### Input parameters

| Parameter | Base case | Range | Reference |
|-----------|-----------|-------|-----------|
| **Assessment of measles immunity (%)** | 84 | 60–100 | Hyle, Ann Intern Med 2017 |
| **Vaccination with MMR (%)** | None | | |
| Vaccinated at pretravel | 47 | 20–100 | Hyle, Ann Intern Med 2017 |
| Exposure to measles while traveling (# exposed/# travelers) | Any international | Any international | 15.1 × 10^-5 to 1.5 × 10^-4 |
| Measles infection, if exposed (%) | | | |
| Probability of infection if non-immune | 90 | 80–100 | CDC Yellow Book 2015 |
| Transmission (#) | From immune | 0–5 | Fiebelkorn, CID 2015 |
| Contacts per imported case | From nonimmune | 0–20 | Fiebelkorn, CID 2015 |
| **Costs (US$)** | | | |
| Cost per imported measles case | 14,600 | 3,300 | Fiebelkorn, CID 2015 and JID 2010; US Dol 2015 |
| Cost per transmitted measles case | 550 | | Ortega-Sanchez, Vaccine 2014 and JID 2010; US Dol 2015 |
| Cost per measles case contact | | | |

### Disclosures

**All authors:** No reported disclosures.

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### 2488. Clinical Implications of Asymptomatic Plasmodium falciparum Infections in Malawi

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**Session:** 277. Global Infections 
Saturday, October 7, 2017: 2:00 PM

**Background.** In Malawi, asymptomatic *Plasmodium falciparum* infections are common and make up a substantial proportion of the infection burden. However, the implications of these infections for disease burden are unknown. We do not know if asymptomatic infections eventually progress to clinical malaria or if they persist without effective treatment. This study aims to characterize asymptomatic infections in a region with high transmission and examine the association between persistent asymptomatic infections and clinical disease.

**Methods.** This study enrolled 120 participants, aged 1–50 years, with uncomplicated malaria (treated with artemether–lumefantrine) and followed them monthly for up to 2 years. Participants presenting with symptoms during follow-up were tested via rapid diagnostic test and treated if positive. Samples from all visits, regardless of symptoms, were tested for parasites using both microscopy and qPCR. Genotyping with *msp1*, *msp2*, and *glurp* was used to differentiate between new and persistent infections. Asymptomatic infections were defined as infections detected when symptoms were absent, and first detected at least 2 weeks before or after a symptomatic episode. Cox frailty models were used to estimate the association between asymptomatic infections and time between clinical malaria episodes; mixed models were used to estimate the odds of clinical symptoms comparing new to persistent infections.

**Results.** Analysis has been completed for 1,702 person months of follow-up time. Asymptomatic infections were detected in 23% of visits. After adjustment for age and season, carriage of asymptomatic infections, the longest of which persisted for 16 months, was associated with decreased risk of clinical malaria (HR 0.45, P < 0.001) in all ages. When asymptomatic infections preceded a clinical episode, newly acquired infections were detected at 9% of the following clinical episodes. After adjustment for age, sex, and season, clinical malaria was more likely to be due to newly acquired infections (OR 1.3, 95% CI 1.2–1.5) than to a persistent infection.

**Conclusion.** In a high-transmission setting, asymptomatic *P. falciparum* infections infrequently developed into clinical disease and may be protective against clinical malaria.

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

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### 2489. Silent Polio Transmission: A Spatial Analysis

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**Session:** 277. Global Infections 
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**Background.** As wild poliovirus is eradicated and countries switch from Oral Polio Vaccine (OPV) to Inactivated Polio Vaccine (IPV) per WHO recommendations, preventing circulation of vaccine-derived poliovirus is a top priority. However, spatial dynamics of OPV transmission are not well understood. Understanding these trends will improve resource targeting in the event of OPV reintroduction in underervaccinated communities. Mexico provides a natural environment to study OPV as it provides IPV routinely and bi-annual OPV campaigns.

**Methods.** Children in three villages near Orixaba, Mexico were randomized to three levels (10%, 30%, 70%) to receive OPV. We measured distance to nearest OPV shedding, and the amount of shedding close to unvaccinated individuals. We used maps to show the proximity and amount of shedding. Distance and density of shedding was analyzed separately using mixed effects logistic regression with random effects for household and time, adjusted for age, gender, area, and running water.

**Results.** The median distance to nearest OPV shedding was 85 meters (IQR 46, 145). The median number of shedding individuals within 200 m was 3 (2, 6). Shedding between household transmission occurred rapidly with unvaccinated individuals shedding on day one of the study (Figure 1). There was little evidence (Odds Ratio [OR] 1.04 [95% Highest Posterior Density (HPD) 0.92, 1.16]) of an association between distance (per 100 m) from OPV shedding and odds of shedding. There was some suggestion that the number of OPV shedding with 200 m may have some effect on unvaccinated shedding with OR 0.93 (HPD 0.84, 1.01) but not at 100 or 500m. Results were consistent across the three villages.

**Conclusion.** Household structure appears to have limited value in predicting transmission of poliovirus shedding. The use of OPV results in rapid but low levels of transmission throughout the community and this would usually go undetected. The only way to avoid this is to not use OPV or to have strong controls such as quarantine, or strict hygiene protocols. After withdrawal of OPV worldwide the decision to reinroduce due to an outbreak should not be taken lightly as it appears a small amount of shedding, and the amount of shedding close to unvaccinated individuals. We used maps to show the proximity and amount of shedding. Distance and density of shedding was analyzed separately using mixed effects logistic regression with random effects for household and time, adjusted for age, gender, area, and running water.

**Figure 1.** Contour Plot: Shedding Over Time.

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

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### 2490. Phylogenetic Analysis of an Unusual Increase in Salmonella enterica serovar Paratyphi A Infection among Travelers Returning from Myanmar

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**Session:** 277. Global Infections  
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**Background.** The proportion of enteric fever cases caused by *Salmonella enterica* subspecies *enterica* serovar Paratyphi A (S. Paratyphi A) has recently been increasing in Asian counties, which is a public health concern. In 2015, an unusual increase in S. Paratyphi A infection among Japanese travelers returning from Myanmar was noted, while there is little information on this trend up until Myanmar.

**Methods.** Isolates from travelers who returned with enteric fever from 2005 to 2015 were analyzed in order to determine country-specific notification rates (epidemiological investigation). The notification rate was defined as cases returning from each country per 100,000 Japanese travelers who visited to the country. S. Paratyphi A isolates collected from 2001 to 2015 were analyzed by whole-genome sequencing (microbiological investigation).

**Results.** Yearly notification trends indicated that enteric fever was potentially endemic to Myanmar (5–16 cases/100,000 travelers); the trends were similar to those observed in India (4–21 cases/100,000 travelers). A rapid increase in S. Paratyphi A infection occurred from 2012–2014 (2–4 cases/100,000 travelers) to 2015 (13 cases/100,000 travelers). A phylogenetic tree, constructed based on analysis of 105 S. Paratyphi A isolates (33 and 30 related to Myanmar and Cambodia, and 42 controls), revealed that most Myanmar- and Cambodia-related isolates formed clusters in the same lineage (Figure 1). Additionally, Myanmar-related isolates from 2015 harbored identical phage type 1 and were genetically closely related (each isolate had 0–10 single-nucleotide polymorphisms (SNPs), mostly within 0–7 SNPs) (Figure 2), yielding a wider SNP range than outbreak-associated isolates from Cambodia in 2013 (within a SNP distance of 0–6).

**Conclusion.** Epidemiological trends and molecular subtyping suggested a possible outbreak of S. Paratyphi A infection occurred in Myanmar in 2015. The recent upsurge of S. Paratyphi A infection in Myanmar is important for travelers and clinicians since infection cannot be prevented by typhoid vaccination.

Figure 1. Polygenetic tree of 105 S. Paratyphi A isolates  
Figure 2. SNP distances of 0–6.

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

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2491. Murine Typhus: a Common Cause of Acute Febrile Illness with Potential for Serious Complications  
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**Background.** Individual cases and outbreaks of murine typhus have been documented in South Texas. We report 90 cases from Hidalgo County, Texas, enumerating complications and comparing results in children and adults.

**Methods.** We reviewed records of 101 patients in three hospitals in Hidalgo County, Texas, who had positive typhus serology (IgG or IgM titer ≥1:128) during 2001–2015 and were categorized as suspected, probable or confirmed murine typhus cases in accord with CDC definitions. We excluded 11 cases because a current infection may have confounded our tabulation of manifestations or there was insufficient information to make a clinical diagnosis.

**Results.** The majority presented with typical typhus: fever, headache, myalgias and fatigue. Rash, thrombocytopenia and elevated hepatic transaminases were frequent (Table). Clinical complications in 25 cases (28%) caused a less typical syndrome, including bronchiolitis, pneumonia, pancreatitis, cholecystitis, mesenteric adenitis, myositis, rhombomyelitis, meningitis and septic shock. Procalcitonin was >0.5 in 10 of 14 (71%) cases. Once the diagnosis was suspected, patients were treated with doxycycline with a rapid response in every case. Generally fever disappeared within 24–36 hours of the first dose.

**Conclusion.** Murine typhus is a common endemic infection in South Texas. Although most patients had a typical syndrome, the disease is multisystem, and complications appeared in 28% of cases. Procalcitonin was usually elevated. Rats and opossums are common reservoirs for Rickettsia typhi, and a search for cases of murine typhus may be warranted in other parts of the US as well, so that treatment with doxycycline can be begun promptly.

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

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**Table: Symptoms, signs, laboratory findings**

| Symptoms                          | Number (%) abnormal |
|-----------------------------------|---------------------|
| Fever (temperature >105.4°F)      | ≥36/36 (100%)       |
| Myalgia                           | ≥15/20 (75%)        |
| Headache                          | ≥23/32 (72%)        |
| Rash                              | ≥18/36 (50%)        |
| Liver enzymes                     | ≥3/6 (50%)          |
| Sign of disease                   | ≥14/54 (26%)        |
| Total                             | ≥90/90 (99%)        |

P-value

| Fever (temperature >105.4°F)      | 1                   |
| Myalgia                           | 0.44                |
| Headache                          | 0.38                |
| Rash                              | 0.12                |
| Liver enzymes                     | 0.22                |

*Comparing pediatric vs. adult cases.

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2492. Direct and Indirect Impact of 13-valent Pneumococcal Conjugate Vaccine (PCV13) on Invasive Pneumococcal Disease (IPD) Among Children and Adults in the U.S.  
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**Session:** 278. Pneumococcal and Pertussis Vaccines  
**Saturday, October 7, 2017: 2:00 PM**

**Background.** In February 2010, PCV13 was introduced for routine use among children < 5 years. In June 2012, PCV13 was recommended for use in series with 23-valent polysaccharide vaccine (PPSV23) for adults ≥19 years with select medical conditions, and in August 2014, for all adults ≥65 years. We evaluated the direct and indirect effects of PCV13 6 years post-introduction on invasive pneumococcal disease (IPD).

**Methods.** IPD cases (isolation of pneumococcus from sterile sites) were identified among residents of Active Bacterial Core surveillance (ABCs) sites during July 2007–June 2016. Rates were serotyped by Quellung, PCR, or whole genome sequencing and classified as PCV13 or non-vaccine type (NVT). Incidence changes were estimated as percent changes (one minus rate ratio) and 95% confidence intervals (95% CI) between pre-PCV13 (2007–2009) and two post-PCV13 periods (July 2014–June 2015 and July 2015–June 2016).

**Results.** ABCs identified 31,190 IPD cases between 2007 and 2015, with 2,750 cases among children < 5 years and 10,930 among those ≥65 years. During the two post-PCV13 periods, overall IPD rates were 33%–62% lower relative to 2007–2009 among all age groups, including <5 years and ≥65 years (Figure). Significant reductions in PCV13-type IPD incidence were observed for all age groups during both post-PCV13 periods, with incidence 84% (95% CI 78, 88%) and 68% (95% CI 63, 73%) lower in 2015–2016 among children < 5 years and adults ≥65 years, respectively. PCV13-type IPD reductions were driven by serotypes 19A and 7E IPD due to non-vaccine types also declined significantly among children < 5 years (−27%, 95% CI −42, 9%), and adults ≥65 years (−24%, 95% CI −34, −14%). PCV13-type IPD incidence did not differ significantly between the two post-PCV13 periods.

**Conclusion.** IPD incidence declined among children and adults in the U.S. following PCV13 introduction among children. The lack of difference in PCV13 rates between 2014–2015 and 2015–2016 suggests no measurable early impact of PCV13 introduction among adults ≥65 years. To date, we found no evidence of significant replacement disease with non-PCV13 types. Further work is needed to explain reductions in non-vaccine type disease observed in the post-PCV13 era.