Data Availability

**All analyses (Figures 1 and 2).**

To analyze change in mortality rate of hosts when infected with evolved versus ancestral bacteria, we used JMP Pro 14 (SAS, Cary, NC). From Excel, we imported: Parasite Tr, Worm Strain, Population, Replicate, and % Change [(evolved-ancestor)/ancestor] into JMP to create a new data table. We then chose these parameters:

Tools 🡪 Fit Model

The “Y” role variable 🡪 % Change

The model effects 🡪 Parasite Tr, Worm Strain

Personality 🡪 Generalized Linear Model

Distribution 🡪 Exponential

Link Function 🡪 Logit

Data file: Mortality\_Change\_P10.xlsx

Once “run” was performed, JMP gave an output of model effects.

Next, we performed contrast tests between variables of interest.

Next to the top heading, “Generalized Linear Model Fit,” there is a red downward-facing arrow. When the arrow is clicked, an option for “Contrast” will come up. These are post-test Tukey’s contrast tests.

**Figure 1a: CB4856**

Contrast tests performed:

* 0:0 (control) with 50:50 + 75:25 + 25:75 (mixed populations combined)
* 100:0 CB4856 with above mixed populations

**Figure 1b: ewIR 68**

Contrast tests performed:

* 0:0 (control) with 50:50 + 75:25 + 25:75 (mixed populations combined)
* 100:0 ewIR 68 with above mixed populations

**Figure 2**

The same GLM analysis was performed as stated above, and then Contrasts were used.

Contrast tests performed:

(CB4856 infected with CB4856-evolved parasites + ewIR 68 with ewIR 68-evolved parasites)

& (CB4856 infected with ewIR 68-evolved parasites + ewIR 68 with CB4856-evolved parasites)