

Supplementary Table 1: Transmission model parameters

Transmission model parameters and variables	Value
State Variables	
Number of susceptible people at time t, S(t)	Dynamic
Number of latently infected people at time t, E(t)	Dynamic
Number of infectious people at time t, I(t)	Dynamic
Number of recovered and immune people at time t, R(t)	Dynamic
Number of people who have lost natural immunity at time t, W(t)	Dynamic
Cumulative number of primary infections at time t, (F(t)	Dynamic
Cumulative number of all infections at time t, C(t)	Dynamic
Transmission model parameters	
Number of latently infected people at time t=0, 1 st January 2021, by age group, $E_a(0)$, $a = 1, 2, \dots, 6$	Inferred from data.
Background transmission, β_0	Inferred from data
Scaling from social to effective contacts at home, β_{home} , school, β_{school} , work, β_{work} and other places, β_{other}	Inferred from data
Maximum increase in transmission due to the introduction of the alpha and beta variants, $L_{\alpha\beta}$, or the delta variant, L_{δ}	Inferred from data
Growth rate of the alpha and beta variants, $\kappa_{\alpha\beta}$, or the delta variant, κ_{δ}	Inferred from data
Midpoint of the sigmoid growth curve for alpha and beta variants, $t_{0\alpha\beta}$, or the delta variant, $t_{0\delta}$	Inferred from data
A factor that translates the initial (1 st Jan -10 th Mar 2021) seroprevalence by age group to initial attack rates, τ	Inferred from data
Infectious period, $1/\gamma$	2.4 days. Chosen to recreate a serial interval of 5.5days [1]
Latent period, $1/\sigma$	3.1 days. The mean incubation period [2] was reduced by two days of pre-symptomatic transmission [3] to give a latency period.
Mean period of complete protection after a natural infection, $1/\omega$	180 days, point estimate based on reinfection studies [4–7]
Relative susceptibility compared to naïve individuals after the loss of complete protection after the first infection, σ_{ω}	$\sigma_{\omega}=0.16$. Point estimate based on reinfection studies [4–7]
c_t – contact rate	1, Equivalent to assuming contacts are back to baseline and stable
v_i - Vaccine effectiveness against transmission (delta variant)	(0%to 35.0%)-dose 1,(0% to 69.0%)-dose 2 [8]
v_a - Vaccine effectiveness against acquisition (delta variant)	(55% to 65%)-dose 1,(65% to 80%)-dose 2[9]

v_d - Vaccine effectiveness against severe disease (delta variant)	(80% to 90%) dose 1, (95% to 99%) -dose 2 [9]
v_μ - Vaccine effectiveness against death (delta variant)	(90%-95%) -dose 1, (95% to 99%) -dose 2 [9]
$1/r_{vp_i}$ - rate of vaccine progression to full efficacy	14 days after each dose ($i = 1,2$) [10]
Observation model parameters and data	
Number of people, by age group, who would test PCR positive on day n , $(P^+)_n$.	Dynamic
Number of people, by age group, who were observed to test PCR positive on day n , $(P_{obs}^+)_n$.	Data
Number of people, by age group, who would test as sero-converted on day n , $(S^+)_n$.	Dynamic
Number of people, by age group, who actually test as sero-converted on day n , $(S_{obs}^+)_n$.	Data
Probability that an infected individual would test PCR positive on day t after infection, $Q_{PCR}(t)$	$Q_{PCR}(t) = f_{onset} Q_\Gamma(\tau)$ where $Q_\Gamma(\tau)$ was the tail function of a gamma distribution fitted to data given in [11] and is the probability function of onset of symptoms post-infection [2].
Probability that an infected individual would be detectably seropositive on day t after infection, $Q_{sero}(t)$	$Q_{sero}(t)$ is linearly increasing over 26 days to saturate at 92.7% sensitivity, based on report delay in seroconversion [11] and maximum sensitivity of serological assay [12].
Relative bias in favour of selecting a PCR positive individual for testing, χ	Inferred from data
Clinical outcome parameters	
The age-dependent probability of death given severe infection, μ_a^D	Inferred from data
The age-dependent probability of critical disease given severe infection, μ_a^C	Inferred from data
The age-dependent probability of severe disease given severe infection, μ_a^S	Inferred from data
Variant specific risk of death, ψ_a^D	Inferred from data
Variant specific risk of critical disease, ψ_a^C	Inferred from data
Variant specific risk of severe disease, ψ_a^S	Inferred from data

References

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