

“Antimicrobial resistance can influence vaccine value, yet it is often missing in economic evaluations. Incorporating standard Antimicrobial resistance mapping and methods in Health Technology Assessment could help ensure policy fully reflects vaccines’ benefits.”

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Examining to what extent evaluation of vaccines incorporates implications for antimicrobial resistance: an Exploratory Review



Background

- Beyond their direct impact on reducing vaccine-preventable disease incidence, they can reduce AMR via multiple mechanisms (e.g., preventing infections, reducing antibiotic use, altering strain ecology).
- Despite this recognition, vaccine economic evaluations often omit AMR pathways, highlighting an important methodological gap and risking undervaluation of vaccines.
- We systematically reviewed peer-reviewed vaccine economic evaluations (2005–2025) and HTA guidance to assess incorporation of AMR pathways using the Jit & Cooper framework (2020)

Methods

- Following PRISMA guidance, we systematically searched Ovid MEDLINE/Embase/EconLit (2005–2025) adapting the inclusion criteria from Nymark *et al.* (2017).
- Inclusion: full economic evaluations of vaccines with AMR-relevant outcomes/pathways.
- Data extraction: vaccine, population, country, model type, time horizon, outcomes, ICERs & thresholds, AMR pathway mapping; CHEERS 2022 appraisal
- Grey literature: HTA manuals from selected high-income jurisdictions: Australia, Canada, Denmark, Germany, Netherlands, Sweden, United Kingdom

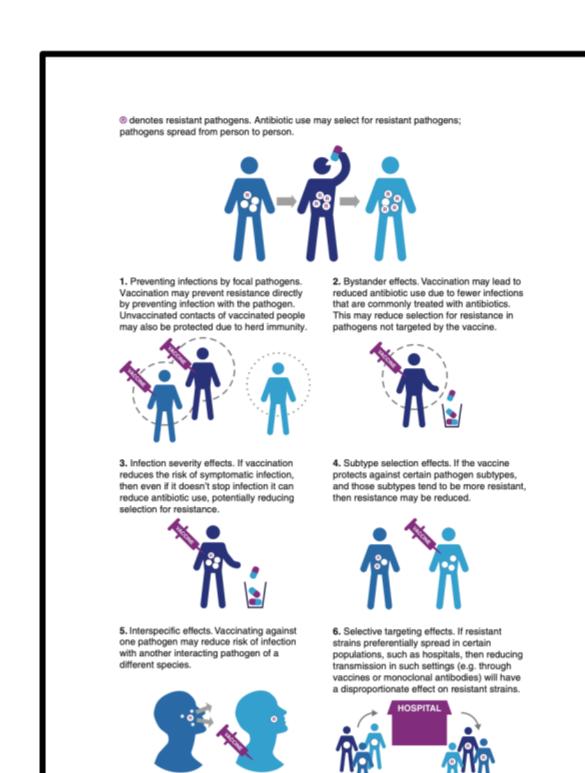


Figure 1. Ways in which vaccines may reduce antimicrobial resistance (Jit & Cooper, 2020)

Key takeaways

1. AMR is under-represented

Only 6/18 (33%) of vaccine economic evaluations explicitly modelled AMR pathways; most studies either omit AMR inputs or capture AMR only indirectly.

2. Including AMR often strengthens vaccine value

Where AMR pathways are modelled, results tend to move toward greater cost-effectiveness (lower ICERs/better value).

3. HTA and methods need to catch up

HTA guidance and reporting standards rarely require AMR mapping or AMR-specific inputs (antibiotic use, resistant cases, serotype dynamics); we need standard extraction fields and targeted methods development (e.g., how to handle selection pressure and when to use dynamic models).

Findings

- AMR inclusion: 6/18 (33%) explicitly modelled AMR pathways; 12/18 (67%) did not model resistance dynamics but sometimes captured AMR-relevant outcomes (e.g., reduced antibiotic prescribing).
- Pathway 1 (preventing focal infections): 6/6 (100%); Pathway 2 (bystander antibiotic reduction): 3/6 (50%); Pathway 4 (subtype selection): 2/6 (33%); Pathway 6 (targeting resistant strains): 1/6 (17%) Pathways 3 & 5: 0/6 (0%)
- Eighteen evaluations were included, covering pneumococcal, influenza, group B streptococcus, typhoid, gonorrhea, and tuberculosis vaccines. Most studies used static models, while dynamic transmission models were applied mainly to influenza, typhoid, gonorrhea, and tuberculosis.
- When AMR was modelled, vaccines were consistently more cost-effective. Pneumococcal DREAMR models projected savings of \$586 million in China and typhoid vaccination in Malawi achieved ICERs of \$300–890/DALY in outbreak contexts. By contrast, studies excluding AMR often reported borderline results, such as \$91,321/QALY for maternal GBS vaccination in the US.
- Grey literature: PBAC (Australia) explicitly referenced AMR; JCVI (U.K.) flagged AMR as a research priority; most manuals do not require AMR modelling.

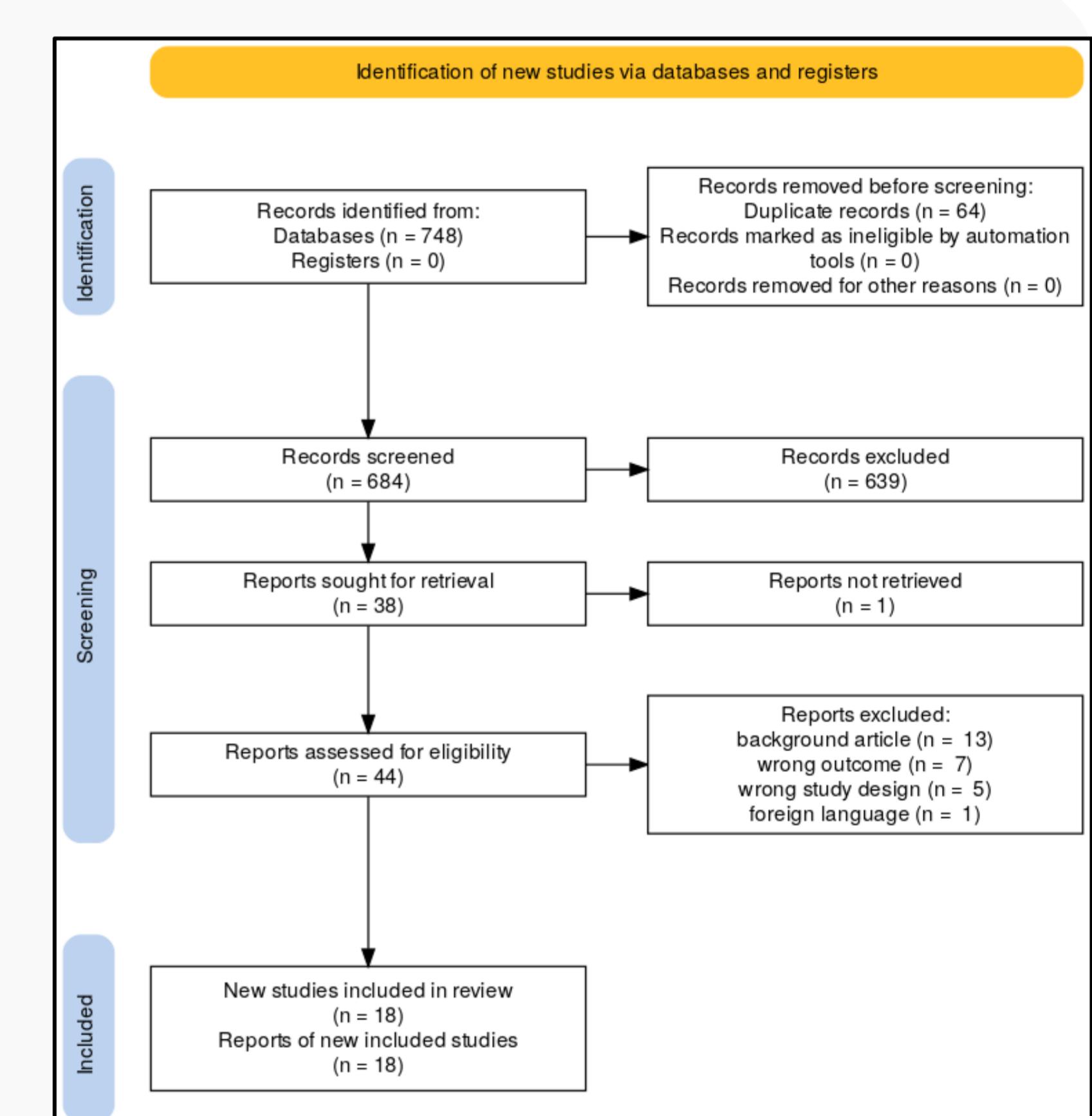


Figure 2. PRISMA 2020 flow diagram of study selection

Discussion & Recommendations

- Excluding AMR pathways likely underestimates vaccine value; inclusion commonly shifts results toward greater cost-effectiveness.
- Excluding AMR risks systematic undervaluation, distorting financing and limiting access to vaccines with AMR benefits. For vaccine development and regulation, these gaps are critical: without explicit standards, combination vaccines, outbreak-use vaccines, and next-generation technologies may be undervalued.
- Future work should prioritize practical methods for including AMR pathways in economic evaluation, especially those outlined by Jit & Cooper, and HTA bodies should establish clearer guidance to ensure decisions reflect vaccines’ full value in mitigating resistance.
- HTA agencies should provide explicit guidance and standardized data extraction items for AMR (e.g., antibiotic use metrics, resistant infections averted, serotype dynamics).
- Practical barriers (data, parametrization, pathways not well understood) explain under-representation — research agendas should prioritize methods development for e.g., selection pressure and strain ecology.



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