**DATA\_EXPLORE:**

**Title:** R-script for data exploration and distribution fitting for all traits

**Legend/Caption:** R-script used for data exploration, histograms, normality tests, q-q lots, and distribution fitting.

**MODELS\_AND\_PLOTS:**

**Title:** R-script for model predictions and data plotting

**Legend/Caption:** R-script used to predict the most parsimonious model using the MuMIN package for all the traits tested in this study. It also contains information on how to plot the data for figure 2, panels B-F.

**FIGURE\_2A:**

**Title:** R-script for plotting figure 2A

**Legend/Caption:** R-script used to plot the data for figure 2A since infectivity (infection rate) is a binomial (1,0) trait and requires further transformation into percentages in order to visualized it.