

EXPLAINING THE ROTAVIRUS SEROTYPE-DISTRIBUTION SHIFT IN CHILDREN AFTER VACCINATION USING A SIMPLE TRANSMISSION MODEL

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BACKGROUND

- Rotavirus causes gastroenteritis in children. The introduction of vaccines protecting children against some rotavirus serotypes induces a redistribution of circulating serotypes in unvaccinated children.
- The mechanisms driving the change in serotype distribution are not well known^{1,2}.
- One hypothesis is that the serotype distribution of the unvaccinated child population will shift toward the serotype distribution of the infected adult population as more children are removed from the infectious population via vaccines³.
- The present model tests this hypothesis.

METHODS

- A dynamic transmission model was developed with two serotypes (1 and 2) circulating in children and in adults but with different pre-vaccination distribution.
- During the pre-vaccination period, the transmission rate from adults to children was lower than the predominant transmission within each population (Figure 1).
- The model assumed closed populations being in equilibrium (no change in demography over time) before the introduction of a vaccine.
- A vaccination against serotype 1 and 2 was introduced into the child population of the model, shifting the serotype distribution to a new post-vaccination equilibrium (Figure 2).
- Default parameters were identified and scenario analyses assessed, testing the model sensitivity to vaccine coverage rates, levels of adult-to-child transmission rates, and relative population sizes.

Figure 1. Virus transmission pathways

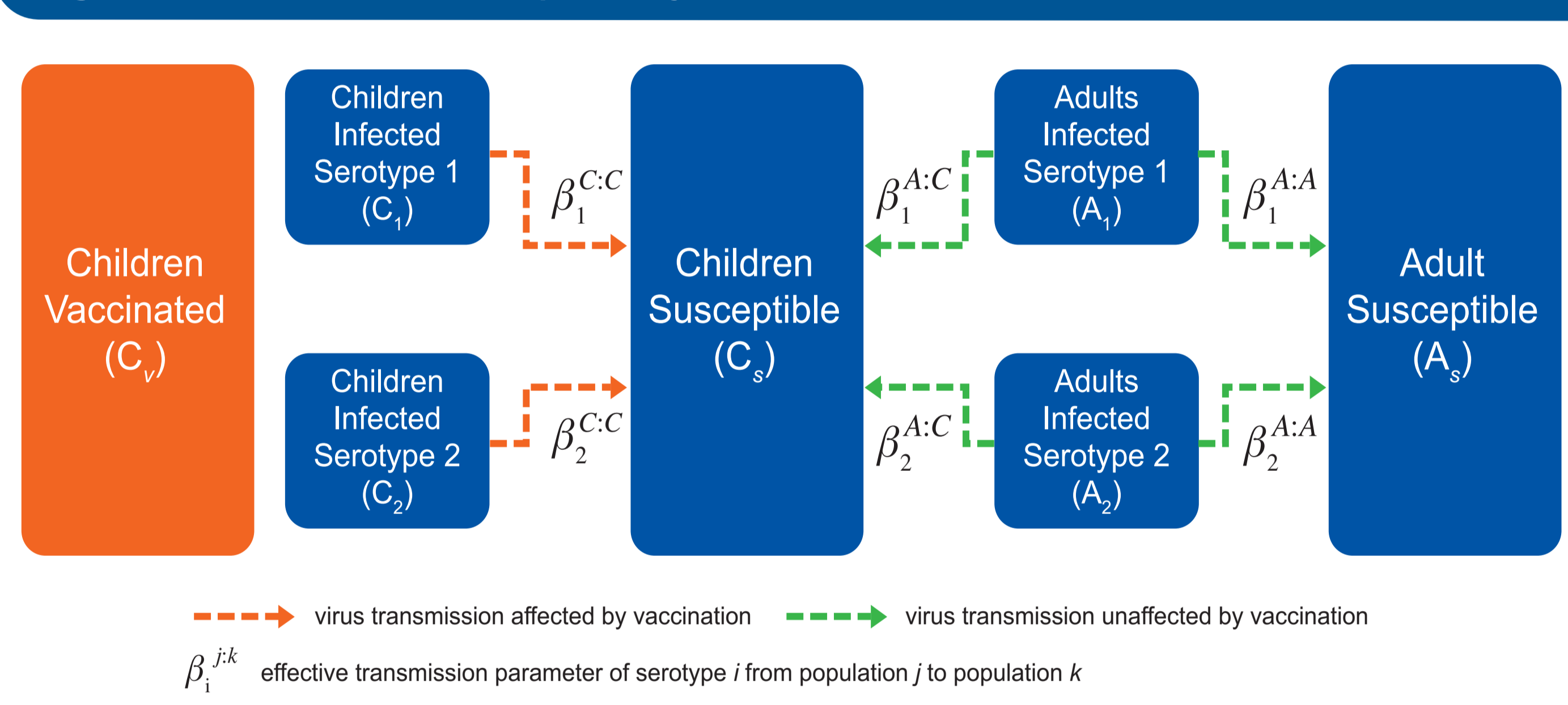
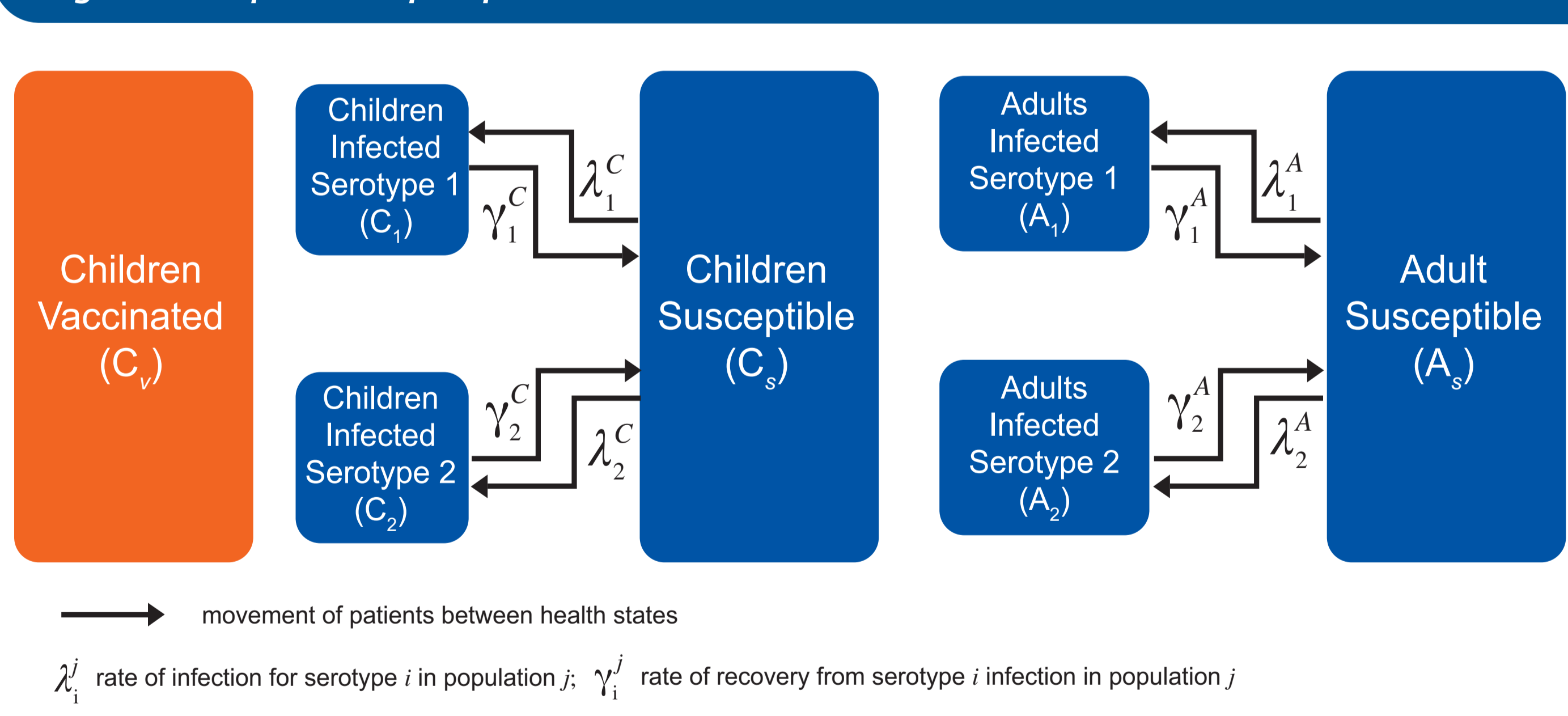


Figure 2. Population perspective



RESULTS

- The distributions between the two serotypes prior to vaccination were 25%:75% in children and 50%:50% in adults, and the proportions infected were 43% and 33%, respectively.
- For the default parameters, 80% vaccine coverage reduced the proportion of children infected by 92% and shifted the child serotype distribution at equilibrium toward the adult distribution to 47%:53% (see Figure 3).
- Similar results were observed for all parameter scenarios, with the serotype distribution in infected children shifting closer to the adult distribution as vaccine coverage increased (see Figure 4 & 5).

Disclosures

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References

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Figure 3. Serotype distribution in children over time

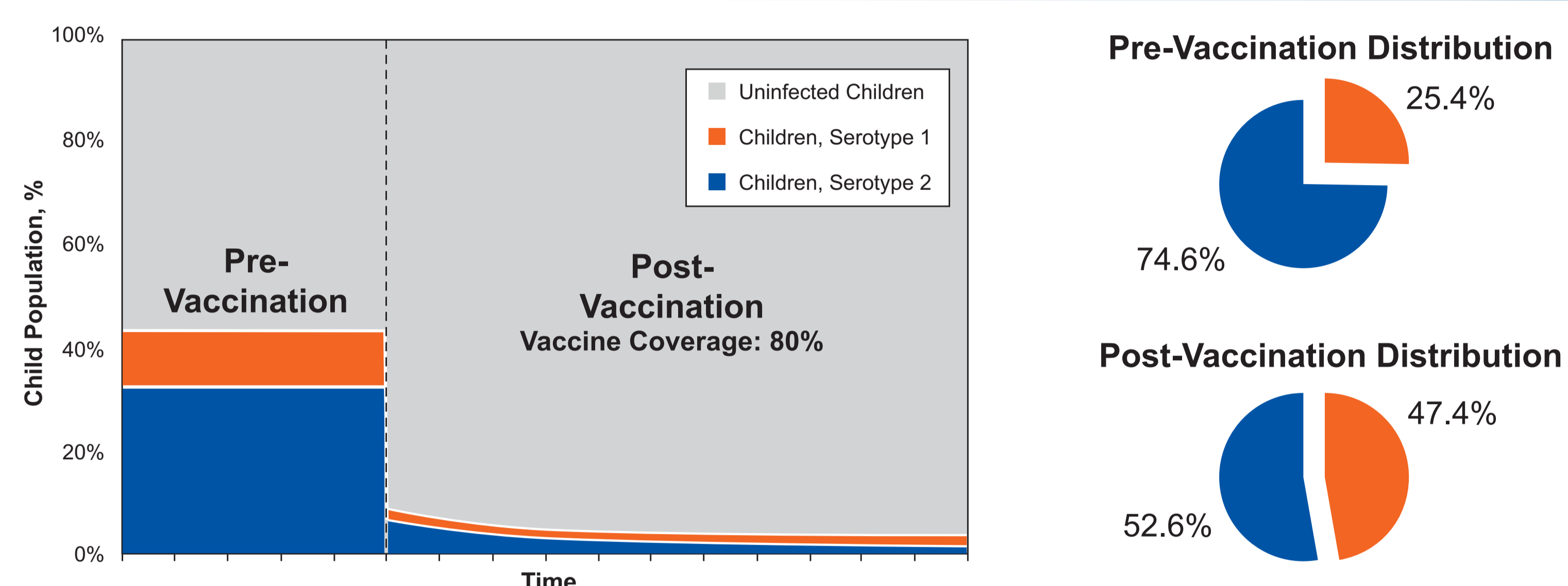


Figure 4. Scenario results on cross infection variation

Vaccine Coverage	20%	50%	80%
% Children infected	22.7%	7.8%	1.9%
Low cross infection (half of baseline adult-to-child transmission)	24.7% (75.3% Serotype 2)	38.8% (61.2% Serotype 2)	47.1% (52.9% Serotype 2)
Baseline cross infection	28.2% (68.3% Serotype 2)	12.3% (58.9% Serotype 2)	3.5% (52.6% Serotype 2)
High cross infection (double baseline adult-to-child transmission)	32.3% (64.8% Serotype 2)	15.5% (57.6% Serotype 2)	4.7% (52.4% Serotype 2)

Serotype distribution: Serotype 1 (orange), Serotype 2 (blue)

Figure 5. Population size variation

Vaccine Coverage	20%	50%	80%
% Children infected	22.7%	7.8%	1.9%
Children = 100, Adults = 50	24.7% (75.3% Serotype 2)	38.8% (61.2% Serotype 2)	47.1% (52.9% Serotype 2)
Children = 100, Adults = 100	28.2% (68.3% Serotype 2)	12.3% (58.9% Serotype 2)	3.5% (52.6% Serotype 2)
Children = 100, Adults = 200	35.6% (62.5% Serotype 2)	18.1% (56.6% Serotype 2)	5.8% (52.2% Serotype 2)

Serotype distribution: Serotype 1 (orange), Serotype 2 (blue)

- For all cross infection levels and population sizes the child serotype distribution shifted to the adult one with higher vaccine coverage.
- Serotype distribution was more sensitive to changes in strength of cross-infection and to the ratio of adults to children distribution at lower vaccine coverage.

CONCLUSIONS

- The model demonstrates that serotype distribution in children after vaccination may be influenced by the adult serotype distribution, with higher vaccine coverage shifting the child distribution closer to the adult distribution.
- These results support the hypothesis that rotavirus exposure from adult populations contributes to observed shifts in rotavirus serotype distributions in children after vaccine introduction.