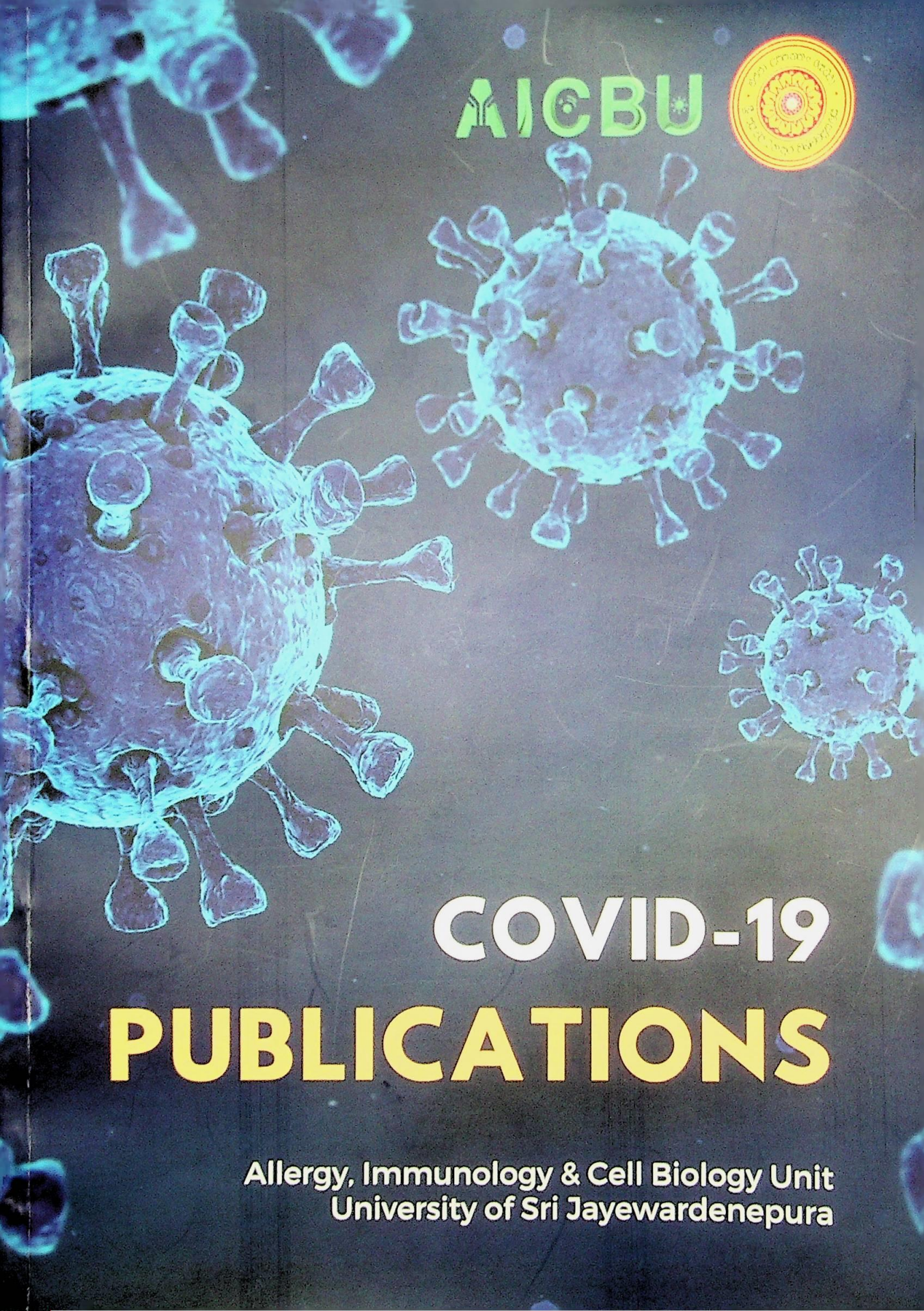


The background of the entire cover is a dark, textured blue-grey. It is populated with several 3D renderings of COVID-19 virus particles. These particles are spherical with a textured surface and numerous spike-like protrusions (glycoprotein spikes) extending from them. The particles are scattered across the cover, with some appearing larger and more detailed than others, creating a sense of depth and focus on the virus.

AICBU



COVID-19

PUBLICATIONS

Allergy, Immunology & Cell Biology Unit
University of Sri Jayewardenepura

ABOUT US

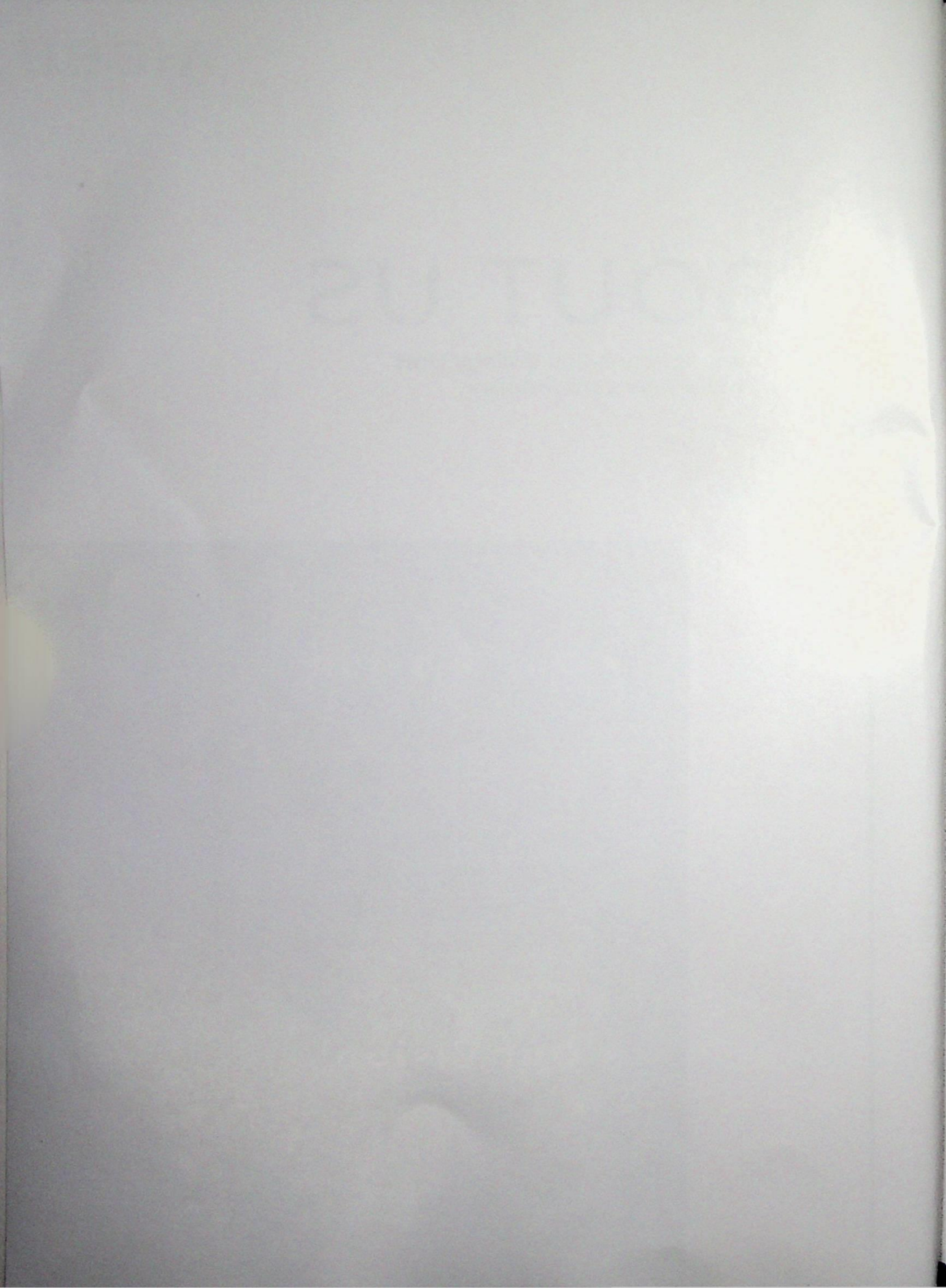
Allergy, Immunology & Cell Biology Unit
University of Sri Jayewardenepura

- **Our Mission**

The mission of the AICBU is to develop human and physical resources, facilitate advanced research and create a world-class innovation platform, while contributing to national development and improving health.

- **Our Vision**

To be a centre of excellence for Allergy, Immunology and Molecular Medicine



A MESSAGE FROM THE DIRECTOR OF OPERATIONS & CLINICAL SERVICES

SARS-CoV-2, the novel coronavirus first detected in Wuhan, China in late 2019 and set off a global pandemic has been an unprecedented challenge to science and humanity. COVID-19 pandemic's devastating impact still hovers over our lives. Containment of this fast-spreading virus required understanding the nature of the virus. This called for a vigorous response and collaboration from scientists worldwide.

When the first patient was detected in Sri Lanka in March 2020, The Allergy Immunology and Cell Biology Unit (AICBU) was already equipped with the necessary facilities and expertise to help in the fight. Our team rose to the occasion and played a significant part in Sri Lanka's management of the pandemic by providing essential data for policy decision-making through our testing, genomic sequencing, and immunogenicity studies for vaccines.

After two and half years, from the month that abruptly changed our lives, we are now moving towards normalcy. As we look back on the achievements and challenges, we can be proud of the work we performed to help our country. I am thankful to our team, who had worked round the clock to carry out this number of research which is summarized in this report. I would like to appreciate the numerous help we received from the Vice-chancellor and the members of academic and non-academic staff. We look forward to making use of this wealth of experience to continue enhancing science and knowledge.

Prof. Chandima Jeewandara

A MESSAGE FROM THE DIRECTOR OF RESEARCH & DEVELOPMENT

The last two years were extremely challenging to everyone, as we had to face the emergence of a completely new virus, we knew nothing about. Initially it created a lot of panic and a sense of doom, as we had to rapidly adapt to the changing environment. The whole global scientific community rose to the occasion by unprecedented amount of whole genomic sequencing to keep track of how the virus is changing, to study disease pathogenesis to understand what the virus does to us and the good and the bad host responses to the virus, to discover how we can treat COVID-19, develop vaccines to prevent COVID-19 and better diagnostics.

We are happy that we were able to contribute to the global effort by keeping track of the virus in Sri Lanka, evaluating better diagnostic methods, disease pathogenesis, drug trials and importantly, to understand the immunogenicity of different COVID-19 vaccines in different populations and their duration of immunogenicity.

Our whole team worked like a well-oiled engine to make this a reality. We were able to do science we never thought was possible by us. We had many disappointments and successes. However, most importantly we learnt so much. The most important lesson being, nothing is impossible if we stand as one.

Prof. Neelika Malavige

scientific reports

SARS-CoV-2 neutralizing antibodies in patients with varying severity of acute COVID-19 illness

Jeewandara C, Jayathilaka D, Gomes L, Wijewickrama A, Narangoda E, Idampitiya D, Guruge D, Wijayamuni R, Manilgama S, Ogg GS, Tan CW, Wang LF, Malavige GN.

Sci Rep. 2021 Jan 21;11(1):2062. doi: 10.1038/s41598-021-81629-2

Impact factor (2021): 4.996

In this study the authors have studied the persistence of SARS-CoV-2 neutralizing antibodies (NABs), and their association with clinical disease severity. A surrogate viral neutralization test was used to evaluate their levels

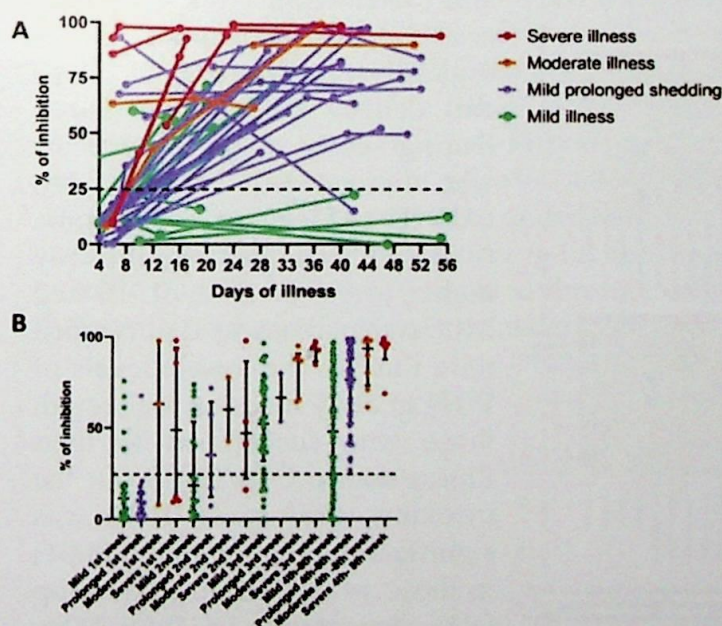


Figure 2. Longitudinal analysis SARS-CoV-2 neutralizing antibodies in patients with varying severity of COVID-19. SARS-CoV-2 NABs were measured in those with severe ($n = 6$), moderate ($n = 5$) and mild/asymptomatic illness ($n = 13$) and also those who had mild illness but with prolonged shedding of the virus ($n = 21$) (A). In order to assess the timing of the NAB responses at different time point, these antibodies were measured in patients with severe pneumonia ($n = 10$), moderate illness ($n = 19$), mild illness ($n = 150$) and prolonged shedding ($n = 82$). The NABs levels were determined in this larger cohort of individuals during the first 3 weeks and during week 4 to 8 of illness (B). The black dotted line indicates the cut-off value of a positive result.

in patients with varying severity of illness, in those with prolonged shedding and those with mild/asymptomatic illness at various time points. Patients with severe or moderate COVID-19 illness had earlier appearance of NABs at higher levels compared to those with mild or asymptomatic illness. This study shows that high levels of NABs during early illness associated with clinical disease severity and that these antibodies declined in 50% of individuals after 3 months since onset of illness.

Similarities and differences between the ‘cytokine storms’ in acute dengue and COVID-19

Dayarathna S, Jeewandara C, Gomes L, Somathilaka G, Jayathilaka D, Vimalachandran V, Wijewickrama A, Narangoda E, Idampitiya D, Ogg GS, Malavige GN.

Sci Rep. 2020 Nov 16;10(1):19839. doi: 10.1038/s41598-020-76836-2.

Impact factor (2021): 4.996

In this study the authors have compared the responses in patients with varying severity of COVID-19 and acute dengue at different time points of illness in

order to determine the similarities and differences in the cytokine and chemokine responses in severe pneumonia and multi-organ dysfunction in COVID-19 and dengue hemorrhagic fever. During early disease, patients who proceeded to develop COVID-19 severe pneumonia (SP) and DHF had significantly higher levels of IL-6, IL-10 and MIP3 α than those who developed mild illness. The lowest levels of IFN γ in early illness were seen in those who succumbed to their illness due to COVID-19. Of the cytokines evaluated, IL-10 was significantly higher ($p < 0.0001$) in those who went on to develop DHF compared to DF. Low IFN γ

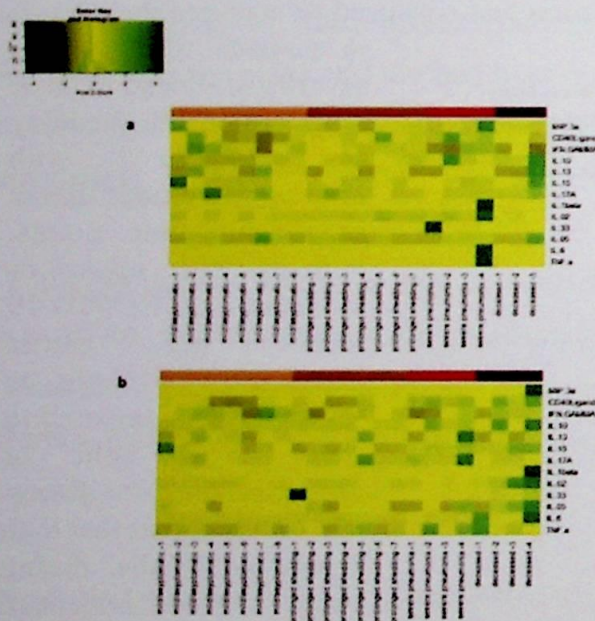


Figure 1. Heat maps representing cytokine and chemokine concentrations in patients with varying severity of COVID19. Each single row represents an individual cytokine or a chemokine level and shown during day 4–9 of illness (time point A) a, and during day 10 to 21 of illness (time point B). In each column represents a different patient.

response to the SARS-CoV2 and high levels of immunosuppressive IL-10 in both COVID-19 and dengue during early illness are indicators of an altered antiviral response potentially contributing to disease severity.



Identification of Novel Candidate CD8⁺ T cell Epitopes of the SARS-CoV2 with Homology to Other Seasonal Coronaviruses

Pushpakumara PD, Madhusanka D, Dhanasekara S, Jeewandara C, Ogg GS, Malavige GN.

Viruses. 2021 May 24;13(6):972. doi: 10.3390/v13060972.

Impact Factor: 5.818

In this study the authors sought to investigate whether the cross-reactive T cell immunity to seasonal coronaviruses (HCoV) may lead to immunopathology or protection during SARS-CoV2 infection. The investigators used IEDB (Immune epitope database) and NetMHCpan (ver. 4.1) to identify candidate CD8⁺ T cell epitopes, restricted through HLA-A and B alleles, thus understanding the influence of cross-reactive T cell responses. Conservation analysis was carried out for these epitopes with HCoVs, OC43, HKU1, and NL63. The authors suggest that it would be crucial to understand T cell responses that are associated with protection, and the differences in the functionality and phenotype of epitope specific T cell responses, presented through different HLA alleles common in different geographical groups, to understand disease pathogenesis.



Dengue and COVID-19: two sides of the same coin

Malavige, G.N., Jeewandara, C. & Ogg, G.S.

J Biomed Sci. 2022 Jul 3;29(1):48. doi: 10.1186/s12929-022-00833-y

Impact Factor: 12.771

In this article, the authors discussed the similarities and differences between the SARS-CoV-2 and the dengue virus (DENV) infections so that lessons learnt so far from studying both infections will be helpful in further understanding their immune- pathogenesis and to develop therapeutic interventions. While there are many similarities between dengue and SARS-CoV-2 infection, there are also key differences especially in long-term disease sequelae. Therefore, it would be important to study the parallels between the immuno-pathogenesis of both infections for development of more effective vaccines and therapeutic interventions.

Dengue	Dengue and COVID-19	COVID-19
Age All ages	Age Older age	Gender Male sex
Immune status Secondary infection	Physiological status Pregnancy	Comorbidities Cardiovascular disease Chronic lung disease Immunosuppression Cancers
Viral factors All four dengue viruses cause severe dengue DENV4 infection milder?	Comorbidities Diabetes Obesity Hypertension Asthma Chronic kidney disease	Viral factors Wide differences in hospitalizations and mortality due to different variants in different countries.

Fig. 1 Risk factors for severe dengue and COVID-19. The common changes are highlighted in the middle box, while those specific to dengue (green box) and COVID-19 (blue box) are shown separately

Seroprevalence of SARS-CoV-2 Infection in the Colombo Municipality Region, Sri Lanka

Jeewandara C, Guruge D, Abyrathna IS, Danasekara S, Gunasekera B, Pushpakumara PD, Madhusanka D, Jayathilaka D, Ranasinghe T, Somathilake G, Tanussiya S, Jayadas TT, Kuruppu H, Thashmi N, Harvie M, Wijayamuni R, Schimanski L, Tan TK, Rijal P, Xiao J, Ogg GS, Townsend A, Malavige GN.

Front Public Health. 2021 Nov 12;9:724398. doi: 10.3389/fpubh.2021.724398.

Impact factor: 6.461

This study showed that the overall sero-positivity rate was 24.46%, while seropositivity by HAT was 18.90%. Although The SARS-CoV-2 infection

detection rates by PCR were highest in the population between the ages of 20–60 years of age, there was no statistically significant difference in the seropositivity rates in different age groups. In conclusion, a high sero-prevalence rate (24.5%) was seen in all age groups in the CMC suggesting that a high level of transmission was seen during this time. The higher PCR positivity rates between the ages of 20–60 are likely to be due to increased testing carried out in the working population. Therefore, the PCR positivity rates, appear to underestimate the true extent of the outbreak and the age groups which were infected.

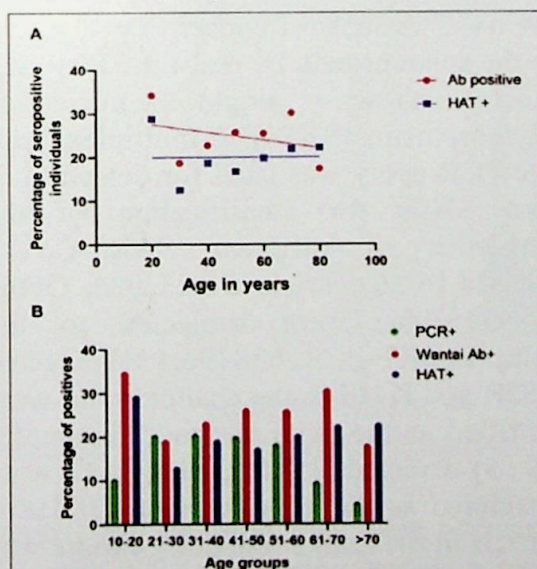


FIGURE 2 | Seropositivity rates and infection rates in different age groups. The seropositivity rates were assessed in each age group by the Wantai total antibody assay (Wantai Ab+) and the HAT assay (HAT+), and the positivity rates of each assay were correlated with the age (A). The PCR positivity rates in each age group and the Wantai (Ab+) and HAT (HAT+) positivity rates were compared in each age group (B).



Surveillance of SARS-CoV-2 variants of concern by identification of single nucleotide polymorphisms in the spike protein by a multiplex real-time PCR

Gomes L, Jeewandara C, Jayadas TP, Dissanayake O, Harvie M, Guruge D, Withanage V, Mahesh PKB, Rajapakse W, Ramachandran R, Dharmarajan V, Pathiraja I, Sanjeevani A, Bandara P, Nanayakkara G, Francis VR, Kithsiri A, Edirisinghe DA, De Silva K, Wijayamuni R, Ogg GS, Waggoner J, Malavige GN.

J Virol Methods. 2022 Feb; 300:114374. doi: 10.1016/j.jviromet.2021.114374.

Impact factor: 2.623

The authors have identified that SARS-CoV-2 variants of concern (VOCs) can be identified by the unique mutations in the spike protein by real-time PCR that

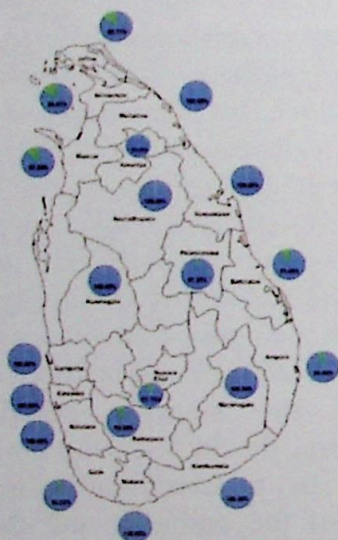


Fig. 1. The prevalence of SARS-CoV-2 variants of concern (VOCs) in 16 districts of Sri Lanka. The delta variant (blue) and the alpha variant (green) are shown.

detect these single nucleotide polymorphisms (SNPs). A multiplex, real-time PCR assay was used for detection of these SNPs for identification of the prevalence of different SARS-CoV-2 VOCs in 16/26 districts in Sri Lanka. Of the 664/934 that were subjected to the multiplex qRT-PCR, 638 (96.1 %) detected L452R and K417 in the channels and were identified as the delta variant. 25 samples (3.9 %) detected N501Y, with K417 were considered as the alpha variant. Of 10/16 districts in Sri Lanka, the delta variant was the only VOC detected. This multiplex real-time qRT-PCR which identifies certain SNPs specific to the VOCs appears

to be a fast, cheaper and less technically demanding method to generate data regarding the spread of different SARS-CoV-2 variants, and is a suitable method for lower income countries, to supplement the data generated by genomic sequencing.

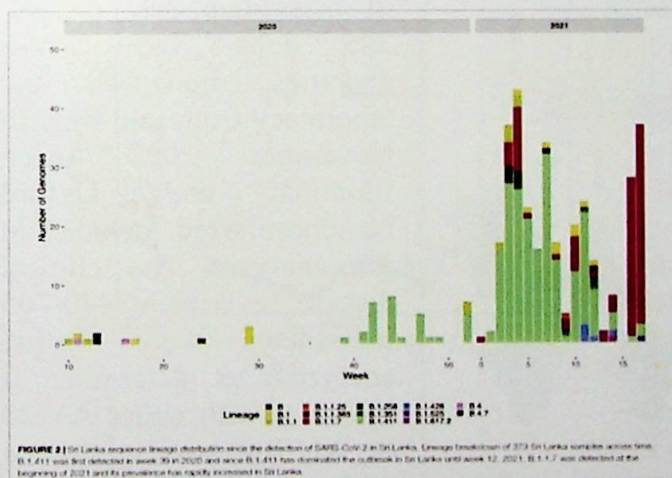
Genomic and Epidemiological Analysis of SARS-CoV-2 Viruses in Sri Lanka

Jeewandara C, Jayathilaka D, Ranasinghe D, Hsu NS, Ariyaratne D, Jayadas TT, Panambara Arachchige DM, Lindsey BB, Gomes L, Parker MD, Wijewickrama A, Karunaratne M, Ogg GS, de Silva TI, Malavige GN.

Front Microbiol. 2021 Sep 16;12:722838. doi: 10.3389/fmicb.2021.722838.

Impact factor: 6.064

In this study the investigators sought to understand the molecular epidemiology of severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) in Sri Lanka, since March 2020, by carrying out genomic sequencing overlaid on available



epidemiological data until April 2021. The B.1.411 lineage was most prevalent, which was established in Sri Lanka and caused outbreaks throughout the country until March 2021. The estimated time of the most recent common ancestor (tMRCA) of this lineage was June 1, 2020 (with 95% lower and upper bounds March 30 to July 27) suggesting that

cryptic transmission may have occurred, prior to a large epidemic starting in October 2020. Returning travelers were identified with infections caused by lineage B.1.258, as well as the more transmissible B.1.1.7 lineage, which has replaced B.1.411 to fuel the ongoing large outbreak in the country. The large outbreak that started in early October, is due to spread of a single virus lineage, B.1.411 until the end of March 2021, when B.1.1.7 emerged and became the dominant lineage.

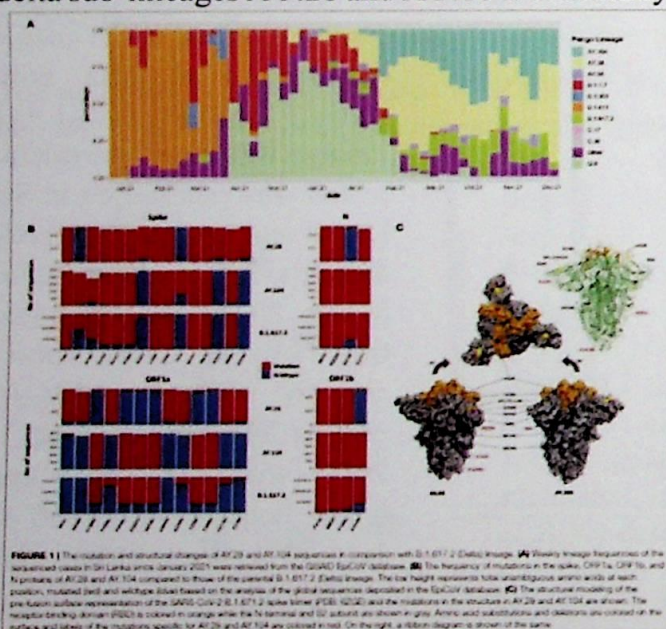
Molecular Epidemiology of AY.28 and AY.104 Delta Sub-lineages in Sri Lanka

Ranasinghe D, Jayathilaka D, Jeewandara C, Gunasinghe D, Ariyaratne D, Jayadas TTP, Kuruppu H, Wijesinghe A, Bary FF, Madhusanka D, Pushpakumara PD, Guruge D, Wijayamuni R, Ogg GS, Malavige GN.

Front Public Health. 2022 Jun 21; 10:873633. doi: 10.3389/fpubh.2022.873633.

Impact factor: 6.461

The worst SARS-CoV-2 outbreak in Sri Lanka was due to the two Sri Lankan delta sub-lineages AY.28 and AY.104. This study further evaluates the mutations



and clinical disease severity of these two sub-lineages. 705 delta SARS-CoV-2 genomes sequenced the laboratory from mid-May to November 2021 using Illumina and Oxford Nanopore were included in the analysis. The clinical disease severity of 440/705 individuals were further analyzed to determine if infection with either AY.28 or AY.104 was associated with more severe disease. Sub-genomic RNA (sg-RNA) expression was analyzed using periscope. There was no difference in the clinical disease severity or duration of hospitalization in individuals infected with these sub lineages. AY.28 and AY.104 appear to have a fitness advantage over the parental delta variant (B.1.617.2), while AY.28 also had a higher expression of sg-RNA compared to other sub-lineages.

PLOS GLOBAL PUBLIC HEALTH

Epidemiological and virological factors determining dengue transmission in Sri Lanka during the COVID-19 pandemic

Dinuka Ariyaratne, Laksiri Gomes, Tibutius T. P. Jayadas, Heshan Kuruppu, Lahiru Kodituwakku, Chandima Jeewandara, Nimalka Pannila Hetti, Anoja Dheerasinghe, Sudath Samaraweera, Graham S. Ogg, Gathsaurie Neelika Malavige

PLOS Global Public Health 2(8): e0000399.

<https://doi.org/10.1371/journal.pgph.0000399>

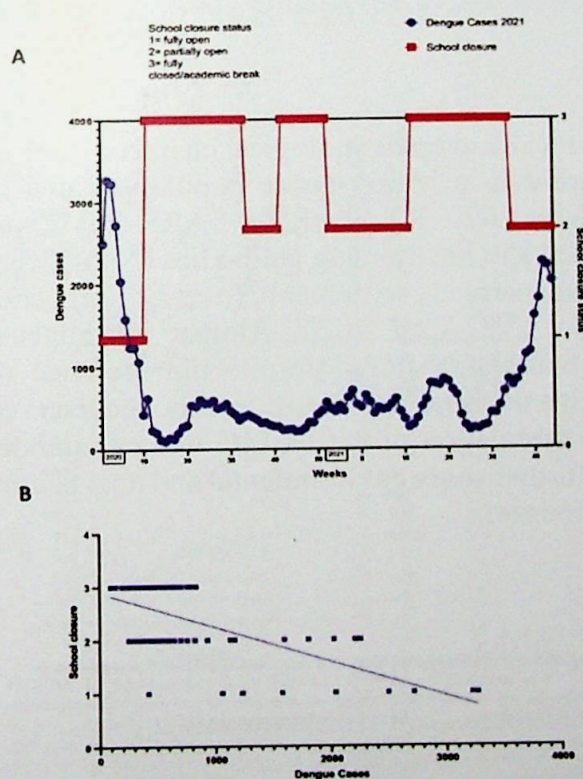


Fig 4. The relationship between number of dengue cases and periods of full and partial school closure in 2021 (A) and the correlation between number of dengue cases and periods of full and partial school closure (B). The number of cases of dengue for 2021 were obtained from DengNet (2) and the SARS-CoV-2 case numbers were obtained from Health Promotion Bureau (5). The data was plotted against school closure data for 2021 from UNESCO (7). School closure status was classified as 1 = fully open, 2 = partially open and 3 = fully closed/academic break. Spearman correlation was calculated (Spearman's $r = -0.4712$, $p < 0.0001$).

<https://doi.org/10.1371/journal.pgph.0000399.g004>

This study sought to identify the contribution of virological factors, human mobility, school closure and mosquito factors in affecting the changes in dengue transmission in Sri Lanka during the COVID-19 pandemic. It was observed that with the onset of the COVID-19 pandemic in early 2020 there was a drastic reduction in the number of dengue cases in Sri Lanka, with an increase towards the end of 2021. To understand the reasons for the differences in the dengue case numbers in 2020 to 2021 compared to previous years, the association between the case numbers in Colombo (which has continuously reported the highest number of cases) with school closures, stringency index, changes in dengue virus (DENV) serotypes and vector densities were investigated.

Transmission dynamics, clinical characteristics and sero-surveillance in the COVID-19 outbreak in a population dense area of Colombo, Sri Lanka April- May 2020

Jeewandara C, Guruge D, Jayathilaka D, Deshan Madhusanka PA, Pushpakumara PD, Tanussiya Ramu S, Sepali Aberathna I, Saubhagya Rasikangani Danasekara DR, Pathmanathan T, Gunatilaka B, Malavige S, Dias Y, Wijayamuni R, Ogg GS, Malavige GN.

PLoS One. 2021 Nov 8;16(11):e0257548.doi:10.1371/journal.pone.0257548.

Impact factor: 3.752

The investigators investigated the clinical and epidemiological characteristics of a SARS-CoV-2 outbreak that occurred in a highly dense population area in Colombo, Sri Lanka from April to May 2020. RT-qPCR for SARS-CoV2 was carried out, SARS-CoV-2 specific total and neutralizing antibodies (Nabs) were assessed in a densely packed, underserved settlement (n = 2722) after identification of the index case on 15th April 2020. Almost all infected individuals developed mild or asymptomatic illness despite the presence of comorbid illnesses. Since the majority of those who were in this underserved settlement were not infected despite circulation of the D614G variant, authors suggest that it would be important to further study environmental and host factors that lead to disease severity and transmission.

Table 2. The presence of SARS-CoV-2 specific total antibodies and neutralizing antibodies in COVID-19 patients, their close contacts and non-close contacts in the Colombo Municipality region.

	SARS-CoV antibody positivity at 11 to 60 days		SARS-CoV antibody positivity at 120 to 160 days	
	Total antibodies	Neutralizing antibodies	Total antibodies	Neutralizing antibodies
COVID-19 RT-qPCR positive patients	59/89 (67.8%)	59/89 (67.8%)	40/65 (61.5%)	26/64 (40.6%)
Close contacts	5/437 (1.1%)	4/437 (0.9%)	7/418 (1.7%)	1/414 (0.2%)
Non-close contacts	23/1539 (1.5%)	0/14	NA	NA

Immune Responses to a Single Dose of the AZD1222/Covishield Vaccine at 16 Weeks in Individuals in Sri Lanka

Jeewandara C, Guruge D, Pushpakumara PD, Kamaladasa A, Aberathna IS, Ramu ST, Gunasekera B, Wijesinghe A, Dissanayake O, Kuruppu H, Ranasinghe T, Jayathilaka D, Dayarathna S, Ekanayake D, Jayamali J, Gamalath N, Mudunkotiwa A, Somathilake G, Dissanayake M, Harvie M, Nimasha T, Madusanka D, Jayadas T, Wijayamuni R, Schimanski L, Rijal P, Tan TK, Townsend A, Ogg GS, Malavige GN.

J Immunol. 2021 Dec 1;207(11):2681-2687. doi:10.4049/jimmunol.2100762.

Impact factor: 5.422

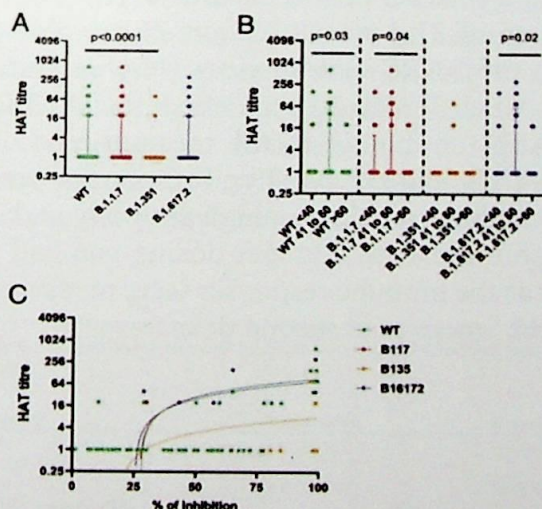


FIGURE 2. Ab responses to the SAR-CoV-2 Wuhan, WT variant, and other variants of concern. Ab responses to the RBD of the WT, B.1.1.7, B.1.351, and B.1.617.2 were determined by HAT in 69 individuals (A) and also in this cohort of individuals when categorized into three age groups (B). The Ab responses for the variants were correlated with the ACE2 receptor-blocking Ab levels, which significantly and positively correlated with the HAT titers for WT (Spearman $r = 0.62$; $p < 0.0001$), B.1.1.7 (Spearman $r = 0.61$; $p < 0.0001$), B.1.351 (Spearman $r = 0.30$; $p = 0.01$), and B.1.617.2 (Spearman $r = 0.64$; $p < 0.0001$) (C). All tests were two-sided. The error bars indicate the median and IQRs.

single dose induced a high frequency of memory T and B cell responses.

This study investigated the immunogenicity of a single dose of vaccine at ≥ 16 weeks post immunization. Severe acute respiratory syndrome coronavirus 2-specific Abs in 553 individuals and Abs to the receptor-binding domain of the Wuhan virus (wild-type) and the variants of concern, angiotensin-converting enzyme 2 receptor blocking Abs ex vivo and cultured IFN- γ T cell (*Homo sapiens*) responses and B cell (*H. sapiens*) ELISPOT responses, were investigated in a sub cohort. Virus-specific Abs were maintained at ≥ 16 wk after receiving a single dose of AZD1222, although levels were lower to variants of concern, especially in older individuals. A

Kinetics of immune responses to the AZD1222/Covishield vaccine with varying dose intervals in Sri Lankan individuals

Jeewandara C, Aberathna IS, Gomes L, Pushpakumara PD, Danasekara S, Guruge D, Ranasinghe T, Gunasekera B, Kamaladasa A, Kuruppu H, Somathilake G, Dissanayake O, Gamalath N, Ekanayake D, Jayamali J, Jayathilaka D, Mudunkotuwa A, Harvie M, Nimasha T, Wijayamuni R, Schimanski L, Rijal P, Tan TK, Dong T, Townsend A, Ogg GS, Malavige GN.

Immun Inflamm Dis. 2022 Apr;10(4):e592. doi: 10.1002/iid3.592.

Impact factor (2021):2.493

In this study the authors have compared antibody and T cell responses in two cohorts with two different dosing gaps for the AZD1222 vaccine; individuals with a dosing gap of 12 weeks, sampled 12 weeks post second dose (cohort 1) and individuals with a median dosing gap of 21.4 weeks (cohort 2) sampled 6 weeks post second dose. Antibodies to the SARS-CoV-2 virus were assessed among individuals as separate cohorts of different dosing schedules. ACE2-blocking antibodies (ACE2-blocking Abs), antibodies to the receptor-binding domain (RBD) of variants of concern (VOC), and ex vivo T cell responses were assessed in a sub-cohort. Both dosing schedules resulted in high antibody and T cell responses post vaccination, although those with a longer dosing gap had a higher magnitude of responses, possibly as the immune responses were measured 6 weeks post second dose compared to 12 weeks post second dose.



Immune responses to a single dose of the AZD1222/Covishield vaccine in health care workers

Jeewandara C, Kamaladasa A, Pushpakumara PD, Jayathilaka D, Aberathna IS, Danasekara DRSR, Guruge D, Ranasinghe T, Dayarathna S, Pathmanathan T, Somathilake G, Deshan Madhusanka PA, Ramu ST, Pramanayagam Jayadas TT, Kuruppu H, Wijesinghe A, Thashmi Nimasha HM, Milroy D, Nandasena AA, Nilanka Sanjeewani PKG, Wijayamuni R, Samaraweera S, Schimanski L, Tan TK, Dong T, Ogg GS, Townsend A, Malavige GN.

Nat Commun. 2021 Jul 29;12(1):4617. doi: 10.1038/s41467-021-24579-7.

Impact factor (2021): 17.69

Several COVID-19 vaccines have received emergency approval. Here the authors assessed the immunogenicity of a single dose of the AZD1222 vaccine, at one month, in a cohort of health care workers (HCWs) (629 naïve and 26 previously infected). 93.4% of naïve HCWs seroconverted, irrespective of age and gender. Haemagglutination test for antibodies to the receptor binding domain (RBD), surrogate neutralization assay (sVNT) and ex vivo IFN γ ELISpot assays were carried out in a sub-cohort. This study showed high seroconversion after one vaccine dose, but also suggested that one vaccine dose may be insufficient to protect against emerging variants

Table 1 Seropositivity rates of a single dose of the ChadOx1 between 28 and 32 days in HCWs who were seronegative at baseline.

Age group	Seropositive	Seronegative	Antibody Index (total antibodies) Median (IQR)
20-29 (n = 100, males = 43)	95 (95%)	5 (5%)	7.5 (4.3-10.7)
30-39 (n = 182, males = 87)	164 (90.1%)	18 (9.9%)	6.1 (3.3-10.9)
40-49 (n = 160, males = 62)	159 (98.7%)	5 (3.1%)	8.8 (4.6-12.1)
50-59 (n = 149, males = 58)	139 (93.2%)	8 (5.4%)	7.4 (3.3-14.7)
>60 (n = 38, males = 11)	31 (81.6%)	7 (18.4%)	8.1 (2.3-12.1)

scientific reports

Immune responses following the first dose of the Sputnik V (Gam-COVID-Vac)

Jeewandara C, Fernando S, Pushpakumara PD, Ramu ST, Kamaladasa A, Gunasekara B, Aberathna IS, Kuruppu H, Ranasinghe T, Dayarathne S, Dissanayake O, Gamalath N, Ekanayake D, Jayamali J, Wijesinghe A, Dissanayake M, Somathilake G, Harvie M, Danasekara S, Jayathilaka D, Wijayatilake HDK, Weerasooriya N, Kekulandara C, Schimanski L, Rijal P, Tan TK, Dong T, Townsend A, Ogg GS, Malavige GN.

Sci Rep. 2022 Feb 2;12(1):1727. doi: 10.1038/s41598-022-05788-6.

Impact factor (2021): 4.996

In this study the authors have investigated the immunogenicity of Gam-COVID-Vac at 4 weeks (327 naïve individuals). 88.7% seroconverted, with significantly lower sero-conversion rates in those over 60 years ($p = 0.004$) and significantly lower than previously seen with AZD1222 ($p = 0.018$). 82.6% developed ACE2 receptor blocking antibodies, although levels were significantly lower than following natural infection ($p = 0.0009$) and a single dose of AZD1222 ($p < 0.0001$). Similar titres of antibodies were observed to the receptor binding domain of WT, B.1.1.7 and B.1.617.2 compared to AZD1222, while the levels for B.1.351 were significantly higher ($p = 0.006$) for Gam-COVID-Vac. 30% developed ex vivo IFN γ ELISpot responses (significantly lower than AZD1222), and high frequency of CD107a expressing T cells along with memory B cell responses. Although single dose of Gam-COVID-Vac was highly immunogenic, administration of a second dose is likely to be beneficial.

Age categories	Positive N (%)	95% CI	Antibody index (median, IQR)
20–40, n = 71	70 (98.59%)	(95.85%, 100%)	6.7 (3.5 to 11.1)
40–59, n = 168	148 (88.10%)	(83.20%, 92.99%)	6.6 (2.4 to 10.5)
≥ 60, n = 88	72 (81.82%)	(73.76%, 89.88%)	3.9 (1.4 to 9.7)

Table 1. Seroconversion rates and antibody titres (given as the antibody index) 4 weeks following a single dose of the Gam-COVID-Vac.



Kinetics of immune responses to SARS-CoV-2 proteins in individuals with varying severity of infection and following a single dose of the AZD1222

Jayathilaka D, Jeewandara C, Gomes L, Jayadas TTP, Kamaladasa A, Somathilake G, Guruge D, Pushpakumara PD, Ranasinghe T, Aberathna IS, Danasekara S, Gunathilaka B, Kuruppu H, Wijewickrama A, Wijayamuni R, Schimanski L, Tan TK, Ogg GS, Townsend A, Malavige GN.

Clin Exp Immunol. 2022 Jun 23;208(3):323-331. doi: 10.1093/cei/uxac009.

Impact Factor: 5.732

This study compared the antibody responses to SARS-CoV-2 following natural infection and following a single dose of AZD1222 (Covishield), in Sri Lankan individuals. The authors assessed the IgG and IgA responses to S1, S2, RBD, and N proteins in patients at 4 weeks and 12 weeks since the onset of illness or following vaccination. Antibodies to the receptor-binding domain of SARS-CoV-2 wild type (WT), α , β , and λ and ACE2 (Angiotensin Converting Enzyme 2) receptor blocking antibodies were also assessed in these cohorts. Vaccinees had significantly less IgA to SARS-CoV-2, but comparable IgG responses to those with natural infection. However, following a single dose vaccine reduced antibody levels to the VOCs, which further declined with time, suggesting the need to reduce the gap between the two doses, in countries experiencing outbreaks due to VOCs.

immunology

Immune responses to Sinopharm/BBIBP-CorV in individuals in Sri Lanka

Jeewandara C, Aberathna IS, Pushpakumara PD, Kamaladasa A, Guruge D, Wijesinghe A, Gunasekera B, Tanussiya S, Kuruppu H, Ranasinghe T, Dayarathne S, Dissanayake O, Gamalath N, Ekanayake D, Jayamali J, Jayathilaka D, Dissanayake M, Madusanka D, Jayadas TT, Mudunkotuwa A, Somathilake G, Harvie M, Nimasha T, Danasekara S, Wijayamuni R, Schimanski L, Rijal P, Tan TK, Dong T, Townsend A, Ogg GS, Malavige GN.

Immunology. 2022 Jun 27. doi: 10.1111/imm.13536.

Impact factor (2021):7.215

There are limited data on the immunogenicity of the Sinopharm/BBIBP-CorV in different populations, antibody responses against different SARS-CoV-2 variants of concern and T cell responses. In this study the immunogenicity of the vaccine, in individuals in Sri Lanka was investigated. SARS-CoV-2-specific antibodies were measured in individuals who were sero-negative at baseline, and ACE2 receptor blocking antibodies, antibodies to the receptor-binding domain (RBD) of the wild-type (WT), alpha, beta and delta variants, ex vivo and cultured IFN γ ELISpot assays, intracellular cytokine secretion assays and B cell ELISpot assays were carried out in a sub cohort of the vaccines at 4 and 6 weeks (2 weeks after the second dose). Sinopharm/BBIBP-CorV appeared to induce a similar level of antibody responses against ACE2 receptor delta and beta as seen following natural infection.

Persistence of antibody and T cell responses to the Sinopharm/BBIBP-CorV vaccine in Sri Lankan individuals

Jeewandara C, Aberathna IS, Pushpakumara PD, Kamaladasa A, Guruge D, Wijesinghe A, Gunasekera B, Tanussiya S, Kuruppu H, Ranasinghe T, Dayarathne S, Dissanayake O, Gamalath N, Ekanayake D, Jayamali J, Jayathilaka D, Dissanayake M, Jayadas TT, Mudunkotuwa A, Somathilake G, Harvie M, Nimasha T, Danasekara S, Wijayamuni R, Schimanski L, Rijal P, Tan TK, Dong T, Townsend A, Ogg GS, Malavige GN.

Immun Inflamm Dis. 2022 Jun;10(6):e621. doi: 10.1002/iid3.621.

Impact factor (2021): 2.493

This study investigated the immune responses in a cohort of Sri Lankan individuals in order to determine the kinetics and persistence of immune responses following the Sinopharm/BBIBP-CorV, SARS-CoV-2 specific total antibodies were measured by enzyme-linked immunosorbent assay, 12 weeks after the second dose of the vaccine. Angiotensin-converting enzyme 2 (ACE2) receptor blocking antibodies (ACE2R-Ab), antibodies to the receptor-binding domain (RBD) of the ancestral virus (WT) and variants of concern, were measured in a sub cohort. T cell responses and memory B cell responses were assessed by ELISpot assays. This study showed that antibody responses declined in all age groups, especially in those ≥ 60 years, while T cell responses persisted. The effect of waning of immunity on hospitalization and severe disease should be assessed by long term efficacy studies.

PLOS GLOBAL PUBLIC HEALTH

Antibody responses to Sinopharm/BBIBP-CorV in pregnant mothers in Sri Lanka

Chandima Jeewandara, K. A. Chintha S. Jayampathi, Thushali Ranasinghe, Inoka Sepali Aberathna, Banuri Gunasekara, Saubhagya Danasekara, Thashmi Nimasha, Heshan Kuruppu, Osanda Dissanayake, Nayanathara Gamalath, Dinithi Ekanayake, Jewantha Jayamali, Gayasha Somathilake, Dinuka Guruge, Ruwan Wijayamuni, Achala Kamaladasa, Graham S. Ogg, Gathsaurie Neelika Malavige

PLOS Global Public Health 2(7): e0000607.
<https://doi.org/10.1371/journal.pgph.0000607>

The authors sought to investigate the antibody responses and, maternal and fetal adverse events following the administration of the Sinopharm/BBIBP-CorV

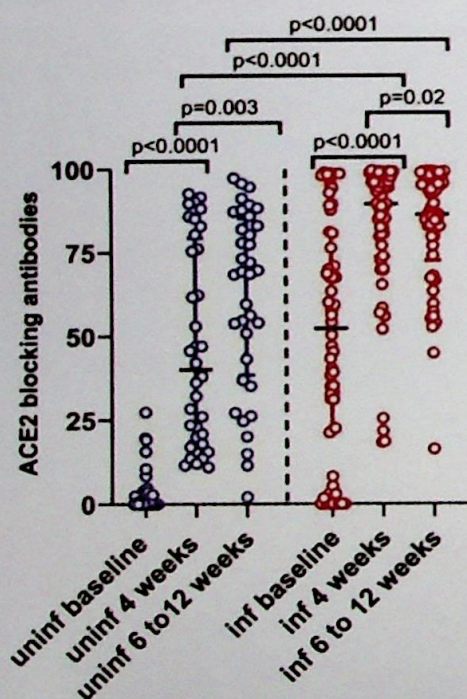


Fig 2. ACE2 blocking antibodies following first and second dose of the sinopharm/BBIBP-CorV vaccine. The ACE2 receptor blocking antibodies were measured by the surrogate virus neutralization test as baseline uninfected ($n = 36$) and infected ($n = 56$) pregnant women. Wilcoxon matched-pairs signed rank test was used to compare the means of the antibody values before and after the vaccine, while the Mann-Whitney U test was used to calculate the differences in antibody responses at each time point in baseline uninfected and infected women. All tests were two-tailed. The boxes indicate the median and the interquartile range.

vaccine in pregnant mothers in Sri Lanka. SARS-CoV-2 receptor binding domain (RBD) specific total antibodies and ACE2 blocking antibodies were measured by ELISA in pregnant mothers who received the vaccine in the first, second and third trimester of pregnancy. The Sinopharm/BBIBP-CorV vaccine appeared safe and induced high seroconversion rates and ACE2 blocking antibodies in pregnant mothers in the second and third trimester in pregnancy. However, the RBD binding antibodies and ACE2 blocking antibodies post-second dose were significantly higher in previously infected pregnant mothers post-second dose, suggesting that two doses of the vaccine are likely to be less immunogenic in previously unexposed individuals.

Comparison of the immunogenicity of five COVID-19 vaccines in Sri Lanka

Jeewandara C, Aberathna IS, Danasekara S, Gomes L, Fernando S, Guruge D, Ranasinghe T, Gunasekera B, Kamaladasa A, Kuruppu H, Somathilake G, Jayamali J, Jayathilaka D, Wijayatilake HDK, Pushpakumara PD, Harvie M, Nimasha T, de Silva SDG, Wijayamuni R, Schimanski L, Rijal P, Tan J, Townsend A, Ogg GS, Malavige GN.

Immunology. 2022 Jun 25: doi: 10.1111/imm.13535

Impact factor (2021):7.215

In this study antibody responses in individuals 3 months post-vaccination in those who had received different vaccines in Sri Lanka was compared in order to determine the antibody responses elicited by different vaccines against SARS-CoV-2. Abs to the receptor binding domain (RBD) of the ancestral (wild type) virus (WT) as well as to variants of concern (VoCs), and ACE2 blocking Abs, were assessed in individuals vaccinated with Moderna, Sputnik V, or Sputnik light and the results were compared with previously reported data on Sinopharm and AZD1222 vaccines. The Moderna vaccine elicited the highest ACE2 blocking antibody levels followed by Sputnik V/AZD1222, while those who received Sinopharm had the lowest levels.

TABLE 1 Percentage of individuals seroconverted based on total RBD antibodies and ACE2 blocking antibodies for SARS CoV-2 at 3 months following full vaccination

Vaccine	Antibody type	Percentage positivity (number of positive individuals/total number) median age (range)			
		All individuals mean age (range)	Age 20 to 39	Age 40 to 59	Age >60
AZD1222	RBD-Abs	100% (299/299) 45 years (21–81)	100% (129/129)	100% (152/152)	100% (18/18)
	ACE2 blocking-Abs	96.2% (65/69) 49 years (24–81)	96.1% (25/26)	92.3% (24/26)	94.1% (16/17)
Sinopharm	RBD-Abs	95.07% (193/203) 47 years (25–72)	96.72% (59/61)	95.0% (114/120)	90.91% (20/22)
	ACE2 blocking-Abs	60.9% (67/110) 47 years (25–72)	65.8% (27/41)	66.6% (32/48)	38.1% (8/21)
Moderna	RBD-Abs	94.2% (214/227) 50 years (22–82)	96% (48/50)	93.7% (121/129)	93.7% (45/48)
	ACE2 blocking-Abs	99.5% (223/224) 50 years (22–82)	100% (48/48)	99.2% (131/132)	100% (44/44)
Sputnik Light (1 dose)	RBD-Abs	94.5% (174/184) 46 years (20–59)	95.5% (43/45)	94.2% (131/139)	0
	ACE2 blocking Abs	74% (37/50) 40 years (20–59)	76% (19/25)	72% (18/25)	0
Sputnik V (2 doses)	RBD-Abs	100% (127/127) 44 years (25–66)	100% (50/50)	100% (77/77)	0
	ACE2 blocking-Abs	97.7% (124/127)	100% (50/50)	96.1% (74/77)	0

Comparison of different sequencing techniques for identification of SARS-CoV-2 variants of concern with multiplex real-time PCR

Ranasinghe D, Jayadas TTP, Jayathilaka D, Jeewandara C, Dissanayake O, Guruge D, Ariyaratne D, Gunasinghe D, Gomes L, Wijesinghe A, Wijayamuni R, Malavige GN.

PLoS One. 2022 Apr 4;17(4):e0265220. doi: 10.1371/journal.pone.0265220.

Impact factor: 3.752

The emergence of different SARS-CoV-2 variants and the continuous evolvement of sub lineages of the delta variant have made it important for all the countries to carry out sequencing of at least >1% of their infections, in order to detect emergence of variants with higher transmissibility and with ability to evade immunity. In this study authors have compared usefulness of a two-step commercially available multiplex real-time PCR assay to detect important single nucleotide polymorphisms (SNPs) associated with the variants and compared the sensitivity, accuracy and cost effectiveness of the Illumina sequencing platform and the Oxford Nanopore Technologies' (ONT) platform. Although the ONT had a slightly higher error rate compared to the Illumina technology, it achieved higher coverage with a lower number of reads, generated less ambiguous bases and was significantly less expensive than Illumina sequencing technology.

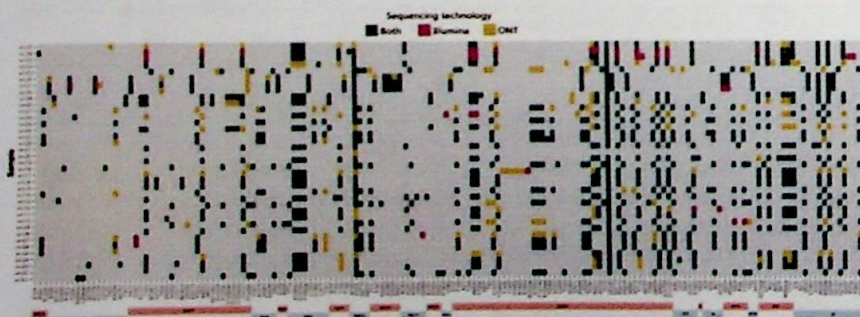


Fig 2. Comparison of amino acid changes detected in SARS-CoV-2 genomes by both sequencing technologies. Annotated amino acid substitutions and deletions detected in each sample ($n = 37$). Mutations colored in green indicates they are synonymously detected by both sequencing technologies, whereas yellow and red indicate mutations detected exclusively by only one technology. The X axis indicates each amino acid, which is denoted by the original amino acid, its position in the protein and the substitution/deletion. Amino acid deletions are denoted by "del".

BMC Infectious Diseases

Sensitivity and specificity of two WHO approved SARS-CoV2 antigen assays in detecting patients with SARS-CoV2 infection

Jeewandara C, Guruge D, Pushpakumara PD, Madhusanka D, Jayadas TT, Chaturanga IP, Aberathna IS, Danasekara S, Pathmanathan T, Jayathilaka D, Somathilaka G, Kuruppu H, Gomes L, Gunasekara V, Wijayamuni R, Ogg GS, Malavige GN.

BMC Infect Dis. 2022 Mar 22;22(1):276. doi: 10.1186/s12879-022-07240-6.

Impact Factor: 3.670

In this study the investigators evaluated two WHO approved SARS-CoV-2 rapid antigen (Ag) detection kits in a large cohort of Sri Lankan individuals because of the concerns regarding their sensitivity and specificity, in different settings. The overall sensitivity of the SD-Biosensor Ag kit was 36.5% and the Abbott Ag test was 50.76%. The Abbott Ag test showed specificity of 99.4% and the SD-Biosensor Ag test 97.5%. Both rapid Ag tests appeared to be highly sensitive in detecting individuals at lower Ct values, in a community setting in Sri Lanka. But the authors suggested that it will be important to further establish the relationship to infectivity.

Table 1 Positivity rate of the SD-Biosensor rapid Ag kit for different RT-qPCR kits at different Ct values

PCR Kit (number of PCR positive samples)	Avg Ct value for PCR	Number of samples used	Sensitivity of the SD-Biosensor Ag kit (%)	95% CI lower limit (%)	95% CI upper limit (%)
SeeGene Kit (n = 505)	< 25	177	76.6	69.5	82.5
	26–30	130	36.2	28.1	45.1
	31–38	198	6.1	3.3	10.6
TAQPATH Kit (n = 186)	< 25	87	71.3	60.4	80.2
	26–30	77	13	6.7	23
	31–38	22	9.5	1.7	31.8
SD-Biosensor RT-qPCR Kit (n = 183)	< 25	61	72.1	59%	82.5
	26–30	51	7.8	2.5%	19.7
	31–38	71	0%	0	6.4



Comparison of two assays to detect IgG antibodies to the receptor binding domain of SARS-CoV-2 as a surrogate marker for assessing neutralizing antibodies in COVID-19 patients

Kamaladasa A, Gunasekara B, Jeewandara C, Jayathilaka D, Wijewickrama A, Guruge D, Wijayamuni R, Tan TK, Ogg GS, Townsend A, Malavige GN.

Int J Infect Dis. 2021 Aug;109:85-89. doi: 10.1016/j.ijid.2021.06.031.

Impact Factor (2021): 12.074

In this study, two assays that are correlated with NABs were compared: the haemagglutination test (HAT) and the surrogate virus neutralization test (sVNT). The specificity of the HAT was >99%, and sensitivity was similar to the sVNT.

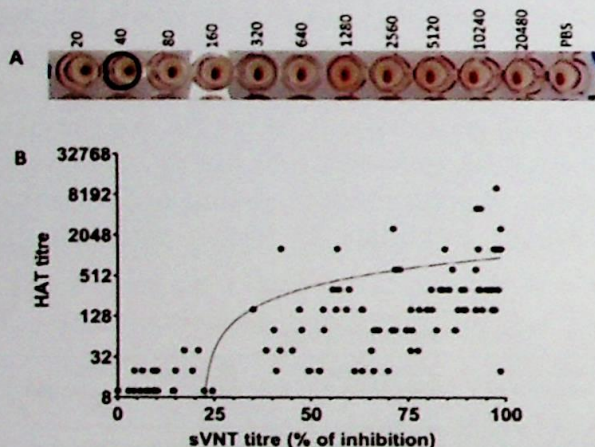


Figure 1. Correlation of antibody levels determined by haemagglutination test (HAT) titration and surrogate virus neutralization test (sVNT). (A) Example of HAT titration carried out on a sample. The HAT titration was conducted using 11 doubling dilutions of the serum from 1:20 to 1:20480 (the titres are indicated as '20', instead of '1:20'). The HAT titre of the sample was determined according to the last well in which the complete absence of teardrop formation was observed (marked with a black solid circle), indicating a titre of 1:40 for this patient. (B) Correlation of antibody levels determined by HAT titre and the percentage inhibition of binding of the RBD to recombinant ACE2 by the serum sample according to the sVNT assay. This correlation was performed with samples obtained from 50 patients belonging to cohort 1 at three time points during the course of illness. Spearman's $r = 0.79$, $P < 0.0001$.

The levels of HAT were significantly and positively correlated with those of the sVNT (Spearman's $r = 0.78$, $P < 0.0001$). Patients with moderate and severe illness had higher HAT titres when compared to those with mild illness. Six of seven patients with severe illness had a titre of >1:640 during the second week of illness, whereas only five of 31 patients with a mild illness had a titre of >1:160 in the second week of illness. In conclusion, the haemagglutination test would be ideal to use as an indicator.

Journal of the Ceylon College of Physicians

Comparison of the analytical sensitivity of three real time PCR kits used in the detection of the SARS-CoV-2

Dayarathna, S., Jayathilaka, D., Jeewandara, C., Wijewickrama, A., Narangoda, E., Idampitiya, D. and Malavige, G.N

Journal of the Ceylon College of Physicians, 51(1), pp.53–57.

DOI: [10.4038/jccp.v51i1.7888](https://doi.org/10.4038/jccp.v51i1.7888)

COVID-19 infection is diagnosed by a real-time Reverse transcriptase Polymerase chain reaction (RT-PCR), which can detect the presence of the SARS-CoV-2 virus as early as day one of symptoms. However, the performance of these kits can vary widely. This study assessed the performance of three different PCR kits from different manufacturers used for diagnosis of COVID-19 in Sri Lanka. The three PCR kits had highly varied sensitivity for the positive with high Ct values (>35) and lower Ct values (Ct values 30-35). This study suggests that the sensitivity of the PCR kits to be thoroughly evaluated prior to their use and for optimum results, kits with higher sensitivity should be used in the compatible machine.



Enhancing immunity in viral infections, with special emphasis on COVID-19: A review

Jayawardena R, Sooriyaarachchi P, Chourdakis M, Jeewandara C, Ranasinghe P.

A review. *Diabetes Metab Syndr.* 2020 Jul-Aug;14(4):367-382. doi: 10.1016/j.dsx.2020.04.015.

Balanced nutrition which can help in maintaining immunity is essential for prevention and management of viral infections. While data regarding nutrition in coronavirus infection (COVID-19) are not available, in this review, authors have aimed to evaluate evidence from previous clinical trials that studied nutrition-based interventions for viral diseases (with special emphasis on respiratory infections), and summarized their observations. This article summarizes the possible benefits of some vitamins, trace elements, nutraceuticals and probiotics in viral infections. Nutrition principles based on these data could be useful in possible prevention and management of COVID-19

BMJ Global Health

Stronger together: a new pandemic agenda for South Asia

Bandara S, Bhaumik S, Sriram V, Saha S, Zia N, Hasan MZ, Malavige GN, Rasali D.

BMJ Glob Health. 2021 Aug;6(8):e006776. doi: 10.1136/bmjgh-2021-006776.

Impact Factor: 8.056

The authors presented a pragmatic ‘Stronger Together’ agenda on critical areas of concern for political, social, medical and public health leaders in South Asia to consider and build on increased time and resources. This article suggested that regional collaborative efforts within existing facilities and building a regional network similar to the Indian SARS-CoV-2 Genome Sequencing Consortia are feasible. The article further elaborated on how the network can also build capacity within each country in the long run making countries self-sufficient to collect data and strengthen regional surveillance. The authors also put forward the idea of linking genomic data with clinical and public health data as well as enabling environmental surveillance so that it will provide a more comprehensive picture of circulating SARS-CoV-2 variants. Authors suggested that this could be an investment, not only for the ongoing pandemic but also for other endemic pathogens and emerging infectious diseases.



COVID-19 Pandemic: lessons learnt and the way forward

Malavige/ Vidyodaya Journal of Science 24 No. 02 (2021) 3-6

<https://journals.sjp.ac.lk/index.php/vjs/article/view/5403>

Although the scientific community had been predicting and preparing for a pandemic for the last 10 years, many policy makers did not envision that a virus could cause such devastation to human life, economies and to the social structure. COVID-19 has taught us many bitter lessons and while moving forward it is important to understand that this current pandemic is yet to end. However, COVID-19 is unlikely to be the last pandemic that we face. Due to certain human activities such as urbanization, deforestation, increased human and animal interactions and climate change, we will see more pandemics emerging in the coming years. Preparedness and anticipation of such an event is the only way forward.

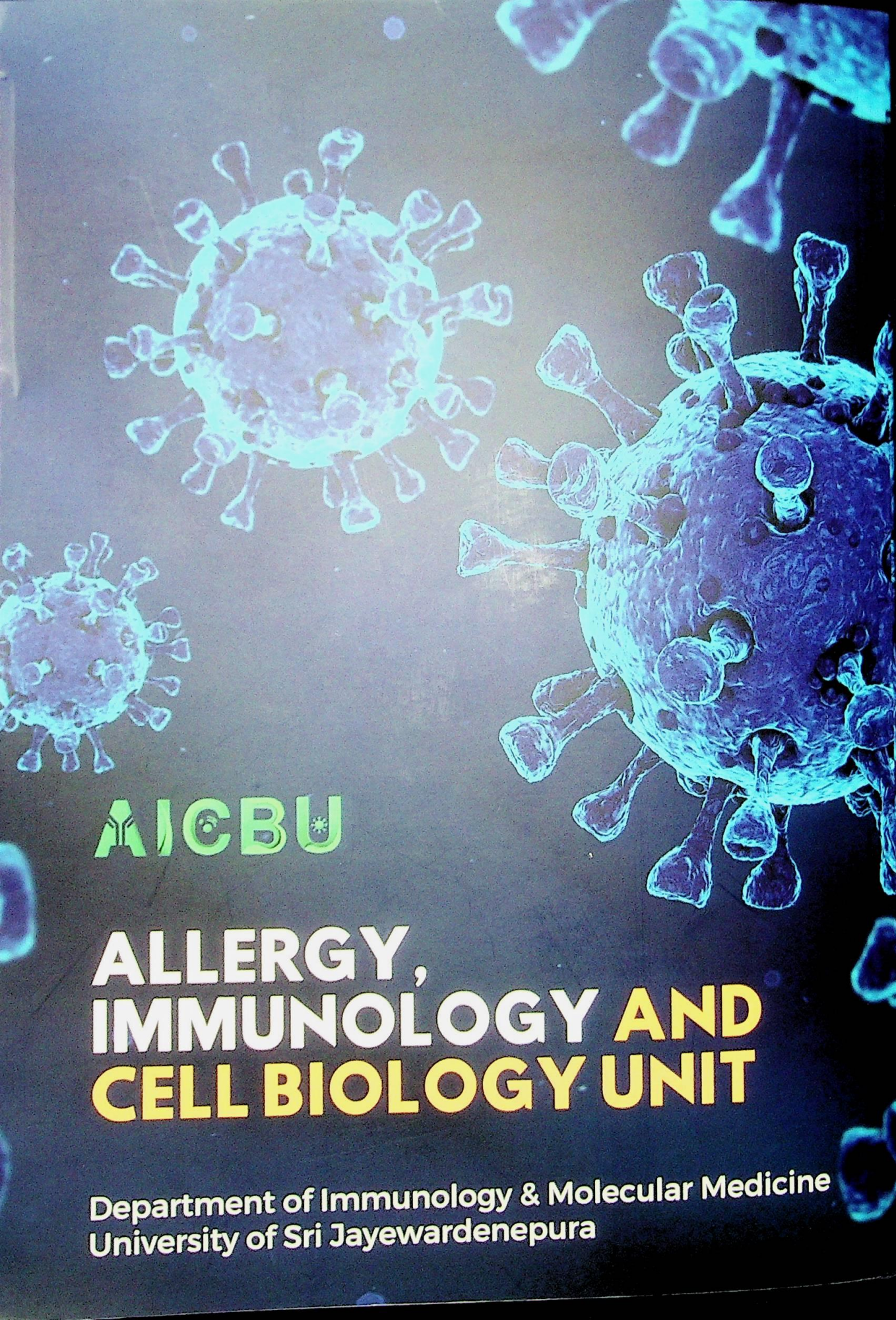
Expansion of SARS-CoV-2 sequencing capacity globally is vital for future control of the COVID-19 pandemic

de Silva TI & Malavige GN

Sri Lanka Journal of Medicine Vol. 30 No.1, 2021

DOI:10.4038/sljm.v30i1.273

In this article the authors discuss about the role played by the viral genomic sequencing during the pandemic and the importance of sharing the sequenced data. They further elaborate on how the sequenced and shared data accelerated the health care response to the SARS-CoV-2 pandemic, worldwide. They also discuss the gaps in the efficiency of sequencing and how these 'Blind Spots' can be devastating in the long run. The authors conclude that enhancing the genomic sequencing capacity would also help to tackle threats posed by the infectious diseases in the future.



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