

misfolded, whereas the baculovirus expression system usually produces proteins with properly folded VLP structures.

Methods: 1. Immunofluorescence assay was for localizing recombinant proteins. 2. High-performance liquid chromatography was for purifying recombinant proteins. 3. Transmission electron microscope was for observing the structure of VLP. 4. Immunogold staining was for confirming the antigenicity of VLP.

Findings: In this study, we produce the original sequence PCV3 Cap (ori-PCV3Cap) and the codon-optimized sequence of the PCV3 Cap (opti-PCV3Cap), respectively. Both recombinant proteins can be successfully produced in the baculovirus expression system, but the yield of opti-PCV3Cap was slightly higher than that of ori-PCV3Cap. Both expressed proteins were further observed to assemble into 17–20 nm particles under transmission electron microscopy and could be recognized by the monoclonal antibody specific to PCV3 Cap in immunogold staining. Furthermore, mutation of the PCV3 Cap within the putative nucleolar localization sequence (NoLS) resulted in reducing protein accumulation in the nucleus and increasing protein extraction efficiency.

Conclusion: All the results indicate that opti-PCV3Cap with the putative NoLS mutation had higher protein yield in the baculovirus expression system and formed a VLP structure as a candidate for PCV3 vaccine.

<https://doi.org/10.1016/j.ijid.2023.04.320>

ASCARIS LUMBRICOIDES AND ASCARIS SUUM PROTEIN PROFILE ANALYSIS WITH R SOFTWARE ENVIRONMENT (MALDIQUANT)

S. Nagorny¹, A. Aleshukina², I. Berezinskaya¹, V. Denisenko², L. Ermakova³, N. Pshenichnaya⁴

¹Rostov Research Institute of Microbiology and Parasitology, Parasitology, Rostov-on-Don, Russian Federation

²Rostov Scientific Research Institute of Microbiology and Parasitology, Microbiology, Rostov-on-Don, Russian Federation

³Rostov Scientific Research Institute of Microbiology and Parasitology, Clinic of infectious and parasitic diseases, Parasitology, Rostov-on-Don, Russian Federation

⁴Central Research Institute of Epidemiology, Department of Infectious Diseases and Epidemiology, Moscow, Russian Federation

Intro: In parasitology, the use of Mass spectrometric analysis is limited by the lack of databases of protein profiles for most parasitic pathogens.

Aim: to study the feasibility of using the R software environment (MALDIquant) to identify differences in the protein profiles of ascaris by the example of *Ascaris lumbricoides* and *Ascaris suum*.

Methods: For the experiment we used 10 species of *A. lumbricoides* and 10 *A. suum*. Head ends of specimens up to 20 mm were used.

Ascaris was washed in 0.9% NaCl, exposure for 24 hours in a solution of 2 antibiotics. The biological material was homogenized mechanically, sonicated (70 kHz for 30 seconds five times in 3 cycles in an alcohol bath (–30 C). Protein profiles were obtained using the Sepsityper Kit 50, in accordance with the instructions based on Microflex LT MALDI–TOF MS (Bruker Daltonics) with FlexControl software (Bruker Daltonics). The result was visualized using Flex analysis 3.3 software (Bruker Daltonics).

Preliminary processing of spectra using the R-MALDIquant package included the following steps: import of the raw spectra into

the R environment; smoothing of spectra; baseline subtraction; spectrum normalization; averaging of repeated spectra; peak detection and peak equalization; creating a matrix of peak intensities; statistical analysis.

Findings: Common patterns for both species ranged from 3100 to 8200 kDa. Differences were noted in the range from 13450 to 14655 kDa.

For the *A.suum* cluster, the coincidence of the mass / charge index with the reference profile was recorded at 100%, and for *A.lumbricoides* – 95–99%.

Discussion: The averaging of the repeated spectra made it possible to obtain reference spectrograms of *Ascaris* and construct dendrograms with two clusters.

Conclusion: Processing mass spectra of *Ascaris* in the software environment R (MALDI quant) made it possible to obtain reference library profiles for species identification

<https://doi.org/10.1016/j.ijid.2023.04.321>

RAPID EMERGENCE OF CANDIDA AURIS IN NORTH ITALY, 2019 TO JULY 2022

C. Sticchi¹, E. Vecchi², S. Ambretti³, C. Gagliotti⁴, E. Ricchizzi⁴, M.L. Moro⁴, G. Diegoli², F. Russo⁵, M. Tonon⁵, R. Raso⁶, F. Maraglino⁷, G. Rezza⁷, M. Sabbatucci^{7,8}

¹Regional Health Agency Liguria, Health prevention, Genoa, Italy

²Emilia-Romagna Region, Directorate General for Personal Care, Health and Welfare, Bologna, Italy

³IRCSS AOU Polyclinic Sant'Orsola-Malpighi, Microbiology Laboratory, Bologna, Italy

⁴Emilia-Romagna Region, Health and social agency, Bologna, Italy

⁵Veneto Region, Directorate for Prevention, Veterinary Food Safety, Venice, Italy

⁶ASL AL, Regional Epidemiology Service for Infectious Diseases (SeREMI), Alessandria, Italy

⁷Ministry of Health, Directorate General Health Prevention, Rome, Italy

⁸Italian National Institute of Health, Infectious Diseases, Rome, Italy

Intro: *Candida auris* represents a serious global health threat. Cases have been reported from over 40 countries in six continents. In Italy, the 1st case was detected in July 2019, never reported to the Ministry of Health (MoH); 2 cases were notified on January and July 2020; 277 cases occurred between November 2020 and October 2021, notified on November 2021 following specific ministerial request; 32 cases were notified November 2021–July 2022. Here we describe the outbreak to raise awareness on this growing threat.

Methods: Cases were notified by the local facilities to regional health authorities and/or the MoH. We defined a confirmed case as a subject infected/colonized by *C. auris* isolated from any type of sample from sterile/non-sterile site. We performed descriptive analysis by R software (version 4.1.1).

Findings: In 4 regions, 312 cases (66% males, median age 59, range 0–76 years) were detected in 12 healthcare facilities, including 34 (11%) deaths. The minority of patients (22%) were colonised. One had history of travel abroad. Over two third were from re-animation and intensive care units. All the environmental samples tested negative. Weekly screening of contacts and instruction of cases were performed at the facilities. Infection prevention and control (IPC) measures were applied locally. The MoH nominated a National Reference Laboratory. Two messages were posted through

the Epidemic Intelligence Information System in 2021. On February 2022, rapid risk assessment declared the risk for further spread high within Italy and low to other countries.

Conclusion: Awareness is crucial to identify *C. auris* colonisation/infection. Appropriate microbiological capacity and ability for patient isolation, prompt case information, strict adherence to IPC measures, periodic screening of contacts, chlorine-based environmental cleaning and reprocessing of medical devices or dedicated equipment, strengthened microbiological and epidemiological surveillance, and prompt notification at both regional and national level are fundamental to stop *C. auris* spread.

<https://doi.org/10.1016/j.ijid.2023.04.322>

PREDICTING THE INTENTIONS TO RECEIVE COVID-19 VACCINE USING THE HEALTH BELIEF MODEL: A CROSS-SECTIONAL STUDY AMONG RESIDENTS OF AN URBAN AREA IN KHARTOUM, SUDAN 2021

T. Abdallah¹, T. Osman², E. Malik²

¹MSF - Belgium, Medical, Khartoum, Sudan

²University of Khartoum, Community medicine, Khartoum, Sudan

Intro: To combat the newly emerging pandemic (Coronavirus disease 2019 (COVID-19)) different preventive measures are advised. World Health Organization recommended vaccination as an important intervention for ending this pandemic. This study aims to understand the willingness and acceptability to take the vaccine using the health belief model.

Methods: A cross-sectional study was conducted during the period January to February 2021 in an urban area of Khartoum, Sudan. The study reached 580 adult individuals. Chi-square test was used to test associations, univariate and multivariate binary logistic regression was used to identify the predictors.

Findings: The Majority of the participants mentioned that they had never been infected by COVID-19 before. (57.4%) believed that they are at risk of infection and most of them did not agree that they are more susceptible to the infection than other people. (83.1%) disagreed that covid-19 complications will be severe for people of their age. (92.6%) of them have heard about the vaccine. (36.9%) of the participants doubted the vaccine effectiveness and (203, 35.0%) believed that it is not safe for them to be vaccinated. (62.9%) of the participants mentioned, they are willing to take the vaccine. Age, perceived susceptibility, being less concerned about getting the disease, perceived vaccine effectiveness and safety, using the vaccine by other people, and doctor advice were significantly predicting the willingness to take the vaccine.

Conclusion: Though most of the participants were willing to take COVID-19 vaccine, many factors were associated and predicted this willingness. These factors should be considered when setting policies and activities to enhance the uptake of the vaccine.

<https://doi.org/10.1016/j.ijid.2023.04.323>

ANTIMICROBIAL SUSCEPTIBILITY AND GENETIC BASIS OF RESISTANCE OF KLEBSIELLA SPP ISOLATED FROM DIARRHEIC AND NON-DIARRHEIC CHILDREN AT HEALTH FACILITIES IN MUKURU INFORMAL SETTLEMENT, NAIROBI, KENYA

C. Wairimu, S. Kariuki

Kenya Medical Research Institute, Centre for Microbiology Research, Nairobi, Kenya

Intro: Antimicrobial resistance (AMR) is a global threat to public health and particularly to children. This study aimed to determine the prevalence of multidrug resistance of fecal *Klebsiella* spp on selected beta lactam (3rd generation cephalosporins and carbapenems) and fluoroquinolone classes of drugs in four health facilities serving the slum communities of Nairobi city in Kenya. Additionally, determine the genetic basis for the multidrug resistance observed.

Methods: This study was a cross sectional laboratory based study where a total of 1171 children below 16 years were selected. 5 grams of stool samples were collected from the participants. Confirmation of *Klebsiella* spp was performed using API 20E; resistance patterns were determined using Kirby – Bauer disk diffusion method; detection of resistance genes was done by conventional PCR; and phylogenetic analysis was performed by (GTG)5 PCR.

Findings: 395 (33.73%) *Klebsiella* spp were isolated, consisting of 365 (92.4%) *Klebsiella pneumoniae* and 30 (7.6%) *Klebsiella oxytoca*. The prevalence of multi-drug resistance (MDR) *K. pneumoniae* and MDR *K. oxytoca* was 64.1 % (234/365) and 96.67 % (29/30) respectively. Third generation cephalosporins, cefotaxime ceftriaxone and ceftazidime showed the highest resistance of 30.7%, 29.9% and 27.4% respectively, whereas carbapenems had the least resistance of 1.6%, each, to *K. pneumoniae*. Genes associated with resistance included bla CTX-M 95.2%, bla OXA-1 66.7%, qnrS 54.1%, qnrB 47.6% and bla NDM-1 7.1%.

Discussion: The carriage of multiple resistance genes demonstrated can be attributed to the presence of resistance determinants such as plasmids, insertion sequences, transposons, integrons. These genes can be transferred to other pathogens and hence aggravating their virulence.

Conclusion: There's need for antimicrobial stewardship, improved (WASH) practices and prioritization of AMR intervention development.

<https://doi.org/10.1016/j.ijid.2023.04.324>

COMPARATIVE PUBLIC HEALTH IMPACT OF ROTAVIRUS VACCINATION IN CHINA

S. Oluwaseun¹, C. Yang², S.J. Si Tu³, Y. Song⁴, F. Han², C. Gu², J. Signorovitch⁴, X.C. Wang³, R. Bian⁵, C. Carias⁶

¹Merck, BARDS-HEDS, North Wales, PA, United States of America

²Analysis Group, Health Economics & Outcomes Research, Beijing, China

³MSD, Outcomes Research, Beijing, China

⁴Analysis Group, Health Economics & Outcomes Research, Boston, MA, United States of America

⁵MSD, Medical Affairs, Beijing, China

⁶Merck, CORE, North Wales, PA, United States of America