Supplemental information

Population immunity predicts evolutionary

trajectories of SARS-CoV-2

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Tables

Table S1: Antigenic data. Related to Figure 1.

We list neutralisation titers, T_i^k, of strains from variant i assayed against human antisera induced by primary immunisation (infection or vaccination) with strains of variant k (columns). Numbers are computed from average values of titer drops ($\Delta T_i^k = T_*^k - T_i^k$) of primary data from refs. 3, 7, 8, 29, 30, 32, 52, 53, 71–85, 85–88, 90; see Table S4. Where no primary data is available, titer drops are inferred by symmetry or (as lower bounds) by genetic similarity (numbers in italics, Methods). Absolute titers T_i^k are shifted by the reference titers $T_*^k = 6.5$, ($k =$ Alpha, Delta, BA.1, BA.2, BA.4/5), $T_*^{\text{vac}} = 7.8$, $T_*^{\text{bst}} = T_*^{\text{biv}} = 9.8$ obtained from refs. 8, 9, 52, 93; see Methods and Figure 1D.

	Alpha	Delta	BA.1	BA.2	BA.4/5	vac	bst	biv
Alpha	6.6	4.7	*< 2.2*	*< 2.2*	*< 2.2*	7.0	*< 9.0*	*< 9.0*
Delta	5.0	6.6	*< 1.8*	*< 1.8*	*< 1.8*	6.1	8.3	*< 8.3*
BA.1	1.5	1.8	6.6	4.7	5.3	2.2	7.1	*7.1*
BA.2	*< 1.5*	*< 1.8*	5.3	6.6	7.3	*< 2.2*	7.4	10.5
BA.4/5	*< 1.5*	*< 1.8*	4.0	5.2	6.6	*< 2.2*	6.4	9.8
BA.4.6	*< 1.5*	*< 1.8*	*< 3.0*	*< 4.2*	5.8	*< 2.2*	6.2	9.4
BA.5.9	*< 1.5*	*< 1.8*	*< 3.0*	*< 4.2*	5.3	*< 2.2*	6.6	*9.4*
BQ.1.1	*< 1.5*	*< 1.8*	1.6	2.9	4.3	*< 2.2*	4.3	7.3
XBB	*< 1.5*	*< 1.8*	1.3	1.6	3.0	*< 2.2*	4.4	6.6
BF.7	*< 1.5*	*< 1.8*	2.9	3.7	5.3	*< 2.2*	5.9	9.5
BM.1.1	*< 1.5*	*< 1.8*	1.9	2.3	3.1	*< 2.2*	4.9	*< 7.8*
BN.1	*< 1.5*	*< 1.8*	3.2	3.0	3.4	*< 2.2*	5.2	*< 7.8*
CH.1	*< 1.5*	*< 1.8*	1.5	1.7	2.7	*< 2.2*	3.6	5.7

Table S2: Ranking of fitness models. Related to Figure 3.

We compare the full fitness model used in the main text (VAC+INF: vaccination + infection + intrinsic selection) with partial models (INF: infection + intrinsic selection, VAC: vaccination + intrinsic selection), and a null model (0: intrinsic selection only). Columns from left to right: vaccination parameter, γ_{vac}, ML values with 95% confidence intervals (γ_1 for Alpha–Delta, γ_2 for all later shifts); infection weight parameter, b, ML values with 95% confidence intervals (b_1 for shifts up to BA.2, b_2 for BA.2–BA.4/5, b_3 for BA.4/5–BQ.1); log likelihood score difference to the null model, ΔL; BIC score difference to the null model, ΔH. The likelihood scores are reported separately for the early shifts (1 to BA.1) and for all shifts (1 to BQ.1).

model	antigenic parameters					scores (early shifts)		scores (all shifts)	
	γ_1	γ_2	b_1	b_2	b_3	ΔL	ΔH	ΔL	ΔH
VAC+INF	1.22 ± 0.03	0.28 ± 0.01	2.4 ± 0.5	5.6 ± 1.0	6.4 ± 1.0	950	-1883	1830	-3638
INF	9.7	-	0.11	0.26	0.3	392	-773	1255	-2492
VAC	1.22	0.42	-	-	-	876	-1741	-3826	7662
0	-	-	-	-	-	0	0	0	0

Table S3: Intrinsic and antigenic selection components. Related to Figure 3.

Selection coefficients between the invading and the ancestral variant, $s = f_{\text{inv}} - f_{\text{anc}}$, and their decomposition into antigenic and intrinsic components are inferred for the full fitness model; all values are time averages for each clade shift. Rows from top to bottom: major clade shifts from 1 to BQ.1. Columns from left to right: average antigenic selection in immune classes of infection ($k =$ Alpha, ..., BA.4/5) and vaccination ($k =$ vac, bst, biv); intrinsic selection (s_0); total selection (s). Selection coefficients are given in units $[10^{-2}\text{d}^{-1}]$; the symbol "<" marks values $s < 0.01\text{d}^{-1}$. We list ML values with 95% confidence intervals (for selection components) or with rms cross-region variation of selection (for the total selection, s).

clade shift	selection coefficients									
	Alpha	Delta	BA.1	BA.2	BA.4/5	vac	bst	biv	s_0	s
1–Alpha	<	-	-	-	-	<	-	-	$8 \pm .1$	8 ± 1
Alpha–Delta	$1 \pm .1$	<	-	-	-	-	$4 \pm .2$	-	$4 \pm .2$	9 ± 2
Delta–BA.1	<	$2 \pm .6$	$-1 \pm .2$	-	-	6 ± 1	$-1 \pm .2$	-	6 ± 1	13 ± 2
BA.1–BA.2	<	<	$1 \pm .4$	<	-	<	$-1 \pm .5$	-	$8 \pm .2$	8 ± 1
BA.2–BA.4/5	<	<	$3 \pm .2$	$3 \pm .2$	<	<	$3 \pm .6$	-	<	8 ± 1
BA.4/5–BQ.1	<	<	<	$1 \pm .2$	$2 \pm .2$	<	$1 \pm .5$	<	<	$5 \pm .3$