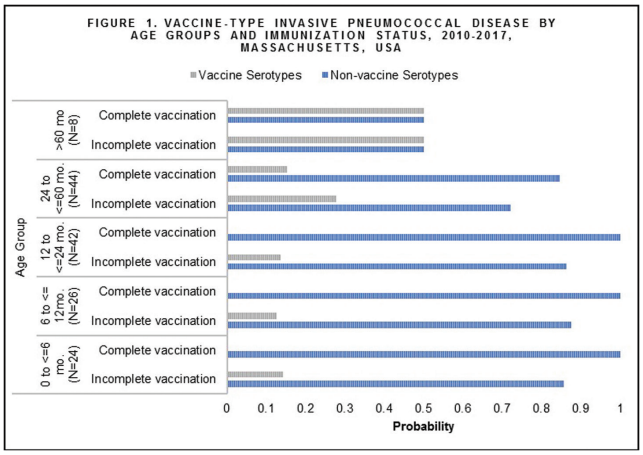
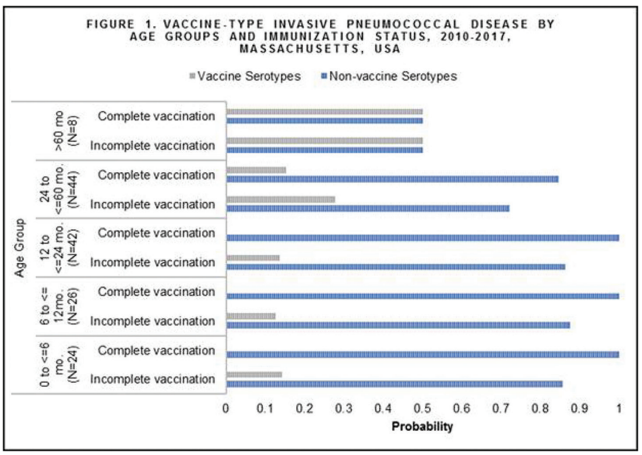
to be due to VT (9%, 95% CI 4–18% vs. 19%, 95% CI 10–31%, respectively). Despite complete immunization, 80 of 144 (55.6%) of all IPD in >60 months was breakthrough IPD (Figure 1). Among children with ≥1 comorbid condition and incomplete PCV13, 4 of 18 (22%) IPD were due to VT. Children with incomplete vaccination and pneumonia were most likely (11/17, 65%) to have VT; however, bacteremia without focus cases with incomplete vaccination were most likely (44/45, 3%) to have NVST (Figure 2). Our algorithm performs with 85% accuracy and 92% precision scores.

Conclusion. IPD due to VT after PCV13 vaccination mostly occurs in older children with incomplete PCV13 immunization, among those with underlying comorbidity, and among those who present with pneumococcal pneumonia. Evaluating the immune response following PCV13 vaccination in children with comorbidity could increase our understanding of breakthrough pneumococcal infections despite vaccination with PCV13.





Disclosures. **All authors:** No reported disclosures.

2556. Retrospective Evaluation of Mismatch From Egg-Based Isolation of Influenza Strains Compared With Cell-Based Isolation and the Possible Implications for Vaccine Effectiveness

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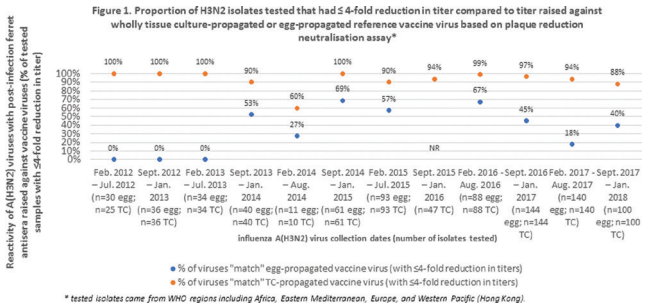
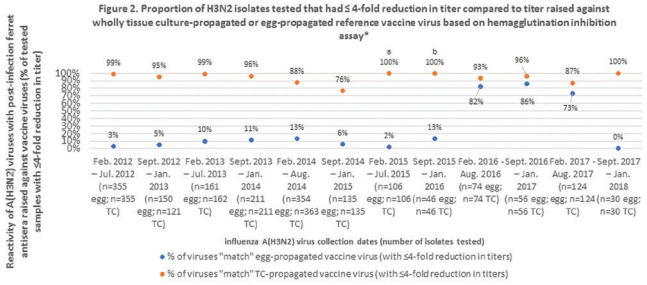
Background. Lower influenza vaccine effectiveness (VE) against circulating H3N2 strains compared with other influenza viruses is partly explained by antigenic mismatch between circulating strains and the vaccine strain (Belongia 2016). This mismatch has recently been linked to a new glycosylation site introduced in the egg-adaptation step (Zost 2017) and HA L194P substitution (Wu 2017) for H3N2. Vaccine manufactured using seed virus wholly grown in mammalian (e.g., Madin–Darby Canine Kidney—MDCK) cells, as with the NH17-18 version of Flucelvax®, avoids these mutations. Preliminary reports suggest that this cell-based vaccine showed greater VE than did similar egg-based vaccines [FDA Statement]. This study aimed to compile existing data on antigenic similarity to measure the degree of match with circulating wild-type isolates of egg- and MDCK-propagated versions of the vaccine H3N2 virus over multiple seasons.

Methods. Using publicly available reports from the Worldwide Influenza Centre, London (Crick), we compiled data on antigenic similarity, defined as H3N2 circulating wild-type virus isolates showing no more than a 4-fold reduction in titer to antisera raised against wholly MDCK- or egg-propagated versions of the vaccine H3N2 viruses. Titers were compared using hemagglutination inhibition (HI) assays and/or plaque reduction neutralization assays (PRNA).

Results. Data from Northern Hemisphere influenza seasons of 2011–2012 to 2017–2018 show a substantially higher proportion of tested circulating influenza H3N2 viruses matched the MDCK-propagated reference viruses than did corresponding egg-propagated reference vaccine viruses (Figures 1 and 2). In half of the seasons evaluated, there was little to no antigenic similarity between circulating viruses and the egg-based vaccine viral seed.

Conclusion. These data suggest higher levels of mismatch have occurred consistently with egg-propagated H3N2 reference viruses compared with MDCK-propagated reference viruses when measured against circulating wild-type isolates and may further explain the potential for lower VE observed against H3N2 historically. Furthermore, these data point to the importance of continuing to utilize cell-derived seeds in creating seasonal influenza vaccines for this strain.





Disclosures. **S. Rajaram**, Seqirus: Employee, Salary. **J. Van Boxmeer**, Seqirus: Employee, Salary. **B. Leav**, Seqirus: Employee and Shareholder, Salary. **P. Suphaphiphat**, Seqirus: Employee, Salary. **I. Iheanacho**, Seqirus: Consultant, Research support. **K. Kistler**, Seqirus: Consultant, Research support.

2557. A Model to Estimate the Potential Impact of Immunizations on Respiratory Syncytial Virus (RSV) Disease Burden Among Infants in the United States

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Background. Respiratory syncytial virus (RSV) is the leading cause of severe respiratory infections among infants worldwide. We developed a mathematical model to estimate the impact of immunizations currently under development on medically attended (MA) RSV infections (RSVi) among infants in the United States.

Methods. We created a spreadsheet-based Decision Tree model to estimate the potential impact of (1) a vaccine given to mothers in their third trimester to indirectly provide protective antibodies to infants during their first RSV season and (2) a monoclonal antibody given to infants at birth during the RSV season (November to April). We measured the annual number of MA-RSVi (hospitalizations, emergency department (ED) visits, and outpatient clinic visits) prevented by immunization before infants reach 6 months of age. Major inputs included population-based rates (from 2000 to 2009) of MA-RSVi in each healthcare setting, immunization uptake, time required to reach partial or full protection, efficacy, and duration of protection. We used 95% confidence intervals of MA-RSVi rates to generate a range of impact estimates.

Results. At baseline (without intervention), we estimated 54,523 RSV-associated hospitalizations (range 45,129–64,148), 141,646 ED visits (range 117,358–166,132) and 410,205 outpatient clinic visits (range 339,535–480,681) occur among infants