

³Zahraa Hospital, Jnah, Lebanon

⁴Ministry of Public Health, Beirut, Lebanon

Purpose: Vaccine acceptance is critical to the success of immunization programs, especially for emerging infectious diseases. This study aims to assess the willingness to receive the COVID-19 vaccine, and the factors associated with this willingness among healthcare workers (HCWs) and non-healthcare workers in Lebanon.

Methods & Materials: A web-based cross-sectional survey was conducted among Lebanese adults aged 18 years and above during November 2020 among Lebanese adults from all Lebanese provinces using a snowball sampling technique. Data were collected using an anonymous Arabic questionnaire that included sociodemographic, health-related variables, intention to receive COVID-19 vaccine, and the Health Belief Model covariates. Multivariable logistic regression analyses were performed to identify the factors associated with the COVID-19 vaccine acceptance among the 2 groups.

Results: A total number of 2802 participants completed the survey. The overall intention to receive a COVID-19 vaccine among the Lebanese adult population was 51.5%. HCWs expressed a higher willingness of getting vaccinated against COVID-19 than non HCWs (65.8% vs. 47%, $p < 0.001$). The factors that are positively associated with the willingness to vaccinate among the general population, non HCWs and HCWs were: older age, being married, living in urban areas, receiving influenza vaccine for this season, higher perception of susceptibility and benefits, concerns related to availability and accessibility of vaccines and recommendation of vaccine from health authorities. However, the previous refusal of any vaccine, concerns about vaccine safety, and side effects impacted negatively this intention. Female gender, importance accounted to religiosity, and concerns about the reliability of the manufacturer were negatively associated with vaccine acceptance among non HCWs. Conversely, good knowledge, vaccine intake by the public, and self-motivation were positively associated with this willingness. Of note, these factors were not significantly associated with such willingness among HCWs.

Conclusion: To control COVID-19 effectively, efforts targeting modifiable factors driving COVID-19 vaccine acceptance are required to increase the acceptance rate among the Lebanese population.

<https://doi.org/10.1016/j.ijid.2021.12.147>

PS09.06 (1072)

Memory B Cell Responses at 16 Weeks Following a Single Dose of AZD1222/Covishield in Sri Lankan Individuals

S.T. Ramu^{1,*}, C. Jeewandara¹, H. Kuruppu¹, P. Pushpakumara¹, M. Harvie¹, S. Dayarathna¹, T. Jayadas¹, T. Ranasinghe¹, I.S. Aberathna¹, S. Danasekara¹, O. Dissanayake¹, N. Gamalath¹, D. Ekanayake¹, J. Jayamali¹, D. Guruge², R. Wijayamuni², G. Ogg³, N. Malavige^{1,3}

¹University of Sri Jayewardenepura, Immunology and Molecular Medicine, Nugegoda, Sri Lanka

²Colombo Municipal Council, Colombo, Sri Lanka

³MRC Weatherall Institute of Molecular Medicine, University of Oxford, Oxford, United Kingdom

Purpose: The dosing interval for AZD1222/Covishield vaccine was prolonged for ≥ 16 weeks, due to short supply in Sri Lanka. As robust secondary immune response depends on the presence of

memory B cell (Bmem), we investigated their frequency following a single dose of the AZD1222.

Methods & Materials: Bmem responses were assessed to S1, S2 and N protein of the SARS-CoV-2 by B cell ELISpot assays in 45 individuals after ≥ 16 weeks of receiving a single dose of the vaccine. The mean ± 2 SD of the background responses was defined as the threshold for positive response of antibody secreting cells (ASCs)/1 million cells.

Results: In this cohort, 40/45 (88.9%) individuals responded to S1, 39/45 (86.7%) to S2 and 36/45 (80%) to N. Responses to S1 ($p < 0.0001$, median 90, IQR 50 to 137.5 ASCs/1 million cells) and S2 ($p = 0.0067$, median 70, IQR 47.5 to 97.5 ASCs/1 million cells) were significantly higher than N (median 50, IQR 22.5 to 80 ASCs/1 million cells). A significant difference in the frequency of responses to S1 ($p = 0.0017$) and S2 ($p = 0.046$), were seen in different age groups, with a higher frequency of ASCs to S1 and S2 proteins in individuals age between 40-60 and > 60 years of age, compared to younger individuals. There was a significant, positive correlation for the frequency of ASCs to S1 (Spearman's $r = 0.49$, $p = 0.0007$), S2 (Spearman's $r = 0.32$, $p = 0.0308$) and N (Spearman's $r = 0.33$, $p = 0.0274$) with age.

Conclusion: 86.7% to 88.9% of individuals had Bmem to the spike protein of the virus, suggesting that a single dose of the vaccine, induced potent Bmem responses. Although 80% of individuals had a low frequency of responses to the N protein, which was not present in the vaccine, this could be due to the presence of cross reactive Bmem responses to N protein of previous beta-coronavirus infections, in older individuals.

<https://doi.org/10.1016/j.ijid.2021.12.148>

Topic 10: Diseases of Animals

PS10.01 (321)

Molecular Detection and Antibigram of *Bacillus cereus* Isolated from Dairy Goat with Mastitis in Malaysia

M.F. Ghazali¹, M.Z. Sukiman¹, M.H. Chai¹, N.M. Mohamad², S.M. Zainal Ariffin^{3,*}

¹Universiti Sultan Zainal Abidin, School of Animal, Aquatic and Environmental Sciences, Faculty of Bioresource and Food Industry, Besut, Terengganu, Malaysia

²Universiti Sultan Zainal Abidin, Centralised Laboratory Management Centre, Besut, Terengganu, Malaysia

³Universiti Putra Malaysia, Department of Veterinary Preclinical Sciences, Faculty of Veterinary Medicine, Serdang, Selangor, Malaysia

Purpose: Mastitis is a major disease frequently reported in dairy goat industry. Mastitis caused by *Bacillus cereus* may (*B. cereus*) be characterised by a very marked degree of tissue damage and subsequently leads to production of abnormal mammary secretions. However, although the used of antibiotic therapy have increased, bacteriological cure rate are low due to emergence of antimicrobial resistance (AMR). The objectives of this study were to determine the prevalence of *B. cereus* in the milk obtained from dairy goat with clinical and subclinical mastitis and to determine the antibiotic susceptibility pattern towards *B. cereus*.

Methods & Materials: A total of 386 lactating does from 37 dairy farms in Malaysia were sampled in this study. All animals were screened and scored for mastitis using the California Mastitis Test (CMT) and 158 goats (307 mammary glands) were identified to be positive for clinical and subclinical mastitis. Identifica-

tion of *B. cereus* was performed using selective medium, biochemical test and polymerase chain reaction (PCR) with primers specific for *bal* gene. The antibiotic susceptibility pattern (AST) of *B. cereus* towards 10 common antibiotics were determined using the disk-diffusion assay.

Results: In this study, 78 (25.4%) out of 307 milk samples from clinical and subclinical mastitis cases were positive for *B. cereus*. Out of 78 milk samples positive for *B. cereus*, 55 were from clinical mastitis cases and 23 were from subclinical mastitis cases. Antibiotic susceptibility test (AST) results showed multidrug resistance pattern with all isolates were fully resistance (100%) towards amoxicillin/ clavulanic acid, cefoxitin, oxacillin and sulphamethazole/ trimethoprim. 59/78 (75.6%) isolates were resistance towards chloramphenicol, ciprofloxacin, clindamycin and streptomycin. 39/78 (50%) and 19/78 (24.3%) of isolates developed resistance towards vancomycin and neomycin respectively.

Conclusion: *B. cereus* isolated from both clinical and subclinical mastitis cases showed high rate of resistance to most tested antibiotics. AST pattern suggest the emergence of Multi-drug Resistant *B. cereus* strain in caprine mastitis cases in Malaysia.

<https://doi.org/10.1016/j.ijid.2021.12.149>

PS10.02 (659)

Molecular Detection of Lumpy Skin Disease Virus in Malaysia 2021

C.K. Khoo*, R. Dahlan, Z. Mat Desa, P.N.A. Syarina, S.S.H. Mohd. Salim, Z. Barker, M.H. Abu Hassan, R. Hassan, F.H. Mohd Saeid

Veterinary Research Institute (VRI), Department of Veterinary Services Malaysia, Ipoh, Malaysia

Purpose: Lumpy skin disease (LSD) is an emerging transboundary notifiable viral disease by the World Organisation for Animal Health (OIE). A member of *Capripoxvirus* within the *Poxviridae* family, LSD virus (LSDV) caused loss of production, infertility, damage to hides and mortality, leading to significant social-economic implications. Originated from the Africa continent, LSD has never been reported in Malaysia before but recently detected in several areas in Asia including Thailand. In May 2021, reports and samples of unknown skin disease in dairy cattle were presented for laboratory diagnosis to confirm provisional LSD clinical diagnosis. This study aims to molecularly detect and confirm the causative agent to enable subsequent control measures to be applied.

Methods & Materials: Three out of 11 dairy cattle from a dairy farm in Perak were showing clinical signs with nodules spotted on the skin of animals. Skin nodule (n=3) and whole blood (n=11) were sampled and tested for LSDV by PCR to confirm the presence of LSDV nucleic acids. The amplicon obtained was subsequently sequenced by Sanger sequencing.

Results: All three skin nodule samples were positive for *Capripoxvirus* by PCR. The nucleotide sequence homology analysis indicates high nucleotide homology to LSDV, confirming the first molecular detection of LSDV in Malaysia. Conversely, all blood samples were negative for *Capripoxvirus* by PCR.

Conclusion: We detected and confirmed the LSD outbreak in Malaysia. Our result indicates transboundary expansion of LSD in the region. This emphasized the importance of tighten border control and lab preparedness to prevent disease introduction and rapid detection of disease. Following this, surveillance, stamping out of the infected animals, suspended the import of animals from infected country and animal movement were carried out and imposed to contain and control the spreading of LSD.

<https://doi.org/10.1016/j.ijid.2021.12.150>

PS10.03 (447)

Spatial Risk Factors Influencing on the Occurrence of Foot and Mouth Disease Outbreaks in Karnataka

V. R.^{1,2,*}

¹ ICAR - National Institute of Veterinary Epidemiology and Disease Informatics, Epidemiology, Bengaluru, India

² ICAR - National Institute of Veterinary Epidemiology and Disease Informatics, Epidemiology, Bengaluru, India

Purpose: Foot and Mouth disease (FMD) is extremely infectious viral disease of cloven-hoofed animals including, cattle, buffalo, sheep, goat, pig and water buffalo and also wild species. The disease is caused by Foot and Mouth Virus (FMDV) belongs to the genus *Aphthovirus* and family *Picornaviridae*. The serotype O is mainly related with cattle in the epidemiology of FMD in Karnataka. In Karnataka, during 1977 to 2014, all 30 districts have reported FMD outbreaks in animals. The present study was aimed to identify the district level spatial risk factors associated with the occurrence of FMD in Karnataka state of India.

Methods & Materials: The 37 years' district outbreak data was collected from the Department of Animal husbandry and Veterinary Services, Hebbal, Karnataka, India. District wise sum of outbreaks was analysed using remote sensed variables along with densities of sheep, goat, cattle and buffalo. Stepwise variable selection was used to select important predictor variables. The predictor variables were selected used in fitting Poisson and negative binomial regression models.

Results: The two predictor variables were selected from the stepwise regression analysis. Based on the Akaike information criterion (AIC), Negative binomial regression model was the best model (AIC=411.27) compared to Poisson regression model (AIC=4656.72). Buffalo density and Bi-annual phase of NDVI was positively associated with occurrence of FMD in Karnataka. The results of the analysis suggest that the spatial variation in occurrence of FMD is influenced by the Buffalo and NDVI.

Conclusion: The spatial analysis of FMD outbreaks and development of risk map will help the policy makers to target vaccination in high risk areas. This will help in reduction of the economic burden of the disease in rural farmers.

<https://doi.org/10.1016/j.ijid.2021.12.151>

PS10.04 (300)

Prevalence of Coagulase-Negative Staphylococci (CoNS) in Healthy and Sick Cat and Dog Populations in Poland

M. Miszczak^{1,*}, A. Korzeniowska-Kowal², A. Wzorek², A. Gamian², L. Szenborn³, K. Rypuła¹, K. Bierowiec¹

¹ Wrocław University of Environmental and Life Sciences, Department of Epizootiology and Clinic of Birds and Exotic Animals, Wrocław, Poland

² Hirszfeld Institute of Immunology and Experimental Therapy, Department of Immunology of Infectious Diseases, Wrocław, Poland

³ Wrocław Medical University, Department of Paediatrics and Infectious Diseases, Wrocław, Poland

Purpose: Coagulase-negative staphylococci (CoNS) constitute a part of the normal microbiota of dogs and cats. These opportunistic