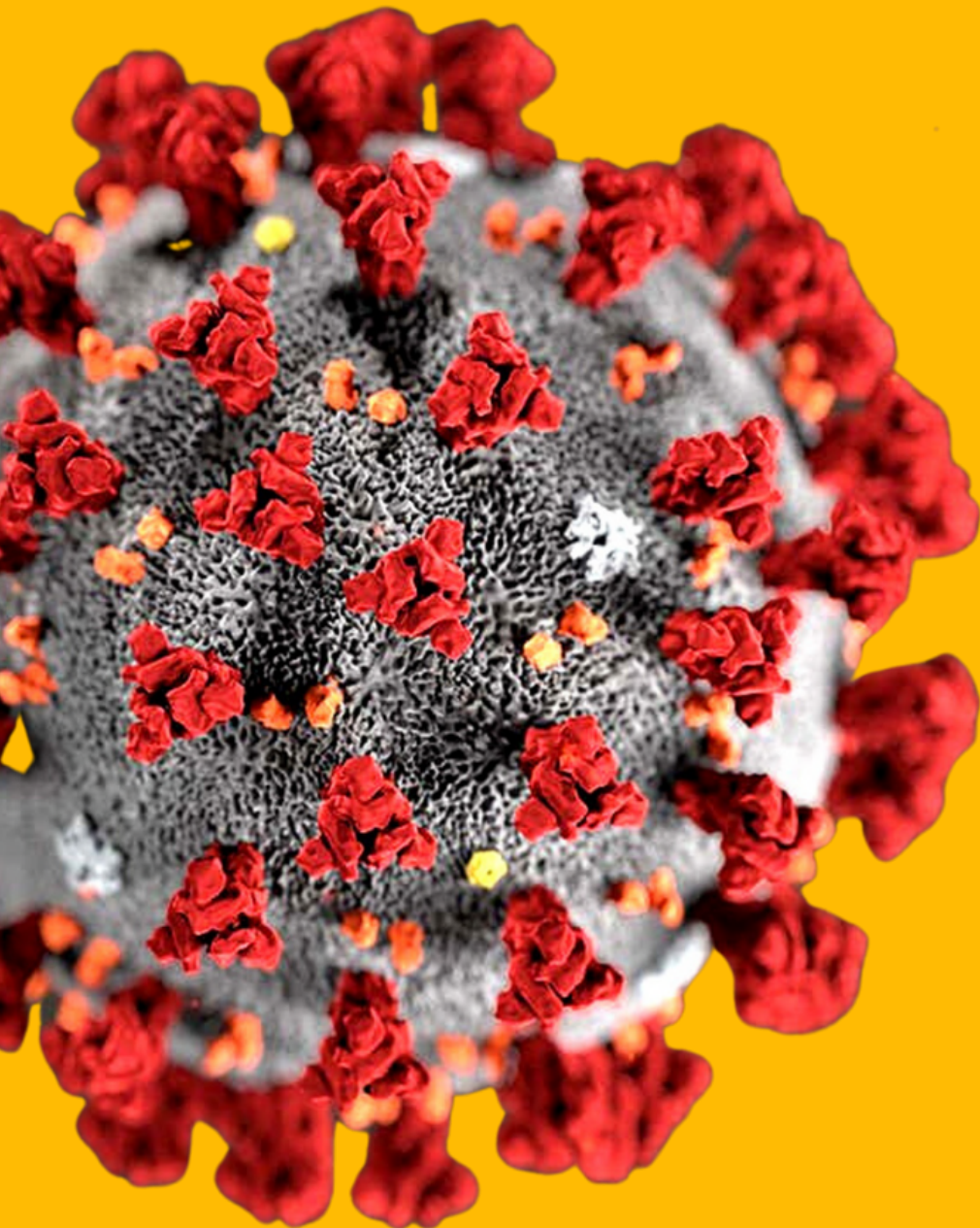


ANNUAL REPORT

ALLERGY, IMMUNOLOGY AND CELL BIOLOGY UNIT
UNIVERSITY OF SRI JAYEWARDENEPURA



2022



A Message from the Director

I take great pleasure in presenting the 2022 Annual Report for the Allergy, Immunology, and Cell Biology Unit.

Over the past year, we were able to maintain the highest standards of care for allergy patients at our clinic, while continuing to excel in research and curating exceptional training programs to nurture the future scientists of Sri Lanka. Our staff worked tirelessly to achieve these outcomes, as evidenced by the vast number of programs, publications, and collaborations that have been generated and are described in this annual report. Their passion, determination, and work ethic are exemplary and, without doubt, a great strength to our nation.

Looking to the future, our primary goals are to become a center of excellence for allergy care in Sri Lanka, maintain our position as a premier immunology research laboratory by expanding on infectious disease surveillance efforts, and augment our education of both budding scientists and the community on contemporary issues in Immunology. This will help us move one step closer towards a healthier nation with an equitable and more inclusive healthcare system.

Prof. Chandima Jeewandara
Professor in Allergy, Immunology, and
Molecular Medicine

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INTRODUCTION

The Allergy, Immunology and Cell Biology Unit (AICBU) was established in 2019. Since then, it has contributed immensely to the needs of Sri Lanka and the international scientific research in the fields of Allergy, Immunology and Molecular Biology. The unit is a part of the University of Sri Jayewardenepura and is headed by two directors: Prof. Chandima Jeewandara, who serves as the Director of Operations and Clinical Services and Prof. Neelika Malavige, who serves as the Director of Research & Development. The AICBU conducts many research studies focused on allergy and infectious diseases and collaborates extensively with many international organizations including the National Institutes of Health (NIH), World Health Organization (WHO), SungKyunKwan University and the University of Oxford. During the COVID-19 pandemic, our team pioneered an effort from the university sector to fight against the virus. Driven by an increasing number of research grants and the excitement of novel findings each term, the team continues to grow rapidly while fulfilling its responsibility of delivering education and training to the scientists of tomorrow as an entity attached to a state university.

OUR MISSION

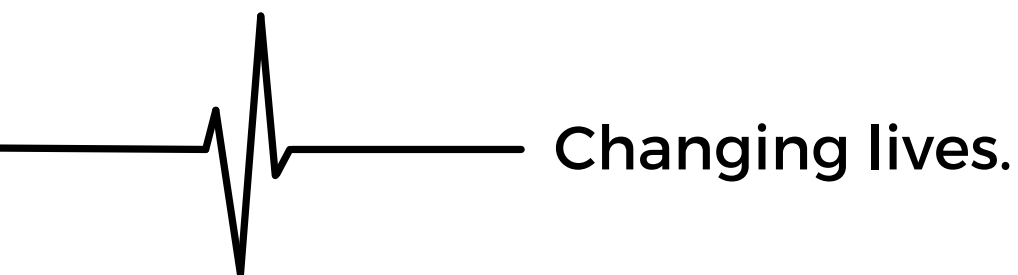
Our mission is to develop human and physical resources and facilitate advanced research to create a world-class innovation platform while contributing to national development and improving health.

OUR VISION

To be a Center of Excellence for Allergy, Immunology and Molecular Medicine.



CLINICAL CARE



Established in 2018, the clinic held at the AICBU is one of the leading referral centres for patients with immunological disorders in Sri Lanka. A team of trained healthcare professionals including professors, medical officers and nurses provide care to patients with the expertise to ensure optimal quality of life while living with allergies.

The clinic was held twice a week at the Family Practice Centre, University of Sri Jayawardenepura from 9am-12pm on Tuesdays and Fridays. The services offered to our patients are listed below:

SERVICES AT THE CLINIC



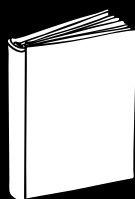
CONSULTATIONS

For patients with food allergy, drug allergy, allergic rhinitis, asthma, atopic dermatitis, chronic urticaria, anaphylaxis and autoimmune disorders.



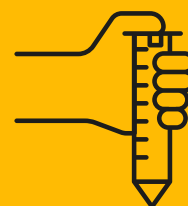
DIAGNOSTIC TESTING

Skin Prick Testing, Intra Dermal Testing, Specific IgE Testing, ISAC ImmunoCAP Testing and Oral Challenge Testing



PATIENT EDUCATION

Offered to patients covering both mental and physical aspects of coping and living with immunological disorders.



EPIPEN DISTRIBUTION

Through the Save A Life project, 886 patients were given epipens and trained free of charge. Careful evaluation was used to select those with anaphylaxis as they need to carry an epipen at all times.

STATISTICS FROM THE CLINIC



1859

Patients



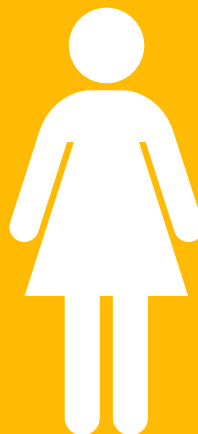
63%
Adults



37%
Children



43%
Male



57%
Female

304

Blood samples collected
for specific IgE testing.



200

ISAC ImmunoCAP
tests performed.

690

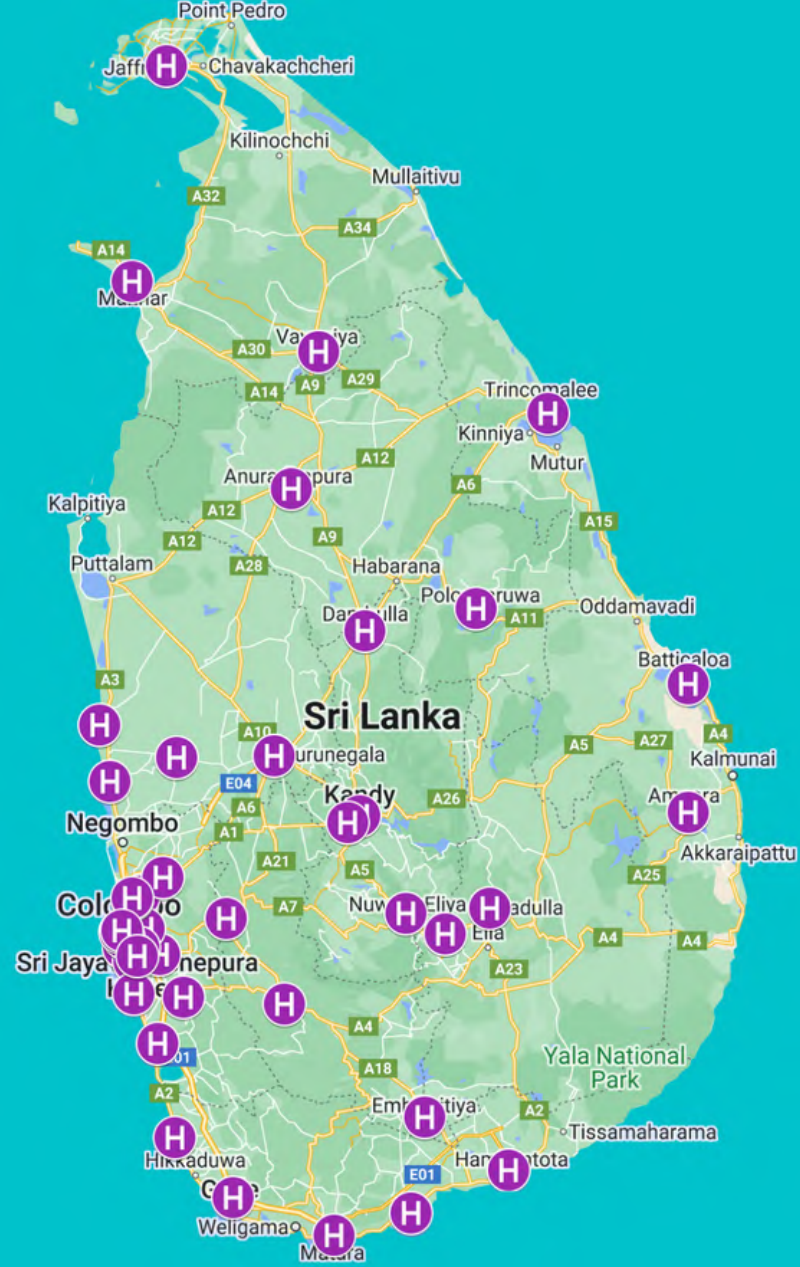
Skin Prick Tests done at a
Concessionary Price to test
for food, drug and
respiratory allergens.



886

Epipens distributed (with
training) free of charge
to those diagnosed with
anaphylaxis.

5



455

Referrals from the private and public sector, GPs and District Medical Officers as follows:

National & Teaching Hospitals

Medical Research Institute
Colombo South Teaching Hospital
National Hospital Sri Lanka
Teaching Hospital Anuradhapura
Teaching Hospital Batticaloa
Lady Ridgeway Hospital for Children
Colombo North Teaching Hospital
University Hospital KDU
Castle Street Hospital for Women
Teaching Hospital Karapitiya
Teaching Hospital Jaffna
National Hospital Kandy
Teaching Hospital Welisara
Teaching Hospital Kuliyapitiya
Teaching Hospital Ratnapura
Dental Institute
Teaching Hospital Peradeniya
De Soysa Hospital for Women
National Cancer Institute Maharagama

Base Hospitals

Homagama BH Marawila BH
Tangalle BH Balapitiya BH
Avissawella BH Horana BH
Panadura BH Welimada BH
Dambulla BH Colombo East BH

Provincial General & District General Hospitals

Kalutara DGH
Hambantota DGH
Kurunegala PGH
Chilaw DGH
Matara DGH
Badulla PGH
Vavuniya DGH
Nuwara Eliya DGH
Gampaha DGH
Ampara DGH
Polonnaruwa DGH
Embilipitiya DGH
Mannar DGH

Other Hospitals

Army Hospital
Navy Hospital
Sri Jayewardanepura GH

MILESTONES

1

We completed the installation and training of the Phadia 250 machine from Thermo Fisher Scientific for the detection of specific IgE.



2

The fully automated autoimmunity diagnostic laboratory was installed and the staff was trained to manage this facility. This includes the IF Sprinter, EUROBlotOne, EUROIMMUN Analyzer I-2P, EUROIMMUN IF Sprinter and the EUROSTAR III Plus Microscope.

UPCOMING PLANS

We hope to be fully operational in conducting allergy and autoimmunity diagnostic testing. In addition to the above testing mentioned, we are planning to commence testing Vitamin D, Total IgE levels and antinuclear antibody.

We also hope to commence biological therapy and immunotherapy for patients with severe disease who are not responding to initial treatment.

RESEARCH

Redefining horizons.

In 2021 and 2022, the AICBU published 29 peer-reviewed journal articles in various renown journals including PLOS Global Public Health, the Journal of Virological Methods, Clinical and Experimental Immunology and the Journal of Biomedical Science. A record of our publications during this period are on the pages that follow and provide an insight into the depth, breadth and success of our research.



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 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.

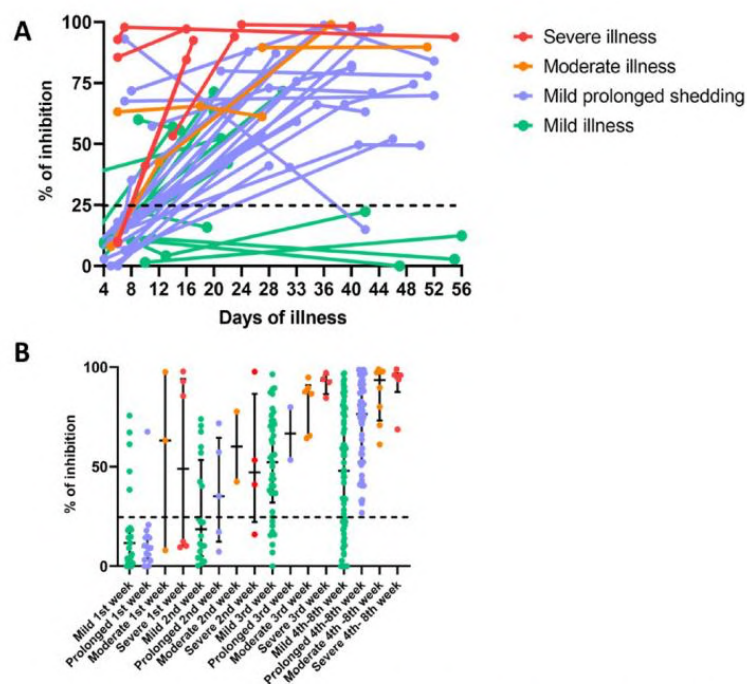


Figure 2. Longitudinal analysis SARS-CoV-2 neutralizing antibodies in patients with varying severity of COVID-19. SARS-CoV-2 NABs were measured in those with severe (n = 6), moderate (n = 5) and mild/asymptomatic illness (n = 13) and also those who had mild illness but with prolonged shedding of the 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.

Identification of Novel Candidate CD8⁺ T cell Epitopes of the SARS-CoV-2 with Homology to Other Seasonal Coronaviruses

Pushpakumara PD, Madhusanka D, Dhanasekara S, Jeewandara C, Ogg GS, Malavige GN. Identification of Novel Candidate CD8⁺ T cell Epitopes of the SARS-CoV2 with Homology to Other Seasonal Coronaviruses, *Viruses*. (2021)

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 HCoV, 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.

Table 1. Predicted CD8⁺ epitopes of the SARS-CoV2 virus restricted through HLA-A alleles.

9mer Peptides with a Peptide Binding Score of ≥0.90						
Protein	HLA-A Allele	Sequence	Score	OC43 % Identity with SARS-CoV2	HKU1 % Identity with SARS-CoV2	NL63 % Identity with SARS-CoV2
Spike	A*02:01	269 ^{YLQRTFL} 277	0.97	44	44	22
Spike	A*24:02	1208 ^{QYKWPWV} 1216	0.95	77	77	77
Spike	A*02:01	978 ^{VLDILSL} 984	0.94	67	67	33
Spike	A*24:02	635 ^{VYSTGSNV} 643	0.93	22	22	22
Spike	A*02:01	109 ^{TLDSKTQSL} 117	0.91	22	22	33
Membrane	A*24:02	95 ^{YFIASFRL} 103	0.91	77	77	77
Nucleocapsid	A*02:01	222 ^{LLLDRLNQL} 230	0.96	33	33	33
NSP2	A*02:01	265 ^{GLNDNILLE} 273	0.92	44	33	44
NSP2	A*24:02	497 ^{TFKLVNKE} 505	0.90	33	22	22
NSP3	A*24:02	726 ^{YYTSNPTTF} 734	0.99	22	22	22
NSP3	A*24:02	1349 ^{NYMPYFTL} 1357	0.98	33	22	11
NSP3	A*24:02	814 ^{YYHTDPS} 824	0.96	11	11	0
NSP3	A*24:02	364 ^{LYDKLVSS} 372	0.95	33	33	11
NSP3	A*24:02	1081 ^{YYKKDSSV} 1089	0.94	33	33	0
NSP4	A*02:01	420 ^{FLNKEMY} 428	0.98	33	33	33
NSP4	A*02:01	359 ^{FLAHQWMV} 367	0.94	44	44	33
NSP4	A*24:02	351 ^{FYLTDVSR} 359	0.92	22	22	22
NSP4	A*24:02	489 ^{LYQPQTS} 494	0.90	66	66	66
NSP5	A*02:06	194 ^{LIQDIQSV} 202	0.95	44	33	11
NSP6	A*02:01	70 ^{FLPSLATV} 78	0.99	33	33	44
NSP6	A*02:01	141 ^{TLMLVLT} 149	0.92	0	0	0
NSP6	A*24:02	84 ^{VYMPASWVM} 92	0.91	0	0	11
NSP7	A*24:02	115 ^{MYASAVVL} 123	0.90	22	22	22
NSP7	A*02:01	12 ^{VLLSVLQQL} 20	0.95	66	66	44
NSP8	A*02:01	152 ^{ALWEIQV} 160	0.98	44	33	22
NSP12	A*24:02	37 ^{TYNDKVG} 45	0.95	66	44	44
NSP12	A*02:01	123 ^{TMDLVYAL} 131	0.93	77	77	77
NSP12	A*02:06	334 ^{FVDGVFFV} 342	0.93	100	100	88
NSP12	A*02:01	854 ^{LMIERFVSI} 862	0.91	88	88	55
NSP13	A*02:01	239 ^{TLVPOEHV} 247	0.95	77	77	44
NSP13	A*24:02	397 ^{VYIGDPAQL} 405	0.91	100	100	77
NSP14	A*02:01	321 ^{LLADKFPVL} 329	0.94	11	11	33
NSP14	A*02:01	176 ^{NLSDRVV} 184	0.93	66	66	77
NSP14	A*02:01	184 ^{VLDWAHGF} 192	0.92	66	44	66
NSP14	A*02:01	494 ^{YLDAYNMM} 502	0.91	44	44	44
NSP15	A*02:06	243 ^{SQLGGLHL} 251	0.96	66	66	66
NSP15	A*02:01	297 ^{LLDDFV} 305	0.95	66	88	88
NSP15	A*02:06	312 ^{SVVSKVVK} 320	0.94	66	66	55
NSP15	A*02:06	181 ^{KVDGVVQQL} 189	0.92	22	22	11
10mer Peptides with a Peptide Biding Score of ≥0.90						
Protein	HLA-A Allele	Sequence	Sore	OC43 % Identity with SARS-CoV2	HKU1 % Identity with SARS-CoV2	NL63 % Identity with SARS-CoV2
Spike	A*24:02	1066 ^{TVYPAQEKNI} 1075	0.94	30	30	10
Spike	A*24:02	159 ^{VYSSANNCTF} 168	0.90	10	30	20
NSP3	A*24:02	717 ^{VYYSNPTTF} 726	0.98	30	40	20
NSP6	A*24:02	242 ^{YDYLVTQEF} 251	0.91	50	50	50

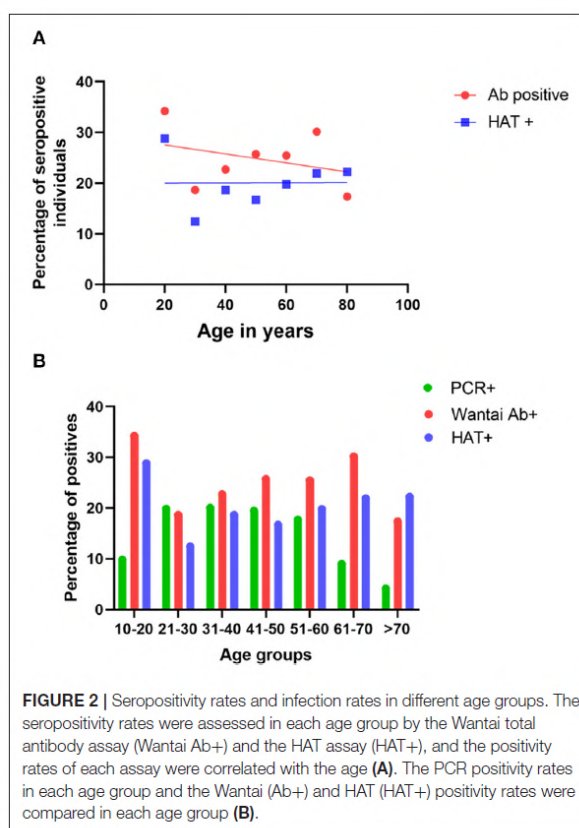
Seroprevalence of SARS-CoV-2 Infection in the Colombo Municipality Region, Sri Lanka

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 seropositivity 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.



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

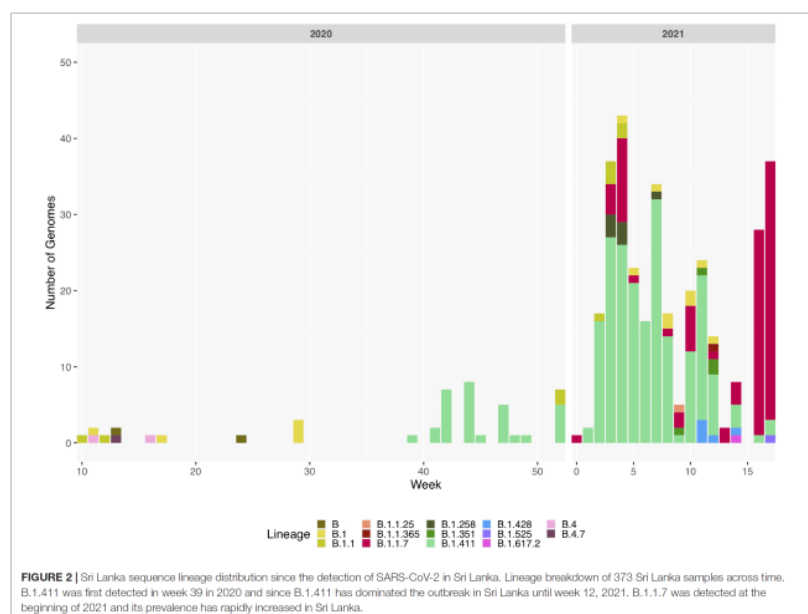
Jeewandara C, Jayathilaka D, Ranasinghe D, Hsu NS, Ariyaratne D, Jayadas TT, Panambara Arachchige DM, Lindsey BB, Gomes L, Parker MD, Wijewickrama, A, Karunaratne M, Ogg GS, de Silva TI, Malavige GN.

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.



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-CoV-2 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.

	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

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.

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

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

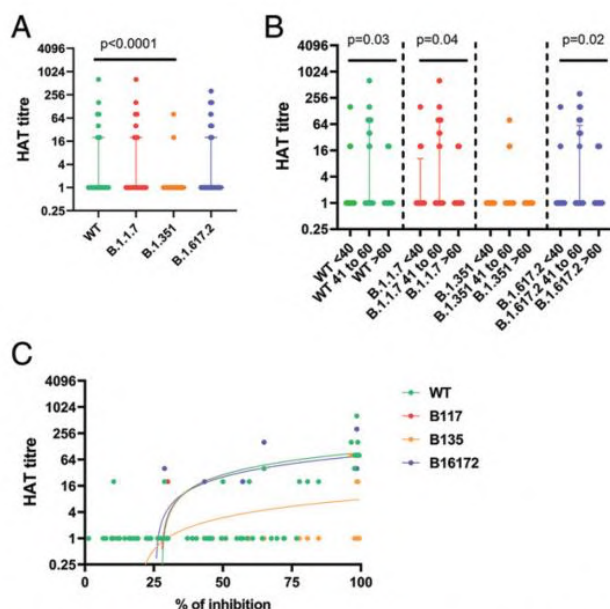


FIGURE 2. Ab responses to the SAR-CoV-2 Wuhan, WT variant, and other variants of concern. Ab responses to the RBD of the WT, B.1.1.7, B.1.351, and B.1.617.2 were determined by HAT in 69 individuals (A) and also in this cohort of individuals when categorized into three age groups (B). The Ab responses 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.

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.

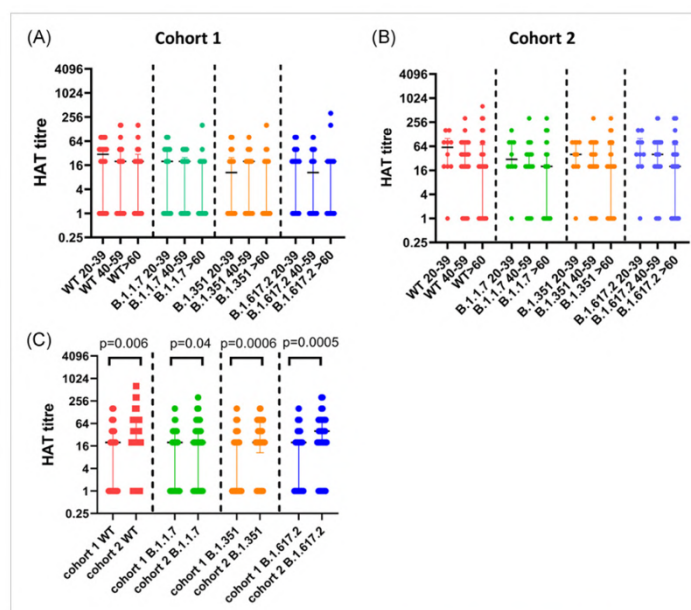


Figure 2

[Open in figure viewer](#) [PowerPoint](#)

Antibodies to the receptor-binding domain (RBD) of the ancestral SARS-CoV-2 virus (WT) and variants of concern (VOC) in cohorts 1 and 2. Antibodies to the RBD of the WT and VOCs were measured in cohort 1 in 20–39 years old ($n = 26$), 40–59 years old ($n = 26$), and >60 years old ($n = 17$) and no significant difference was seen between the different age groups for responses to the RBDs of different VOCs (A). Antibodies to the RBD of the WT and VOCs were also measured in cohort 2 in 20–39 years old ($n = 10$), 40–59 years old ($n = 32$), and >60 years old ($n = 28$) and no significant difference was seen between the different age groups for responses to the RBDs of different VOCs (B). The hemagglutination test (HAT) titres for the WT, B.1.1.7, B.1.351, and B.1.617.2 were compared between the two cohorts (C). Individuals in cohort 2 had significantly higher HAT titres to the WT and all VOCs analyzed by the Mann–Whitney test. All tests were two-tailed. The lines indicate the median and the interquartile range

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 Sanjeevani 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)

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.

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.

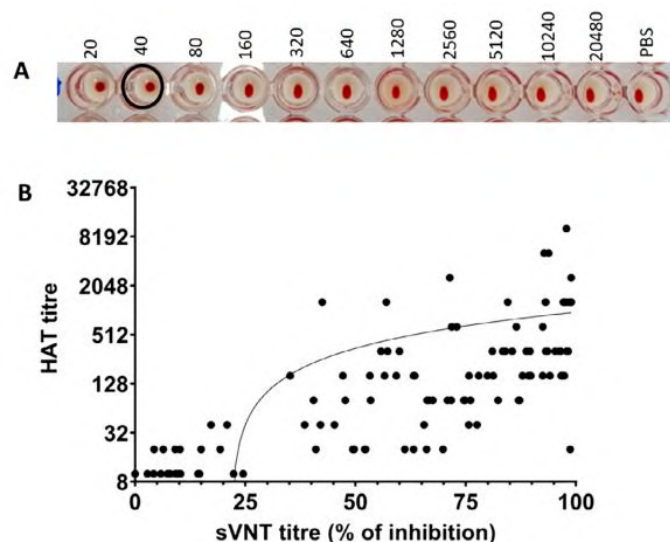


Figure 1. Correlation of antibody levels determined by haemagglutination test (HAT) titration and surrogate virus neutralization test (sVNT). (A) Example of HAT titration carried out on a sample. The HAT titration was conducted using 11 doubling dilutions of the serum from 1:20 to 1:20 480 (the titres 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 $r = 0.79$, $P < 0.0001$.

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.

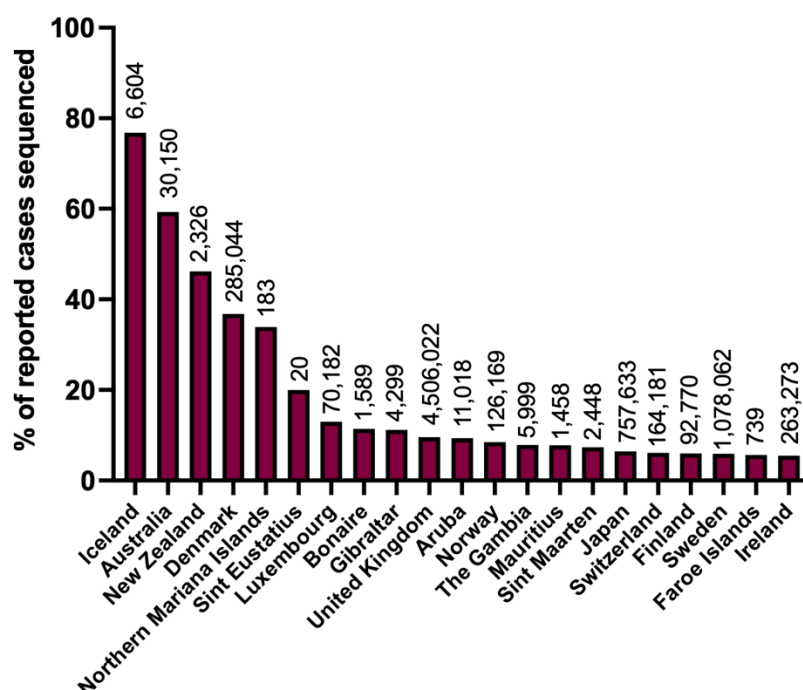


Figure 2. Percentage of total reported SARS-CoV-2 cases sequenced by each country.

Regional Variation in Dengue Virus Serotypes in Sri Lanka and Its Clinical and Epidemiological Relevance

Jayadas, T. T., Kumanan, T., Gomes, L., Jeewandara, C., Malavige, G. N., Ranasinghe, R., Jadi, R. S., Ramasamy, R., & Surendran, S. N. (2021). Regional Variation in Dengue Virus Serotypes in Sri Lanka and Its Clinical and Epidemiological Relevance. *Diagnostics*, 11(11), pp. 2084.

<https://doi.org/10.3390/diagnostics11112084>

Although Dengue is a significant infectious disease in Sri Lanka, identification of the infecting dengue virus (DENV) serotype has mostly only been done in Colombo district in the Western Province. In this study Dengue patients at the Jaffna Teaching Hospital in the city of Jaffna. In the recruited individuals 107 and 112 were positive for the NS1 antigen in 2018 and 2019 respectively. qRT-PCR was subsequently used to determine their virus serotype and the data was related to their clinical characteristics. In both years, DENV1 and DENV2 were the most common serotypes and infectious with multiple serotypes was not detected. In 2018 compared to 2019, DENV3 was significantly more prevalent among the Jaffna patients. However, in 2019 compared to 2018, DENV1 was the more prevalent serotype among these patients. DENV1 genotype-I and DENV3 genotype-I were identified in Jaffna patients in 2018 through limited genomic sequencing. Among the serotyped patients from Jaffna, Dengue was more prevalent in working age persons and males.

Table 1

DENV serotypes identified in the Jaffna district in relation to year, patient age group and gender.

Category	DENV Serotype				Total
	DENV1 (%)	DENV2 (%)	DENV3 (%)	DENV4 (%)	
Year					
2018	26 (24)	60 (56)	15 (14)	6 (6)	107
2019	60 (53)	48 (43)	2 (2)	2 (2)	112
Total	86	108	17	8	219
Age group					
14–20	29 (41)	34 (48)	5 (7)	3 (4)	71
21–60	53 (40)	64 (48)	11 (8)	5 (4)	133
≥61	4 (27)	10 (67)	1 (6)	0 (0)	15
Gender					
Male	45 (36)	64 (51)	9 (7)	8 (6)	126
Female	41 (44)	44 (47)	8 (9)	0 (0)	93
Total	86	108	17	8	219

[Open in a separate window](#)

The number of patients infected with each serotype and the corresponding percentage of the respective totals in parentheses are shown.

In 2019, DENV1 and DENV2 were the predominant serotypes in Colombo district. However, DENV1 and DENV3 were significantly more prevalent in Colombo in comparison to Jaffna in the same year. The differences in serotype prevalent in the two districts may be due to the salinity tolerant *Aedes* strains that are widespread in the Jaffna peninsula. These differences have implications for dengue epidemiology and vaccination. Significant associations between virus serotypes and clinical characteristics were not identified in the Jaffna patients.

Aedes larval bionomics and implications for dengue control in the paradigmatic Jaffna peninsula, northern Sri Lanka

Surendran, S. N., Jayadas, T. T., Thiruchenthoooran, V., Raveendran, S., Tharsan, A., Santhirasegaram, S., Sivabalakrishnan, K., Karunakaran, S., Ponnaiah, B., Gomes, L., Malavige, G. N., & Ramasamy, R. (2021). *Aedes* larval bionomics and implications for dengue control in the paradigmatic Jaffna peninsula, northern Sri Lanka. *Parasites & Vectors*, 14, p. 162.

<https://doi.org/10.1186/s13071-021-04640-6>

In a bid to control endemic arboviral diseases by gaining information for the development of more effective larval sources reduction measures, the larval bionomics of *Aedes* mosquitos was investigated in the Jaffna peninsula in northern Sri Lanka. To achieve this, the habitats of preimaginal stages of *Aedes* mosquitos were surveyed and ovitrap collections were conducted in densely populated areas of the Jaffna peninsula. Productivities of *Aedes* larvae were then analyzed against habitat characteristics, rainfall and dengue incidence. Adults emergin from the collected larvae were also tested for dengue virus (DENV).

In the field habitat collections and ovitraps, only *Aedes aegypti*, *Ae. albopictus* and *Ae. vittatus* were identified. These species differed in their preferences for field habitats and concomitant presence of the three species was observed in the field habitats and ovitraps. The most predominant species in both the field habitat and ovitrap collections was *Aedes aegypti* followed by *Ae. albopictus* and *Ae. vittatus*. The preferred field habitats for *Ae. aegypti* were tires and open drains, although larval productivity was noticeably higher in discarded plastic containers. Larval productivity in the field habitats significantly correlated with rainfall in the preceding month and inversely correlated with the salinity of the habitat. DENV serotype 2 was found in *Ae. aegypti* collected from ovitraps in the city of Jaffna. High Breteau, House and Container indices of 5.1, 5.1 and 7.9% respectively were seen in the field habitat surveys and ovitrap indices of upto 92% were observed in Jaffna city.

Table 1

Aedes larvae presence in different types of habitats

Type of habitat	Number of sampled habitats	Habitat salinity range (ppt salt)	Data for all <i>Aedes</i> species together			Data for each <i>Aedes</i> species separately					
			No. of larvae collected	No. of positive habitats	HPR	<i>Ae. aegypti</i>			<i>Ae. albopictus</i>		
No. of larvae collected	No. of positive habitats	HPR				No. of larvae collected	No. of positive habitats				
Domestic wells	519	0-8	213	9	0.2	145	9	0.2	68	2	
Open surface drains	194	0-3	390	35	2.3	390	35	2.5	0	0	
Cement water storage tanks	235	0	383	14	0.8	144	11	0.7	162	7	
Discarded plastic and paper cups	490	0	754	51	1.3	578	50	1.4	143	13	
Discarded metal containers	338	0	83	6	0.2	83	6	0.2	0	0	
Discarded plastic containers	515	0-5	1372	69	1.7	737	59	1.6	556	32	
Discarded glass and	114	0	21	1	0.1	21	1	0.1	0	0	

[Open in a separate window](#)

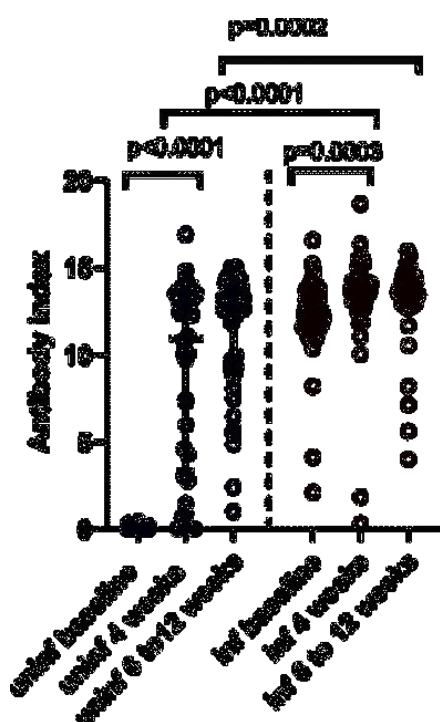
HPR, Habitat preference ratio; ppt, parts per thousand

Overall, through the *Aedes* larval indices, a high potential for Dengue epidemics was identified in populated areas of the peninsula. Numerous constraints to current *Aedes* larval source reduction methods used to control Dengue in the region were identified. These included improper littering practices, failure to implement existing Dengue control guidelines, vertical transmission of DENV in vector mosquitoes and preimaginal development in brackish water, open surface drains and domestic wells that provide potable water. Other resource-constrained tropical coastal zones across the globe are likely to have similar shortcomings in arboviral disease control.

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

Jeewandara C, Jayampathi KC, Ranasinghe T, Aberathna IS, Gunasekara B, Danasekara S, Nimasha T, Kuruppu H, Dissanayake O, Gamalath N, Ekanayake D, Jayamali J, Somathilake G, Guruge D, Wijayamuni R, Kamaladasa A, Graham GS, Malavige GN. Antibody responses to Sinopharm/BBIBP-CorV in pregnant mothers in Sri Lanka. *PLoS Global Public Health* 2(7) (2022)

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 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 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.

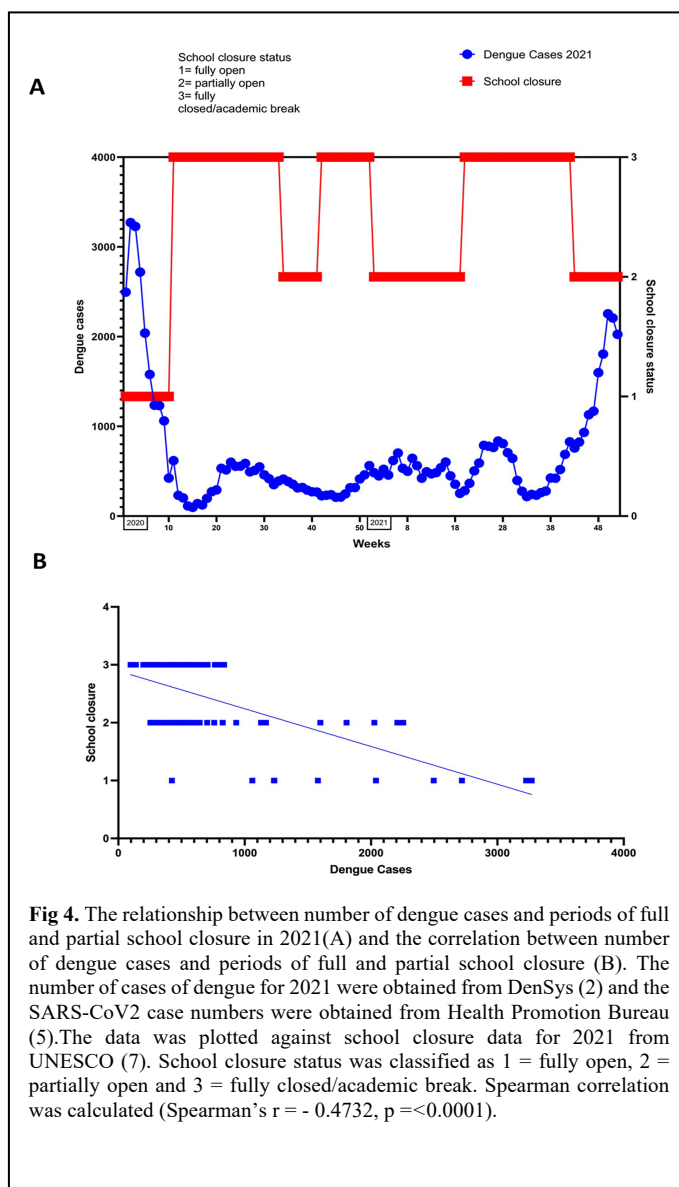
Fig 1. Antibody responses to the receptor binding domain of SARS-CoV-2 virus, following first and second dose of the Sinopharm/BBIBP-CorV vaccine.

SARS-CoV-2 specific total antibodies were measured in baseline uninfected ($n = 36$) and infected ($n = 58$) pregnant women by ELISA, at baseline, 4 weeks from the first dose and 6 to 12 weeks following the second dose (2 to 8 weeks following the second dose). Wilcoxon matched pairs signed rank test was used to compare the means of the antibody indexes, 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 infected and uninfected women. All tests were two-tailed. The lines indicate the median and the inter quartile range.

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

Ariyaratne, D., Gomes, L., Jayadas, T.T.P., Kuruppu, H., Kodituwakku, L., Jeewandara, C., Pannila Hetti, N., Dheerasinghe, A., Samaraweera, S., Ogg, G. and Malavige, G., 2022. Epidemiological and virological factors determining dengue transmission in Sri Lanka during the COVID-19 pandemic. PLOS Global Public Health, 2(8), p.e0000399.

PLOS Global Public Health 2(8): e0000399
<https://doi.org/10.1371/journal.pgph.0000399>



The authors found that a combination of virological, human mobility, school closure and mosquito factors drove 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 behind the differences in the dengue case numbers in 2020 and 2021 compared to previous years, associations between the case numbers in Colombo, the school closures stringency index, changes in dengue virus (DENV) serotypes and vector densities were investigated.

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

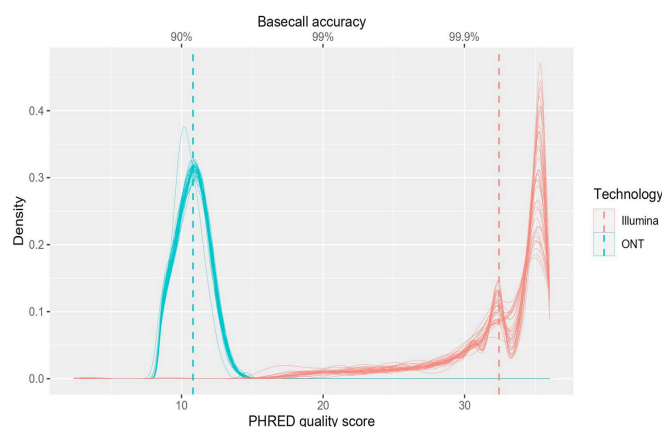


Fig 1. PHRED base call quality score distribution of samples sequenced by Illumina and ONT.

Distribution plot of PHRED (probability of error per base call in a log scale) quality score (x axis) and error probability (secondary x axis) derived from the PHRED score for the data set sequenced from Illumina (n = 37) and ONT (n = 37). The scores of ONT are shown in blue and Illumina in red. The mean PHRED scores/error probability are shown with the dashed line for each technology. The mean PHRED scores averaged at 32.35 in Illumina reads and 10.78 in ONT.

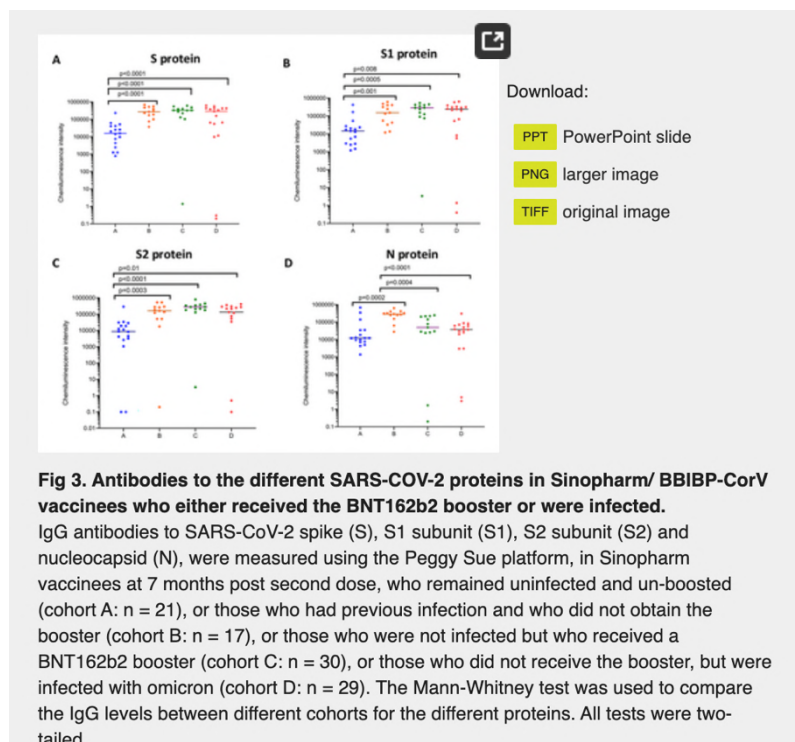
The emergence of different SARS- CoV-2 variants and the continuous evolvement of sub lineages of the delta variant have made it important for all countries to carry out sequencing of at least >1% of their infections, in order to detect emergence of variants with higher transmissibility and the ability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

Comparison of the kinetics and magnitude of antibody responses to different SARS-CoV-2 proteins in Sinopharm/BBIBP-CorV vaccinees following the BNT162b2 booster or natural infection

Jeewandara C, Aberathna IS, Dayarathna S, Nimasha T, Ranasinghe T, Jayamali J, Kamaladasa A, Karunananda M, Perera L, Ogg GS, Malavige GN. Comparison of the kinetics and magnitude of antibody responses to different SARS-CoV-2 proteins in Sinopharm/BBIBP-CorV vaccinees following the BNT162b2 booster or natural infection, PLoS One, 13;17 (2022)

This study focused on investigating the antibody responses to different proteins of SARS-CoV-2 virus in Sinopharm/BBIBP-CorV vaccinees which has not been done previously. The study investigated antibody responses to different SARS-CoV-2 proteins at 2 weeks, 3 months, and 6 months post-second dose in previously infected (n = 20) and uninfected (n = 20) Sinopharm/BBIBP-CorV vaccinees. The IgG antibodies to the S, S1 and S2 and N proteins were several fold higher in those who had natural infection compared to uninfected individuals at all time points. The authors then compared the persistence of antibody responses and effect of natural omicron infection or BNT162b2 booster in Sinopharm/BBIBP-CorV vaccinees. Additionally, total antibodies to the

RBD, ACE2 blocking antibodies and antibody responses to different SARS-CoV-2 proteins were measured in Sinopharm vaccinees at 7 months post second dose, including those who remained uninfected and not boosted (n = 21), or those who had previous infection and who did not obtain the booster (n = 17), those who were not infected, but who received a BNT162b2 booster (n = 30), or those who did not receive the booster but were infected with omicron (n = 29). At 7 months post second dose uninfected (no booster) had the lowest antibody levels to the RBD, while omicron infected vaccinees showed significantly higher anti-RBD antibody levels (p = 0.04) than vaccinees who received the booster. Only 14.3% in Cohort A had ACE2 blocking antibodies, while frequencies of 100%, 85.7% and 100% were observed in naturally infected individuals, those who received the booster and omicron infected individuals. Analyzing antibody levels to the N protein pre-vaccination, naturally infected individuals were found to have the highest levels. Overall, these data suggest that those previously infected Sinopharm/BBIBP-CorV vaccinees have a robust antibody response, 7 months post vaccination, while vaccinees who were naturally infected with omicron had a similar immune response to those who received the booster. The importance of investigating implications for subsequent clinical protection was noted.



Persistence of immune responses to the Sinopharm/BBIBP-CorV vaccine

Jeewandara C, Aberathna IP, Pushpakumara PD, Kamaladasa A, Guruge D, Wijesinghe A, Gunasekara B, Ramu ST, Kuruppu H, Ranasinghe T, Dayarathna S, Dissanayake O, Gamlath N, Ekanayake D, Jayamali J, Jayathilaka D, Dissanayake M, Jyadas 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 NG.

Immun Inflamm Dis. 2022; 10:e621. doi.org/10.1002/iid3.621

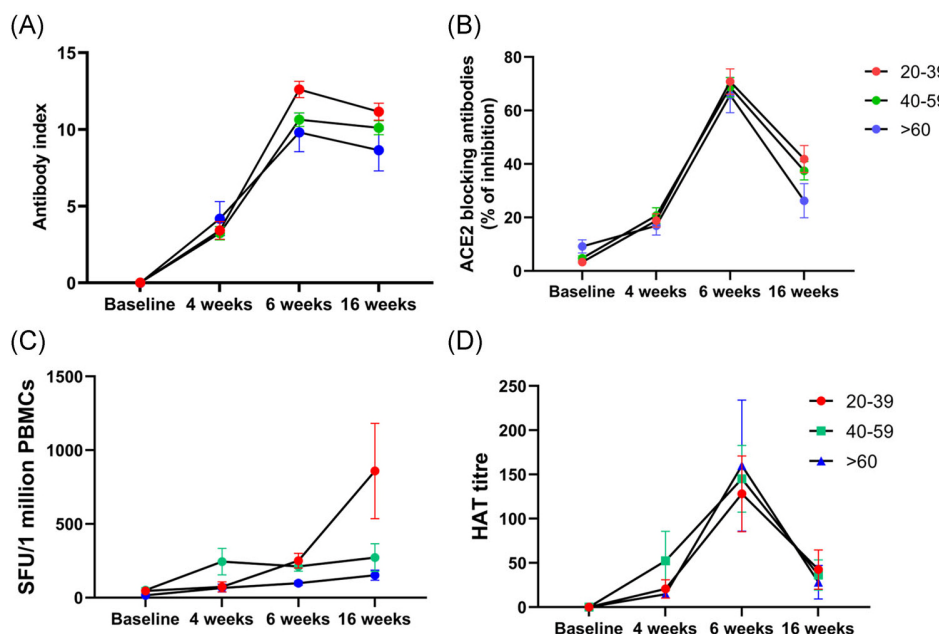


FIGURE 3 Kinetics of antibody and T cell responses over time. SARS CoV-2 total antibodies were measured in 174 individuals, (49 in 20–39, 10 in the 40–59 and 17 in ≥60 years age group), at baseline, 4 weeks after the first dose, 6 weeks (2 weeks after the 2nd dose) and at 16 weeks (12 weeks post 2nd dose) after the second dose by ELISA.

This study was done to determine the kinetics and persistence of immune responses following the Sinopharm/BBIBP-CorV vaccine. SARS-CoV-2 specific total antibodies were measured in a cohort of Sri Lankan individuals aged 20–39 years ($n = 61$), 40–59 years ($n = 120$) and those ≥ 60 years of age ($n = 22$) 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 also measured in a sub cohort. Additionally, T cell and memory B cell responses were assessed by ELISpot assays. A total of 193/203 (95.07%) of individuals had detectable SARS-CoV-2 specific total antibodies, while 67/110 (60.9%) had ACE2R-Ab. A total of 14.3%–16.7% individuals in the 20–39 age groups had detectable antibodies to the RBD of the WT and variants of concern, while the positivity rates of those ≥ 60 years of age was $<10\%$. A total of 14/49 (28.6%) had Interferon gamma ELISpot responses to overlapping peptides of the spike protein, while memory B cell responses were detected in 9/20 to the S1 recombinant protein. The total antibody levels and ACE2R-Ab declined from 2 to 12 weeks from the second dose, while ex vivo T cell responses remained unchanged. The decline in ACE2R-Ab levels was significant among the 40–59 ($p = .0007$) and ≥ 60 ($p = .005$) age groups. According to the observations, antibody responses declined in all age groups, especially in those ≥ 60 years, while T cell responses persisted. It is suggested to assess the effect of waning immunity on hospitalization and severe disease through long term efficacy studies.

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, Gunasekara B, Kamaladasa A, Kuruppu H, Somathilake G, Dissanayake O, Gamlath 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

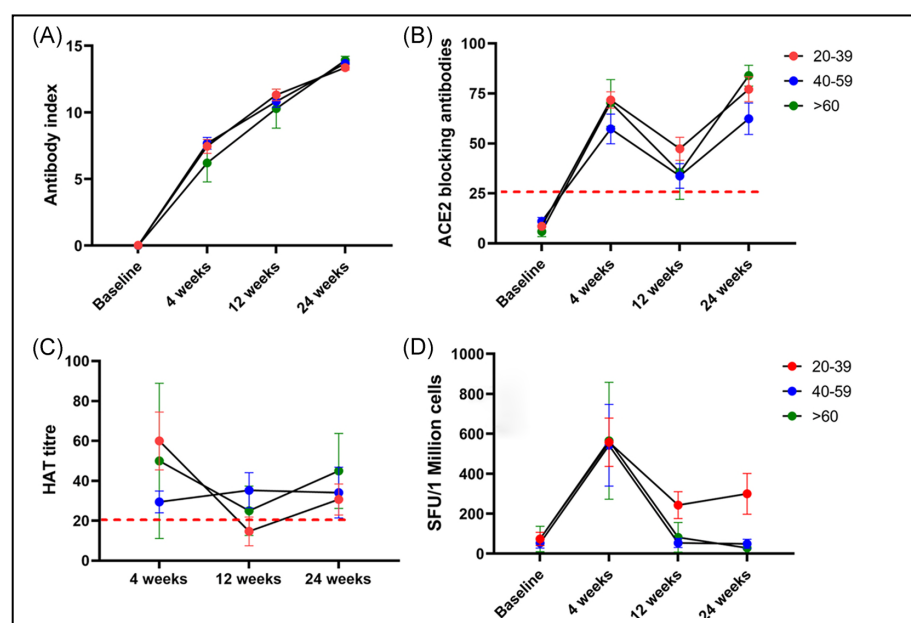


FIGURE 4 Kinetics of antibody and T cell responses over time in cohort 1 (dosing gap of 12 weeks). SARS-CoV-2 total antibodies were measured in 171 individuals (73 in the 29–39 age group, 87 in the 40–59 age group, and 11 in the >60 age group), at baseline, 4 weeks after the first dose, 12 weeks post first dose, and 12 weeks post second dose by ELISA

In this study, the authors 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, however those with a longer dosing gap had responses that were of a higher magnitude, possibly as the immune responses were measured 6 weeks post second dose compared to 12 weeks post second dose.

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, Gamlath 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 to the RBD of 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 showed a high frequency of CD107a expressing T cells along with memory B cell responses. It was understood that 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 infection. 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 vaccines had 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.

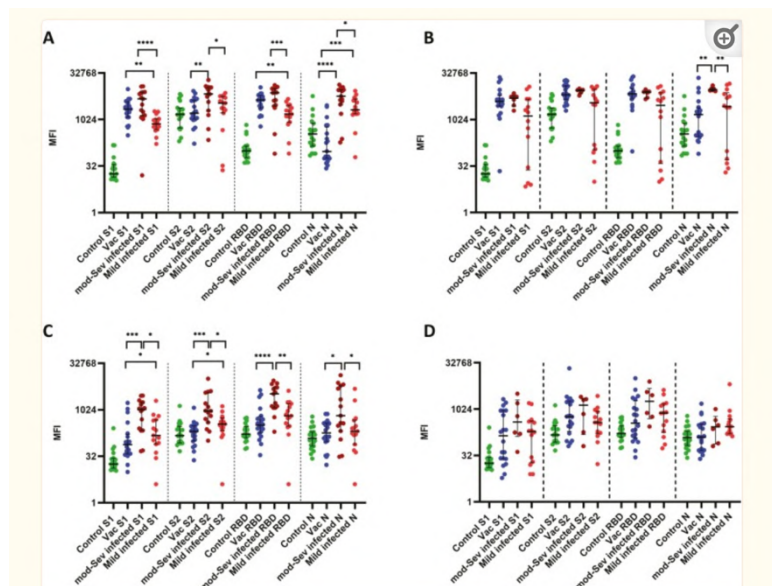


Figure 1.

IgG and IgA antibody levels to S1, S2, RBD, and N protein of SARS-CoV-2 in individuals following natural infection and following a single dose of the AZD1222 vaccine. IgG antibodies to S1, S2, RBD, and N protein was measured by Luminex assays at 4 weeks in those with mild illness ($n = 15$), moderate/severe illness ($n = 15$), vaccinees ($n = 20$) and controls ($n = 19$) (A) and again at 12 weeks in those with mild illness ($n = 14$), moderate/severe illness ($n = 6$), vaccinees ($n = 20$) (B). IgA antibodies were also measured in the above groups at 4 weeks (C) and at 12 weeks (D). The Kruskal-Wallis test was used to determine the difference between the antibody levels between the three different groups (two-tailed) followed by multiple comparisons using two-stage step-up procedure of Benjamini, Krieger, and Yekutieli while controlling the false discovery rate (FDR). The lines indicate the median and the interquartile range.

Sensitivity and specificity of two WHO approved SARS-CoV-2 antigen assays in detecting patients with SARS-CoV-2 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. Sensitivity and specificity of two WHO approved SARS-CoV2 antigen assays in detecting patients with SARS-CoV2 infection, BMC Infectious Disease, 22;22(1):276. (2022)

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 detection kits in a large cohort of Sri Lankan individuals because of concerns regarding their sensitivity and specificity in different settings. The overall sensitivity of the SD Biosensor and Abbott Ag kits were 36.5% and 50.76% respectively. The Abbott Ag test showed specificity of 99.4% while the SD Biosensor Ag test had 97.5% specificity. Both rapid Ag tests appeared to be highly sensitive in detecting individuals at lower Ct values, in a community setting in Sri Lanka however the authors commented on the importance of further establishing 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

Efficacy of rupatadine in reducing the incidence of dengue hemorrhagic fever in patients with acute dengue: A randomized, double blind, placebo-controlled trial

Malavige GN, Jeewandara C, Wijewickrama A, Gunasinghe D, Sameera DM, Chathurika G, Vimalachandran V, Jayarathna G, Perera Y, Wanigatunga C, Dissanayake H, Prathapan S, Narangoda Z, Idampitiya D, Gomes L, Wickramanayake S, Sahabandu P, Graham S, Ogg. (2022) Efficacy of rupatadine in reducing the incidence of dengue haemorrhagic fever in patients with acute dengue: A randomised, double blind, placebo-controlled trial. PLOS NEGLECTED TROPICAL DISEASES

<https://doi.org/10.1371/journal.pntd.0010123>

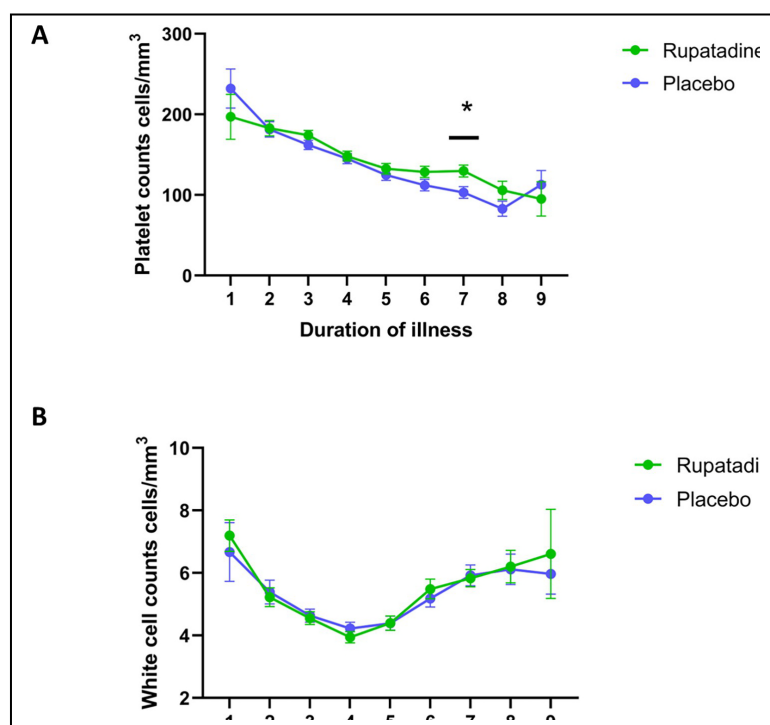


Fig 2. The change in the platelet counts and white cell counts in patients with acute dengue infection. Platelet counts were measured daily in patients with acute dengue infection who were on rupatadine 40mg daily (n = 123) or a placebo daily (n = 126). Data shown for day 9 includes only 6 patients on rupatadine and 7 patients on the placebo as many recovered and were not followed up until this time (A). Total white cell counts were also measured daily in patients with acute dengue infection who were on rupatadine 40mg daily (n = 123) or a placebo daily (n = 126) (B). Differences between the two arms of treatment were done using multiple unpaired nonparametric t tests. The lines indicate the mean, and the error bars the standard error of the mean. All tests were two-tailed.

In the past, Rupatadine has been observed to reduce endothelial dysfunction in vitro, reducing vascular leak in dengue mouse models. It has also been known to reduce the extent of pleural effusion and thrombocytopenia. Hence, this study was set up to determine the efficacy of Rupatadine in reducing the incidence of dengue hemorrhagic fever (DHF) in patients with acute dengue. The clinical trial was carried out by recruiting the patients within three days since the onset of illness to either the treatment arm of oral rupatadine which was 40 mg for 5 days (n = 123) or the placebo arm (n = 126) in an out-patient setting in Sri Lanka. Clinical and laboratory features were measured daily to assess development of DHF and other complications. 12 (9.7%) patients developed DHF in the treatment arm compared to 22 (17.5%) who were on the placebo although this was not significant (p = 0.09, relative risk 0.68, 95% CI 0.41 to 1.08). Rupatadine also significantly reduced (p = 0.01) the proportion of patients with platelet counts <50,000 cells/mm³ and significantly reduced (p = 0.04) persisting vomiting, headache and hepatic tenderness (p<0.0001) in patients. There was a significant difference in the duration of illness (p = 0.0002) although the proportion of individuals who required hospital admission in both treatment arms were similar. Finally, Rupatadine appeared to be safe, well-tolerated and showed a trend towards reducing the proportion of patients with acute dengue who developed DHF. Its usefulness when used in combination with other treatment modalities should be explored.

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. Molecular Epidemiology of AY.28 and AY.104 Delta Sub-lineages in Sri Lanka, Frontiers Public Health (2022)

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

Impact factor: 6.461

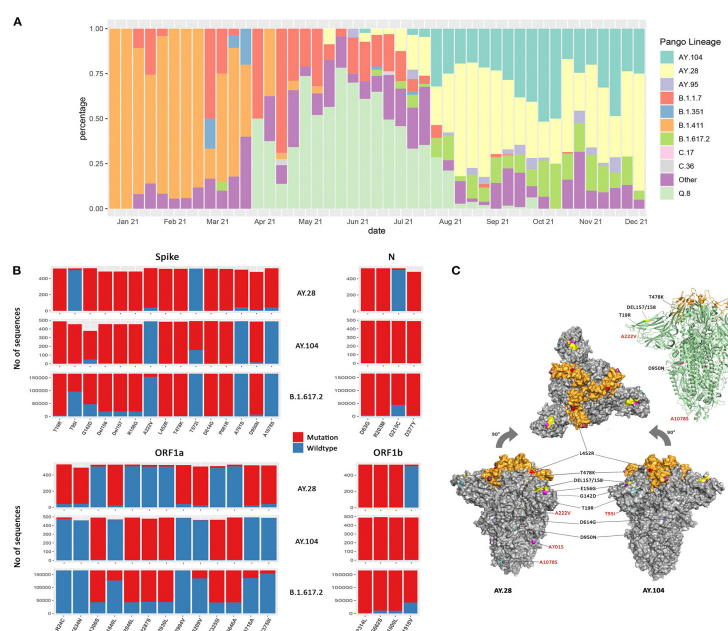


FIGURE 1 | The mutation and structural changes of AY.28 and AY.104 sequences in comparison with B.1.617.2 (Delta) lineage. (A) Weekly lineage frequencies of the sequenced cases in Sri Lanka since January 2021 were retrieved from the GISAID EpiCoV database. (B) The frequency of mutations in the spike, ORF1a, ORF1b, and N proteins of AY.28 and AY.104 compared to those of the parental B.1.617.2 (Delta) lineage. The bar height represents total unambiguous amino acids at each position, mutated (red) and wildtype (blue) based on the analysis of the global sequences deposited in the EpiCoV database. (C) The structural modeling of the pre-fusion surface representation of the SARS-CoV-2 B.1.671.2 spike trimer (PDB: 6ZGE) and the mutations in the structure in AY.28 and AY.104 are shown. The receptor-binding domain (RBD) is colored in orange while the N-terminal and S2 subunit are shown in gray. Amino acid substitutions and deletions are colored on the surface and labels of the mutations specific for AY.28 and AY.104 are colored in red. On the right, a ribbon diagram is shown of the same.

The worst SARS-CoV-2 outbreak in Sri Lanka was due to two Sri Lankan delta sub-lineages AY.28 and AY.104. This study further evaluates the mutations and clinical severity of these two sub lineages. 705 delta variant genomes were sequenced at the laboratory using Illumina and Oxford Nanopore analysis from mid-May to November 2021. 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 also 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.

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, Sanjeewani A, Bandara P, Nanayakkara G, Francis VR, Kithsiri A, Edirisinghe DA, De Silva K, Wijayamuni R, Ogg GS, Waggoner J, Malavige GN. Surveillance of SARS-CoV-2 variants of concern by identification of single nucleotide polymorphisms in the spike protein by a multiplex real-time PCR, *Journal of Virology Methods* (2022)

JVirol methods.2022 Feb;300:114374.doi:10.1016/j.jviromet.2021.114374

Impact factor: 2.623

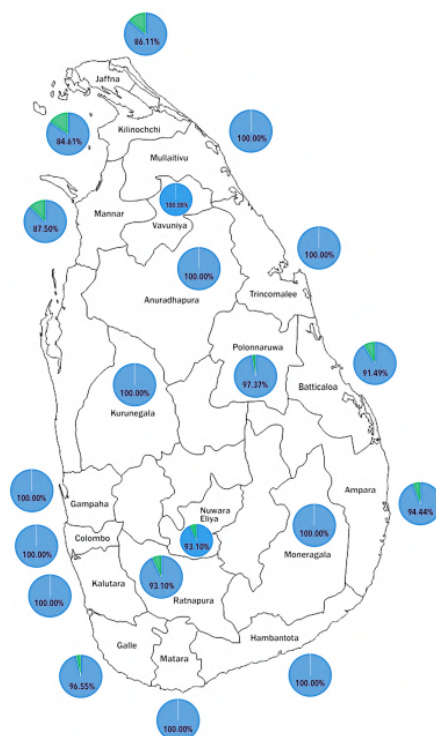


Fig. 1. The prevalence of alpha variant (green) compared to delta variant (blue) in each district of Sri Lanka. The different SARS-CoV-2 va

In this study, a multiplex, real-time PCR assay was used for the detection of single nucleotide polymorphisms (SNPs) with the aim of identifying the prevalence of different SARS-CoV-2 variants of concern (VOCs) in 16 out of 26 districts in Sri Lanka. The reason for conducting this research was because even though active surveillance SARS-CoV-2 VOCs is necessary for proper outbreak control measures, numerous lower income countries find it difficult to detect VOCs through carrying out genomic sequencing only, due to scarce resources.

Results concluded that 664 SNPs out of the 934 that were subjected to multiplex qRT-PCR, 638 (96.1%) detected L452R and K417 in the channels and these were identified as the delta variant. 25 samples (3.9%) detected N501Y, with K417 and this was identified as the alpha variant. The delta variant was the only VOC to be recognized in 10 out of 16 districts in Sri Lanka. Research from this study concluded that multiplex real-time qRT-PCR which identifies specific SNPs specific to the VOCs appear to be a fast, cheap and less technically challenging method to generate data related to the spread of different SARS-CoV-2 variants. In addition, it is a suitable method for lower income countries that are financially challenged, to supplement data produced by genomic sequencing.



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

Malavige, G.N., Jeewandara, C. & Ogg, G.S. Dengue and COVID-19: two sides of the same coin
Journal of Biomedical Science. (2022)

J Biomed Sci.2022 Jul 3;29(1): 48.doi: 10.1186/s12929-022-00833-y
Impact Factor: 12.771

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

In this study, the similarities, and differences between two diseases, dengue and COVID-19, are thoroughly discussed to help us form a better understanding of the two infections, their immunopathogenesis and how to develop therapeutic interventions for the general public. This research is based on the double burden of dengue and COVID-19 outbreaks in Asian and Latin American countries which took a huge toll on the healthcare system of these developing countries.

Evidence suggested that SARS-CoV-2 infects individuals through the respiratory route, while the dengue virus (DENV) infects individuals following a bite of a dengue infected mosquito of the *Aedes* species. Hence, the viral entry route is the key difference between dengue and COVID-19. There are also key differences in the long-term effects people experience due to the two diseases. Anyhow, there are also numerous similarities between dengue and SARS-CoV-2 infections and the similarities outweigh the differences. Both infections result in systemic infection, and portray similar clinical presentations such as headache, myalgia, fever and gastrointestinal symptoms. Both diseases are distinguished by a delayed and impaired type I IFN response and a proinflammatory immune response. Individuals with severe illness were identified to have delayed virus specific T cell responses as well, and it was found that fluctuating endothelial dysfunction leads to increased vascular permeability and coagulation abnormalities. Therefore, it is important to study the parallels between the immunopathogenesis of both dengue and COVID-19 for the development and manufacture of more efficacious vaccines and therapeutic interventions.

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

Jeewandara, C., Aberathna, I. S., Danasekara, S., Gomes, L., Fernando, S., Guruge, D., Ranasinghe, T., Gunasekera, B., Kamaladasa, A., Kuruppu, H., Somathilake, G., Jayamali, J., Jayathilaka, D., Wijayatilake, H. D., Pushpakumara, P. D., Harvie, M., Nimasha, T., de Silva, S. D., Wijayamuni, R., Schimanski, L., Rijal, P., Tan, J., Townsend, A., Ogg, G. S., & Malavige, G. N. (2022). Comparison of the immunogenicity of five COVID-19 vaccines in Sri Lanka. *Immunology*, 167(2), pp. 263-274. <https://doi.org/10.1111/imm.13535>

Impact Factor: 7.215

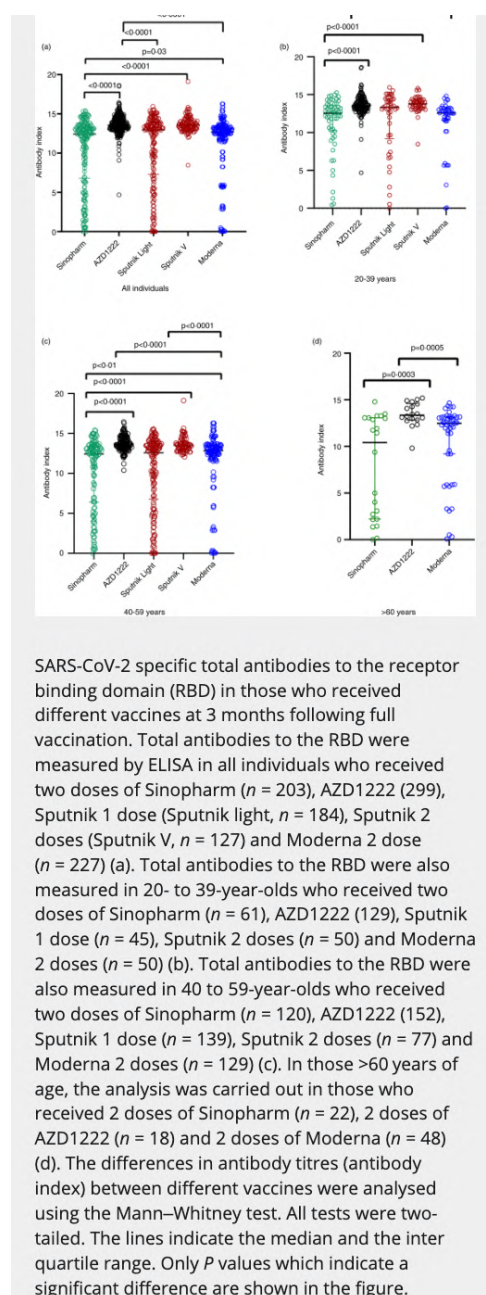
Antibodies to the receptor binding domain (RBD) of wild type (WT) SARS-CoV-2 and variants of concern (VoCs) along with ACE2 blocking antibodies were quantified in Sri Lankan individuals 3 months post-vaccination with Moderna (n=225), Sputnik V (n=128) or Sputnik light (n= 184), to better understand the antibody responses elicited by the different vaccines against the virus. The results were compared with those from previous studies on Sinopharm and AZD1222 vaccinees. A positive response to ACE2 blocking antibodies was seen in 99.5% of Moderna, >94% of AZD1222 or Sputnik V, >70% of Sputnik light and >60% of Sinopharm vaccine recipients. ACE2 blocking antibody levels were highest in Moderna vaccinees, followed by Sputnik V/AZD1222 (equal), Sputnik light and Sinopharm in descending order.

All Moderna vaccinees had antibodies to the RBD of the WT, Alpha and Beta variants. Their positivity rate for the delta variant was 80%. Sputnik V vaccinees showed higher positivity rates for the WT and VoCs when compared to those who received AZD1222. On the other hand, recipients of the Sinopharm vaccine had the lowest positivity rates which were <16.7%.

Although total antibodies to the BD were highest for the Sputnik and AZD1222 vaccinees, the Moderna vaccine surpassed these groups and the Sinopharm group (which had the lowest) when looking at the quantity of ACE2 blocking antibodies elicited.

It became evident that further studies would be needed to understand the effects on clinical outcomes.

FIGURE 1



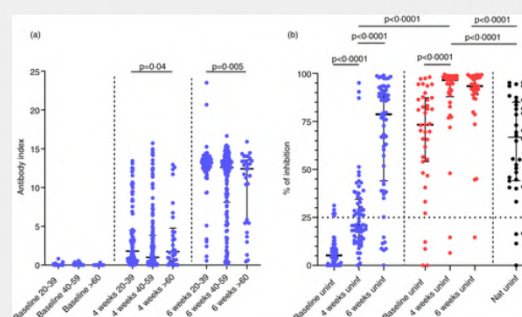
Immune responses to Sinopharm/BBIBP-CorV in individuals in Sri Lanka

Jeewandara, C., Aberathna, I. S., Pushpakumara, P. D., Kamaladasa, A., Guruge, G., 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, T. T., Mudunkotuwa, A., Somathilake, G., Harvie, M., Nimasha, T., Danasekara, S., Wijayamuni, R., Schimanski, L., Rijal, P., Tan, T. K., Dong, T., Townsend, A., Ogg, G. S., & Malavige, G. N. (2022). Immune responses to Sinopharm/BBIBP-CorV in individuals in Sri Lanka. *Immunology* (167)2, pp. 275-285. <https://doi.org/10.1111/imm.13536>

Impact Factor: 7.215

Given that antibody and T cell responses elicited by the Sinopharm/BBIBP-CorV vaccine against different SARS-CoV-2 variants of concern have not been extensively studied in different populations, we investigated this in Sri Lankan individuals. Antibodies specific to SARS-CoV-2 were measured in 282 individuals who were seronegative at baseline. Assays to detect ACE2 receptor blocking antibodies, assays to detect antibodies to the receptor-binding domain (RBD) of the wild-type (WT), alpha, beta and delta variants, ex vivo IFN γ ELISpot assays, cultured ELISpot assays, intracellular cytokine secretion assays and B cell ELISpot assays were also carried out in a sub cohort of the vaccinees at 4 and 6 weeks (2 weeks after the second dose). Although 95 percent of the vaccinees seroconverted, the seroconversion rate was significantly lower ($p < 0.001$) in individuals > 60 years (93.3%) compared to those who were 20-39 years (98.9%). At 6 weeks, 81.25% had ACE2 receptor blocking antibodies and there was no difference in the antibody titres between vaccine and convalescent sera ($p = 0.44$). Additionally, although there was no difference in antibodies to the RBD of beta and delta compared to convalescent sera, vaccinees had significantly less ($p < 0.0001$) antibodies to the RBD of WT and alpha. 27.7% of 46.4% of vaccinees showed ex vivo IFN γ and cultured ELISpot responses respectively and flow cytometry showed IFN γ and CD107a responses. Overall, the Sinopharm/BBIBP-CorV vaccine appeared to elicit an antibody response similar in magnitude against the ACE2 receptor, delta and beta variants as observed following natural infection.

FIGURE 1



SARS-CoV-2 specific antibody responses (total antibodies and ACE2 receptor blocking antibodies) in those who received the Sinopharm/BBIBP-CorV vaccine. (a) SARS-CoV-2 specific total antibodies were measured by ELISA in 20- to 39-year-old individuals ($n = 89$), 40- to 59-year olds ($n = 163$) and > 60 years olds ($n = 30$) at 4 weeks following the first dose and again at 6 weeks (2 weeks after the second dose). (b) ACE2 receptor blocking antibodies were measured by the surrogate neutralizing antibody assay in a sub cohort of these individuals ($n = 64$) at 4 and 6 weeks, in a cohort of individuals ($n = 38$), who were found to be seropositive for SARS-CoV-2 at the time of recruitment and in a cohort of naturally infected individuals 6 weeks following onset of illness ($n = 36$). The differences in the total antibody titres between different age groups was determined by the Kruskal-Wallis test. the differences in ACE2 receptor blocking antibodies at baseline uninfected and infected individuals were assessed by the Wilcoxon matched-pairs signed ranked test. all tests were two sided. the error bars indicate the median and the interquartile ranges. Baseline uninfected individuals: Blue, baseline infected individuals: Red, naturally infected unvaccinated individuals: Black

Universities



THE UNIVERSITY
of NORTH CAROLINA
at CHAPEL HILL



DukeNUS
Medical School

Centre for
Outbreak Preparedness

Governmental Agencies



MINISTRY OF HEALTH
Sri Lanka

WHO



Research Institutes



CREID
Centers for Research in
Emerging Infectious Diseases



Asian-American
Centers for
Arbovirus
Research and
Enhanced
Surveillance

Nonprofit Organizations



Research Projects





FUNDING

Research Grants

TOTAL

LKR 2.375 Billion

WHO

USD 1.635 Million

Seroprevalence Studies in Colombo

USD 150,000

Seroprevalence Studies Islandwide

USD 220,000

AgRDT

USD 1,200,000

Sequencing

USD 200,000

NIH

USD 267,000/yr
for 7 years

SKKU

USD 333,333/yr
for 7 years

World Bank

USD 27,000

Other Grants

USD 555,000

Generated Funds

**PCR, RAT and
Allergy Testing**

LKR 143 Million

39

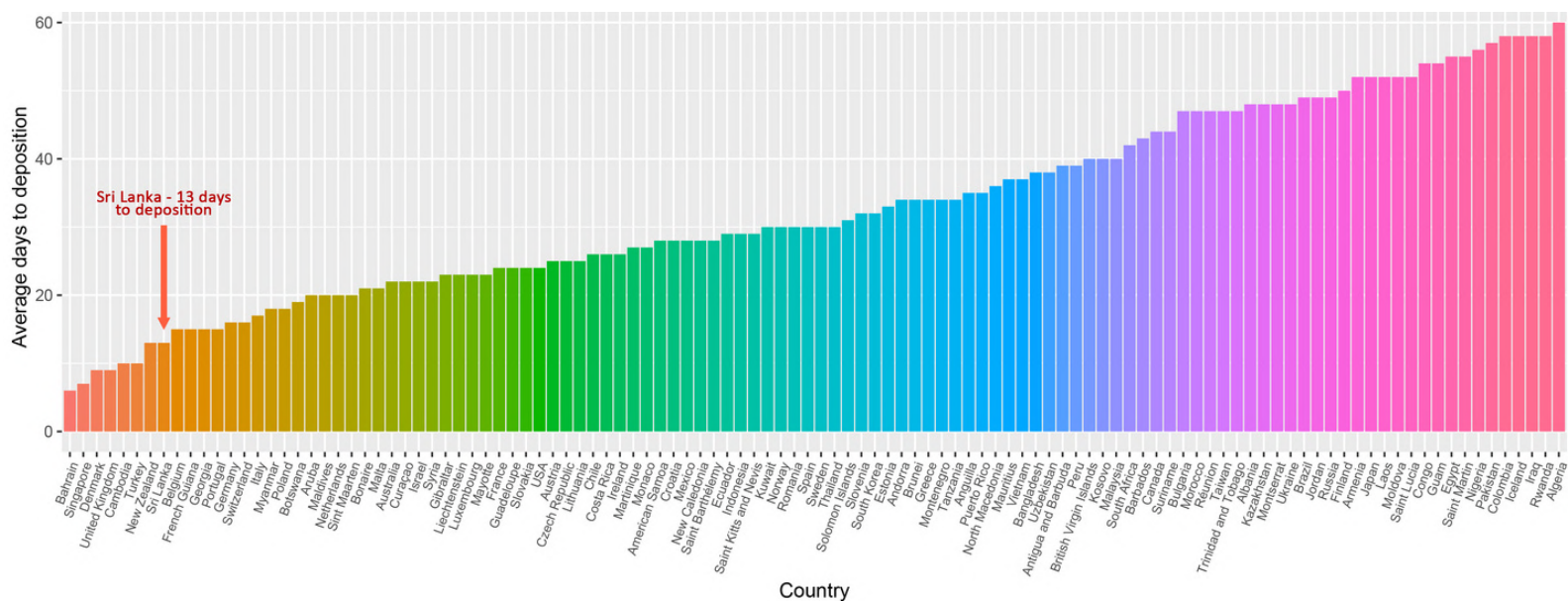
NEXT

GENERATION SEQUENCING

The future is here.

The AICBU was the first laboratory in Sri Lanka to introduce Oxford Nanopore Sequencing, the second to own a benchtop next-generation genome sequencing machine and the first to purchase an Illumina NextSeq 550 and iSeq 100. The team conducted Sri Lanka's first COVID-19 Whole Genome Sequencing run on 18th April 2020 using this technology. Since then, it has carried out over 75 sequencing runs to produce over 3032 high-quality genomic datasets. 76.8% of this data was generated using Oxford Nanopore sequencing and the remainder using Illumina.

During the four major outbreaks in Sri Lanka since March 2020, the team was able to identify and report every lineage that drove the outbreak within a very short time. This is reflected in GISAID Data Deposition statistics which indicate that Sri Lanka was one of the countries with the lowest average number of days to deposit sequences, surpassing developed countries such as the USA and Norway.



NEXT

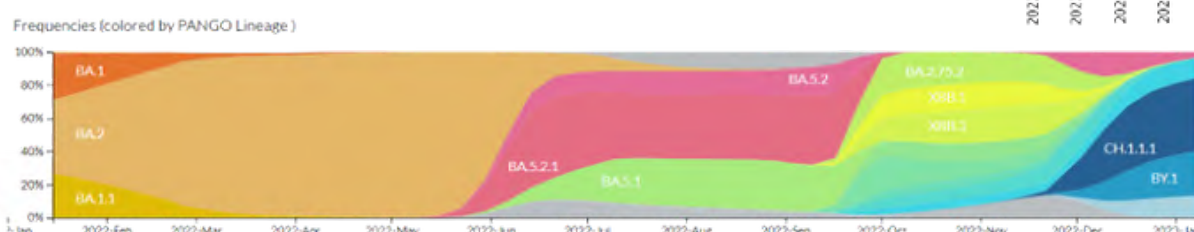
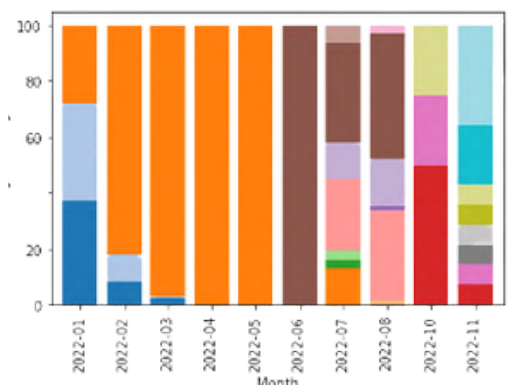
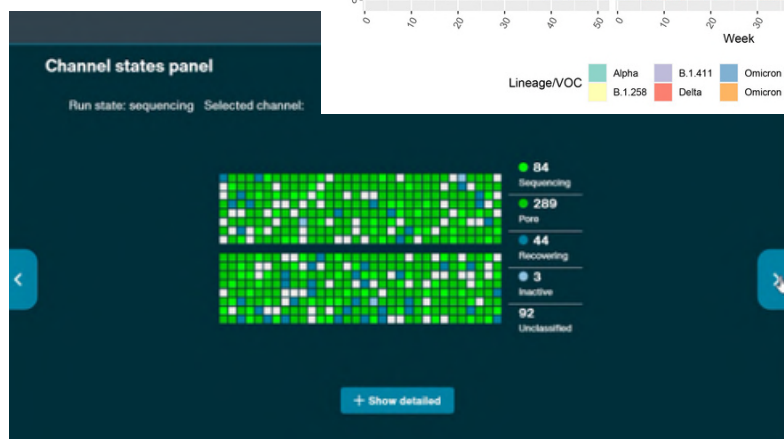
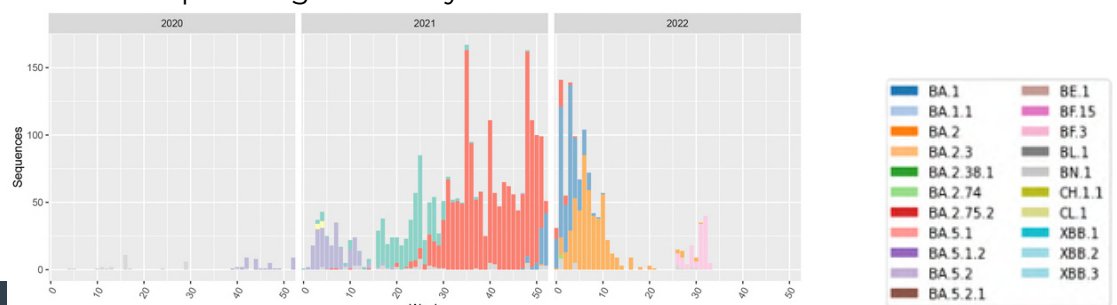
GENERATION SEQUENCING

The future is here.

The unit is 1 of just 4 laboratories in the government sector that have the capacity to conduct genome sequencing of SARS-CoV-2 in Sri Lanka and more than 94% of genomes uploaded to GISAID in the country are from the AICBU thanks to its 5 genome sequencers and GPU-powered bioinformatics setup specially dedicated to Oxford Nanopore Sequencing. Additionally, during the Delta-wave in Sri Lanka, we were able to train 183 medical laboratory technologists from the Ministry of Health.

At present, our research efforts are focused on the following areas:

- Genomic and epidemiological analysis of the SARS-CoV-2 virus in Sri Lanka <https://nextstrain.org/community/aicbu/ncov/srilanka>
- Genomic and epidemiological analysis of the Dengue virus in Sri Lanka
- Using JSON to manage Nextstrain for Sri Lanka <https://github.com/aicbu/ncov>
- Sub-genomic RNA (sgRNA) expression in SARS-CoV-2 ARTIC network using amplicon nanopore sequencing data
- Bacterial genome sequencing
- 16S microbiome sequencing and analysis



COVID-19

Leading the fight

During the COVID-19 pandemic, the AICBU assisted the Government of Sri Lanka with the national COVID-19 response by rendering diagnostic and other services to the Ministry of Health. A statistical overview of these services can be found below.

220,764

PCR Tests Done

15,000

Variant PCR Tests Done

9640

Antibody Tests Done

3032

SARS-CoV-2 Sequencing

Tests Done (USJ Contribution >94%)

nextstrain.org/community/aicbu/ncov/srilanka

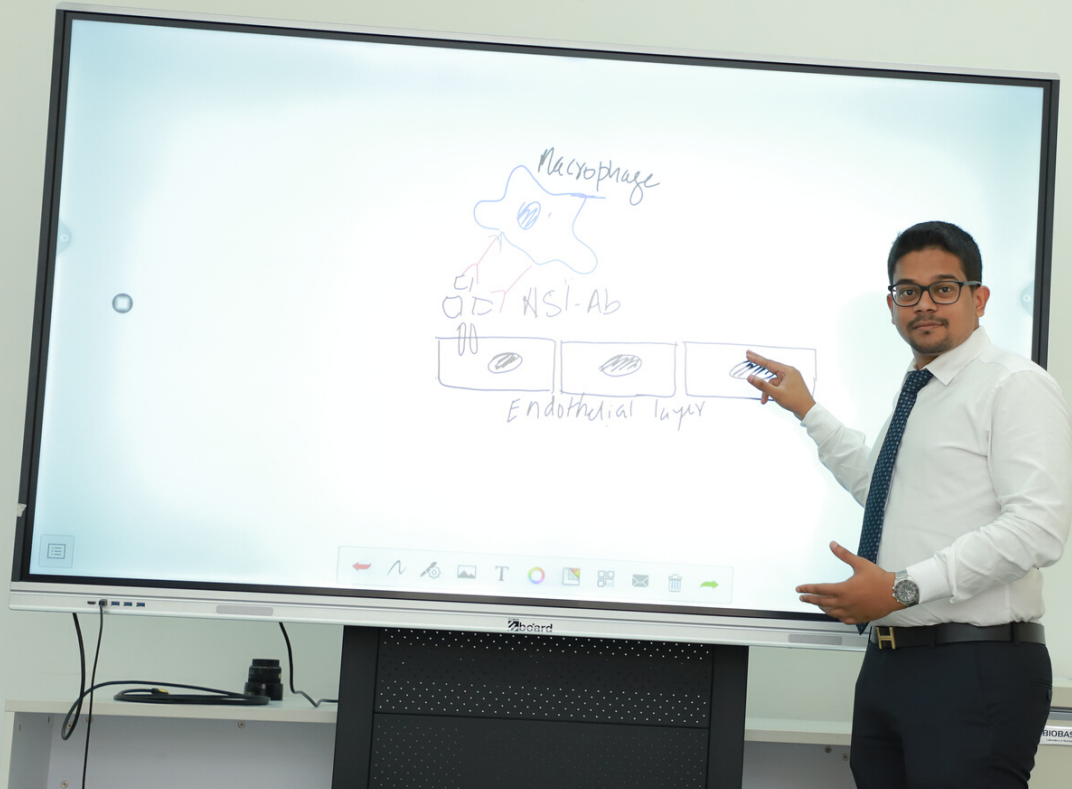
24,000

Sequence PCR Tests Done

(600 Selected Samples x 40 Runs)







EDUCATION

Sharing our knowledge.

MSc Course

In 2022, the Department of Immunology and Molecular Medicine started laying the foundation for the MSc in Immunology program in collaboration with the AICBU. The program, which is a hybrid course featuring online lectures on weekday evenings and on-site practicals on weekends, is scheduled to commence in March 2023 following final approval from the University Grants Commission at the end of February. Students will be offered a 2-year course covering 60 credits, of which 25 credits is dedicated to research.

BSc Course

In 2023, the unit will collaborate further with the Department of Immunology and Molecular Medicine by contributing to the final year specialisation in Immunology for the BSc (Hons) in Human Biology degree program. The first undergraduate student has already joined and the AICBU hopes to welcome more students through the upcoming intakes. This will be facilitated by the Faculty of Medical Sciences which is in this final stage of approval to open up a direct entry level for the course- a change that will see 5-10 students taking up Immunology as a specialisation per intake.

Other Courses

Apart from the aforementioned courses, the AICBU also contributes to teaching and examination of the MBBS degree program conducted by the Faculty of Medical Sciences and the BSc in Nursing, BSc in Medical Laboratory Science and BSc in Pharmacology conducted by the Faculty of Allied Health Sciences.

TRAINING

Developing skillsets.



Graduate Interns

The AICBU and Department of Immunology and Molecular Medicine were requested to provide training to Medical Laboratory Science Graduate Interns who were attached to the Ministry of Health and posted at government hospitals. Training was carried out from 11th October 2021 to 18th February 2022 and 183 trainees took part in the program. Participants were split into 10 groups and each group underwent 2 weeks of lectures, demonstrations and hands-on training in PCR, Swabbing, Phlebotomy, Sequencing and other molecular diagnostic techniques.

Undergraduate Training

In 2022, five students from the Faculty of Applied Sciences underwent a 10-week training program with the AICBU as part of a mandatory internship in their degree program. Further to commendations received from these interns, their department allocated six more students for training at the AICBU in 2023. These interns are currently completing their internship at the unit.

Other Training Programs

As the most experienced PCR testing laboratory in Sri Lanka, the AICBU has trained numerous Medical Laboratory Technologists from hospitals and universities while empowering several virologists to establish laboratories in their respective institutions including the Infectious Disease Hospital (IDH) and Sri Jayewardenepura Hospital.

With its progressive outlook on the scientific landscape in Sri Lanka, the unit also tailored a 6-week training program to cater to demand from high school students attending both local and international schools. The program was a great success and provided excellent exposure to students who participated in 2022.



Prof. Neelika Malavige

Director of Research and Development

Professor in Immunology and Molecular Medicine



Prof. Chandima Jeewandara

Director of Operations and Clinical Services

Professor in Allergy, Immunology and Molecular Medicine



Mr. Laksiri Gomes

Senior Research Scientist



Dr. Deshni Jayathilaka

Post-doctoral Research Scientist



Dr. Pradeep Darshana

Post-doctoral Research Scientist



Dr. Tibutius Thanesh

Post-doctoral Research Scientist



Dr. Dinuka Ariyaratne

Graduate Student/ Lecturer



Dr. Thushali Ranasinghe

Graduate Student/ Lecturer



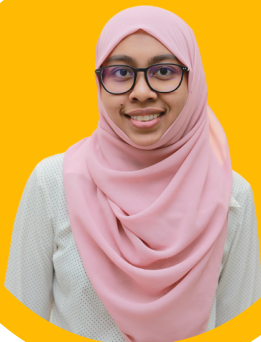
Ms. Shashika Dayaratna

Graduate Student/ Lecturer



Ms. Sepali Aberathna

Graduate Student/ Lecturer



Ms. Shyrar Ramu

Graduate Student/Project Coordinator



**Ms. Saubhagya
Danasekara**

Field Research Coordinator



Dr. Dumni Gunasinghe

Graduate Student



Mr. Heshan Kuruppu

Graduate Student



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Ms. Jeewantha Jayamali

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Mr. Rajitha Perera

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Dr. Hashini Colambage

Demonstrator



**Dr. Deneshan
Peranantharajah**

Demonstrator



Dr. Nayanathara Gamalath
Demonstrator



Dr. Dinithi Ekanayake
Demonstrator



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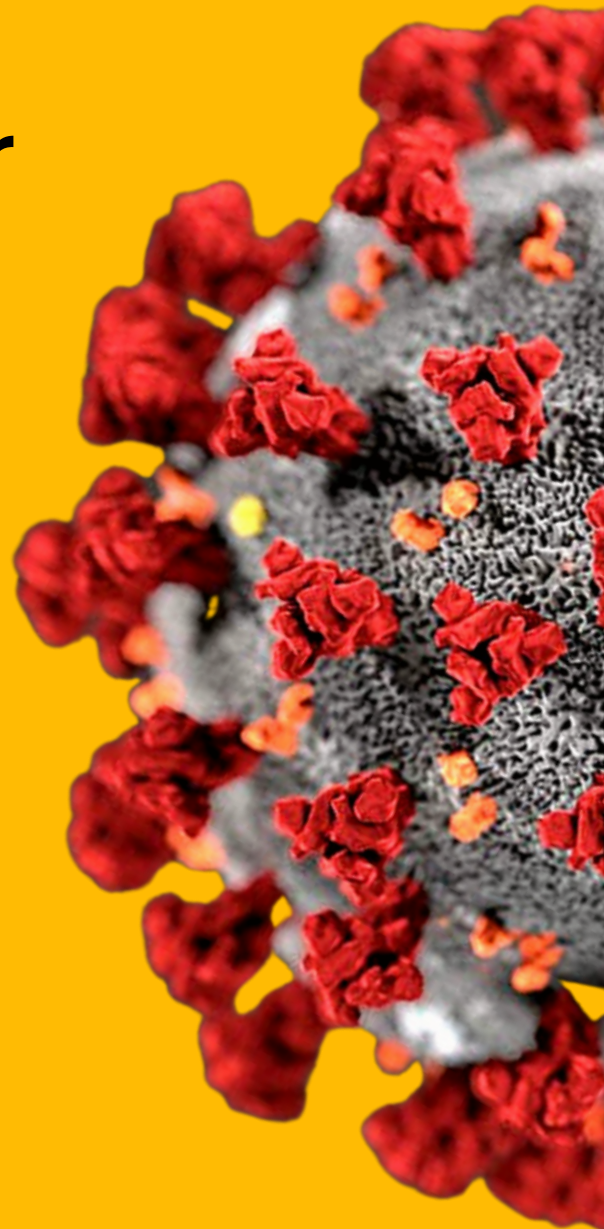


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We thank you for
your ongoing
support of our
clinical services,
education and
research.



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