#### [PPC2]

# UNDERGRADUATE DENTAL STUDENTS' MANAGEMENT OF DEEP CARIES – A COMPARISON TO BEST PRACTICE

#### Mohammed Adam, Kunal Agarwal, Nicholas Longridge University of Liverpool, Pembroke Place, Liverpool, UK, L3 5PS

We aimed to compare the attitudes and behaviours of final year undergraduate dental students at a UK institution towards managing deep caries (tooth decay) to currently accepted best practice.

Dental caries is reportedly the most prevalent disease globally affecting over 2.4 billion people. Unmanaged, carious lesions can progress rapidly into deeper layers of the tooth ultimately leading to pulpal necrosis indicating complex and costly endodontic treatment or extraction. Pulpitis, a common sequela of caries, can have a significant deleterious effect on quality of life.

Attitudes and understanding towards the management of deep caries previously focused on an infection-based ideology, resulting in complete caries removal that may now be considered overtreatment. Contemporary clinical and histological evidence has shifted treatment towards minimally invasive procedures to manage the dynamic metabolic process. Nonetheless, dentists' attitudes and studies have demonstrated differing viewpoints towards preferred caries removal techniques.

Modern undergraduate curricula should be evidence-based, reflecting current best practice, but research developments can take time to transition into undergraduate teaching and textbooks. It is crucial to understand the attitudes and behaviours of prospective dentists to understand gaps within undergraduate curricula and inform future education.

A previously validated cross-sectional survey was identified and modified following validation by an expert panel and focus group. It was delivered electronically to final year undergraduate dental students at an institute in the United Kingdom.

The results demonstrated a lack of understanding concerning correct terminology with varying levels of understanding and attitudes towards management of deep caries. Although in most cases preferred management was in line with best practice, many students chose alternative options and were hesitant about leaving carious tissue.

We conclude that our data reveals a need for regular revision of curricula with greater incorporation of minimally invasive techniques in the management of deep caries to reflect international consensus.

## [PPC3]

## RAPID DETECTION OF PATHOGENIC BACTERIA BASED ON WHOLE GENOME SEQUENCE

Mingzhen Tian<sup>1</sup>, Bo Cao<sup>1</sup>, Shanghao Zhang<sup>2</sup>, Wei Ma<sup>3</sup>

<sup>1</sup>Shanghai Jiao Tong University, College of Basic Medical Sciences, 227 South Chongqing Road, Shanghai, China <sup>2</sup>Shanghai Jiao Tong University, School of Life Sciences and Biotechnology, 800 Dongchuan Road, Shanghai, China <sup>3</sup>Shanghai Jiao Tong University, Skate Key Laboratory of Microbial Metabolism, 800 Dongchuan Road, Shanghai, China

Bacteria are the causative agent of many human diseases, but it is always a difficult problem to determine the type of pathogen quickly. At present, based on the traditional bacterial isolation and analysis technology, it generally takes 5-7 days to provide important information such as the type of pathogenic bacteria to clinicians, which not only seriously affects the therapeutic effect, but also leads to the abuse of antibiotics and the increase of bacterial resistance.

In this experiment, BLAST local alignment algorithm was used to find the feature gene sequences of common pathogenic bacteria in order to establish a rapid detection system of common pathogenic bacteria in clinical practice. We have developed a complete, rapid, and accurate feature gene screening process. Through four rounds of screening at different levels, we have completed the determination of the optimal feature genes of 12 clinically common pathogenic bacteria. In addition, we used big data omics analysis to screen primer fragments, and obtained feature primer pairs of *Klebsiella pneumonia, Escherichia coli,* and *Pseudomonas aeruginosa*. We verified the specificity of the feature primers obtained in different strains and clinical samples, which proved their good specificity and universality.

The results obtained by us are of great help to the rapid detection of pathogenic bacteria based on gene diagnosis in the future, to effectively alleviate the abuse of antibiotics and the increase of bacterial resistance.

### [PPC4]

# A SYSTEMATIC REVIEW OF OUTCOME MEASURES REPORTED IN RANDOMISED CLINICAL TRIALS OF THE EFFICACY OR SAFETY OF INTERVENTIONS IN COMMUNITY-ACQUIRED PNEUMONIA

Ahmed Kouta, Alexandros Mathioudakis, Timothy Felton, Suzanne Vertsapen, Paul Dark, Kimme Hyrich

Department of Medical Sciences, University of Manchester, Oxford Rd, Manchester M13 9PL

Community-acquired pneumonia (CAP) is one of the leading causes of death worldwide, killing 2.5 million people globally each year. There is room for improvement however in the efficiency of community-acquired pneumonia research, as outcome measure selection for research in this area is not standardised. Lack of outcome measure standardisation leads to outcome heterogeneity which reduces the comparability of data assessing the same disease. The use of, and types of outcomes used in CAP trials is currently unknown. Therefore, this systematic literature review reports outcome measures used in CAP trials with the aim of assessing the use of outcomes. This information will inform the next steps in creating a standardised core outcome set, in the hope of increasing CAP research relevance and comparability.

This systematic literature review was part of a bigger pneumonia wide systematic literature review of outcome measures which has been registered with PROSPERO (PROSPERO ID: CRD42019147411). Cochrane and PubMed databases were searched for CAP trials measuring the efficacy or safety of interventions between January 1<sup>st</sup> 2010 and December 31<sup>st</sup> 2019, with English transcripts. Verbatim outcomes were extracted and categorised into overarching outcome domains.

Seventy-four trials were eligible for data extraction. There was a total of 425 outcome measures, which were characterised into 41 outcome domains. No outcome domains were present in more than 75% of trials, and only one outcome domain-adverse events was present in more than 50% of trials. Eighty-five % of outcome domains were present in no more than a quarter of trials.

There is significant outcome heterogeneity within CAP trials, and a lack of consensus on any outcomes. As such, the development of a core outcome set is recommended, which will set a minimum standardised set of outcomes for future CAP trials to report.

## [PPC5]

# MAGNITUDE AND SENSITIVITY PATTERN OF METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS IN A TERTIARY CARE HOSPITAL IN JAIPUR

Navya Sharma<sup>1</sup>, Niketa Gupta<sup>2</sup>, Rekha Bachhiwal<sup>2</sup> <sup>1</sup>Dr D Y Patil Medical College, Hospital & Research Centre, Pune, Maharashtra, 411018 <sup>2</sup>Department of Microbiology, SMS Medical College and attached group of Hospital, Jaipur, Rajasthan, India, 302021

Antimicrobial resistance (AMR) is a growing global health problem. *Staphylococcus aureus* is the commonest bacterium associated with community acquired and nosocomial infections. Methicillin-resistant strains are increasingly being reported worldwide.

In this study, we determined the prevalence and antimicrobial susceptibility pattern of Methicillin-resistant *Staphylococcus aureus* (MRSA), isolated from various clinical specimens from a tertiary care hospital. The study comprised of 500 strains of *Staphylococcus aureus* isolated from various clinical specimens using standard microbiological procedures. From these isolates, methicillin resistant strains were screened, and their antimicrobial susceptibility pattern was detected according to CLSI 2020 guidelines.

Out of 500 strains a total of 328 strains were found to be methicillin resistant. In this study all MRSA strains were vancomycin sensitive and majority of the MRSA strains were linezolid susceptible. However, vancomycin intermediate and linezolid resistant strains have been reported in some studies, but not found in our study.

Multidrug resistant strains of MRSA are increasing day by day. This is a subject of concern in the present therapeutic scenario especially in the developing countries. There should be close monitoring of antimicrobial susceptibility pattern of MRSA strains with special reference to vancomycin and linezolid and these drugs should be used judiciously.