Report 49: Growth, population distribution and immune escape of Omicron in England[+]

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[+]. *Updated 20-12-2021 to: (a) correct accidental transposition of S+ and S- columns in Table 3; (b) correct incorrect total S+ and S- numbers given on page 5; (c) correct the labelling of the 18-20 age band in Table 1; (d) clarify that VE analysis excluded reinfections; (e) provide separate estimates of the reinfection relative risk for vaccinated and unvaccinated cases; (f) add a comment on page 5 that the crude ratios of hospitalisations to cases give no information on severity on their own due to the differences in the age distribution of Omicron and Delta cases.*

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Summary

To estimate the growth of the Omicron variant of concern (1) and its immune escape (2–9) characteristics, we analysed data from all PCR-confirmed SARS-CoV-2 cases in England excluding those with a history of recent international travel. We undertook separate analyses according to two case definitions. For the first definition, we included all cases with a definitive negative S-gene Target Failure (SGTF) result and specimen dates between 29/11/2021 and 11/12/2021 inclusive. For the second definition, we included cases with a positive genotype result and specimen date between 23/11/2021 and 11/12/2021 inclusive. We chose a later start date for the SGTF definition to ensure greater specificity of SGTF for Omicron.

We used logistic and Poisson regression to identify factors associated with testing positive for Omicron compared to non-Omicron (mostly Delta) cases. We explored the following predictors: day, region, symptomatic status, sex, ethnicity, age band and vaccination status. Our results suggest rapid growth of the frequency of the Omicron variant relative to Delta, with the exponential growth rate of its frequency estimated to be 0.34/day (95% CI: 0.33-0.35) [2.0 day doubling time] over the study period from both SGTF and genotype data. The distribution of Omicron by age, region and ethnicity currently differs markedly from Delta, with 18–29-year-olds, residents in the London region, and those of African ethnicity having significantly higher rates of infection with Omicron relative to Delta.

Hospitalisation and asymptomatic infection indicators were not significantly associated with Omicron infection, suggesting at most limited changes in severity compared with Delta.

To estimate the impact of Omicron on vaccine effectiveness (VE) for symptomatic infection we used conditional Poisson regression to estimate the hazard ratio of being an Omicron case (using SGTF definition) compared with Delta, restricting our analysis to symptomatic cases and matching by day, region, 10-year age band, sex and ethnicity. We found a significant increased risk of an Omicron case compared to Delta for those with vaccine status AZ 2+weeks post-dose 2 (PD2) , Pfizer 2+w PD2, AZ 2+w post-dose 3 (PD3) and PF 2+w PD3 vaccine states with hazard ratios of 1.86 (95%CI: 1.67-2.08), 2.68 (95%CI: 2.54-2.83), 4.32 (95%CI: 3.84-4.85) and 4.07 (95%CI: 3.66-4.51), respectively, where PD3 states are categorised by the dose 1/2 vaccine used. Depending on the Delta VE estimates used (10), these estimates translate into Omicron VE estimates of between 0% and 20% PD2 and between 55% and 80% PD3 against Omicron, consistent with other estimates (11). Similar estimates were obtained using genotype data, albeit with greater uncertainty.

To assess the impact of Omicron on reinfection rates we relied on genotype data, since SGTF is associated with a higher observed rate of reinfection, likely due to reinfections typically having higher Ct values than primary infections and therefore being subject to a higher rate of random PCR target failure. Controlling for vaccine status, age, sex, ethnicity, asymptomatic status, region and specimen date and using conditional Poisson regression to predict reinfection status, Omicron was associated with a 5.41 (95% CI: 4.87-6.00) fold higher risk of reinfection compared with Delta. This suggests relatively low remaining levels of immunity from prior infection.

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1. Methods

1. 1 Data

We analysed UKHSA and NHS data from all PCR-confirmed SARS-CoV-2 cases in England with no history of recent international travel. In addition to genotype data, we used S-gene target failure (SGTF) as a proxy for Omicron infection, given the 69-70 Spike deletion present in that variant. SGTF was only scored for PCR tests with Ct values under 30 for other targets, to minimise the risk of false negatives. SGTF results by this definition were available for approximately 40% of pillar 2 cases in England in the analysis period.

Given the SGTF and genotyping data, we undertook two analyses defining an Omicron case as either: (1) having a positive result from the SGTF analysis and specimen date between 29/11/2021 and 11/12/2021 inclusive; or (2) having a positive genotype result and specimen date between 23/11/2021 and 11/12/2021 inclusive. Our analysis was undertaken using data provided by the UK Health Security Agency (UKHSA) on 15th December 2021. We restricted our analysis to Pillar 2 cases where sex, age and symptom status was known (98% and 93% of cases in the genotype and S-gene analysis respectively).

The UKHSA England COVID-19 line-list was linked via National Health service (NHS) number to the National Immunisation Management System (NIMS) database, the SGTF results database, NHS hospital episode data and a separate list of known reinfections. We excluded cases which were not able to be linked to NIMS (due to an invalid NHS number), and where age, region, symptom status or an SGTF or genotype result were not available. A total of 93% of both genotyped and SGTF cases met these criteria. Cases associated with documented recent overseas travel were also excluded. Specimen date was taken to be the *last* reported specimen date for each unique NHS number across all linked datasets. Reinfections were identified as two positive test results for the same individual 90 or more days apart.

Data access: While all data used in this analysis were anonymised, the individual-level nature of the data used risks individuals being identified, or being able to self-identify, if it is released publicly. Requests for access to the underlying source data should be directed to UKHSA.

1.2 Statistical analysis

Exploratory analysis: To estimate factors associated with Omicron cases relative to Delta cases, we fitted logistic regression models to all Omicron cases (using our two separate case definitions as above), using the following predictor variables: Day of test specimen, NHS region, symptomatic status, vaccination status, reinfection status, age band (0-12, 13-17, 18-29, 30-49, 50-69, 70+), sex, ethnic group. We did not explore interactions, given total Omicron case numbers included in the analysis remains relatively small.

Vaccine effectiveness (VE) for symptomatic infection: Given the current differences between Omicron and Delta in their distribution by age, region and ethnic group, it is important to control for confounders and interactions when estimating VE. We therefore used conditional Poisson regression to estimate the association between vaccination status and the odds of being an Omicron case relative to Delta cases, using vaccination status as the predictor, and stratifying by using a stratum variable defined as the interaction between day, region, sex, 10-year age band and ethnic group (approximately 11,000 strata). Only symptomatic cases with no evidence of reinfection were included in this analysis, to produce estimates compatible with previous VE studies. Conditional Poisson regression (12) was used in preference to conditional logistic regression due to the relatively high

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frequencies of Omicron in the dataset, which made odds-ratios a poorer approximation to hazard ratios.

Hazard ratios for vaccination status can be translated into predicted vaccine effectiveness estimates via the equation $VE(Omicron) = 1 - HR\ [1\text{-}VE(Delta)]$, where HR is the hazard ratio estimated for a particular vaccination class.

Reinfection risk: To assess the impact of Omicron on reinfection rates we relied on genotype data, since SGTF is associated with a higher observed rate of reinfection, likely due to reinfections typically having higher Ct values than primary infections and therefore being subject to a higher rate of random PCR target failure. We used conditional Poisson regression (12) to predict reinfection status, evaluating the hazard ratio for reinfection associated with Omicron versus Delta cases, with strata defined by the interaction of vaccine status, 10-year age-band, sex, ethnicity, asymptomatic status, region and specimen date.

1.3 Ethical approval

Surveillance of COVID-19 testing and vaccination is undertaken under Regulation 3 of The Health Service (Control of Patient Information) Regulations 2002 to collect confidential patient information (https://www.legislation.gov.uk/uksi/2002/1438/regulation/3/made) under Sections 3(i) (a) to (c), 3(i)(d) (i) and (ii) and 3(3). Data were shared with the investigators as part of the UK's emergency response to the COVID-19 pandemic, via the SPI-M subcommittee of the UK Scientific Advisory Group for Emergencies (SAGE). Ethics permission was sought for the study via Imperial College London's standard ethical review processes and the study was approved by the College's Research Governance and Integrity Team (ICREC reference: 21IC6945).

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2. Results

2.1 Risk factors for Omicron relative to Delta

A total of 208,947 S+ and 15,087 S- cases with complete data were included in the SGTF analysis, and 142,340 Delta and 6,184 Omicron cases were included in the genotype analysis. Figure 1 shows the growth in log-odds frequency over time. The frequency of S- in the SGTF data set was 20% on 10th December.

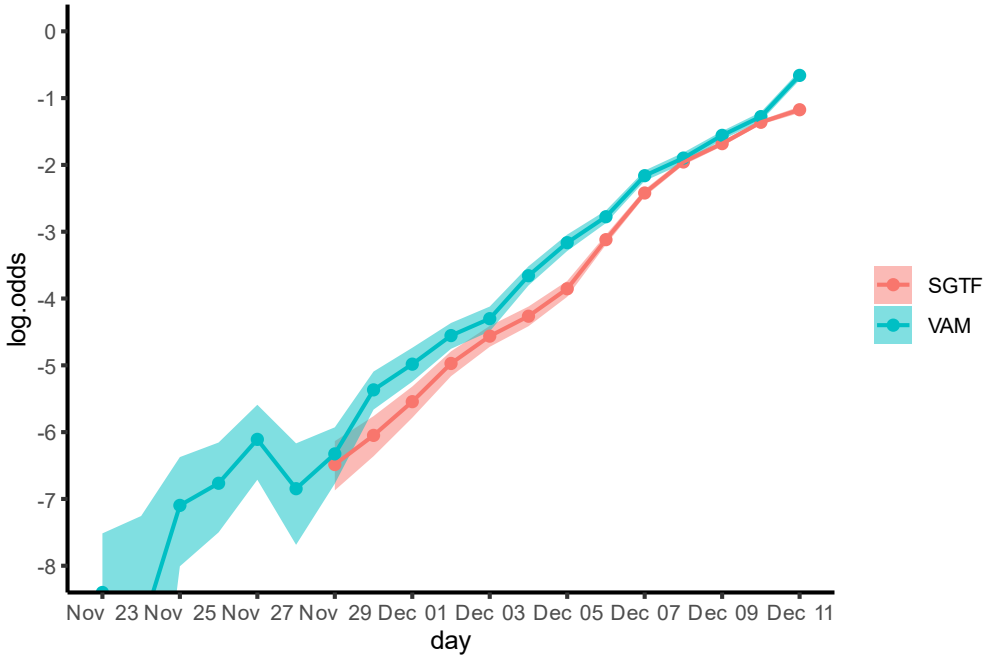

Figure 1: log-odds of Omicron frequency among incident PCR-positive cases from November 23rd to December 11th 2021 in England from SGTF and genotype (VAM) data, with exact binomial 95% confidence intervals.

Table 1 presents the results of the exploratory logistic regression using SGTF data. Results were very similar for genotype data (table not shown). Both analyses suggest rapid growth of the log odds frequency of the Omicron variant relative to Delta, with exponential growth rate estimates of 0.45/day (95%CI: 0.44-0.46) [1.5 day doubling time] and 0.43/day (95%CI: 0.42-0.44) [1.6 day doubling time] obtained from genotype and SGTF data, respectively. Given the frequency of Omicron exceeded 20% by the last time point examined, the exponential growth rate of frequency (as compared with log odds frequency) was estimated to be somewhat lower, at 0.34/day (95% CI: 0.33-0.35) [2.0 day doubling time] from both SGTF and genotype data, calculated using Poisson rather than logistic regression. There is some sign of the growth rate of log odds frequency of SGTF slowing between December 8th and 11th (Figure 1), but only to a rate of approximately 0.3/day [2.3 day doubling time].

The distribution of Omicron by age, region and ethnicity currently differs markedly from Delta, with 18-29 year-olds, the London region, and those of African ethnicity having significantly higher rates of infection with Omicron relative to Delta. Hence the crude ratios of hospitalisations to cases shown give no information on severity on their own since risk of hospitalisation increases markedly with age. Hospitalisation and asymptomatic infection indicators were not significantly associated with Omicron infection, suggesting at most limited changes in severity compared with Delta. Vaccination classes were generally associated with Omicron infection, but VE was formally assessed using conditional logistic regression (see below). Omicron was also significantly associated with reinfection, but this is also better examined using Poisson regression to estimate hazard ratios of reinfection (see below).

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Table 1. Estimates from the logistic regression predicting SGTF from all cases with S-gene target results. Numbers of S+ and S- cases are shown for each stratum, together with the log OR and OR estimates (with 95% confidence intervals in parentheses) and associated p-values. Results with p<0.05 are shown in red. Vaccination states not shown (see Tables 2 and 3).

Class	Variable	S+	S-	log(OR)	OR	p-value
Time	Day	208947	15087	0.43 (0.42-0.44)	1.54 (1.53-1.55)	<1e-6
NHS Region	London	21585	5976	0	1	-
	East of England	27986	2274	-0.85 (-0.91--0.79)	0.43 (0.4-0.46)	<1e-6
	Midlands	41223	1645	-1.53 (-1.59--1.46)	0.22 (0.2-0.23)	<1e-6
	North East and Yorkshire	45631	811	-2.32 (-2.41--2.24)	0.1 (0.09-0.11)	<1e-6
	North West	34726	1998	-1.11 (-1.17--1.04)	0.33 (0.31-0.35)	<1e-6
	South East	27405	1985	-0.85 (-0.92--0.79)	0.43 (0.4-0.45)	<1e-6
	South West	10391	398	-1.47 (-1.58--1.35)	0.23 (0.21-0.26)	<1e-6
Symptoms	symptomatic	119284	8171	0	1	-
	asymptomatic	89663	6916	-0.02 (-0.06-0.02)	0.98 (0.95-1.02)	0.4348
Sex	Female	109240	8454	0	1	-
	Male	99707	6633	0.04 (0-0.08)	1.04 (1-1.08)	0.052
Ethnic group	White British	165715	8746	0	1	-
	African	2459	1851	2.29 (2.2-2.38)	9.86 (9.03-10.77)	<1e-6
	Any other Asian background	2511	232	0.02 (-0.14-0.18)	1.02 (0.87-1.2)	0.7791
	Any other Black background	400	163	1.75 (1.5-1.99)	5.73 (4.5-7.28)	<1e-6
	Any other ethnic group	2016	194	0.16 (-0.01-0.34)	1.18 (0.99-1.4)	0.0733
	Any other mixed background	1702	208	0.62 (0.45-0.8)	1.87 (1.57-2.23)	<1e6
	Any other White background	14215	1249	0.03 (-0.04-0.1)	1.03 (0.96-1.11)	0.4512
	Bangladeshi/British Bangladeshi	1228	64	-0.69 (-0.98--0.41)	0.5 (0.38-0.66)	<1e5
	Caribbean	1430	571	1.53 (1.4-1.66)	4.6 (4.04-5.25)	<1e-6
	Chinese	1228	138	0.34 (0.13-0.55)	1.4 (1.14-1.73)	0.002
	Indian/British Indian	4735	410	0.04 (-0.08-0.16)	1.04 (0.93-1.18)	0.4926
	Irish	1036	105	-0.07 (-0.31-0.16)	0.93 (0.74-1.17)	0.5444
	Pakistani/British Pakistani	3215	159	-0.14 (-0.32-0.04)	0.87 (0.73-1.04)	0.1415
	Unknown	2815	507	0.32 (0.21-0.43)	1.38 (1.24-1.54)	<1e6
	White and Asian	1864	147	0.33 (0.12-0.54)	1.39 (1.13-1.71)	0.0022
	White and Black African	747	110	1.05 (0.79-1.31)	2.86 (2.21-3.69)	<1e6
	White and Black Caribbean	1631	233	0.93 (0.76-1.1)	2.53 (2.13-3.01)	<1e-6
Reinfection status	Not reinfection	206321	13586	0	1	-
	Reinfection	2626	1501	1.88 (1.79-1.97)	6.55 (5.99-7.15)	<1e-6
Hospital status	No hospital attendance	207555	15063	0	1	-
	Hospital attendance	1392	24	-0.05 (-0.49-0.39)	0.95 (0.61-1.47)	0.8275
Age band	18-29	23853	5931	0	1	-
	0-12	56239	792	-1.93 (-2.02--1.84)	0.15 (0.13-0.16)	<1e-6
	13-17	19423	746	-1.18 (-1.28--1.08)	0.31 (0.28-0.34)	<1e-6
	30-49	74532	5634	-1.06 (-1.11--1.01)	0.35 (0.33-0.36)	<1e-6
	50-69	32417	1800	-1.13 (-1.21--1.06)	0.32 (0.3-0.35)	<1e-6
	70+	2483	184	-1.43 (-1.61--1.26)	0.24 (0.2-0.28)	<1e-6

2.2 Vaccine effectiveness

Table 2 and 3 show ORs for vaccination states associated with Omicron cases versus Delta cases from the conditional regression using SGTF data, for two different sets of estimates of VE for Delta: (a) a cohort analysis undertaken at Imperial College (publication in preparation), and from a test negative case control [TNCC] study undertaken by UKHSA (updated version of (10)).

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Table 2: Vaccination state related estimated hazard ratios for Omicron relative to Delta, estimated VE against symptomatic infection for Delta from a whole population cohort analysis for England (Ferguson et al, in preparation) and predicted resulting VE values for Omicron. VE estimates only shown for hazard ratios with p<0.05 (in red). D1, D2 and D3 states are post-dose 1, 2 and 3, respectively. Dose 3 states all received a mRNA booster and are distinguished by the dose 1/2 vaccine used. Numbers in vaccination state names (14, 21) refer to days since dose. Analysis restricted to symptomatic cases with no evidence of reinfection.

Vaccination category	S+	S-	Mean delay since last dose (days)	Hazard ratio	Delta VE (%)	Omicron VE (%)	p-value
None	49716	1547	-	1			-
AZ:D1:<21	3	0	4	-			0.936
AZ:D1:21+	832	34	233	1.16 (0.89-1.51)			0.266
AZ:D2:<14	65	7	6	2.62 (1.5-4.61)	46 (44.8-47.2)	-42 (-154-21)	<1e-3
AZ:D2:14+	32887	1676	178	1.86 (1.74-1.98)	25 (24.3-25.7)	-39 (-50--30)	<1e-6
AZ:D3:<14	4926	250	5	1.86 (1.67-2.08)	53.9 (52.5-55.2)	14 (1-25)	<1e-6
AZ:D3:14+	1192	230	36	4.32 (3.84-4.85)	89.7 (88.9-90.4)	55 (46-63)	<1e-6
PF:D1:<21	1250	44	9	1.02 (0.81-1.28)			0.866
PF:D1:21+	6706	362	90	1.46 (1.34-1.6)	33.1 (32.7-33.6)	2 (-7-11)	<1e-6
PF:D2:<14	391	28	5	1.36 (1.04-1.78)	66.7 (66.2-67.3)	55 (40-66)	0.026
PF:D2:14+	17544	2888	141	2.68 (2.54-2.83)	55.9 (55.5-56.3)	-18 (-26--11)	<1e-6
PF:D3:<14	890	60	6	2.49 (2.06-3.01)	65.4 (64.5-66.4)	14 (-7-31)	<1e-6
PF:D3:14+	1801	288	48	4.07 (3.66-4.51)	88.6 (88.1-89.1)	54 (46-60)	<1e-6

Table 3: As Table 2 but using UKHSA TNCC-based estimates of VE for Delta (10)

Vaccination category	S+	S-	Mean delay since last dose (days)	Hazard ratio	Delta VE (%)	Omicron VE (%)	p-value
None	49716	1547	-	1			-
AZ:D1:<21	3	0	4	-			0.936
AZ:D1:21+	832	34	233	1.16 (0.89-1.51)			0.266
AZ:D2:<14	65	7	6	2.62 (1.5-4.61)	51.7 (49.7-53.7)	-27 (-132-31)	<1e-3
AZ:D2:14+	32887	1676	178	1.86 (1.74-1.98)	43.7 (43-44.4)	-5 (-13-3)	<1e-6
AZ:D3:<14	4926	250	5	1.86 (1.67-2.08)	84 (82.9-85.1)	70 (65-75)	<1e-6
AZ:D3:14+	1192	230	36	4.32 (3.84-4.85)	93.8 (93.3-94.3)	73 (67-78)	<1e-6
PF:D1:<21	1250	44	9	1.02 (0.81-1.28)			0.866
PF:D1:21+	6706	362	90	1.46 (1.34-1.6)	51.4 (50.5-52.2)	29 (21-36)	<1e-6
PF:D2:<14	391	28	5	1.36 (1.04-1.78)	67.8 (66.7-68.8)	56 (41-68)	0.026
PF:D2:14+	17544	2888	141	2.68 (2.54-2.83)	69.8 (69.4-70.2)	19 (13-24)	<1e-6
PF:D3:<14	890	60	6	2.49 (2.06-3.01)	78.1 (76.7-79.3)	45 (30-57)	<1e-6
PF:D3:14+	1801	288	48	4.07 (3.66-4.51)	94.3 (93.9-94.6)	77 (72-80)	<1e-6

2.3 Reinfection

Controlling for vaccine status, age, sex, ethnicity, asymptomatic status, region and specimen date, Omicron was associated with a 5.41 (95% CI: 4.87-6.00) fold higher relative risk of reinfection compared with Delta. The relative risks were 6.36 (95% CI: 5.23-7.74) and 5.02 (95% CI: 4.47-5.67) when estimated separately for unvaccinated and vaccinated cases, respectively.

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3. Discussion

The growth rates estimated for Omicron translate into doubling times of under 2.5 days, even allowing for the potentially slowing of growth up to 11th December. These estimates are consistent or even faster than doubling times reported from South Africa (13). Assuming an exponentially distributed generation time of 5.2 days and that R=1 currently for Delta, reproduction number (R) estimates for Omicron are above 3 for the SGTF and genotype analyses, and above 2.5 even for the period 8th-10th December. Shorter assumed generation times will give lower R estimates.

The distribution of Omicron by age, region and ethnicity currently differs markedly from Delta, indicating Omicron transmission is not yet uniformly distributed across the population. However, we note that given its immune evasion, the age distribution of Omicron infection in the coming weeks may continue to differ from that of Delta. London is substantially ahead of other English regions in Omicron frequency.

We find strong evidence of immune evasion, both from natural infection, where the risk of reinfection is 5.41 (95% CI: 4.87-6.00) fold higher for Omicron than for Delta, and from vaccine-induced protection. Our VE estimates largely agree with those from UKHSA's TNCC study (11) and predictions from predicting VE from neutralising antibody titres (4,14), suggesting very limited remaining protection against symptomatic infection afforded by two doses of AZ, low protection afforded by two doses of Pfizer, but moderate to high (55-80%) protection in people boosted with an mRNA vaccine.

Our estimate of the hazard ratio for reinfection relative to Delta also supports previous analysis of reinfection risk in South Africa (15). Prior to Omicron, the SIREN cohort study of UK healthcare workers estimated that SARS-CoV-2 infection gave 85% protection against reinfection over 6 months (16), or a relative risk of infection of 0.15 compared with those with no prior infection. Our hazard ratio estimate would suggest the relative risk of reinfection has risen to 0.81 [95%CI: 0.73-1.00] (*i.e.* remaining protection of 19% [95%CI: 0-27%]) against Omicron.

We find no evidence (for both risk of hospitalisation attendance and symptom status) of Omicron having different severity from Delta, though data on hospitalisations are still very limited.

There are several limitations of this analysis. While case numbers are increasing quickly, there are still limits in our ability to examine interactions between the variables considered. The distribution of Omicron differed markedly from Delta across the English population at the time this analysis was conducted, likely due to the population groups in which it was initially seeded, which increases the risks of confounding in analyses. SGTF is an imperfect proxy for Omicron, though SGTF had over 60% specificity for Omicron over the date range analysed in the SGTF analysis (and close to 100% by 10th December). Intensified contact tracing around known Omicron cases may have increased case ascertainment over time, potentially introducing additional biases.

Our analysis reinforces the still emerging but increasingly clear picture that Omicron poses an immediate and substantial threat to public health in England and more widely.

4. Acknowledgements

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5. Bibliography

1. World Health Organization. Classification of Omicron (B.1.1.529): SARS-CoV-2 Variant of Concern [Internet]. 2021 [cited 2021 Dec 15]. Available from: https://www.who.int/news/item/26-11-2021-classification-of-omicron-(b.1.1.529)-sars-cov-2-variant-of-concern

2. Ikemura N, Hoshino A, Higuchi Y, Taminishi S, Inaba T, Matoba S. SARS-CoV-2 Omicron variant escapes neutralization by vaccinated and convalescent sera and therapeutic monoclonal antibodies. medRxiv [Internet]. 2021 Dec 14 [cited 2021 Dec 15];2021.12.13.21267761. Available from: https://www.medrxiv.org/content/10.1101/2021.12.13.21267761v1

3. Schubert M, Bertoglio F, Steinke S, Heine PA, Ynga-Durand MA, Zuo F, et al. Human serum from SARS-CoV-2 vaccinated and COVID-19 patients shows reduced binding to the RBD of SARS-CoV-2 Omicron variant in comparison to the original Wuhan strain and the Beta and Delta variants. medRxiv [Internet]. 2021 Dec 13 [cited 2021 Dec 15];2021.12.10.21267523. Available from: https://www.medrxiv.org/content/10.1101/2021.12.10.21267523v1

4. Gardner BJ, Kilpatrick AM. Estimates of reduced vaccine effectiveness against hospitalization, infection, transmission and symptomatic disease of a new SARS-CoV-2 variant, Omicron (B.1.1.529), using neutralizing antibody titers. medRxiv [Internet]. 2021 Dec 12 [cited 2021 Dec 15];2021.12.10.21267594. Available from: https://www.medrxiv.org/content/10.1101/2021.12.10.21267594v2

5. Dejnirattisai W, Shaw RH, Supasa P, Liu C, Stuart AS, Pollard AJ, et al. Reduced neutralisation of SARS-COV-2 Omicron-B.1.1.529 variant by post-immunisation serum. medRxiv [Internet]. 2021 Dec 11 [cited 2021 Dec 15];2021.12.10.21267534. Available from: https://www.medrxiv.org/content/10.1101/2021.12.10.21267534v1

6. Rössler A, Riepler L, Bante D, Laer D von, Kimpel J. SARS-CoV-2 B.1.1.529 variant (Omicron) evades neutralization by sera from vaccinated and convalescent individuals. medRxiv [Internet]. 2021 Dec 11 [cited 2021 Dec 15];2021.12.08.21267491. Available from: https://www.medrxiv.org/content/10.1101/2021.12.08.21267491v1

7. Wilhelm A, Widera M, Grikscheit K, Toptan T, Schenk B, Pallas C, et al. Reduced Neutralization of SARS-CoV-2 Omicron Variant by Vaccine Sera and Monoclonal Antibodies. medRxiv [Internet]. 2021 Dec 13 [cited 2021 Dec 15];2021.12.07.21267432. Available from: https://www.medrxiv.org/content/10.1101/2021.12.07.21267432v4

8. Lu L, Wing-Yee Mok B, Chen L, Man-Chun Chan J, Tak-Yin Tsang O, Hoi-Shiu Lam B, et al. Neutralization of SARS-CoV-2 Omicron variant by sera from BNT162b2 or Coronavac vaccine recipients. medRxiv [Internet]. 2021 Dec 14 [cited 2021 Dec 15];2021.12.13.21267668. Available from: https://www.medrxiv.org/content/10.1101/2021.12.13.21267668v1

9. Ikemura N, Hoshino A, Higuchi Y, Taminishi S, Inaba T, Matoba S. SARS-CoV-2 Omicron variant escapes neutralization by vaccinated and convalescent sera and therapeutic monoclonal antibodies. medRxiv [Internet]. 2021 Dec 14 [cited 2021 Dec 15];2021.12.13.21267761. Available from: https://www.medrxiv.org/content/10.1101/2021.12.13.21267761v1

10. Lopez Bernal J, Andrews N, Gower C, Gallagher E, Simmons R, Thelwall S, et al. Effectiveness of Covid-19 Vaccines against the B.1.617.2 (Delta) Variant. New England Journal of Medicine

[Internet]. 2021 Aug 12 [cited 2021 Dec 15];385(7):585–94. Available from: https://www.nejm.org/doi/full/10.1056/nejmoa2108891

11. Andrews N, Stowe J, Kirsebom F, Toffa S, Rickeard T, Gallagher E, et al. Effectiveness of COVID-19 vaccines against the Omicron (B.1.1.529) variant of concern. medRxiv [Internet]. 2021 Dec 14 [cited 2021 Dec 15];2021.12.14.21267615. Available from: https://www.medrxiv.org/content/10.1101/2021.12.14.21267615v1

12. Armstrong BG, Gasparrini A, Tobias A. Conditional Poisson models: A flexible alternative to conditional logistic case cross-over analysis. BMC Medical Research Methodology [Internet]. 2014 Nov 24 [cited 2021 Dec 16];14(1):1–6. Available from: https://bmcmedresmethodol.biomedcentral.com/articles/10.1186/1471-2288-14-122

13. Grabowski F, Kochańczyk M, Lipniacki T. Omicron strain spreads with the doubling time of 3.2—3.6 days in South Africa province of Gauteng that achieved herd immunity to Delta variant. medRxiv [Internet]. 2021 Dec 9 [cited 2021 Dec 15];2021.12.08.21267494. Available from: https://www.medrxiv.org/content/10.1101/2021.12.08.21267494v1

14. Khoury DS, Steain M, Triccas J, Sigal A, Davenport MP, Cromer D. Analysis: A meta-analysis of Early Results to predict Vaccine efficacy against Omicron. medRxiv [Internet]. 2021 Dec 14 [cited 2021 Dec 15];2021.12.13.21267748. Available from: https://www.medrxiv.org/content/10.1101/2021.12.13.21267748v1

15. Pulliam JRC, Schalkwyk C van, Govender N, Gottberg A von, Cohen C, Groome MJ, et al. Increased risk of SARS-CoV-2 reinfection associated with emergence of the Omicron variant in South Africa. medRxiv [Internet]. 2021 Dec 2 [cited 2021 Dec 15];2021.11.11.21266068. Available from: https://www.medrxiv.org/content/10.1101/2021.11.11.21266068v2

16. Hall VJ, Foulkes S, Charlett A, Atti A, Monk EJM, Simmons R, et al. SARS-CoV-2 infection rates of antibody-positive compared with antibody-negative health-care workers in England: a large, multicentre, prospective cohort study (SIREN). The Lancet [Internet]. 2021 Apr 17 [cited 2021 Dec 15];397(10283):1459–69. Available from: http://www.thelancet.com/article/S0140673621006759/fulltext