The Incubation Period of Cholera: A Systematic Review Supplement

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1 Basic Model

Our models follow the approach for analysis of coarse data from *Reich et al*[1] with small modifications. In general, we used maximum likelihood estimates for exploring and comparing basic models. In the final analysis we used a Bayesian framework, which gave nearly identical point estimates of the key quantiles and parameters of the incubation period distributions, but with slightly larger, 95% credible intervals.

The Bayesian model used the doubly censored likelihood from *Reich et al*[1] with weakly-informative prior distributions on log of the median (μ), and the log-log of the dispersion ($log(\phi)$).

$$\mu \sim N(0, 100)$$
$$log(\phi) \sim N(0, 100)$$

We sampled from the posterior distribution with the Metropolis-Hastings Algorithm using the MCMCPack package in R and ran 3 chains for at least 100,000 iterations after a 50,000 iteration burn in period.[2] We visually assessed convergence of the three chains and used a scale reduction factor,[3] $\hat{R}$, of less than 1.01 as a measure of convergence.

2 Differences Between Strains

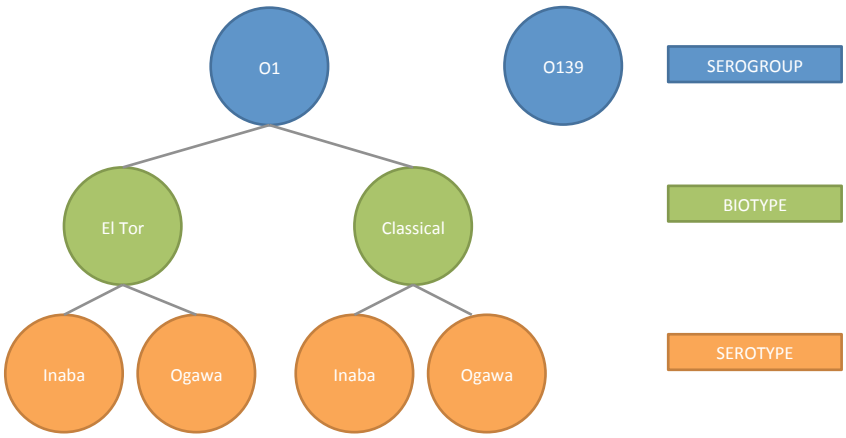

Figure 1: **Relationships between the various strains of** *Vibrio cholerae* **considered in this manuscript.**

To explore differences the incubation period between strain groups (i.e. serogroups, biotypes, and serotypes), we fit log-normal models to the data. For each strain classification, we fit two models, one model with separate parameters for each type, and one with shared parameters for each type. We used Bayes Information Criteria (BIC), and Akaike's Information Criteria (AIC/AICc) to compare the fit of the two models. An overview of these model comparisons are shown below. From this we find evidence for differences between strains before adjusting for study specific variables like study type.

Table 1: **Comparisons between models of the incubation period of subgroups of cholera strains. We estimated joint and separate models for each strain differentiation and compared AIC, AICc, and BIC for models that (1) assume that strains have the same distributions and (2) allow each strain to have a different distribution.**

Model	nLL	n	DF	AIC	AICc	BIC	ΔAICc	ΔBIC
Serogroup (Shared)	1367.60	323	2	2739.19	2739.23	2746.75		
Serogroup (Sep)	1358.74	323	4	2725.47	2725.60	2740.58	13.63	6.17
O1	1219.57	294	2	2443.14	2443.18	2450.51		
O139	139.16	29	2	282.33	282.87	285.06		
Biotype (Shared)	1179.80	255	2	2363.60	2363.60	2370.60		
Biotype (Sep)	1170.40	255	4	2348.70	2348.90	2362.90	14.70	7.80
El Tor	681.60	173	2	1367.10	1367.20	1373.40		
Classical	488.80	82	2	981.60	981.70	986.40		
Classical-Serotype (Shared)	488.80	82	2	981.60	981.70	986.40		
Classical-Serotype (Separate)	482.70	82	4	973.40	973.90	983.00	7.80	3.40
Inaba (Classical)	282.30	46	2	568.50	568.80	572.20		
Ogawa (Classical)	200.40	36	2	404.90	405.20	408.00		
El Tor-Serotype (Shared)	614.90	107	2	1233.70	1233.80	1239.10		
El Tor-Serotype (Separate)	604.20	107	4	1216.30	1216.70	1227.00	17.10	12.00
Inaba (El Tor)	81.30	32	2	166.70	167.10	169.60		
Ogawa (El Tor)	522.80	75	2	1049.70	1049.90	1054.30		
O1 (Shared)	1219.57	294	2	2443.14	2443.18	2450.51		
O1 (Separate)	1209.3	294	4	2426.66	2426.80	2441.40	16.38	9.11
O1-Experimental	561.82	91	2	1127.63	1127.80	1132.65		
O1-Observational	647.52	203	2	1299.03	1299.09	1305.66		

2.1 Alternative Parametric Models

In addition to fitting our data to a log-normal distribution we explored the fit of Weibull, and gamma distributions. The fit of the each of these models to O1 and O139 are shown below in Table 2. While there is statistical support (by likelihood ratio test) for the use of the gamma distribution for *V. cholerae* O1, there are no clinically relevant differences in the resulting estimates, and we chose to follow conventionally used and more familiar log-normal distribution.[4,5]

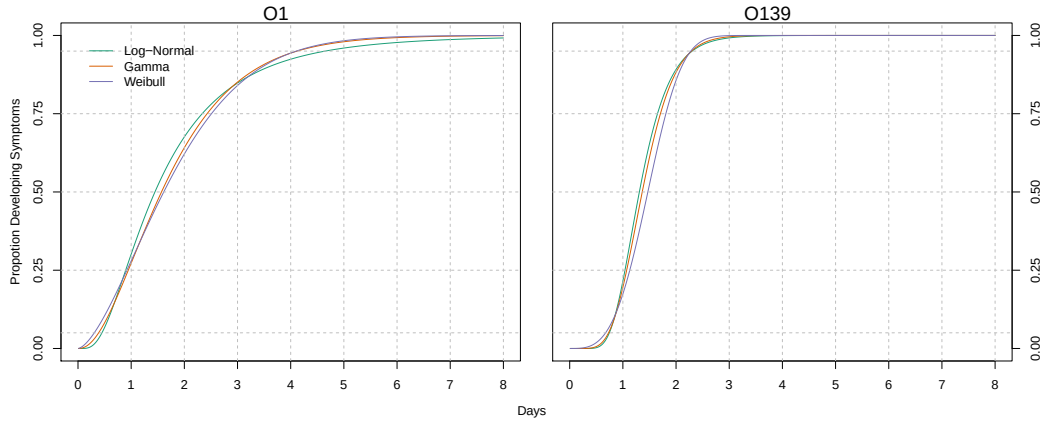

Figure 2: **Comparison of maximum likelihood estimate incubation period distributions with log-normal, Weibull, and gamma distributions.**

Table 2: **Comparison of -2 log likelihood for different parametric models**

	Log-Normal	**Gamma**	**Weibull**
O1	2439.1	2416.7	2422.4
O139	278.3	278.9	280.0

2.2 Hierarchical Models

We explored hierarchical Bayesian models to investigate whether adjusting for study type (i.e. observational vs. experimental) could explain the differences between strains of different biotypes and serotypes. To do this we modeled the mean of natural logarithm of time ($log(T)$), and the log of its standard deviation. We built two models, one that adjusted for biotype and the other that adjusted for serotypes within each biotype. We fit each model with only an intercept and indicator for the strain type (e.g. biotype), and noted whether the 95% CIs of the parameters associated with strain type crossed zero. Next we included an indicator variable which took the value of one when the study was observational and zero if it was experimental. If the parameter associated with the strain type in the model with the study type indicator crossed zero, this suggests that the variability between strains can be accounted for by study type.

In general the differences between strains came through differences in the variance model, not the mean model (i.e. the alphas below, not the betas in the code shown in Figure 3). We found that differences between biotypes (El Tor and classical), and classical serotypes (Ogawa and Inaba) could be explained by study type. While the differences between El Tor serotypes were attenuated after adjustment for study type, they remained significant.

We fit these models in JAGS,[6] and ran three parallel chains for each model and assessed convergence in the same manner at the first model described above. It should be noted that in these models we reduced all doubly censored data to singly interval censored data to ease computations. With this singly reduced data, we were able to almost exactly replicate the results presented in the main text.

```
model
{
    for (i in 1:study) {
        for (j in offset[i]:(offset[i + 1] - 1)) {
            ## next two lines deal with censoring
            y[j] ~ dinterval(log.t[j], log.lim.s[j, 1:2])
            log.t[j] ~ dnorm(mu[i], tau[i])
        }
    }
    for (k in 1:study) {
        mu[k] <- beta0 + beta.bt * bt[k]  #modeling the mean of log.t
        alpha.re[k] ~ dnorm(0.0, tau.l.sigma)
        l.sigma[k] <- alpha0 + alpha.bt * bt[k] + alpha.obs *
            is.obs[k] #modeling the log sd of log.t
        sigma[k] <- exp(l.sigma[k])
        tau[k] <- 1/(sigma[k] * sigma[k])
    }
    beta0 ~ dnorm(0.0, 0.001)
    alpha0 ~ dnorm(0.0, 0.001)
    alpha.bt ~ dnorm(0.0, 0.001)
    beta.bt ~ dnorm(0.0, 0.001)
    alpha.obs ~ dnorm(0.0, 0.001)
    sigma.l.sigma ~ dunif(0.001, 10)
    tau.l.sigma <- 1/(sigma.l.sigma * sigma.l.sigma)
}
```

Figure 3: JAGS code for Biotype Model

2.3 Non-parametric Models

We fit O1 and O139 data using a non-parametric maximum likelihood estimate for doubly interval censored data using the self-consistent estimator, as implemented in the R package, interval.[7] This estimator proposed, by Turnbull, divides the distribution into areas with equal statistical support, shown as rectangles. We visually compared the non-parametrically estimated distribution of incubation periods to those fit with maximum likelihood techniques. As seen below in Figure 4, the distributions match reasonably well.

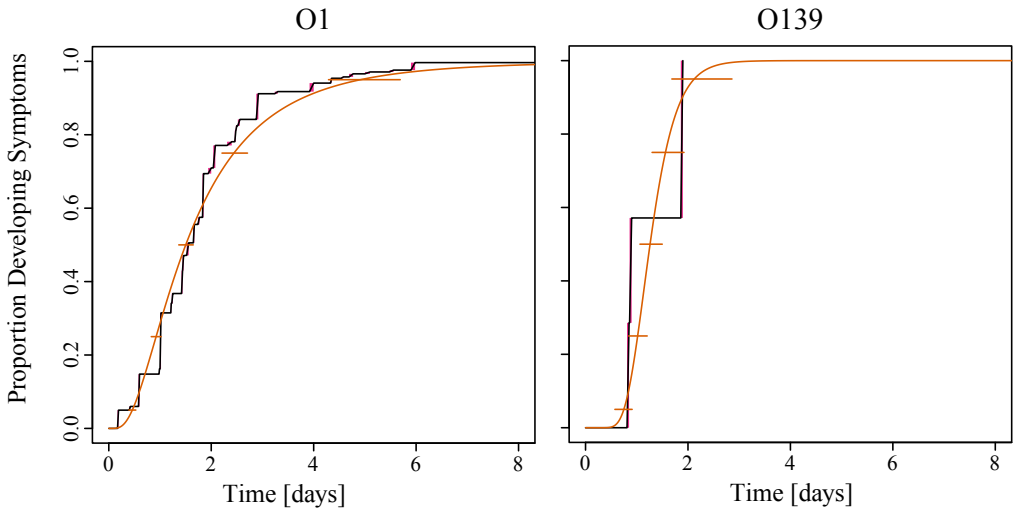

Figure 4: **Orange line is the parametric fit used in the paper and the black line represents the non-parametric maximum likelihood estimate based on the method of Turnbull. Pink rectangles represent areas of equal support by the data.**

3 Full Results by Strain and Study Type

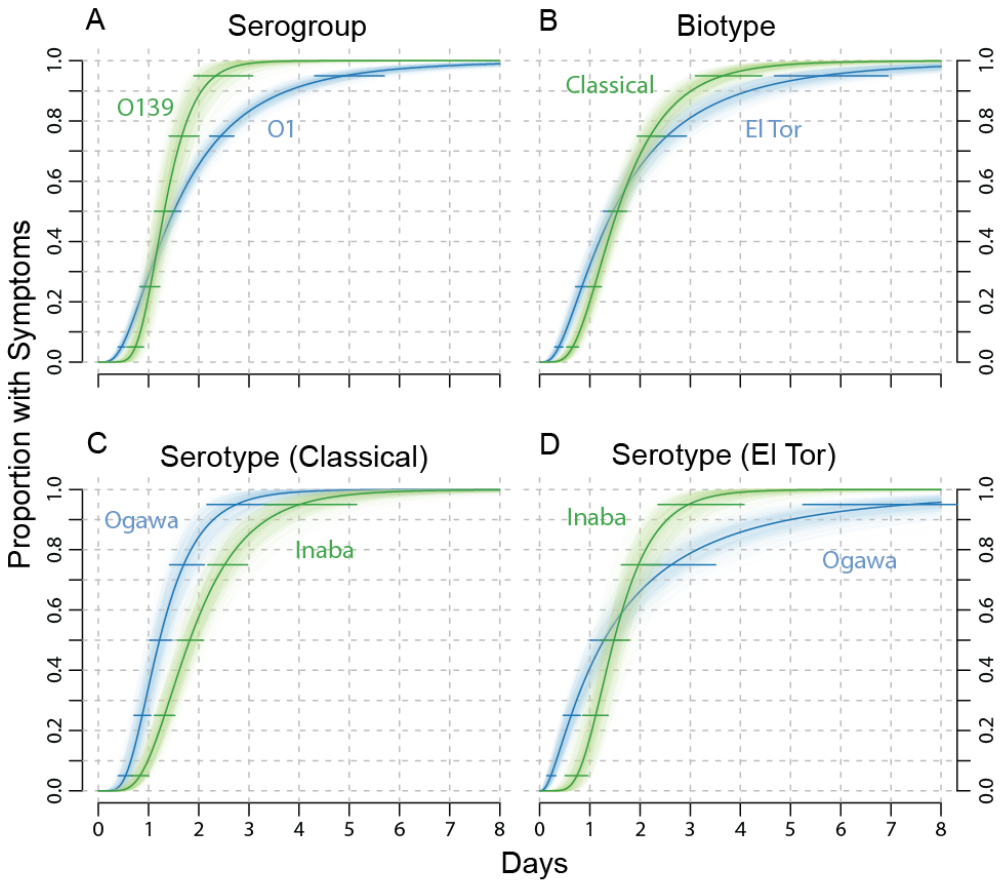

Figure 5: **Incubation period distributions by serogroup (A), biotype (B), and serotype (C,D). 95% credible intervals shown with horizontal bars, and light colored lines represent draws from the joint posterior distribution of parameters.**

Table 3: **Estimates of 5th, 25th, 50th (median), 75th, and 95th percentiles, and dispersion for the incubation periods of cholera by serogroup, biotype, and serotype within biotype. 95% credible intervals are shown in parentheses. The numbers of observations are shown under the column labeled n, and the number and type (experimental or observational) of studies from which the observations came from are labeled s_{exp} and s_{obs}. * indicates that one study had both two different serotypes.**

	n	s_{exp}	s_{obs}	n_{exp}	n_{obs}	5^{th} **percentile**	25^{th} **percentile**	50^{th} **percentile**	75^{th} **percentile**	95^{th} **percentile**	**dispersion**
All	323	8	9	120	203	0.5 (0.4,0.5)	0.9 (0.8,1.0)	1.4 (1.3,1.6)	2.3 (2.1,2.5)	4.4 (3.9,5.0)	1.98 (1.87,2.11)
O1	294	5	9	91	203	0.5 (0.4,0.5)	0.9 (0.8,1.0)	1.5 (1.3,1.6)	2.3 (2.1,2.6)	4.7 (4.1,5.4)	2.04 (1.92,2.19)
O139	29	3	0	29	0	0.7 (0.6,0.9)	1.0 (0.9,1.2)	1.3 (1.1,1.5)	1.7 (1.4,2.0)	2.3 (1.9, 3.1)	1.42 (1.31,1.54)
Inaba	78	4	1	55	23	0.8 (0.7,0.9)	1.2 (1.1,1.4)	1.7 (1.5,1.9)	2.3 (2.1,2.6)	3.6 (3.1,4.4)	1.59 (1.48,1.74)
Ogawa	111	1	3	36	75	0.3 (0.2,0.4)	0.7 (0.6,0.8)	1.3 (1.1,1.5)	2.3 (1.9,2.8)	5.6 (4.4,7.5)	2.46 (2.21,2.85)
El Tor	173	2	5	9	164	0.4 (0.3,0.5)	0.8 (0.7,1.0)	1.5 (1.3,1.7)	2.5 (2.2,2.9)	5.6 (4.7,6.9)	2.27 (2.08,2.53)
Classical	82	3	0	82	0	0.7 (0.5,0.8)	1.1 (0.9,1.2)	1.5 (1.4,1.7)	2.2 (1.9,2.5)	3.6 (3.1,4.5)	1.68 (1.57,1.85)
Inaba (Classical)	46	3*	0	46	0	0.8 (0.6,1.0)	1.3 (1.1,1.5)	1.8 (1.6,2.1)	2.5 (2.2,3.0)	4.0 (3.3,5.2)	1.62 (1.48,1.82)
Ogawa (Classical)	36	3*	0	36	0	0.5 (0.4,0.7)	0.9 (0.7,1.0)	1.2 (1.0,1.5)	1.7 (1.4,2.1)	2.7 (2.2,3.8)	1.64 (1.48,1.92)
Inaba (El Tor)	32	2	1	9	23	0.7 (0.5,1.0)	1.1 (0.9,1.4)	1.5 (1.2,1.8)	2.0 (1.6,2.4)	3.0 (2.4,4.1)	1.52 (1.37,1.81)
Ogawa (El Tor)	75	0	3	0	75	0.2 (0.1,0.3)	0.6 (0.5,0.8)	1.3 (1.0,1.6)	2.6 (2.0,3.5)	7.4 (5.2,11.5)	2.89 (2.46,3.62)
Experimental	120	-	-	-	-	0.7 (0.6,0.8)	1.1 (1.0,1.2)	1.5 (1.4,1.6)	2.1 (1.9,2.3)	3.3 (2.9,3.9)	1.63 (1.54,1.76)
Observational	203	-	-	-	-	0.4 (0.3,0.4)	0.8 (0.7,0.9)	1.4 (1.2,1.5)	2.4 (2.1,2.7)	5.2 (4.4,6.4)	2.26 (2.08,2.52)
O1(No ET Ogawa)	219	5	6	91	128	0.7 (0.6,0.8)	1.1 (1.0,1.2)	1.5 (1.4,1.7)	2.1 (1.9,2.4)	3.5 (3.0,4.1)	1.64 (1.54,1.78)
All (No ET Ogawa)	248	8	6	120	128	0.7 (0.6,0.8)	1.1 (1.0,1.2)	1.5 (1.4,1.7)	2.1 (2.0,2.3)	3.4 (3.1,3.8)	1.62 (1.54,1.71)

4 Sensitivity Analyses

4.1 Serogroup definition

This section presents tables of likelihood-based and Bayesian estimates of incubation periods including and excluding observations made before serogroup definitions existed.[8]

Table 4: **Estimates without data from before serogroup classification, Bayesian**

	p5	p25	p50	p75	p95	disp
All	0.5 (0.4,0.5)	0.9 (0.8,1)	1.4 (1.3,1.6)	2.3 (2.1,2.5)	4.4 (3.9,5)	2 (1.9,2.1)
O1	0.5 (0.4,0.5)	0.9 (0.8,1)	1.5 (1.4,1.6)	2.4 (2.2,2.7)	4.9 (4.3,5.7)	2.1 (1.9,2.2)
O139	0.7 (0.6,0.9)	1 (0.9,1.2)	1.3 (1.1,1.5)	1.7 (1.4,2)	2.3 (1.9,3.1)	1.4 (1.3,1.6)
Inaba	0.8 (0.7,0.9)	1.2 (1.1,1.4)	1.7 (1.5,1.9)	2.3 (2.1,2.6)	3.6 (3.1,4.4)	1.6 (1.5,1.7)
Ogawa	0.3 (0.2,0.4)	0.7 (0.6,0.8)	1.3 (1.1,1.5)	2.3 (2,2.8)	5.6 (4.4,7.5)	2.5 (2.2,2.8)
ElTor	0.4 (0.3,0.5)	0.8 (0.7,1)	1.5 (1.3,1.7)	2.5 (2.2,2.9)	5.6 (4.7,6.9)	2.3 (2.1,2.5)
Classical	0.7 (0.5,0.8)	1.1 (0.9,1.2)	1.5 (1.4,1.7)	2.2 (1.9,2.5)	3.6 (3.1,4.4)	1.7 (1.6,1.9)
Inaba (Classical)	0.8 (0.6,1)	1.3 (1.1,1.5)	1.8 (1.6,2.1)	2.5 (2.2,3)	4 (3.3,5.2)	1.6 (1.5,1.8)
Ogawa (Classical)	0.5 (0.4,0.7)	0.9 (0.7,1)	1.2 (1,1.5)	1.7 (1.4,2.1)	2.7 (2.2,3.8)	1.6 (1.5,1.9)
Inaba (El Tor)	0.7 (0.5,1)	1.1 (0.9,1.4)	1.5 (1.2,1.8)	2 (1.6,2.4)	3 (2.4,4.1)	1.5 (1.4,1.8)
Ogawa (El Tor)	0.2 (0.1,0.3)	0.6 (0.5,0.8)	1.3 (1,1.6)	2.6 (2,3.5)	7.4 (5.2,11.5)	2.9 (2.5,3.6)
Experimental	0.7 (0.6,0.8)	1.1 (1,1.2)	1.5 (1.4,1.6)	2.1 (1.9,2.3)	3.3 (2.9,3.9)	1.6 (1.5,1.8)
Observational	0.4 (0.3,0.4)	0.8 (0.7,0.9)	1.4 (1.2,1.5)	2.4 (2.1,2.7)	5.2 (4.4,6.4)	2.3 (2.1,2.5)
O1 (No ET Ogawa)	0.7 (0.6,0.8)	1.1 (1,1.2)	1.5 (1.4,1.7)	2.1 (1.9,2.4)	3.5 (3,4.1)	1.6 (1.5,1.8)
All (No ET Ogawa)	0.7 (0.6,0.8)	1.1 (1,1.2)	1.5 (1.4,1.7)	2.1 (2,2.3)	3.4 (3.1,3.8)	1.6 (1.5,1.7)

Table 5: **Estimates with data from before serogroup classification, Bayesian**

	p5	p25	p50	p75	p95	disp
All	0.5 (0.4,0.5)	0.9 (0.8,1)	1.4 (1.3,1.6)	2.3 (2.1,2.5)	4.4 (3.9,5.0)	2 (1.9,2.1)
O1	0.4 (0.4,0.5)	0.9 (0.8,1)	1.4 (1.3,1.6)	2.3 (2.1,2.6)	4.7 (4.1,5.4)	2 (1.9,2.2)
O139	0.7 (0.6,0.9)	1 (0.9,1.2)	1.3 (1.1,1.5)	1.7 (1.4,2)	2.3 (1.9,3.1)	1.4 (1.3,1.6)
Inaba	0.8 (0.7,0.9)	1.2 (1.1,1.4)	1.7 (1.5,1.9)	2.3 (2.1,2.6)	3.6 (3.1,4.4)	1.6 (1.5,1.7)
Ogawa	0.3 (0.2,0.4)	0.7 (0.6,0.8)	1.3 (1.1,1.5)	2.3 (2,2.8)	5.6 (4.4,7.5)	2.5 (2.2,2.8)
ElTor	0.4 (0.3,0.5)	0.8 (0.7,1)	1.5 (1.3,1.7)	2.5 (2.2,2.9)	5.6 (4.7,6.9)	2.3 (2.1,2.5)
Classical	0.7 (0.5,0.8)	1.1 (0.9,1.2)	1.5 (1.4,1.7)	2.2 (1.9,2.5)	3.6 (3.1,4.4)	1.7 (1.6,1.9)
Inaba (Classical)	0.8 (0.6,1)	1.3 (1.1,1.5)	1.8 (1.6,2.1)	2.5 (2.2,3)	4 (3.3,5.2)	1.6 (1.5,1.8)
Ogawa (Classical)	0.5 (0.4,0.7)	0.9 (0.7,1)	1.2 (1,1.5)	1.7 (1.4,2.1)	2.7 (2.2,3.8)	1.6 (1.5,1.9)
Inaba (El Tor)	0.7 (0.5,1)	1.1 (0.9,1.4)	1.5 (1.2,1.8)	2 (1.6,2.4)	3 (2.4,4.1)	1.5 (1.4,1.8)
Ogawa (El Tor)	0.2 (0.1,0.3)	0.6 (0.5,0.8)	1.3 (1,1.6)	2.6 (2,3.5)	7.4 (5.2,11.5)	2.9 (2.5,3.6)
Experimental	0.7 (0.6,0.8)	1.1 (1,1.2)	1.5 (1.4,1.6)	2.1 (1.9,2.3)	3.3 (2.9,3.9)	1.6 (1.5,1.8)
Observational	0.4 (0.3,0.4)	0.8 (0.7,0.9)	1.4 (1.2,1.5)	2.4 (2.1,2.7)	5.2 (4.4,6.4)	2.3 (2.1,2.5)
O1 (No ET Ogawa)	0.7 (0.6,0.8)	1.1 (1,1.2)	1.5 (1.4,1.7)	2.1 (1.9,2.4)	3.5 (3,4.1)	1.6 (1.5,1.8)
All (No ET Ogawa)	0.7 (0.6,0.8)	1.1 (1,1.2)	1.5 (1.4,1.7)	2.1 (2,2.3)	3.4 (3.1,3.8)	1.6 (1.5,1.7)

Table 6: **Estimates without data from before serogroup classification, Likelihood**

	p5	p25	p50	p75	p95	disp
All	0.5 (0.4,0.5)	0.9 (0.8,1)	1.4 (1.3,1.6)	2.3 (2.1,2.5)	4.4 (3.9,5)	2 (1.9,2.1)
O1	0.5 (0.4,0.5)	0.9 (0.8,1)	1.5 (1.4,1.6)	2.4 (2.2,2.7)	4.9 (4.2,5.6)	2 (1.9,2.2)
O139	0.8 (0.6,0.9)	1 (0.8,1.2)	1.3 (1,1.5)	1.5 (1.2,1.9)	2.1 (1.5,2.6)	1.4 (1.2,1.5)
Inaba	0.8 (0.7,0.9)	1.3 (1.1,1.4)	1.7 (1.5,1.9)	2.3 (2,2.6)	3.6 (3,4.2)	1.6 (1.5,1.7)
Ogawa	0.3 (0.2,0.4)	0.7 (0.6,0.8)	1.3 (1.1,1.5)	2.3 (1.9,2.8)	5.6 (4.1,7)	2.4 (2.1,2.8)
ElTor	0.4 (0.3,0.5)	0.8 (0.7,1)	1.5 (1.3,1.7)	2.5 (2.2,2.9)	5.6 (4.5,6.7)	2.3 (2,2.5)
Classical	0.7 (0.5,0.8)	1.1 (1,1.2)	1.5 (1.4,1.7)	2.2 (1.9,2.5)	3.6 (3,4.3)	1.7 (1.5,1.8)
Inaba (Classical)	0.8 (0.7,1)	1.3 (1.1,1.5)	1.8 (1.6,2.1)	2.5 (2.1,2.9)	3.9 (3.1,4.8)	1.6 (1.4,1.8)
Ogawa (Classical)	0.5 (0.4,0.7)	0.9 (0.7,1)	1.2 (1,1.4)	1.7 (1.4,2)	2.7 (2,3.4)	1.6 (1.4,1.8)
Inaba (El Tor)	0.8 (0.5,1)	1.1 (0.9,1.4)	1.5 (1.2,1.8)	2 (1.6,2.4)	2.9 (2.1,3.7)	1.5 (1.3,1.7)
Ogawa (El Tor)	0.2 (0.1,0.3)	0.6 (0.5,0.8)	1.3 (1,1.6)	2.6 (1.9,3.3)	7.2 (4.5,9.9)	2.9 (2.3,3.4)
Experimental	0.7 (0.6,0.8)	1.1 (1,1.2)	1.5 (1.3,1.6)	2.1 (1.9,2.3)	3.3 (2.9,3.8)	1.6 (1.5,1.7)
Observational	0.4 (0.3,0.4)	0.8 (0.7,0.9)	1.4 (1.2,1.5)	2.4 (2,2.7)	5.2 (4.2,6.2)	2.3 (2,2.5)
O1 (No ET Ogawa)	0.7 (0.6,0.8)	1.1 (1,1.2)	1.5 (1.4,1.7)	2.1 (1.9,2.4)	3.4 (2.9,4)	1.6 (1.5,1.8)
All (No ET Ogawa)	0.7 (0.6,0.8)	1 (0.9,1.1)	1.4 (1.3,1.5)	2 (1.8,2.1)	3.1 (2.7,3.4)	1.6 (1.5,1.7)

Table 7: **Estimates with data from before serogroup classification, Likelihood**

	p5	p25	p50	p75	p95	disp
All	0.5 (0.4,0.5)	0.9 (0.8,1)	1.4 (1.3,1.6)	2.3 (2.1,2.5)	4.4 (3.9,4.9)	2 (1.9,2.1)
O1	0.4 (0.4,0.5)	0.9 (0.8,1)	1.4 (1.3,1.6)	2.3 (2.1,2.6)	4.6 (4,5.3)	2 (1.9,2.2)
O139	0.7 (0.6,0.9)	1 (0.9,1.2)	1.3 (1.1,1.5)	1.6 (1.3,2)	2.3 (1.7,2.9)	1.4 (1.3,1.6)
Inaba	0.8 (0.7,0.9)	1.3 (1.1,1.4)	1.7 (1.5,1.9)	2.3 (2,2.6)	3.6 (3,4.2)	1.6 (1.5,1.7)
Ogawa	0.3 (0.2,0.4)	0.7 (0.6,0.8)	1.3 (1.1,1.5)	2.3 (1.9,2.8)	5.6 (4.1,7)	2.4 (2.1,2.8)
El Tor	0.4 (0.3,0.5)	0.8 (0.7,1)	1.5 (1.3,1.7)	2.5 (2.2,2.9)	5.6 (4.5,6.7)	2.3 (2,2.5)
Classical	0.7 (0.5,0.8)	1.1 (1,1.2)	1.5 (1.4,1.7)	2.2 (1.9,2.5)	3.6 (3,4.3)	1.7 (1.5,1.8)
Inaba (Classical)	0.8 (0.7,1)	1.3 (1.1,1.5)	1.8 (1.6,2.1)	2.5 (2.1,2.9)	3.9 (3.1,4.8)	1.6 (1.4,1.8)
Ogawa (Classical)	0.5 (0.4,0.7)	0.9 (0.7,1)	1.2 (1,1.4)	1.7 (1.4,2)	2.7 (2,3.4)	1.6 (1.4,1.8)
Inaba (El Tor)	0.8 (0.5,1)	1.1 (0.9,1.4)	1.5 (1.2,1.8)	2 (1.6,2.4)	2.9 (2.1,3.7)	1.5 (1.3,1.7)
Ogawa (El Tor)	0.2 (0.1,0.3)	0.6 (0.5,0.8)	1.3 (1,1.6)	2.6 (1.9,3.3)	7.2 (4.5,9.9)	2.9 (2.3,3.4)
Experimental	0.7 (0.6,0.8)	1.1 (1,1.2)	1.5 (1.4,1.6)	2.1 (1.9,2.3)	3.3 (2.9,3.8)	1.6 (1.5,1.7)
Observational	0.4 (0.3,0.4)	0.8 (0.7,0.9)	1.4 (1.2,1.5)	2.4 (2,2.7)	5.2 (4.2,6.2)	2.3 (2,2.5)
O1 (No ET Ogawa)	0.7 (0.6,0.8)	1.1 (1,1.2)	1.5 (1.4,1.7)	2.1 (1.9,2.4)	3.4 (2.9,4)	1.6 (1.5,1.8)
All (No ET Ogawa)	0.7 (0.6,0.8)	1.1 (1,1.2)	1.5 (1.4,1.7)	2.1 (2,2.3)	3.4 (3,3.8)	1.6 (1.5,1.7)

4.2 Observational vs. Experimental Data

Here we show the fitted distributions of data stratified by strain and study type. While some of these categories are fit with limited data, they provide some insight into the differences between observational and experimental incubation periods in the literature.

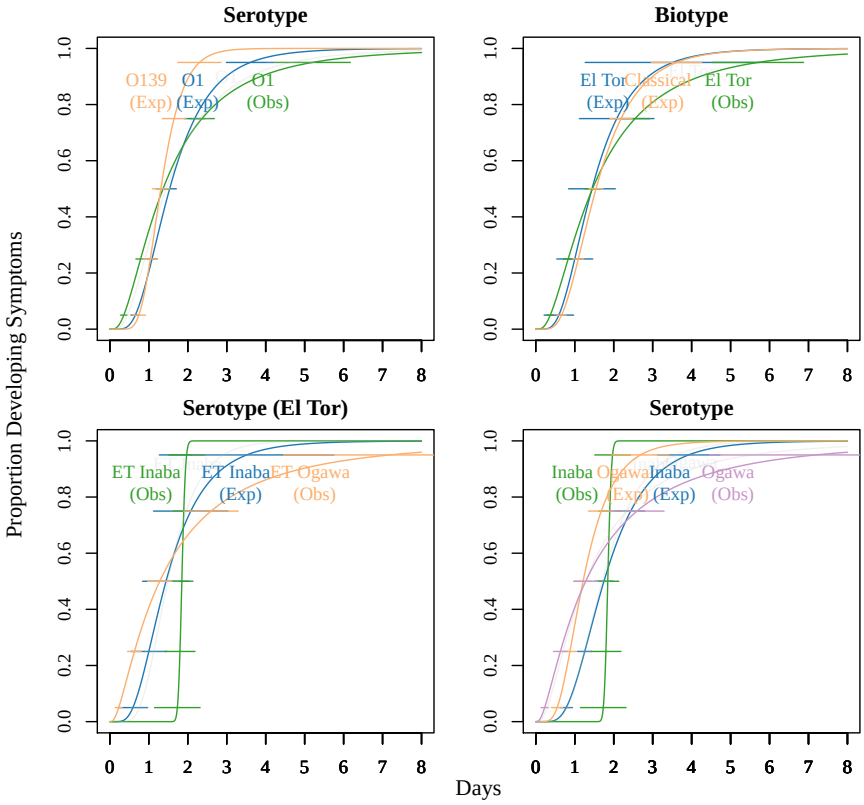

Figure 6: **Fitted incubation period cumulative distribution functions by strain and study type with asymptotic 95% confidence intervals.**

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