

## Web Material

### **Assessment of the Status of Measles Elimination in the United States, 2001–2014**

#### **Web Appendix 1**

Explanation for assumption of finite chains of transmission: Methods 1–3 assume that all chains of transmission are finite, and thus point estimates of  $R$  obtained with these methods will always be  $<1$  (1, 2). This assumption is appropriate in a setting where endemic transmission of measles has been interrupted, as is the case for the U.S. (3), and it does not preclude an evaluation of trends in  $R$  over time. Importantly, upper confidence limits of these estimates may exceed 1, allowing for exclusion of the possibility of endemic transmission. In addition, point estimates of  $R_{index}$  calculated using Method 4 may exceed 1.

## Web Appendix 2

Sensitivity analyses: Method 1 assumes that all outbreaks must be linked to an imported case. When this approach is applied to all chains of transmission, including those in which the imported primary case was not identified (e.g., a short-term visitor who left the country before developing symptoms),  $R$  may be overestimated, as you are essentially including non-imported cases without their associated importation. Thus, all analyses were conducted twice, either including or excluding chains without an identified imported source. These analyses showed that, except for Method 1, estimates of  $R$  and  $R_{index}$  were generally larger when analyses were limited to chains with an identified imported source; excluding cases with an unknown source increases the proportion of total cases that are imported and yields a lower  $R$  for Method 1.

Larger outbreaks and those of longer duration may be more likely than smaller chains and single cases to be reported, which may affect  $R$  estimates using Methods 2 and 3. Similarly, smaller chains and singleton cases may be more likely to be false-positives. To account for this,  $R$  was estimated after discarding chains of transmission below a minimum size and duration; we considered minimum chain sizes of 1–5 cases and minimum chain duration from 0–4 generations of spread. These analyses showed that estimates of  $R$  based on the size of outbreaks were lower when single-case chains were included in the analysis, and increasingly larger as analyses were restricted to larger chain sizes (Supplementary Table 1). Estimates of  $R$  based on the duration of outbreaks were smaller when single-case chains were included in the analysis, but otherwise fairly constant (Supplementary Table 2).

All  $R$  and  $R_{index}$  estimates in these sensitivity analyses remained  $<1$ .

**Web Table 1.** Sensitivity analyses for minimum chain size used to estimate the effective reproduction number,  $R$ , for measles in the United States, for all chains and for only those with an identified link to an importation — 2001–2014

| Minimum Chain Size Considered | All Chains      |            | Chains With an Identified Imported Source Only |            |
|-------------------------------|-----------------|------------|--|------------|
|                               | Estimate of $R$ | 95% CI     | Estimate of $R$                                | 95% CI     |
| 1                             | 0.66            | 0.62, 0.70 | 0.70   | 0.66, 0.74 |
| 2                             | 0.78            | 0.73, 0.83 | 0.79   | 0.74, 0.84 |
| 3                             | 0.82            | 0.77, 0.87 | 0.82   | 0.77, 0.88 |
| 4                             | 0.84            | 0.79, 0.90 | 0.84   | 0.79, 0.90 |
| 5                             | 0.86            | 0.80, 0.92 | 0.86   | 0.80, 0.92 |

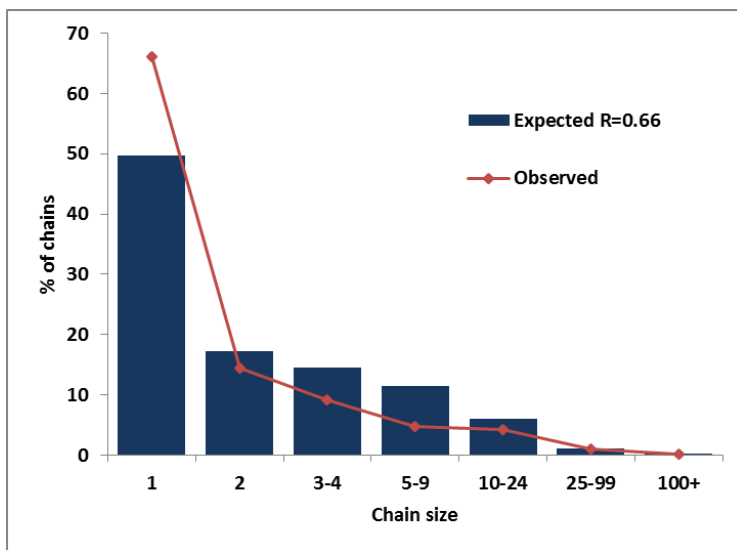
CI, confidence interval.

**Web Table 2.** Sensitivity analyses for minimum number of generations of spread used to estimate the effective reproduction number,  $R$ , for measles in the United States, for all chains and for only those with an identified link to an importation — 2001–2014

| Minimum Generations of Spread Considered | All Chains      |            | Chains With an Identified Imported Source Only |            |
|--|-----------------|------------|--|------------|
|  | Estimate of $R$ | 95% CI     | Estimate of $R$                                | 95% CI     |
| 0  | 0.45            | 0.40, 0.49 | 0.49   | 0.45, 0.54 |
| 1  | 0.59            | 0.53, 0.66 | 0.60   | 0.53, 0.67 |
| 2  | 0.54            | 0.47, 0.63 | 0.55   | 0.47, 0.64 |
| 3  | 0.61            | 0.50, 0.72 | 0.61   | 0.51, 0.72 |
| 4  | 0.66            | 0.53, 0.80 | 0.66   | 0.53, 0.80 |

CI, confidence interval.

**Web Figure 1.** Observed and expected distribution of chain sizes with an identified link to an importation, according to the effective reproduction number,  $R$ , United States 2001–2014



## References

1. De Serres G, Gay NJ, Farrington CP. Epidemiology of transmissible diseases after elimination. *Am J Epidemiol.* 2000;151(11):1039–1048; discussion 49–52.
2. Gay NJ, De Serres G, Farrington CP, et al. Assessment of the status of measles elimination from reported outbreaks: United States, 1997–1999. *J Infect Dis.* 2004;189(suppl 1):S36–S42.
3. Papania MJ, Wallace GS, Rota PA, et al. Elimination of endemic measles, rubella, and congenital rubella syndrome from the Western hemisphere: the US experience. *JAMA Pediatr.* 2014;168(2):148–155.