

Containment scenarios for post-spillover transmission chains of avian influenza H5N1 from poultry to humans

In the format provided by the
authors and unedited

This supplemental provides additional details of model parameterisation and results of sensitivity analysis for relevant scenarios.

Table of Contents

1.	<i>Contact matrices and population demographics.....</i>	<i>1</i>
2.	<i>Distribution of incubation period, serial interval, and infectious period.....</i>	<i>7</i>
3.	<i>Additional Results: self-isolation begins 2 days after symptom onset.....</i>	<i>8</i>
4.	<i>Sensitivity Analyses: Part A.....</i>	<i>13</i>
5.	<i>Sensitivity Analyses: Part B.....</i>	<i>19</i>
	Part B1. Self-isolation begins 2 days after symptom onset.....	19
	Part B2. Self-isolation begins 1 day after symptom onset.....	20
6.	<i>Sensitivity Analyses: Part C.....</i>	<i>21</i>
	Part C1. Self-isolation begins 2 days after symptom onset.....	21
	Part C2. Self-isolation begins 1 day after symptom onset.....	22
7.	<i>Sensitivity Analysis: Part D.....</i>	<i>23</i>
	Part D1. Self-isolation begins 2 days after symptom onset.....	23
	Part D2. Self-isolation begins 1 day after symptom onset.....	25

1. Contact matrices and population demographics

We used contact patterns from the CONNECT study to construct age-stratified contact matrices for households, within poultry farms, and the general community. For poultry farm employees, two matrices were constructed. The first captured contacts among poultry farm employees (ages ≥ 20 years), based on reported work-related interactions. The second captured contacts with the general community, derived by summing contact matrices across all activities outside the work setting, such as transport, leisure, and other activities. For the general community (non-poultry employees), the contact matrix was derived by subtracting the average number of household contacts from the total number of daily contacts, thereby isolating non-household interaction patterns.

We assumed daily contact counts followed a negative binomial distribution, where the average number of contacts per age group was taken as the sum of age-specific average contacts reported in CONNECT study.¹ As the CONNECT study did not report variances, we estimated the standard deviation by multiplying the average total number of daily contacts by the coefficient of variation (CV=standard deviation divided by the mean) from a previous work.² Using this estimated standard deviation, we parameterised the negative binomial distribution for each age group using the mean-dispersion parameterisation: $p = \mu/\sigma^2$ and $k = \mu p/(1 - p)$, where μ is the mean and σ is the standard deviation. The same age-specific value of p was applied across the three contact matrices (within poultry farms, poultry farmers and general community, and with non-poultry farmers), adjusting the

dispersion parameter k accordingly. This assumption leveraged the property that convolution of independent negative binomial random variables with the same p results in a negative binomial distribution: $\sum_j Nb(k_j, p) = Nb(\sum_j k_j, p)$.

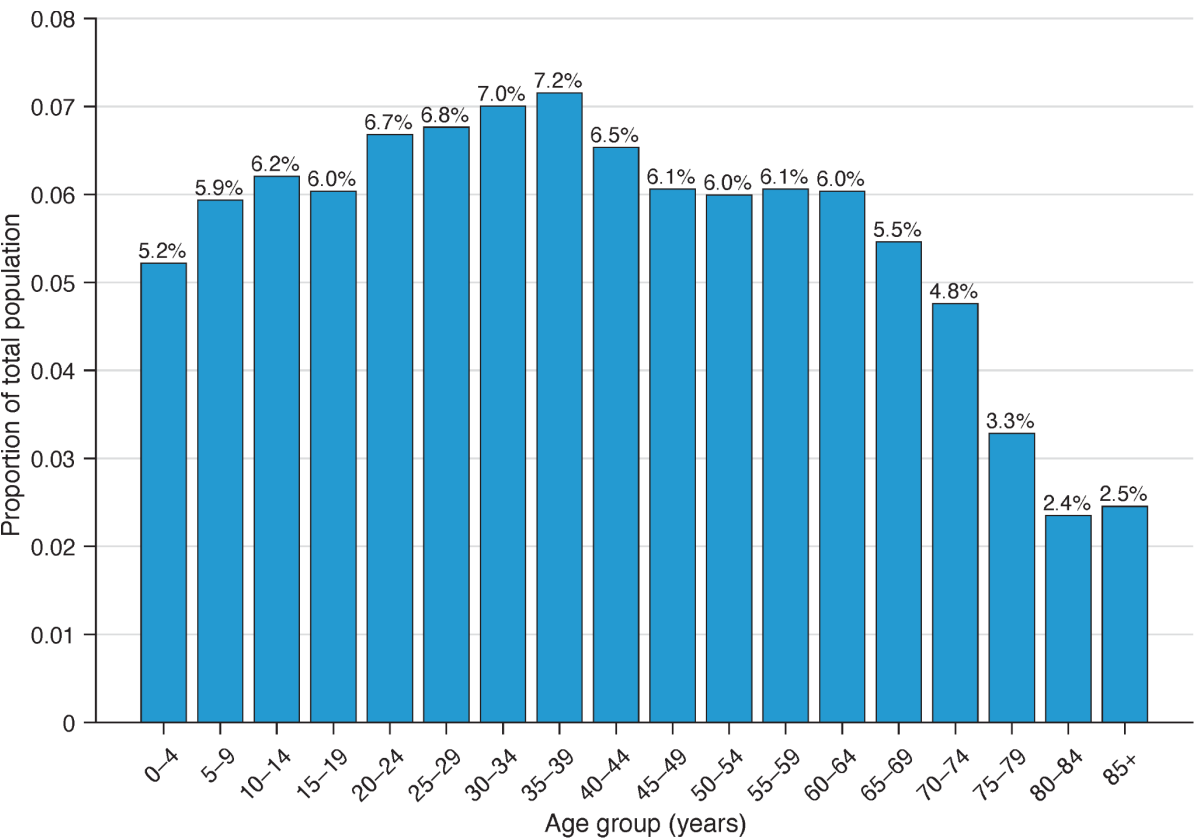


Figure A1. Age distribution of Abbotsford, BC, Canada, based on the 2021 Census³ used for model parameterisation.

Table A1. Distribution of the household sizes used for model parameterisation.³

Total number of households	Household size	No. Household
53235	1 person	13195
	2 persons	16375
	3 persons	7280
	4 persons	7680
	5 or more persons	8820
Average per household	2.8	

Table A2. Number of operations with a range of employees in the poultry and egg industry in Abbotsford Census subdivision, BC, Canada.⁴

Number of poultry farms	Proportion	Number of employees
85	64.89%	1-4
28	21.37%	5-9
12	9.16%	10-19
3	2.29%	20-49
3	2.29%	50-99

Table A3. Age distribution of poultry farmers based on US data for animal breeders from 2015 to 2024.⁵

Age	Proportion
20 to 24 years	3.75%
25 to 34 years	23.75%
35 to 44 years	32.50%
45 to 54 years	18.75%
55 to 64 years	12.50%
65 years and over	8.75%

Table A4. Distribution and proportion of daily number of contacts between individuals from different age groups for the general (non-poultry farmers) population, derived from CONNECT study in Canada.

Age of index	Negative Binomial		Age of contact																
	k	p	0-4	5-9'	10-14'	15-19	20-24	25-29	30-34	35-39	40-44	45-49	50-54	55-59	60-64	65-69	70-74	75-79	≥80
0-4	0.9941	0.2556	0.44	0.10	0.02	0.01	0.03	0.04	0.09	0.06	0.06	0.04	0.04	0.03	0.02	0.01	0.01	0.00	0.00
5-9	1.5098	0.2368	0.08	0.47	0.07	0.01	0.01	0.06	0.04	0.06	0.05	0.04	0.07	0.01	0.01	0.01	0.01	0.00	0.00
10-14	1.7570	0.2179	0.01	0.08	0.50	0.05	0.02	0.05	0.11	0.05	0.04	0.03	0.02	0.01	0.01	0.01	0.00	0.00	0.00
15-19	1.8407	0.2277	0.01	0.01	0.13	0.22	0.08	0.07	0.14	0.10	0.07	0.05	0.04	0.04	0.01	0.01	0.01	0.01	0.01
20-24	1.5025	0.1634	0.01	0.01	0.02	0.05	0.18	0.13	0.14	0.10	0.10	0.11	0.05	0.04	0.03	0.02	0.01	0.01	0.01
25-29	1.5352	0.1587	0.01	0.03	0.03	0.03	0.10	0.15	0.14	0.13	0.10	0.07	0.07	0.07	0.03	0.02	0.01	0.01	0.01
30-34	1.8732	0.1748	0.01	0.03	0.07	0.05	0.09	0.11	0.12	0.11	0.09	0.08	0.07	0.08	0.04	0.03	0.02	0.01	0.01
35-39	1.8041	0.1742	0.02	0.03	0.05	0.03	0.06	0.11	0.13	0.14	0.12	0.09	0.08	0.08	0.03	0.02	0.01	0.01	0.01
40-44	1.5004	0.1390	0.03	0.07	0.05	0.03	0.08	0.09	0.12	0.12	0.10	0.09	0.08	0.08	0.03	0.02	0.01	0.01	0.01
45-49	1.5321	0.1390	0.05	0.03	0.06	0.04	0.09	0.08	0.10	0.11	0.10	0.09	0.09	0.09	0.04	0.03	0.02	0.01	0.01
50-54	1.3720	0.1440	0.03	0.03	0.04	0.03	0.07	0.07	0.10	0.09	0.09	0.09	0.09	0.10	0.06	0.04	0.03	0.02	0.02
55-59	1.3439	0.1719	0.02	0.02	0.02	0.03	0.05	0.09	0.10	0.10	0.09	0.09	0.11	0.11	0.07	0.05	0.03	0.02	0.02
60-64	1.1822	0.2328	0.02	0.02	0.02	0.02	0.05	0.08	0.11	0.08	0.06	0.07	0.11	0.12	0.10	0.06	0.05	0.02	0.03
65-69	1.1408	0.2555	0.01	0.00	0.00	0.01	0.05	0.07	0.10	0.07	0.07	0.07	0.09	0.11	0.08	0.11	0.09	0.04	0.04
70-74	1.1967	0.3226	0.00	0.01	0.01	0.02	0.04	0.06	0.08	0.07	0.05	0.07	0.09	0.11	0.09	0.11	0.10	0.05	0.06
75-79	1.2939	0.3366	0.00	0.01	0.03	0.03	0.03	0.06	0.09	0.04	0.05	0.08	0.08	0.08	0.07	0.10	0.08	0.09	0.09
≥80	1.2016	0.3816	0.00	0.00	0.00	0.02	0.01	0.05	0.05	0.07	0.04	0.05	0.12	0.09	0.08	0.10	0.08	0.09	0.14

Table A5. Distribution and proportion of daily number of contacts between poultry farmers and general population from different age groups, derived from CONNECT study in Canada.

Age of index	Negative Binomial		Age of contact																
	k	p	0-4	5-9'	10-14'	15-19	20-24	25-29	30-34	35-39	40-44	45-49	50-54	55-59	60-64	65-69	70-74	75-79	≥80
20-24	0.3359	0.1634	0.00	0.00	0.03	0.10	0.25	0.15	0.10	0.05	0.08	0.08	0.04	0.04	0.03	0.02	0.01	0.01	0.00
25-29	0.2244	0.1587	0.01	0.00	0.01	0.03	0.16	0.29	0.15	0.09	0.05	0.03	0.05	0.05	0.03	0.02	0.01	0.01	0.00
30-34	0.2887	0.1748	0.03	0.01	0.02	0.04	0.06	0.18	0.18	0.10	0.07	0.09	0.07	0.08	0.03	0.03	0.01	0.00	0.00
35-39	0.3248	0.1742	0.03	0.02	0.03	0.04	0.07	0.12	0.16	0.16	0.10	0.08	0.06	0.04	0.03	0.03	0.02	0.01	0.01
40-44	0.2689	0.1390	0.01	0.03	0.03	0.04	0.09	0.12	0.13	0.10	0.12	0.10	0.08	0.07	0.03	0.02	0.02	0.01	0.01
45-49	0.2315	0.1390	0.01	0.00	0.09	0.03	0.08	0.07	0.07	0.08	0.09	0.10	0.11	0.10	0.05	0.04	0.04	0.02	0.01
50-54	0.2194	0.1440	0.01	0.03	0.01	0.05	0.08	0.09	0.07	0.09	0.06	0.09	0.09	0.12	0.07	0.05	0.03	0.03	0.03
55-59	0.4067	0.1719	0.02	0.01	0.01	0.04	0.07	0.10	0.09	0.07	0.08	0.07	0.11	0.12	0.10	0.06	0.03	0.02	0.02
60-64	0.5252	0.2328	0.01	0.02	0.02	0.03	0.07	0.08	0.09	0.06	0.06	0.05	0.09	0.11	0.12	0.09	0.06	0.02	0.03
65-69	0.8122	0.2555	0.01	0.00	0.01	0.01	0.04	0.06	0.08	0.05	0.05	0.06	0.09	0.11	0.10	0.13	0.11	0.04	0.04
70-74	1.1017	0.3226	0.00	0.00	0.00	0.02	0.04	0.05	0.08	0.07	0.04	0.07	0.09	0.11	0.09	0.11	0.10	0.05	0.06
75-79	1.0467	0.3366	0.00	0.01	0.00	0.01	0.04	0.06	0.10	0.05	0.05	0.08	0.08	0.08	0.06	0.09	0.09	0.10	0.10
≥80	1.1806	0.3816	0.00	0.00	0.00	0.02	0.01	0.05	0.05	0.07	0.04	0.05	0.12	0.08	0.08	0.10	0.08	0.09	0.13

Table A6. Distribution and proportion of daily number of contacts between poultry farmers from different age groups in the workplace, derived from CONNECT study in Canada.

Age of index	Negative Binomial		Age of contact												
	k	p	20-24	25-29	30-34	35-39	40-44	45-49	50-54	55-59	60-64	65-69	70-74	75-79	≥80
20-24	1.1877	0.1634	0.11	0.13	0.17	0.13	0.12	0.14	0.06	0.05	0.03	0.02	0.01	0.01	0.01
25-29	1.3945	0.1587	0.08	0.14	0.16	0.15	0.12	0.09	0.09	0.08	0.04	0.03	0.01	0.01	0.01
30-34	1.5588	0.1748	0.11	0.11	0.12	0.13	0.12	0.09	0.09	0.09	0.05	0.04	0.02	0.02	0.01
35-39	1.4310	0.1742	0.07	0.12	0.15	0.16	0.13	0.09	0.09	0.09	0.03	0.03	0.02	0.01	0.01
40-44	1.1701	0.1390	0.05	0.11	0.14	0.17	0.11	0.12	0.10	0.10	0.04	0.02	0.01	0.01	0.01
45-49	1.1652	0.1390	0.07	0.09	0.12	0.14	0.14	0.11	0.11	0.11	0.04	0.03	0.02	0.01	0.01
50-54	1.0549	0.1440	0.03	0.08	0.11	0.11	0.12	0.11	0.11	0.11	0.07	0.06	0.04	0.02	0.03
55-59	0.9672	0.1719	0.04	0.08	0.11	0.11	0.10	0.12	0.12	0.12	0.07	0.05	0.04	0.02	0.03
60-64	0.6924	0.2328	0.04	0.08	0.12	0.09	0.08	0.09	0.13	0.14	0.08	0.05	0.04	0.02	0.03
65-69	0.3955	0.2555	0.03	0.11	0.16	0.13	0.10	0.08	0.09	0.10	0.05	0.05	0.03	0.02	0.03
70-74	0.1135	0.3226	0.05	0.06	0.07	0.09	0.09	0.08	0.08	0.09	0.11	0.09	0.10	0.04	0.05
75-79	0.2443	0.3366	0.03	0.03	0.04	0.04	0.09	0.09	0.10	0.11	0.14	0.13	0.08	0.06	0.06
≥80	0.0244	0.3816	0.00	0.00	0.00	0.00	0.17	0.00	0.00	0.37	0.18	0.00	0.18	0.00	0.10

2. Distribution of incubation period, serial interval, and infectious period

Using reported estimates for the incubation period and serial interval, we obtained the distributions of these parameters that were used to determine the infectious period distribution. For each infected individual, the incubation and infectious periods were sampled from their corresponding distributions (Figure A2).

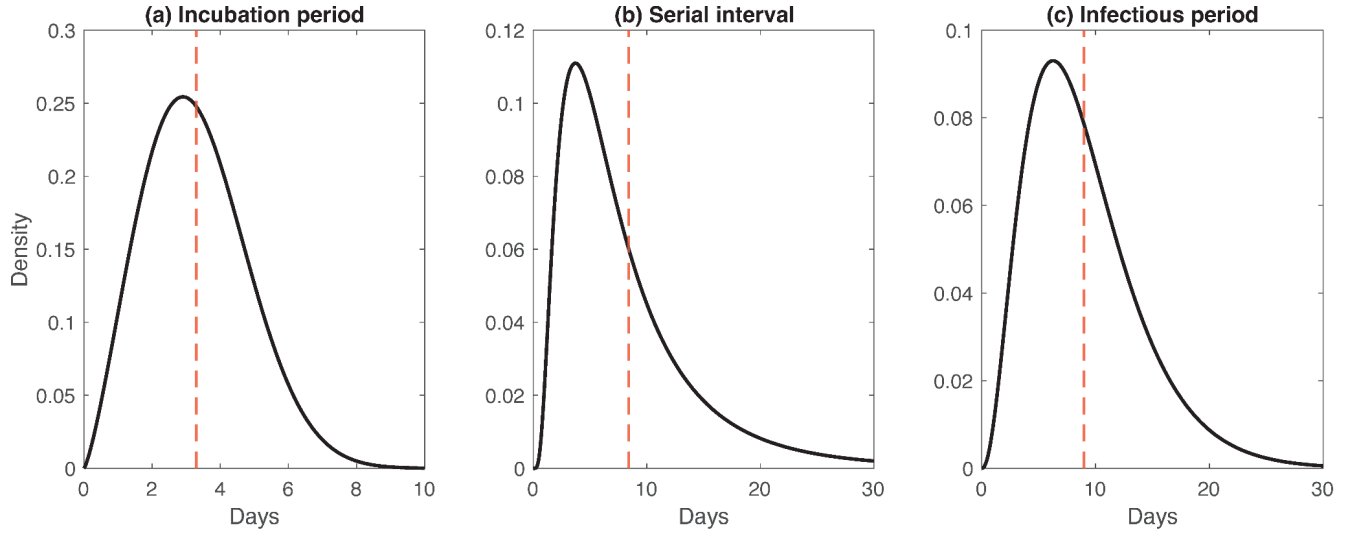


Figure A2. Distributions of serial interval (a), incubation period (b), and infectious period (c). The mean and standard deviation for these distributions are provided in Table 1 of the main text. The red dashed line indicates the mean of distribution.

To derive the distribution of infectious period (T_{IP}), we performed deconvolution in the frequency domain under the assumption that the serial interval (T_{SI}) is the sum of the incubation period (T_{Inc}) and half of the infectious period, that is $T_{SI} = T_{Inc} + T_{\frac{1}{2}IP}$, where $T_{\frac{1}{2}IP}$ is the half infectious period random variable. Given the distribution of serial interval and incubation period, the corresponding probability density functions (f) satisfy the convolution relation

$$f_{SI} = (f_{Inc} * f_{\frac{1}{2}IP})(t) = \int_{-\infty}^{+\infty} f_{Inc}(\tau) f_{\frac{1}{2}IP}(t - \tau) d\tau.$$

Applying Fourier transforms (denoted by $F\{\cdot\}$) to both distributions, gives

$$F\{f_{SI}\}(\omega) = F\{f_{Inc}\}(\omega) \cdot F\left\{f_{\frac{1}{2}IP}\right\}(\omega).$$

We then divided the transformed serial interval by the transformed incubation period to obtain

$$F\left\{f_{\frac{1}{2}IP}\right\}(\omega) = \frac{F\{f_{SI}\}(\omega)}{F\{f_{Inc}\}(\omega)}.$$

From this, we obtained the distribution of half the infectious period by inverse transform $F^{-1}\left\{f_{\frac{1}{2}IP}\right\}$.

The resulting distribution was rescaled to obtain the full infectious period (i.e., $T_{IP} = 2T_{\frac{1}{2}IP}$). Because division in the frequency domain can be numerically unstable when $F\{f_{Inc}\}(\omega)$ is close to zero, we used regularisation and then fitted a Gamma distribution to the deconvolved infectious period distribution using penalised least squares.

3. Additional Results: self-isolation begins 2 days after symptom onset

Distribution of transmission chains

This section presents the distribution of transmission chains with a maximum number of generations across all simulations.

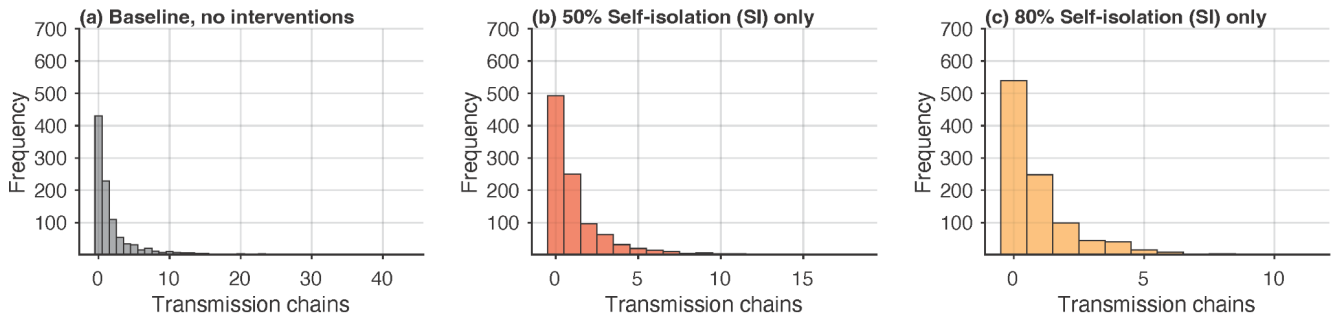


Figure A3. Distribution of transmission chains. Panel (a) shows the frequency of simulations in which transmission chains persisted for a maximum number of generations without interventions among $n = 1,000$ Monte Carlo realisations. Panels (b) and (c) illustrate the distribution of transmission chains with self-isolation at 50% and 80% compliance, respectively. Generation 0 corresponds to the index case being infected by the reservoir.

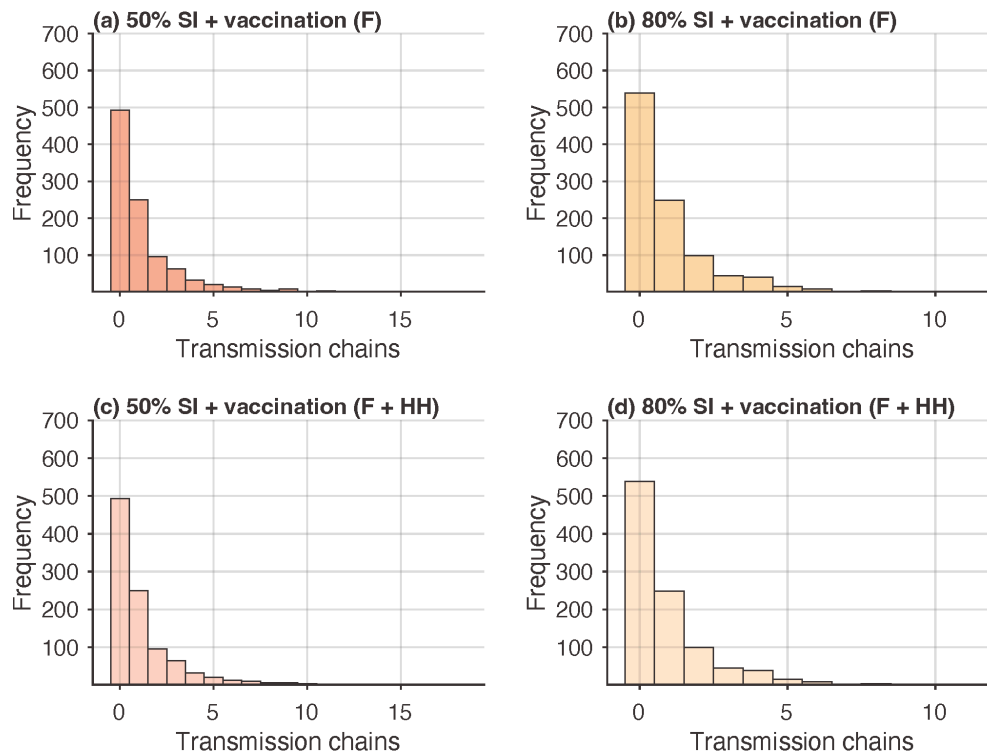


Figure A4. Distribution of transmission chains with reactive vaccination. Panels (a) and (b) show the distribution of transmission chains across generations among $n = 1,000$ Monte Carlo realisations under reactive vaccination of farmers only, with 50% and 80% self-isolation compliance, respectively. Panels (c) and (d) show corresponding results when both farmers and their households were vaccinated. Generation 0 corresponds to the index case being infected by the reservoir.

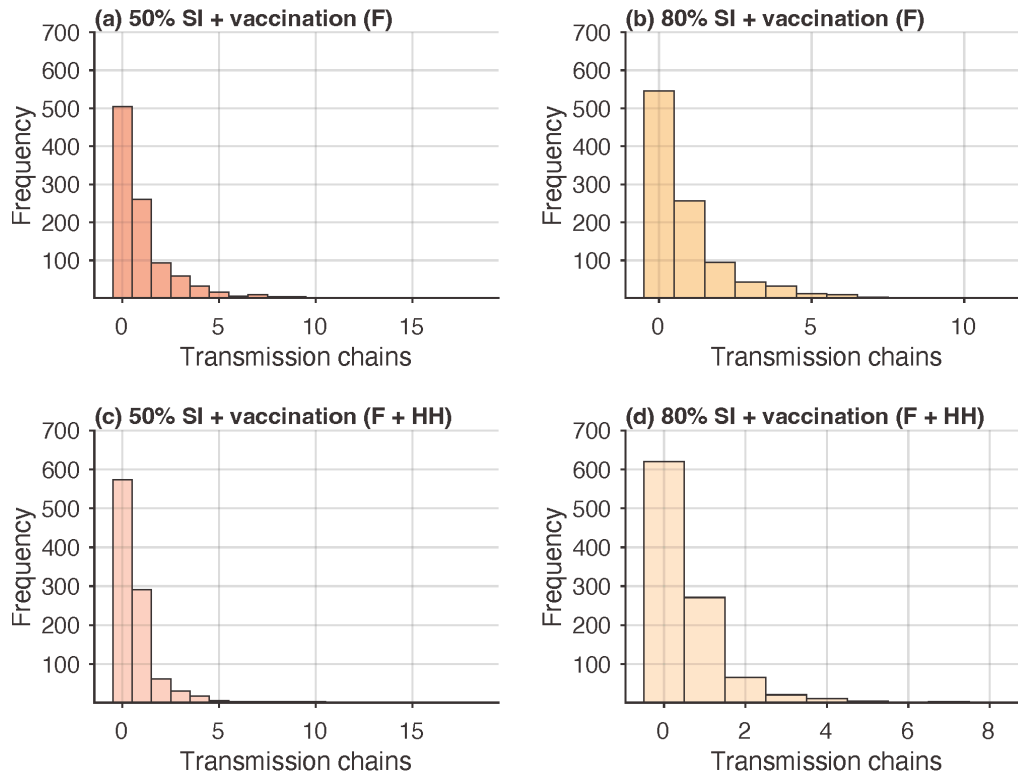


Figure A5. Distribution of transmission chains with preemptive vaccination. Panels (a) and (b) show the distribution of transmission chains across generations among $n = 1,000$ Monte Carlo realisations under preemptive vaccination of farmers only, with 50% and 80% self-isolation compliance, respectively. Panels (c) and (d) show corresponding results when both farmers and their households were vaccinated. Generation 0 corresponds to the index case being infected by the reservoir.

Distribution of outbreak sizes

This section presents the distribution of outbreak sizes for simulations in which at least one secondary case was generated by the index case, and thus transmission chains persisted for at least one generation.

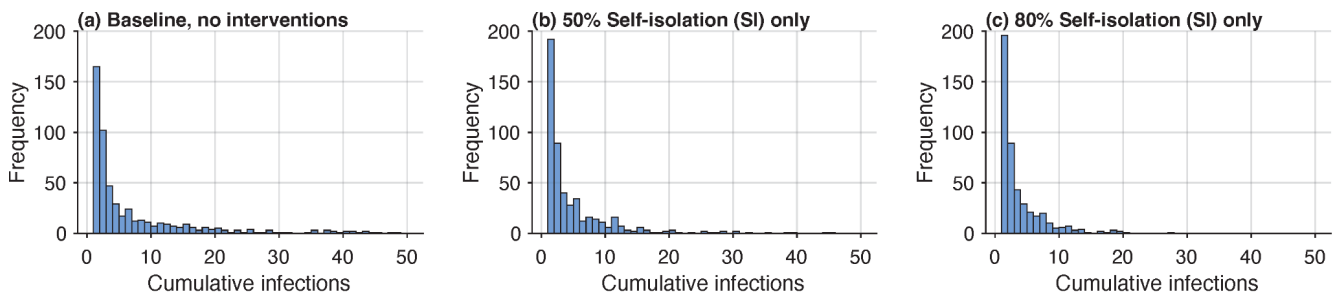


Figure A6. Distribution of cumulative infections in simulations with at least one secondary case. Panels (a), (b), and (c) show this distribution among $n = 1,000$ Monte Carlo realisations over a one-year time horizon under three scenarios: (a) no interventions; (b) self-isolation with 50% compliance, and (c) self-isolation with 80% compliance.

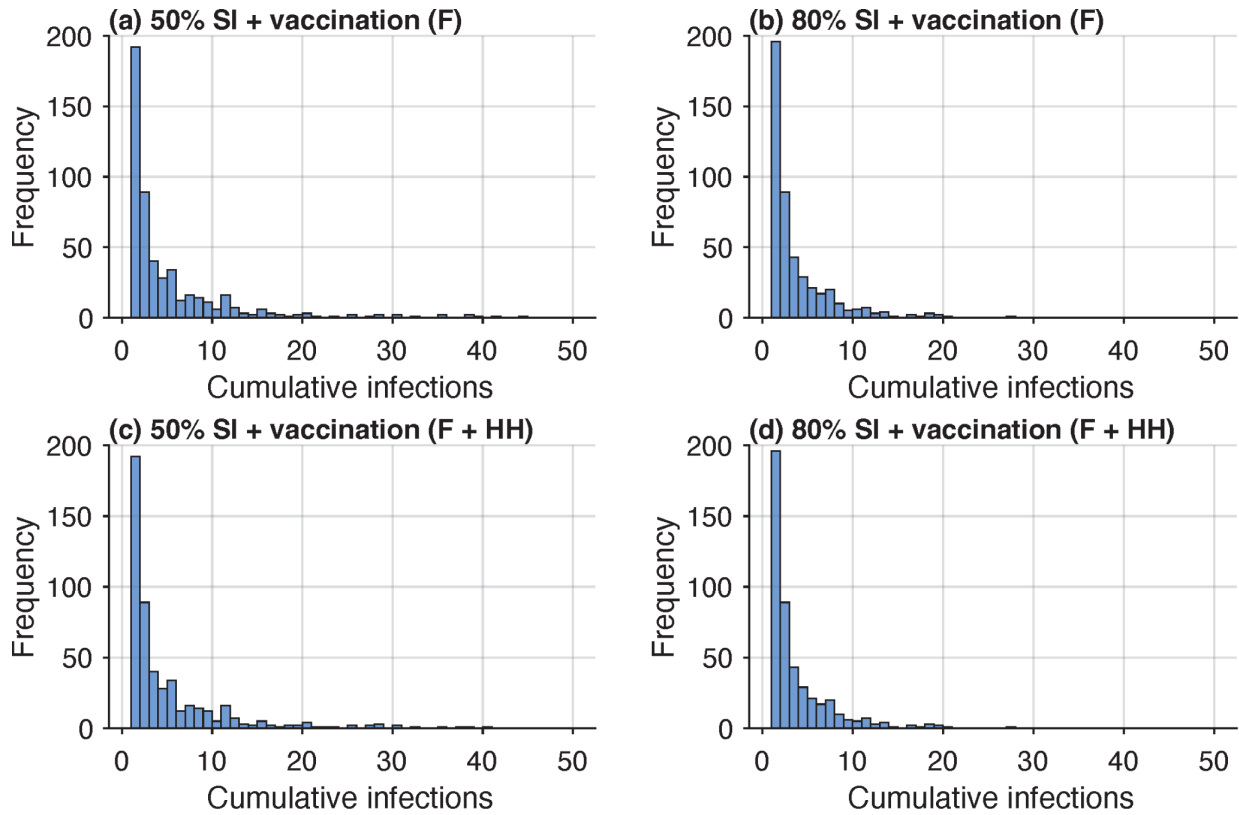


Figure A7. Distribution of cumulative infections in simulations with at least one secondary case under reactive vaccination scenarios. Panels (a) and (b) show the distribution among $n = 1,000$ Monte Carlo realisations over a one-year horizon with 50% and 80% self-isolation compliance, respectively, when only farmers were vaccinated. Panels (c) and (d) show the corresponding distributions when both farmers and their households were vaccinated.

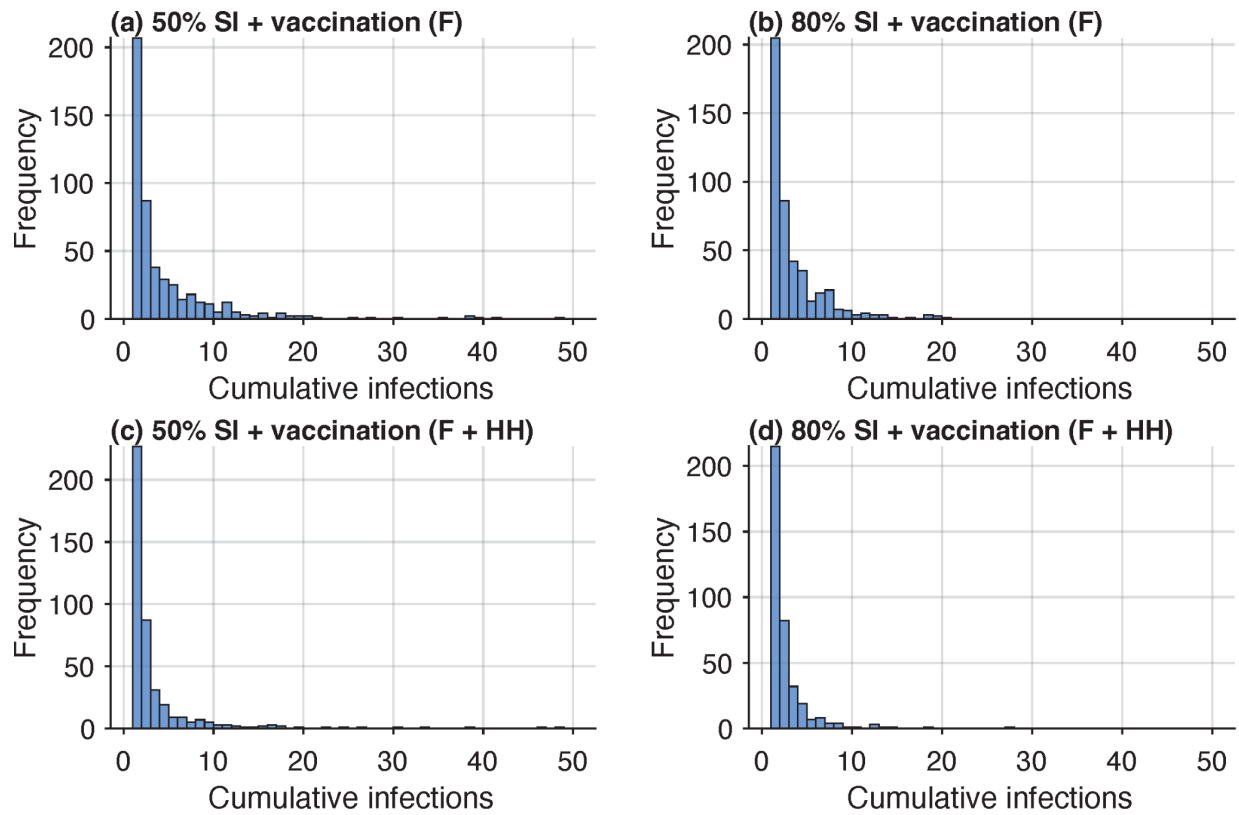


Figure A8. Distribution of cumulative infections in simulations with at least one secondary case under preemptive vaccination scenarios. Panels (a) and (b) show the distribution among $n = 1,000$ Monte Carlo realisations over a one-year horizon with 50% and 80% self-isolation compliance, respectively, when only farmers were vaccinated. Panels (c) and (d) show the corresponding distributions when both farmers and their households were vaccinated.

4. Sensitivity Analyses: Part A

This section presents the results of sensitivity analyses for scenarios in which 50% of infected individuals experienced asymptomatic infection, and self-isolation started 1 day after the onset of symptoms.

Transmission chain survival and effect of self-isolation

In the absence of interventions, 43% of simulations generated no secondary cases, 39% persisted for 1–3 generations, and only 18% produced transmission chains that persisted beyond 3 generations (**Figure A9**). The longest baseline chain exceeded 40 generations.

Introducing self-isolation of symptomatic cases one day after symptom onset reduced the persistence of transmission. With 50% compliance, the probability of survival beyond 3 generations declined to 8% (56% reduction compared to baseline), and to 4% at 80% compliance (78% reduction) (**Figure A9**). As in the two-day self-isolation scenario (main text), no simulations accumulated sufficient mutations to reach the epidemic threshold ($R_0=1$). The distributions of transmission chains are shown in Figures A11-A13.

Among chains exceeding 3 generations, the mean cumulative incidence over a one-year time horizon was 65 cases (95% CI: 35–113) without interventions (**Figure A9**). Self-isolation reduced this to 15 cases (95% CI: 12–17) at 50% compliance and 11 cases (95% CI: 8–13) at 80% compliance. Outbreak size distributions for simulations with secondary cases are shown in Figures A14-A16.

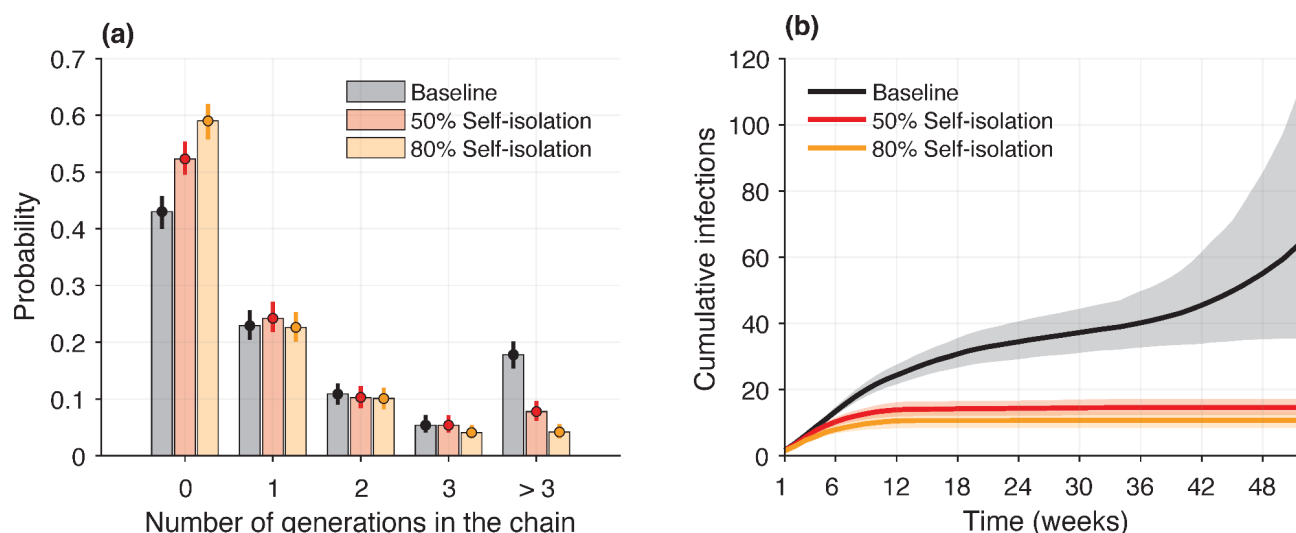


Figure A9. Probability of transmission chains across generations and cumulative number of infections. Panel (a) shows the probability that transmission chains persisted for a maximum number of generations under the baseline (no interventions) and under self-isolation with 50% and 80% compliance. Generation 0 corresponds to the index case being infected by the reservoir. Panel (b) shows cumulative number of infections for simulations in which transmission chains extended beyond three generations among $n = 1,000$ Monte Carlo realisations. Lines denote the mean cumulative infections; shaded bands indicate 95% bootstrap confidence intervals obtained by resampling simulations within each scenario.

Targeted vaccination

Reactive vaccination, whether targeting farmers alone or including their households, had little effect on interrupting transmission chains compared to self-isolation alone (**Figure A10**). In contrast, preemptive vaccination substantially reduced transmission persistence. Vaccinating farmers only resulted in 6% of transmission chains persisting beyond three generations under 50% compliance and 4% under 80% compliance. Extending vaccination to farmers' households further increased the probability of no secondary cases to 60% and reduced persistence beyond three generations to 4% under 50% self-isolation compliance. At 80% compliance, 67% of simulations showed no secondary cases, and only 2% persisted beyond three generations.

Reactive vaccination also produced minimal change in cumulative infections. However, preemptive vaccination reduced mean cumulative cases to 4.6 (95% CI: 3.3–6.4) and 3.3 (95% CI: 2.2–4.8) under farmer-only vaccination at 50% and 80% self-isolation compliance, respectively. Including households further lowered cumulative cases to 3.3 (95% CI: 2.3–4.5) and 2.5 (95% CI: 1.5–4.0) under 50% and 80% compliance (**Figure A10**).

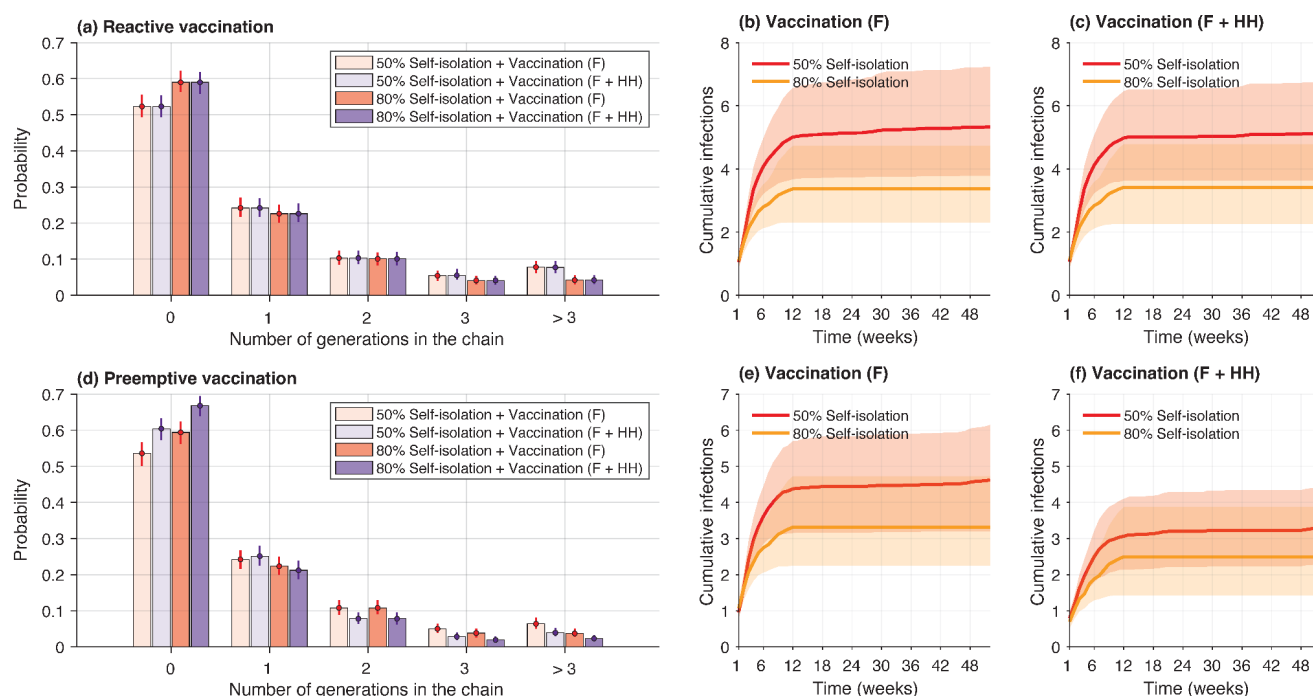


Figure A10. Probability of transmission chains across generations and cumulative number of infections under self-isolation and vaccination strategies. Panels (a) and (d) show the probability that transmission chains persisted for a maximum number of generations under reactive (a) and preemptive (d) vaccination. Generation 0 corresponds to the index case being infected by the reservoir. In Panels (a) and (d), bars (and overlaid points) show the estimated probability (i.e., proportion of simulations) from Monte Carlo simulations ($n = 1,000$ per scenario). Error bars indicate 95% bias-corrected and accelerated bootstrap confidence intervals based on 1,000 bootstrap resamples of simulations for each scenario. Panels (b), (c), (e), and (f) show the mean cumulative number of infections and corresponding 95% confidence intervals over a one-year horizon under 50% and 80% self-isolation compliance, with reactive (b,c) and preemptive (e,f) vaccination. Two vaccination strategies were compared: targeting farmers only (F) or farmers and their households

(F+HH). Lines denote the mean cumulative infections across simulations with transmission chains extended beyond three generations, and shaded bands indicate 95% bootstrap confidence intervals.

Distribution of transmission chains

All figures in this section correspond to the scenarios for self-isolation beginning 1 day after symptom onset, with 50% of infected individuals experiencing asymptomatic infection.

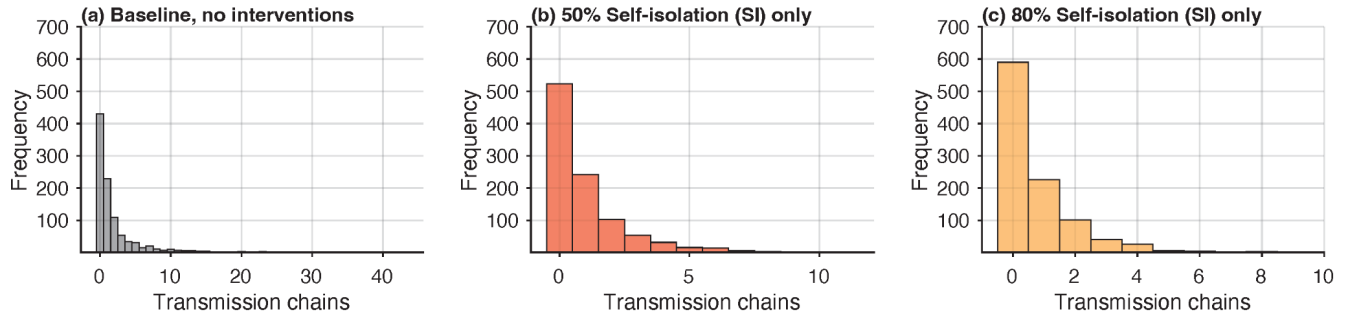


Figure A11. Distribution of transmission chains. Panel (a) shows the frequency of simulations in which transmission chains persisted for a maximum number of generations without interventions among $n = 1,000$ Monte Carlo realisations. Panels (b) and (c) illustrate the distribution of transmission chains with self-isolation at 50% and 80% compliance, respectively. Generation 0 corresponds to the index case being infected by the reservoir.

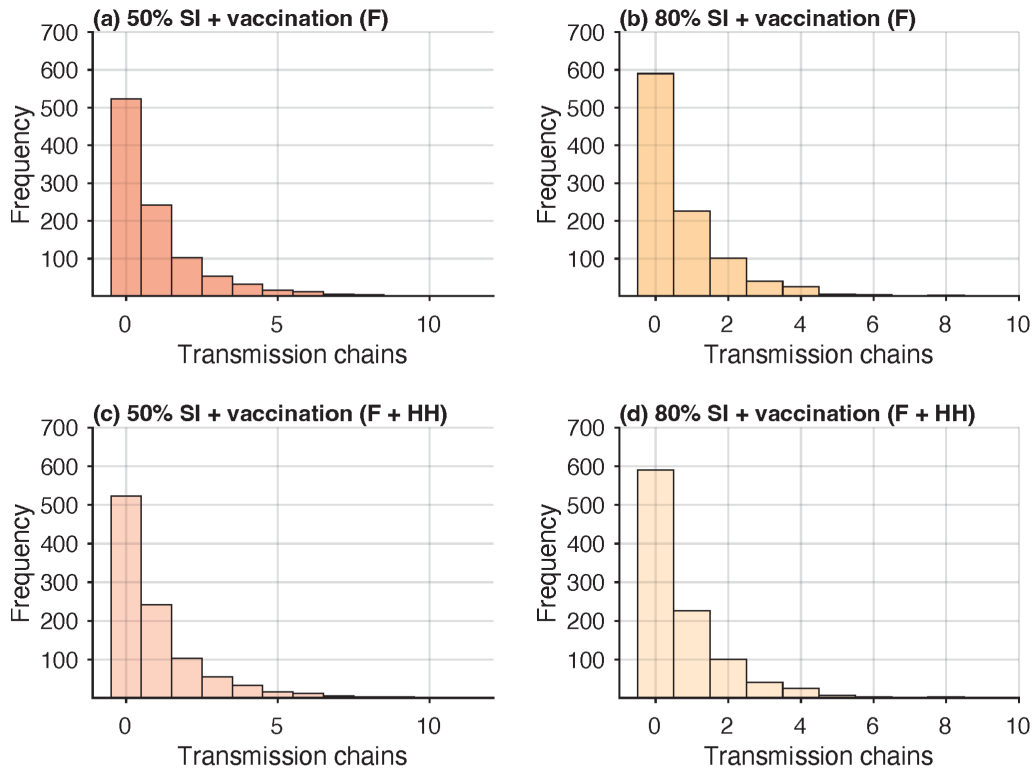


Figure A12. Distribution of transmission chains with reactive vaccination. Panels (a) and (b)

show the distribution of transmission chains across generations among $n = 1,000$ Monte Carlo realisations under reactive vaccination of farmers only, with 50% and 80% self-isolation compliance, respectively. Panels (c) and (d) show corresponding results when both farmers and their households were vaccinated. Generation 0 corresponds to the index case being infected by the reservoir.

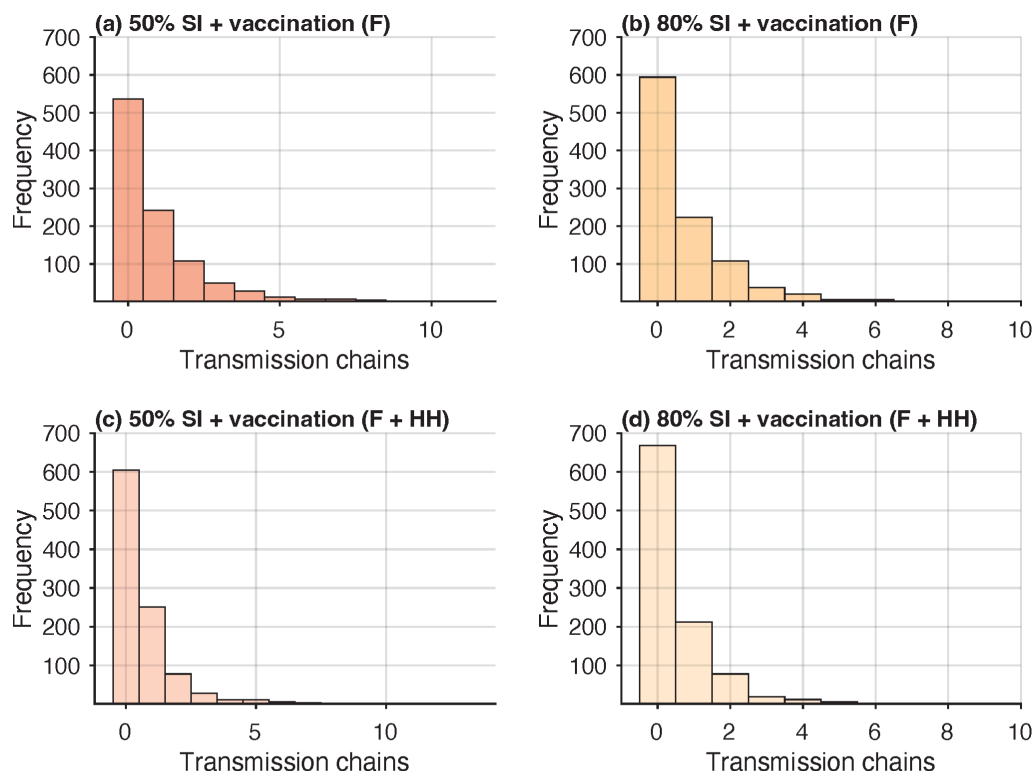


Figure A13. Distribution of transmission chains with preemptive vaccination. Panels (a) and (b) show the distribution of transmission chains across generations among $n = 1,000$ Monte Carlo realisations under preemptive vaccination of farmers only, with 50% and 80% self-isolation compliance, respectively. Panels (c) and (d) show corresponding results when both farmers and their households were vaccinated. Generation 0 corresponds to the index case being infected by the reservoir.

Distribution of outbreak sizes

All figures in this section correspond to the scenarios for self-isolation beginning 1 day after symptom onset, with 50% of infected individuals experiencing asymptomatic infection.

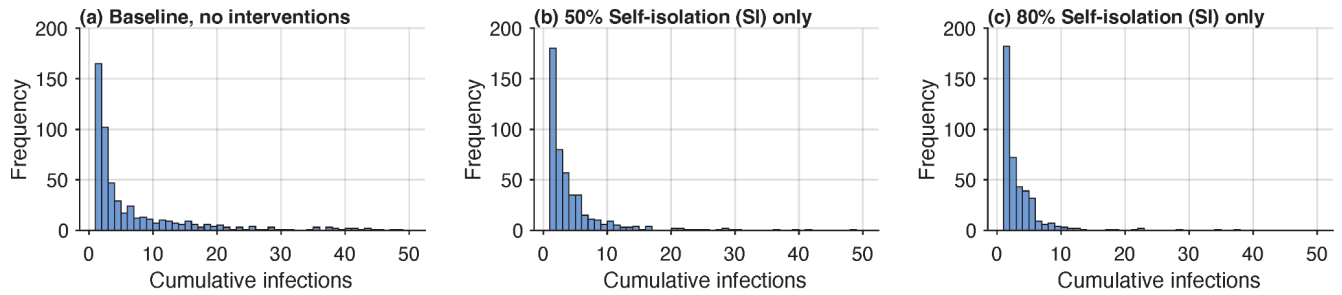


Figure A14. Distribution of cumulative infections in simulations with at least one secondary case. Panels (a), (b), and (c) show this distribution among $n = 1,000$ Monte Carlo realisations over a one-year time horizon under three scenarios: (a) no interventions; (b) self-isolation with 50% compliance, and (c) self-isolation with 80% compliance.

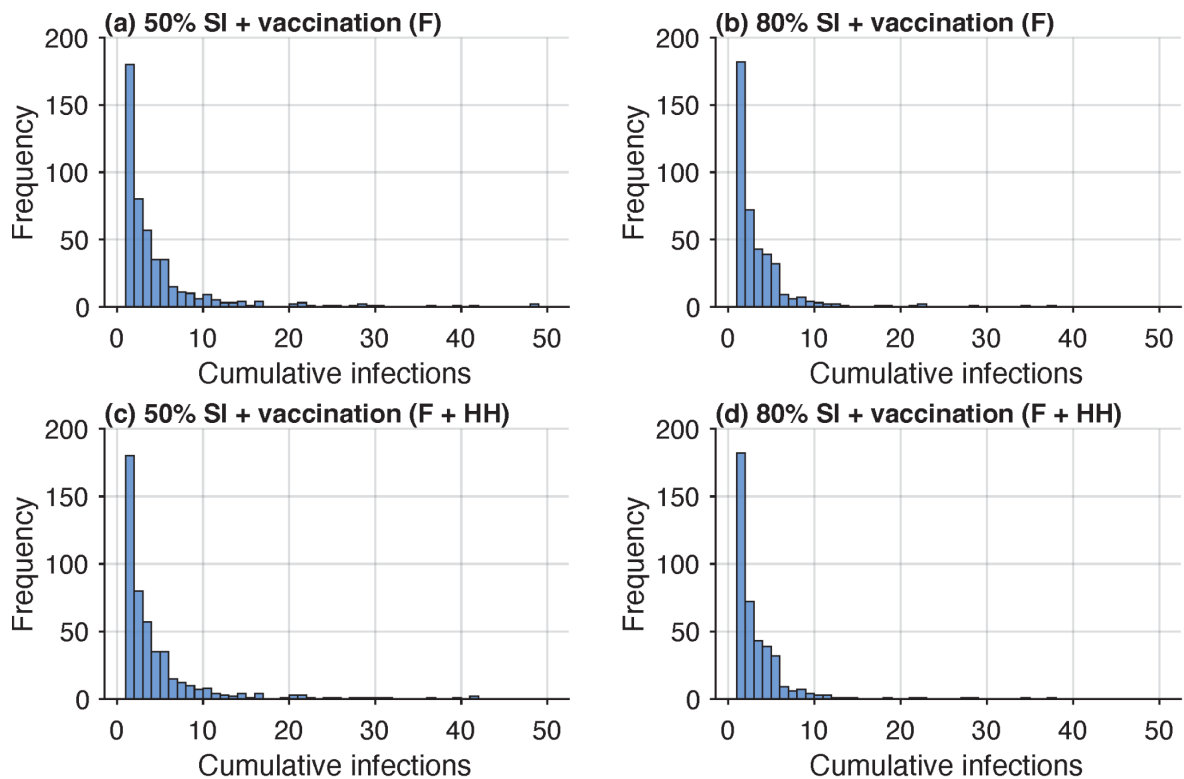


Figure A15. Distribution of cumulative infections in simulations with at least one secondary case under reactive vaccination scenarios. Panels (a) and (b) show the distribution among $n = 1,000$ Monte Carlo realisations over a one-year horizon with 50% and 80% self-isolation compliance, respectively, when only farmers were vaccinated. Panels (c) and (d) show the corresponding distributions when both farmers and their households were vaccinated.

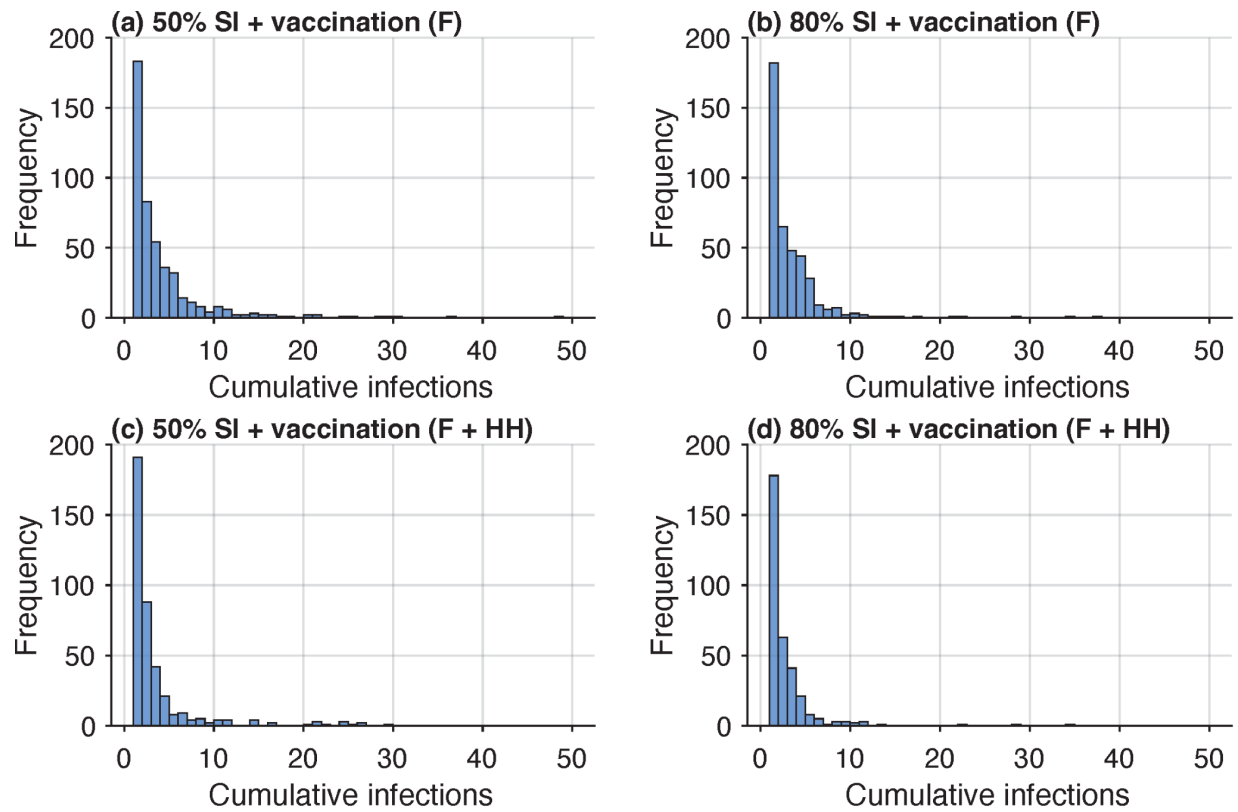


Figure A16. Distribution of cumulative infections in simulations with at least one secondary case under preemptive vaccination scenarios. Panels (a) and (b) show the distribution among $n = 1,000$ Monte Carlo realisations over a one-year horizon with 50% and 80% self-isolation compliance, respectively, when only farmers were vaccinated. Panels (c) and (d) show the corresponding distributions when both farmers and their households were vaccinated.

5. Sensitivity Analyses: Part B

This section presents the results of sensitivity analyses for vaccination with 50% protection against infection, but no protection against symptomatic disease.

Part B1. Self-isolation begins 2 days after symptom onset

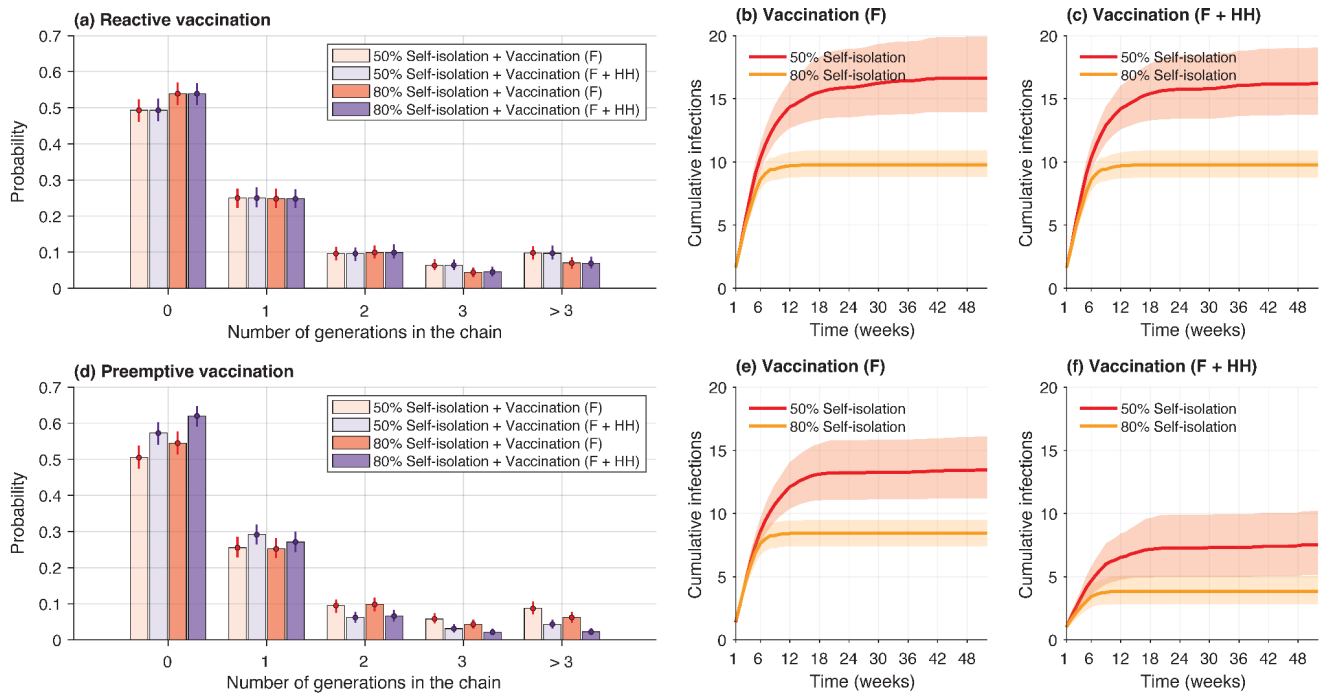


Figure A17. Probability of transmission chains across generations and cumulative number of infections under self-isolation and vaccination strategies. Panels (a) and (d) show the probability that transmission chains persisted for a maximum number of generations under reactive (a) and preemptive (d) vaccination. Generation 0 corresponds to the index case being infected by the reservoir. In Panels (a) and (d), bars (and overlaid points) show the estimated probability (i.e., proportion of simulations) from Monte Carlo simulations ($n = 1,000$ per scenario). Error bars indicate 95% bias-corrected and accelerated bootstrap confidence intervals based on 1,000 bootstrap resamples of simulations for each scenario. Panels (b), (c), (e), and (f) show the mean cumulative number of infections and corresponding 95% confidence intervals over a one-year horizon under 50% and 80% self-isolation compliance, with reactive (b,c) and preemptive (e,f) vaccination. Two vaccination strategies were compared: targeting farmers only (F) or farmers and their households (F+HH). Lines denote the mean cumulative infections across simulations with transmission chains extended beyond three generations, and shaded bands indicate 95% bootstrap confidence intervals.

Part B2. Self-isolation begins 1 day after symptom onset.

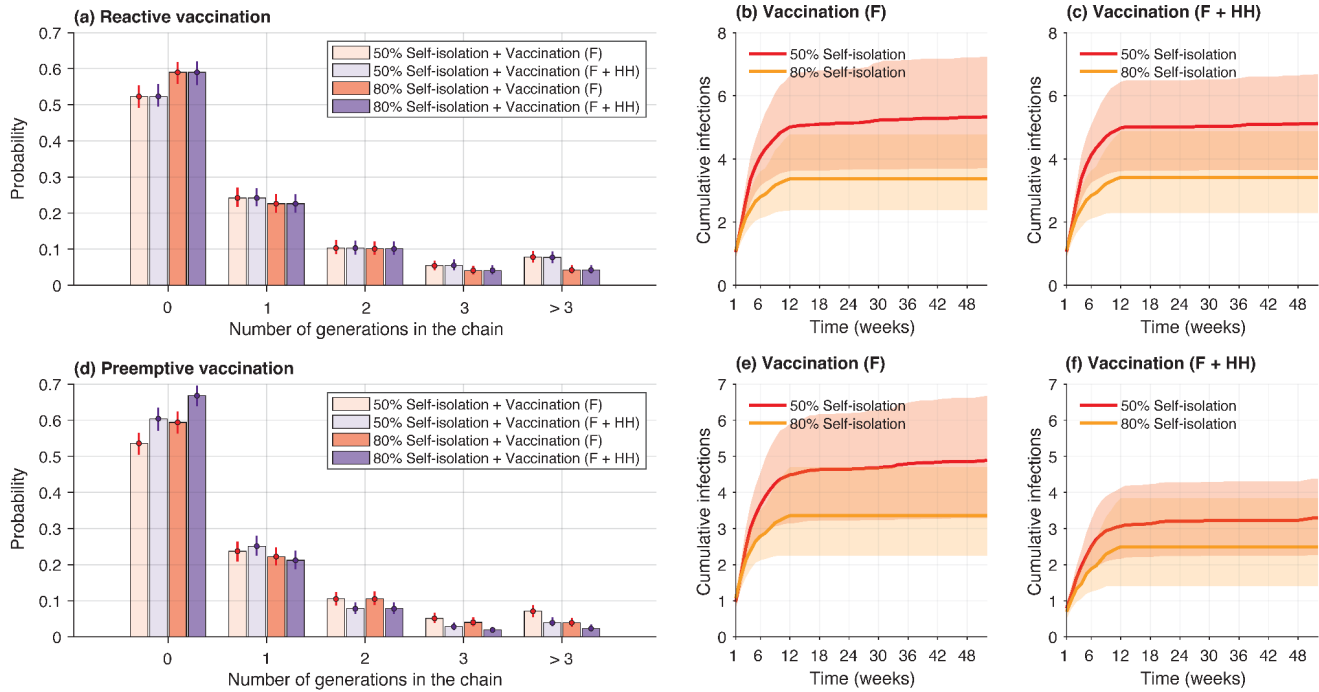


Figure A18. Probability of transmission chains across generations and cumulative number of infections under self-isolation and vaccination strategies. Panels (a) and (d) show the probability that transmission chains persisted for a maximum number of generations under reactive (a) and preemptive (d) vaccination. Generation 0 corresponds to the index case being infected by the reservoir. In Panels (a) and (d), bars (and overlaid points) show the estimated probability (i.e., proportion of simulations) from Monte Carlo simulations ($n = 1,000$ per scenario). Error bars indicate 95% bias-corrected and accelerated bootstrap confidence intervals based on 1,000 bootstrap resamples of simulations for each scenario. Panels (b), (c), (e), and (f) show the mean cumulative number of infections and corresponding 95% confidence intervals over a one-year horizon under 50% and 80% self-isolation compliance, with reactive (b,c) and preemptive (e,f) vaccination. Two vaccination strategies were compared: targeting farmers only (F) or farmers and their households (F+HH). Lines denote the mean cumulative infections across simulations with transmission chains extended beyond three generations, and shaded bands indicate 95% bootstrap confidence intervals.

6. Sensitivity Analyses: Part C

This section presents the results of sensitivity analyses for vaccination with 85% protection against symptomatic disease, but no protection against infection.

Part C1. Self-isolation begins 2 days after symptom onset

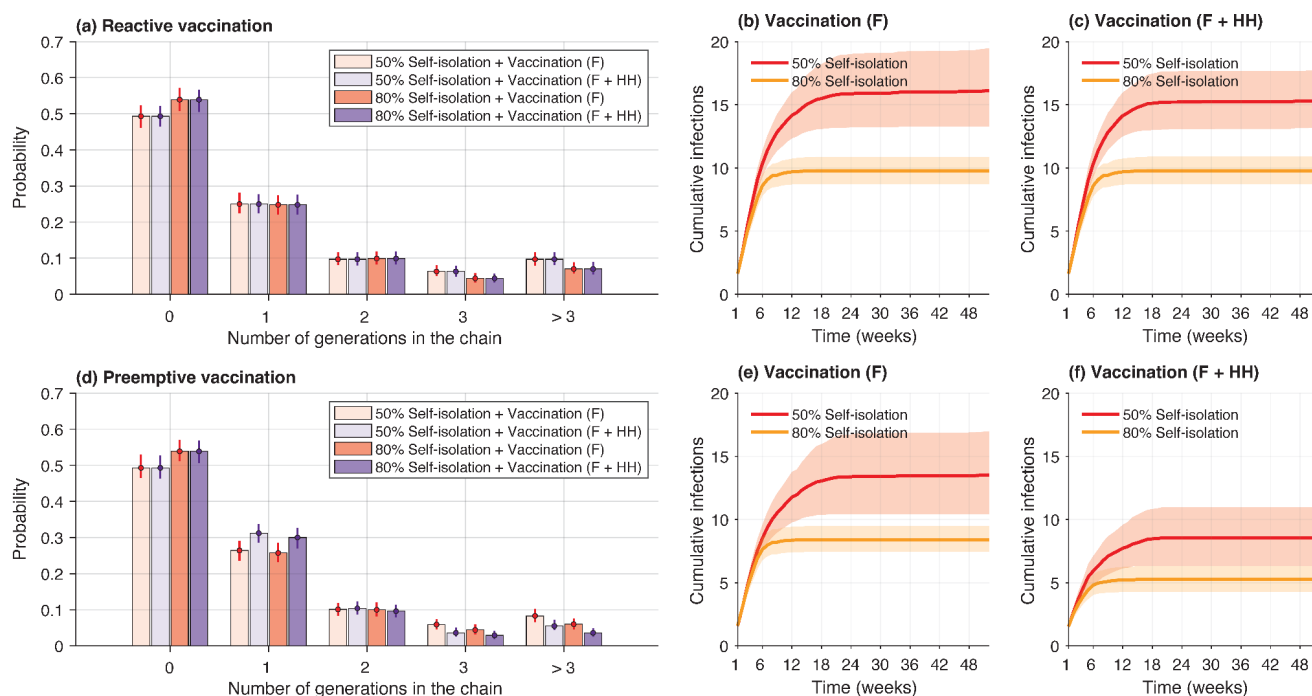


Figure A19. Probability of transmission chains across generations and cumulative number of infections under self-isolation and vaccination strategies. Panels (a) and (d) show the probability that transmission chains persisted for a maximum number of generations under reactive (a) and preemptive (d) vaccination. Generation 0 corresponds to the index case being infected by the reservoir. In Panels (a) and (d), bars (and overlaid points) show the estimated probability (i.e., proportion of simulations) from Monte Carlo simulations ($n = 1,000$ per scenario). Error bars indicate 95% bias-corrected and accelerated bootstrap confidence intervals based on 1,000 bootstrap resamples of simulations for each scenario. Panels (b), (c), (e), and (f) show the mean cumulative number of infections and corresponding 95% confidence intervals over a one-year horizon under 50% and 80% self-isolation compliance, with reactive (b,c) and preemptive (e,f) vaccination. Two vaccination strategies were compared: targeting farmers only (F) or farmers and their households (F+HH). Lines denote the mean cumulative infections across simulations with transmission chains extended beyond three generations, and shaded bands indicate 95% bootstrap confidence intervals.

Part C2. Self-isolation begins 1 day after symptom onset.

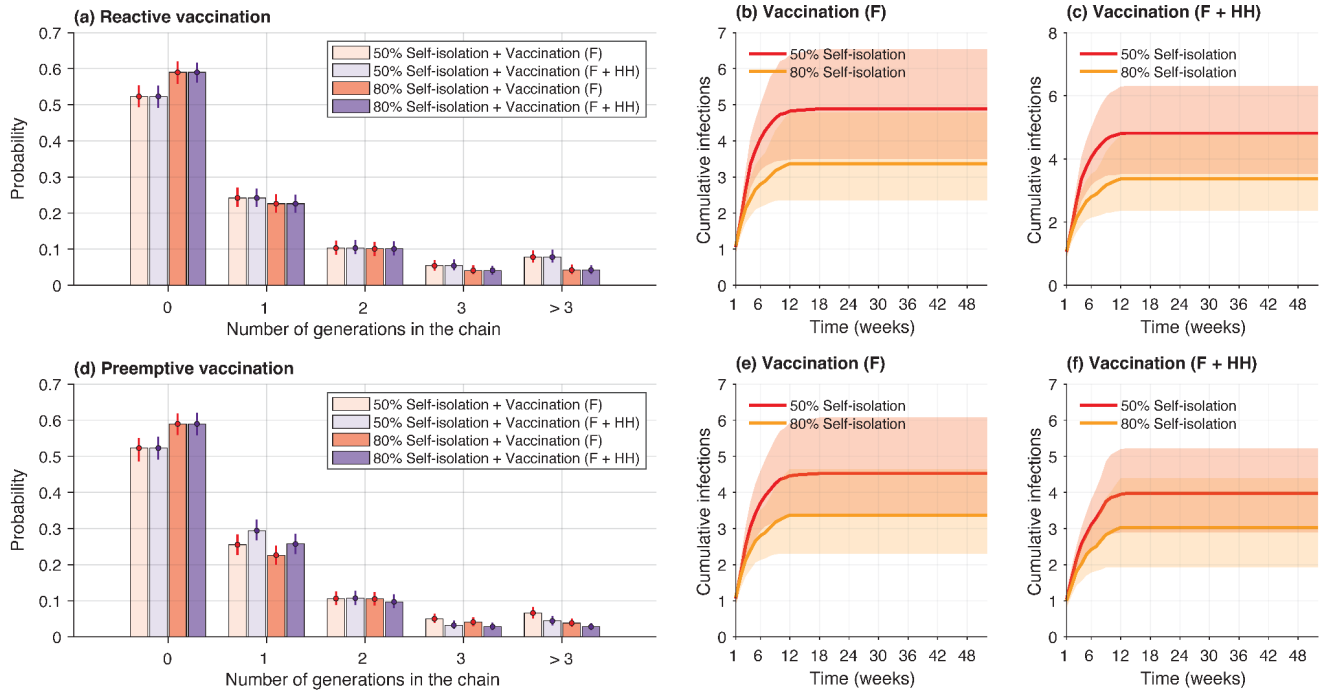


Figure A20. Probability of transmission chains across generations and cumulative number of infections under self-isolation and vaccination strategies. Panels (a) and (d) show the probability that transmission chains persisted for a maximum number of generations under reactive (a) and preemptive (d) vaccination. Generation 0 corresponds to the index case being infected by the reservoir. In Panels (a) and (d), bars (and overlaid points) show the estimated probability (i.e., proportion of simulations) from Monte Carlo simulations ($n = 1,000$ per scenario). Error bars indicate 95% bias-corrected and accelerated bootstrap confidence intervals based on 1,000 bootstrap resamples of simulations for each scenario. Panels (b), (c), (e), and (f) show the mean cumulative number of infections and corresponding 95% confidence intervals over a one-year horizon under 50% and 80% self-isolation compliance, with reactive (b,c) and preemptive (e,f) vaccination. Two vaccination strategies were compared: targeting farmers only (F) or farmers and their households (F+HH). Lines denote the mean cumulative infections across simulations with transmission chains extended beyond three generations, and shaded bands indicate 95% bootstrap confidence intervals.

7. Sensitivity Analysis: Part D

This section presents sensitivity analyses for scenarios in which coverage of target populations (poultry farmers alone or poultry farmers and their households) was achieved within two weeks following introduction of the index case. We assumed that 50% of infected individuals experienced asymptomatic infection. Vaccination was assumed to have 50% protection against infection and 85% protection against symptomatic disease. Compared with a six-week delay in reactive vaccination, a two-week delay reduced the probability of extended multi-generation transmission chains and, consequently, lowered the cumulative number of infections. These outcomes approached those observed under preemptive vaccination scenarios, particularly when self-isolation was initiated one day after symptom onset.

Part D1. Self-isolation begins 2 days after symptom onset

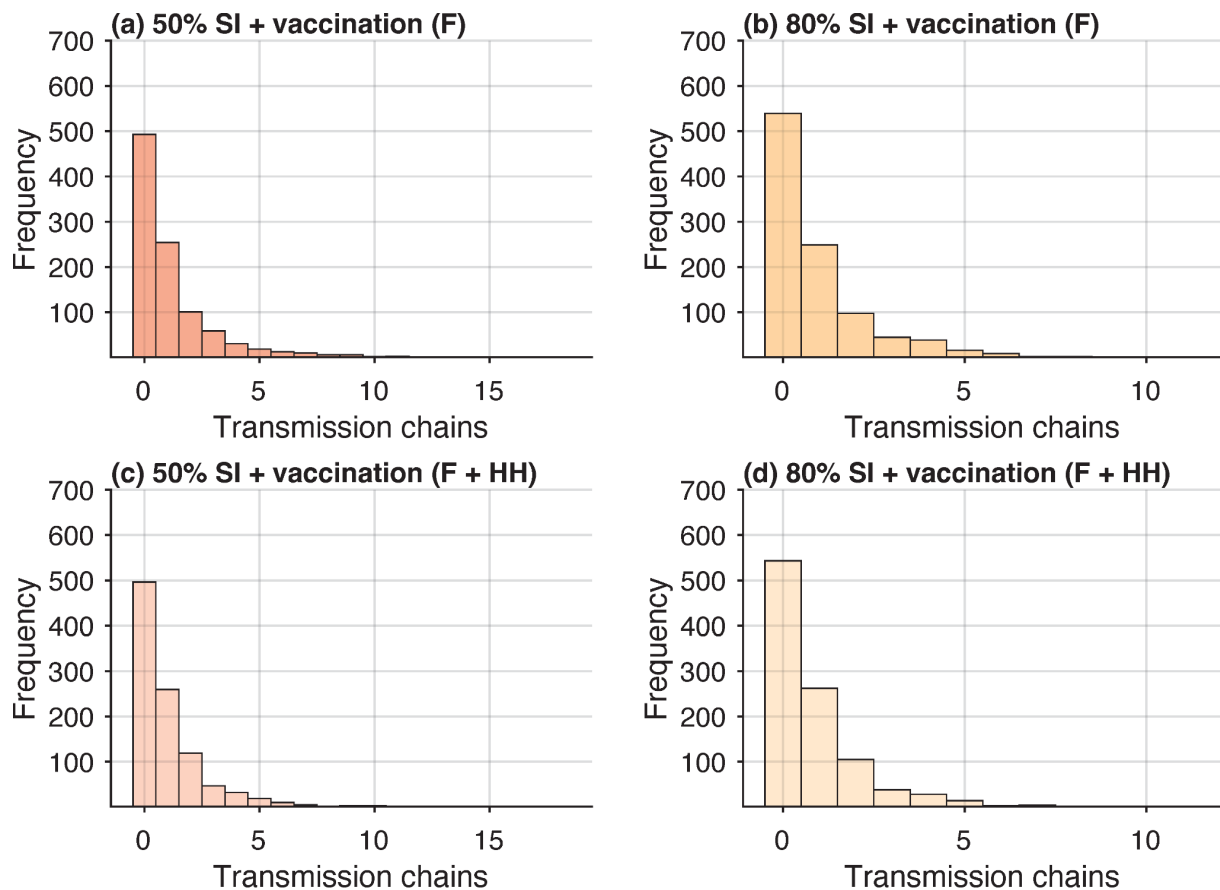


Figure A21. Distribution of transmission chains with reactive vaccination. Panels (a) and (b) show the distribution of transmission chains across generations among $n = 1,000$ Monte Carlo realisations under 2-week delay reactive vaccination of farmers only, with 50% and 80% self-isolation compliance, respectively. Panels (c) and (d) show corresponding results when both farmers and their households were vaccinated. Generation 0 corresponds to the index case being infected by the reservoir.

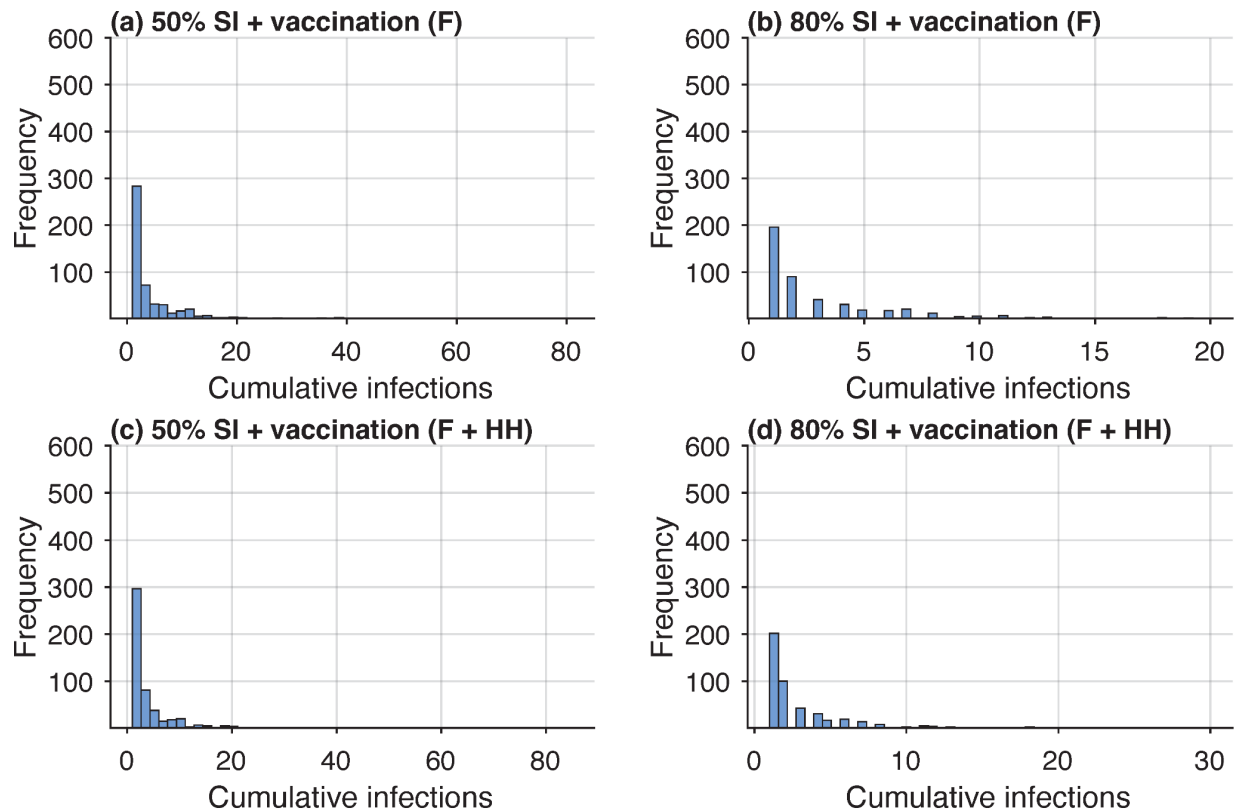


Figure A22. Distribution of cumulative infections in simulations with at least one secondary case under 2-week delay in reactive vaccination scenarios. Panels (a) and (b) show the distribution among $n = 1,000$ Monte Carlo realisations over a one-year horizon with 50% and 80% self-isolation compliance, respectively, when only farmers were vaccinated. Panels (c) and (d) show the corresponding distributions when both farmers and their households were vaccinated.

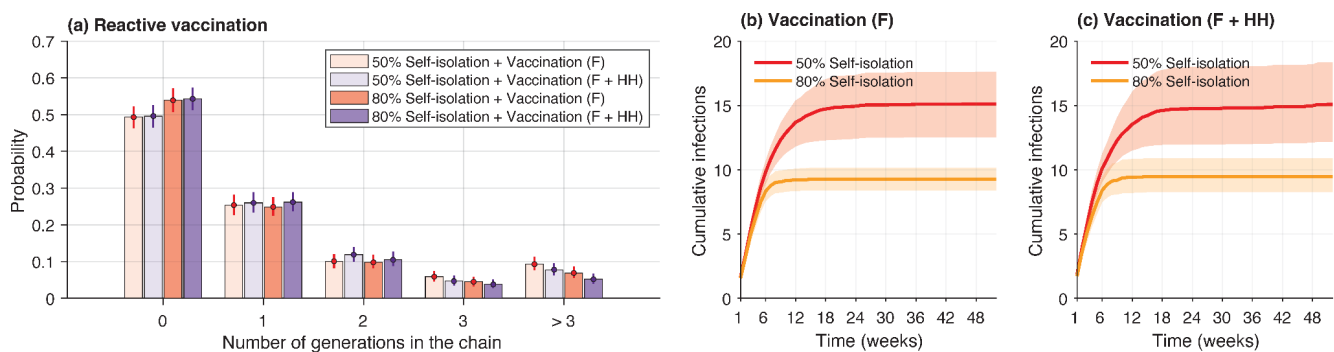


Figure A23. Probability of transmission chains across generations and cumulative number of infections under self-isolation and vaccination strategies. Panels (a) and (d) show the probability that transmission chains persisted for a maximum number of generations under reactive (a) and preemptive (d) vaccination. Generation 0 corresponds to the index case being infected by the reservoir. In Panels (a) and (d), bars (and overlaid points) show the estimated probability (i.e., proportion of simulations) from Monte Carlo simulations ($n = 1,000$ per scenario). Error bars indicate 95% bias-corrected and accelerated bootstrap confidence intervals based on 1,000 bootstrap resamples of simulations for each scenario. Panels (b), (c), (e), and (f) show the mean cumulative

number of infections and corresponding 95% confidence intervals over a one-year horizon under 50% and 80% self-isolation compliance, with reactive (b,c) and preemptive (e,f) vaccination. Two vaccination strategies were compared: targeting farmers only (F) or farmers and their households (F+HH). Lines denote the mean cumulative infections across simulations with transmission chains extended beyond three generations, and shaded bands indicate 95% bootstrap confidence intervals.

Part D2. Self-isolation begins 1 day after symptom onset

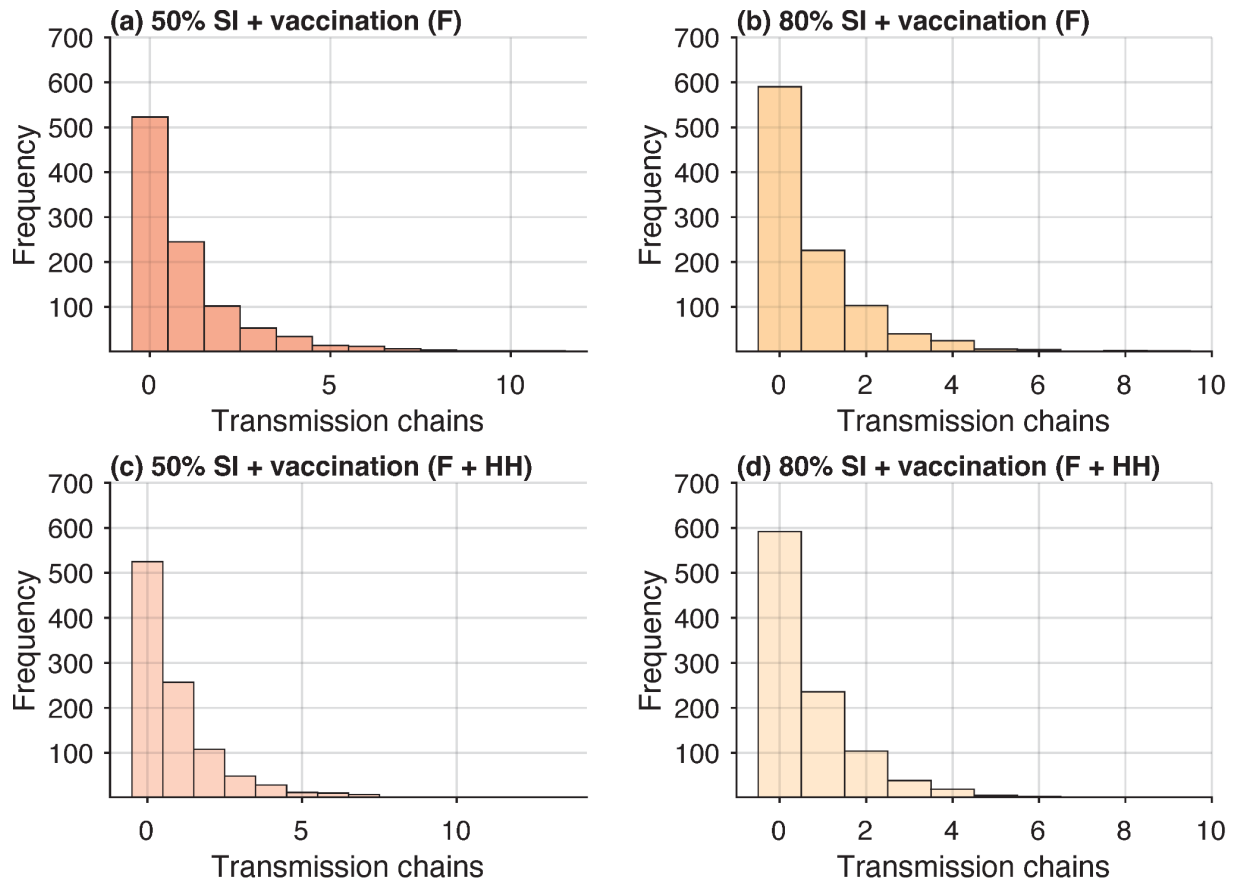


Figure A24. Distribution of transmission chains with reactive vaccination. Panels (a) and (b) show the distribution of transmission chains across generations among $n = 1,000$ Monte Carlo realisations under 2-week delay reactive vaccination of farmers only, with 50% and 80% self-isolation compliance, respectively. Panels (c) and (d) show corresponding results when both farmers and their households were vaccinated. Generation 0 corresponds to the index case being infected by the reservoir.

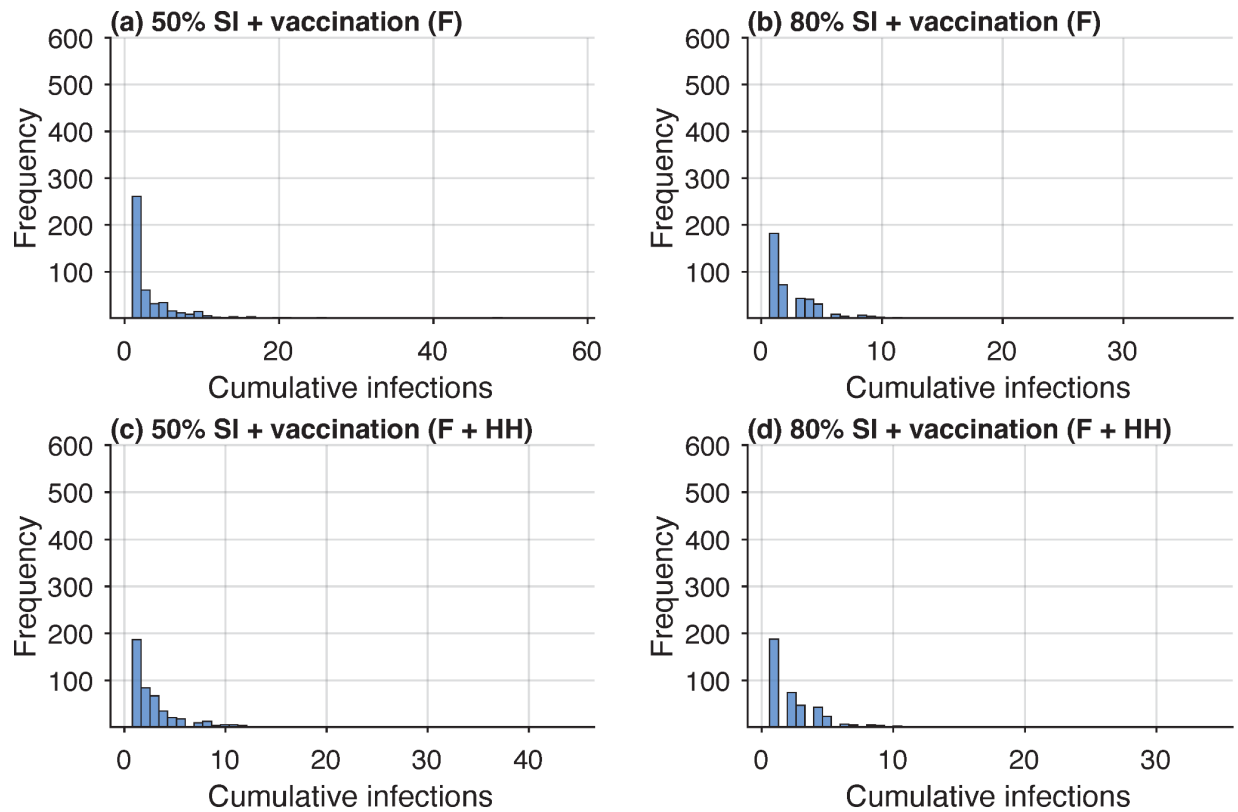


Figure A25. Distribution of cumulative infections in simulations with at least one secondary case under 2-week delay in reactive vaccination scenarios. Panels (a) and (b) show the distribution among $n = 1,000$ Monte Carlo realisations over a one-year horizon with 50% and 80% self-isolation compliance, respectively, when only farmers were vaccinated. Panels (c) and (d) show the corresponding distributions when both farmers and their households were vaccinated.

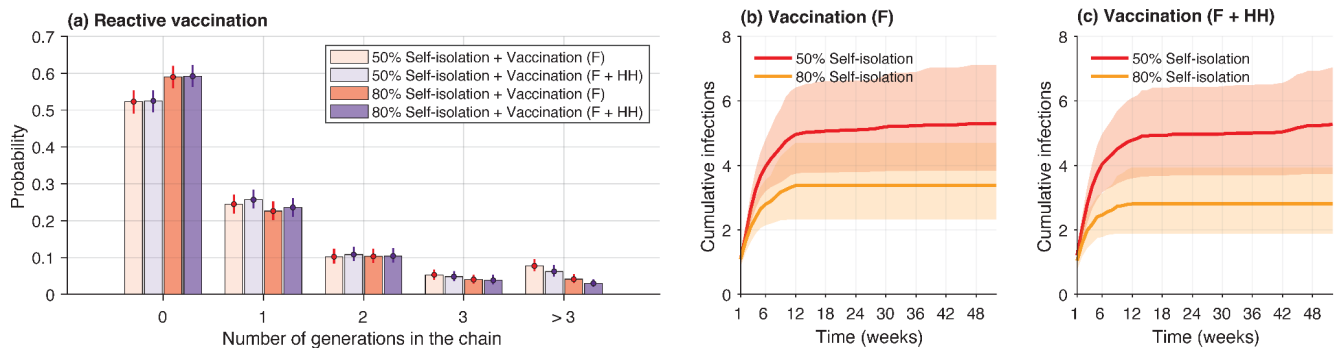


Figure A26. Probability of transmission chains across generations and cumulative number of infections under self-isolation and vaccination strategies. Panels (a) and (d) show the probability that transmission chains persisted for a maximum number of generations under reactive (a) and preemptive (d) vaccination. Generation 0 corresponds to the index case being infected by the reservoir. In Panels (a) and (d), bars (and overlaid points) show the estimated probability (i.e., proportion of simulations) from Monte Carlo simulations ($n = 1,000$ per scenario). Error bars indicate 95% bias-corrected and accelerated bootstrap confidence intervals based on 1,000 bootstrap resamples of simulations for each scenario. Panels (b), (c), (e), and (f) show the mean cumulative number of infections and corresponding 95% confidence intervals over a one-year horizon under 50%

and 80% self-isolation compliance, with reactive (b,c) and preemptive (e,f) vaccination. Two vaccination strategies were compared: targeting farmers only (F) or farmers and their households (F+HH). Lines denote the mean cumulative infections across simulations with transmission chains extended beyond three generations, and shaded bands indicate 95% bootstrap confidence intervals.

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