countries including USA, Spain, Portugal, Panama, Mexico, Columbia, Argentina, Brazil, Australia and New Zealand.

In England and Wales, the maternal vaccination programme was well received both by pregnant women and the media. A survey showed that 93% of women would choose to be vaccinated during their pregnancy, with only 3% saying they would not. Pregnant mothers said midwives and GPs were their preferred source of information when being offered the vaccine.

Uptake of the early vaccine was 70–75% in the period 2013–2018. Since the outbreak ending in 2012 there was a sharp fall in numbers of whooping cough cases, although there was a slight rise again in 2016. There have also been a further 14 deaths, but of these only two had mothers who had been vaccinated. Infants born to vaccinated mothers had a lower risk of hospitalisation, ICU admission and death.

Helen concluded by saying that despite the success of childhood immunisation programmes, pertussis remains a global public health concern. Additional strategies are required to optimise control and protect infants at highest risk of severe disease. Immunising pregnant women has been shown to be a highly effective strategy in protecting young infants in the first months of life. However, challenges remain in achieving consistent high coverage in the target groups. There are also questions remaining concerning the optimal timing of vaccination for the best clinical protection, the longer-term impact of this approach, and the optimal infant/booster schedule.

Transmission dynamics of norovirus in a paediatric hospital

Dr Kathryn Harris (Clinical Scientist, Great Ormond Street Hospital, London) was the penultimate speaker of the day, and gave a fascinating talk on norovirus and the transmission dynamics in a paediatric hospital, stating that there are around 17 million community cases per year, which costs the NHS around £115 million a year. Immunocompetent patients will display winter peaks, with acute vomiting lasting about a day, and they will become dehydrated but have an excellent prognosis. Immunocompromised patients, on the other hand, suffer year-round with infections lasting weeks rather than days. The virus will cause dysfunction of the intestinal barrier and can lead to chronic infection, perhaps resulting in death.

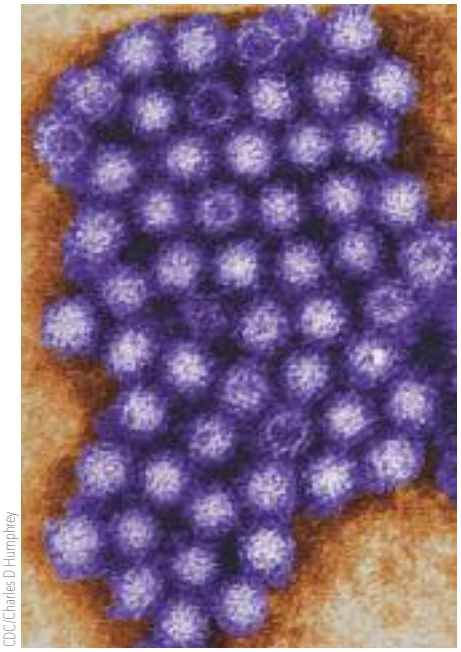
The norovirus genome has been sequenced and genotype can be determined from the protein on the virion. The most common genotype identified between July 2014 and February 2016 in Great Ormond Street Hospital was G11.P21_G11.3. Norovirus

capsid sequencing can help differentiate between genotypes and aid better understanding of infection and transmission dynamics in paediatrics where there is a high numbers of immuno-compromised patients.

A cohort study was conducted where the tertiary referral hospital had 350 beds, with 60% single isolation rooms and no A&E. Residual specimen (when available) from norovirus-positive patients between 1 July 2014 and 17 February 2016 was submitted for whole-genome sequencing (WGS). A total of 205 norovirus PCR-positive patients were identified and in 189 cases WGS was performed. Approximately 59% of the patients were profoundly immunocompromised, with a median age of two.

With the aid of WGS and the addition of deep sequencing the full norovirus genome plus sequence clusters can be identified. The sequencing clusters can support epidemiology and show any possible links between wards and departments. The clusters identified links between shared staff, equipment and the use of common areas.

In this study there appeared to be linked transmission in 44% of cases. 33% of new cases were acquired from another patient despite isolation nursing and stringent IPC measures. 43% of nosocomial infections remain unknown, even with WGS, so wider sampling of patients, the environment, staff and visitors is needed. Now sequencing costs and technologies that allow rapid turnaround times are decreasing, WGS can be used routinely to control nosocomial infections.



CDC/Charles D Humphrey

Ultrastructural morphology displayed by a cluster of norovirus virions (coloured transmission electron microscopy [TEM] image).

The vaginal microbiome and sexually transmitted infections

Professor Janneke van de Wijgert (University of Liverpool, Institute of Infection and Global Health) gave the final presentation of the day, beginning by discussing the types of organisms found in the vaginal microbiome (VMB); the commensals that rarely cause infection (eg lactobacilli), followed by the pathobionts that sometimes cause infection (eg streptococci, staphylococci, enterococci and Enterobacteriaceae), and finally the pathogens such as *Chlamydia trachomatis* and *Neisseria gonorrhoeae*, which almost always cause infection.

Many diagnostic scales have been developed to define the vaginal microbiota, and prior to 2002 these were based on clinical observations as well as laboratory findings, set down in the Amsel criteria (1983) and the Nugent score (1991). From these studies, it has been observed that for a bacterial vaginosis (BV) infection discharge is not always present, and now diagnosis is made using the laboratory findings and not the symptomatic ones.

Since 2002, molecular technologies have become more widely available and affordable with 16S ribosomal gene sequencing being a popular diagnostic tool, even though it does not identify virus, yeast and protozoa, along with the fact that it may not prove useful when pathogens/pathobionts are present in low concentrations.

Professor van de Wijgert continued to discuss the VMB composition and the molecular data of decreasing diversity from a healthy microbiome to severe dysbiosis dominated by *Gardnerella vaginalis*. Lactobacilli are widely thought to predominate in the healthy vagina although Professor van de Wijgert's meta-analysis suggested that while *Lactobacillus crispatus* predominated in Caucasian women, *L. iners* was the predominant species in African women.

Studies on the mucosal biofilms that have been found in the vagina using fluorescence *in situ* hybridisation (FISH) techniques have shown that in healthy biomes lactobacilli form a loose network of bacteria, while those found in the unhealthy biomes are formed of a dense biofilm containing both *G. vaginalis* and *Atopobium vaginae* on the mucosal surfaces. Once these are treated with metronidazole there is only partial resolution and the infection inevitably returns. A hypothesis has developed from these finding suggesting that *G. vaginalis* is an important 'scaffolding' for biofilm development, but this has yet to be confirmed.

Globally, there is a high prevalence

The prize for winning the Trade Quiz was awarded to Rhian James from Singleton Hospital, Swansea, who will also be invited to attend the Annual Scientific Conference in RAF Hendon in May next year as a guest of the BSMT.

of dysbiosis, the majority being asymptomatic with no sequelae. However, sequelae can develop even when asymptomatic; for example, the acquisition of HIV/STI and onwards transmission, pelvic inflammatory disease, infertility with lower success rate of IVF, miscarriage, preterm birth and finally invasive post-abortion, maternal and neonatal infections.

The HELIUS VMB study in Amsterdam looked at the prevalence of dysbiosis. This looked at a random group of asymptomatic volunteer women of many different ethnicities, aged 18–35 years. 61.5% were found to have a normal microbiome, dominated by *L. crispatus*, *L iners* and more rarely other lactobacilli. 32.2% had BV and interestingly 6.2% had other dysbiosis. This study gave more evidence for the existence of aerobic vaginosis, a dysbiosis dominated by pathobionts such as streptococci, staphylococci and *Escherichia coli*, and the authors compared this to a random group of sex workers in Rwanda, and had to take into consideration a range of risk factors from condomless sex, STIs from new partners, menses and vaginal douching.

It was found that dysbiosis was frequently followed by infection and it also seemed that the higher the Nugent score the greater the risk of acquiring HIV. Disruption of the cervico-vaginal barrier appeared to be associated with increasing bacterial diversity, leading to mucus alteration, an increase in cell death resulting in cytoskeleton alteration, increasing proteolytic activity, and release

of pro-inflammatory cytokines. This has led to further study looking at cytokine interaction in the vaginal microbiome. It was found that lactobacilli have an anti-inflammatory cytokine profile in the vagina and both BV and pathobionts had pro-inflammatory cytokines in the vagina linking to increased risk of infection with HIV.

Professor van de Wijgert went on to discuss HIV prevention, looking at VMB and PrEP drug metabolism, where trials have shown discrepant results which could be due exclusively to poor adherence by those taking part, or the hypothesis that dysbiosis is associated with bacteria depleting tenofovir.

Finally, Professor van de Wijgert considered the implications of this work for future diagnosis and treatment. In terms of diagnosis, the need to differentiate dysbiosis types and establish whether or not a biofilm is present and to differentiate these from vaginal candidiasis, trichomoniasis and cervical STIs. In terms of treatment we need to look at the effects of different antibiotics on VMB/pathobionts, and look at how the entire vaginal niche is affected. Vaginal probiotics, and indeed hormones, whether topical or systemic, may have an adjunct role. As in other fields of clinical microbiology, how to treat vaginal biofilms is an enduring issue.

Annual Scientific Conference 2019

Clinical microbiology continues to advance at a rapid rate and culture and the newer molecular methods are proving to be a powerful combination, yielding insights both about the aetiology of different diseases and their treatment. Next year's BSMT Annual Scientific Conference on respiratory tract infections will continue these themes.

The conference will be held at the Royal Air Force Museum, Hendon, London on Thursday 16 May (please note change of venue and day). A greatly expanded trade exhibition will enable delegates to get a good overview both of improved culture media and the newer molecular technologies.

Dr Mark Wilks is Clinical Scientist in Microbiology at Barts Health NHS Trust. Copies of all presentations given at the Autumn Symposium in Liverpool may be found on the BSMT website (www.bsmt.org.uk).

The BSMT Annual Scientific Conference 2019, entitled *Respiratory Microbiology – A Day of Inspiration*, will be held on Thursday 16 May at the Royal Air Force Museum, Hendon (please note change of venue and day).

Tales from the exhibition

The BSMT Autumn Symposium was supported by a wide range of commercial sponsors, which represent a vital symbiotic relationship that enables this series of BSMT events to flourish and go from strength to strength. The following is a review of some of the expertise on show to delegates in Liverpool.

altona Diagnostics

altona Diagnostics is focused on bringing to market high-quality molecular test systems for the detection and quantification of a broad range of infectious disease pathogens. At BSMT, altona presented the AltoStar series of reagents, platforms and bespoke software which enables an advanced 'sample to result' CE-marked automated workflow for RT-PCR testing. Also on show was the RealStar infectious disease kit range, with a common protocol and validated on a broad range of RT-PCR instrumentation, which are designed to offer users real confidence in results.

BioConnections

BioConnections focused on two key areas at the recent BSMT meeting. The Resist product range including Resist 4 OKNV is a 15-minute lateral flow test that confirms the Big Four carbapenemases (KPC, NDM, OXA & VIM) as accurately as the top molecular assays, without the need for instrumentation so at a fraction of the cost. Broth Micro Dilution (BMD) is the international gold standard for antimicrobial sensitivity testing (AST). This is the product that the company has introduced to the UK over the past few years. Manufactured in Germany by Merlin Diagnostika, Micronaut BMD products can be used without equipment or automated, or even linked to MALDI-TOF MS. BMD is the only acceptable method for AST of colistin. The Merlin BMD Colistin strip is already in use in many UK laboratories.

The AltoStar series of reagents, platforms and bespoke software from **altona Diagnostics** offers automated workflow for RT-PCR testing.

The BIOFIRE from **bioMérieux**, a rapid syndromic multiplex PCR system.

bioMérieux

A global leader in *in vitro* diagnostics for more than 50 years, bioMérieux has always been driven by a pioneering spirit and unrelenting commitment to improve public health worldwide. At BSMT in Liverpool this October, the company presented some of its innovative diagnostic solutions. VITEK SOLUTIONS – a complete automated ID/AST platform, the only completely integrated platform for identification and antimicrobial susceptibility testing, designed to move microbiology forward; VIRTUO – a fully automated instrument for blood culture analysis; VIDAS 3 – a benchtop immunoassay system with full traceability and automation; and, the BIOFIRE system – a rapid syndromic multiplex PCR that integrates sample preparation, amplification, detection and analysis.

Bruker

Bruker is the leader in matrix-assisted laser desorption/ionisation (MALDI)-based microbial identification, and the MALDI Biotyper (MBT) is the globally recognised

Resist 4 OKNV, a 15-minute lateral flow test from **BioConnections**.

Bruker is continually adding workflows based on the MALDI Biotyper.

solution for routine usage in the microbiology laboratory. The company is continually adding workflows based on the MBT, including MBT Sepsityper for direct identification from positive blood cultures and subsequent resistance testing. Bruker also markets molecular tests for yeasts and carbapenemase-producing Enterbacteriaceae (CPE), along with the IR Biotyper, for strain typing to target hygiene management. Bruker additionally offers Micronaut for antimicrobial susceptibility testing of bacteria and yeasts. These *in vitro* diagnostics are used in routine laboratories in the fields of human medicine and other microbiology markets. Visitors to the company's stand at BSMT were able to talk to representatives about all of these exciting products.

Launch Diagnostics

Launch Diagnostics has a large range of products and instrumentation for the microbiology and infectious disease laboratory, from rapid tests to multiplex molecular biology assays, with various instruments to complement the assays. The company recently introduced a number of new, advanced instruments and assays to its portfolio. The VirClia chemiluminescence monotest from Vircell includes an extensive range of infectious disease serology tests in a simple-to-use monotest format; and from Abacus Diagnostica, a rapid molecular assay with an innovative instrument employing a simple-to-use reagent concept from sample to result on a plastic test chip.

The VirClia GSD, available from **Launch Diagnostics**.

Mast has produced AST products since 1957.

Mast Group

Mast Group is an independent, market-leading manufacturer and supplier of diagnostic products for clinical, industrial and veterinary testing. Mast has produced antibiotic susceptibility test (AST) products since 1957 and utilises this expertise to assist the ongoing battle against antibiotic resistance. However, the product range has been expanded greatly and Mast now supplies a huge variety of customers in hospital, private clinical, public health and veterinary laboratories, as well as blood banks, food and water testing facilities, and pharmaceutical companies.

MWE

At the recent BSMT meeting in Liverpool, MWE showcased Sigma GBS, a transport device complete with swab and selective enrichment broth designed for the isolation of *Streptococcus agalactiae* (group B *Streptococcus* [GBS]) from pregnant women. Prevention of early onset GBS infections would benefit from more adequate detection methods by optimising specimen collection and processing procedures. It has been proven that without the use of selective enrichment broth, as many as 50% of GBS-positive women have false-negative culture results. With this in mind, MWE developed Sigma GBS to help tackle the issue of false-negative GBS results, offering patients accurate results, saving lives and improving outcomes.

Sigma GBS was developed by **MWE** to help tackle the issue of false-negative GBS results.

National Collection of Type Cultures

The National Collection of Type Cultures (NCTC) is one of four Culture Collections operated by Public Health England. Founded in 1920, it is the longest-established collection of its type, and serves as a United Nations Educational, Scientific and Cultural Organization (UNESCO) Microbial Resource Centre (MIRCEN). NCTC holds almost 6000 type and reference bacterial strains, many of medical, scientific and veterinary importance. The strains support academic, health, food and veterinary institutions and are used in microbiology laboratories and research institutes worldwide. All strains are available in a freeze-dried format, and DNA from over 150 strains is available via the online catalogue.

NCTC, Public Health England

All **NCTC** strains are available in a freeze-dried format

The 2D Datamatrix on show from **Pro-Lab Diagnostics**.

One of the RIDA QUICK range of rapid diagnostic tests for the detection of various pathogens from **R-Biopharm Rhone**.

The UF-5000 from **Sysmex** represents the latest in urinalysis technology.

Pro-Lab Diagnostics

Pro-Lab Diagnostics was pleased once again to support the BSMT Autumn Symposium. Showcasing in Liverpool was 2D Datamatrix Barcoded Microbank, and what the company believes is the latest breakthrough in rapid bacterial ID using FTIR technology. Demonstrations could be arranged for delegates' own laboratory or by visiting the Pro-Lab training facilities.

Qiagen

Qiagen is the leading global provider of Sample to Insight solutions to transform biological materials into valuable molecular insights. Qiagen sample technologies isolate and process DNA, RNA and proteins from blood, tissue and other materials. Assay technologies make these biomolecules visible and ready for analysis. Bioinformatics software and knowledge bases interpret data to report relevant, actionable insights. Automation solutions tie these together in seamless and cost-effective molecular testing workflows. Qiagen provides these workflows to more than 500,000 customers around the world in molecular diagnostics (human healthcare), applied testing (forensics, veterinary testing and food safety), pharma (pharmaceutical and biotechnology companies) and academia (life sciences research).

R-Biopharm Rhone

R-Biopharm Rhone is a daughter company of R-Biopharm-AG, and this year celebrates its 30th year as a leading diagnostics developer and manufacturer. Product technologies include the RIDA QUICK range of rapid diagnostic tests for the detection of various pathogens. RIDA SCREEN ELISA assays are also validated for use with automated platforms. RIDA GENE PCR assays offer a wide range of tests covering respiratory, enteric, STI, transplant and microbiome targets. All are capable of being processed on the majority of PCR systems, offering a complete range of flexible solutions for today's laboratory. All R-Biopharm assays are CE/IVD marked for clinical diagnostics use.

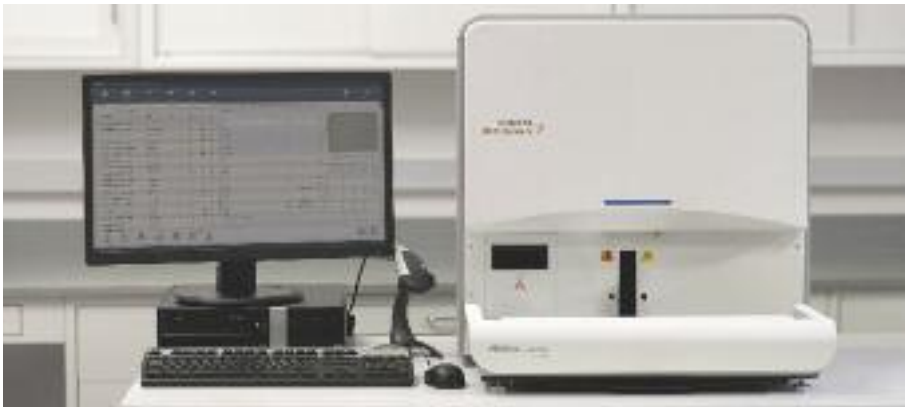
Siemens Healthineers

The VERSANT kPCR Molecular System is a flexible molecular diagnostics platform that enables the laboratory to process multiple sample types, run up to six assays per sample, and consolidate Siemens Healthineers' molecular tests, IVD assays from other manufacturers, and laboratory developed tests (LDTs) on one platform. This user-friendly system reduces manual labour, allowing personnel to spend time on other value-added activities, while providing outstanding assay performance and choice with a broad IVD menu. Elsewhere, do less and see more with a truly digital automated urinalysis system that sets the new standard for accuracy and efficiency. The new Atellica UAS 800 analyser is a truly digital automated urinalysis system, and lets you manage more samples with less staff in shorter time, while never compromising on high-quality results. The system is a completely automated urine sediment analyser designed to minimise the need for manual microscopy.

Sysmex UK

Sysmex UK offers fully automated urinalysis workflow solutions on a premium level. Analysing native urine without any pretreatment prevents the known sources of error inherent in conventional urinary sediment analysis. Urinary tract infection (UTI) information and bacterial differentiation is provided in less than a minute, and the integrated body fluid mode is available at the flick of a switch, and delivers seven diagnostic parameters in BF mode. The UF-5000, based on Sysmex's renowned flow cytometry (FFC), represents the latest in urinalysis technology. It can be used as a standalone analyser or as part of the modular UN-Series for a truly walkaway, seamless urinalysis workplace solution from sample loading to result.

The QIAstatDx instrument was **Qiagen**'s feature product at the BSMT symposium.



Siemens Healthineers offers user-friendly systems that reduce the need for manual input.