Supporting Information

In the full-sibling feral-larvae trials, and in the the trial using the genetically homogeneous laboratory strain, we reared larvae on artificial diet after the main experiment was over, to keep track of which individuals became infected with the virus. Note that infected larvae are easily identifiable because their integument becomes extremely fragile, leading to the release of viral particles (Dwyer, Elkinton, & Buonaccorsi 1997). For any dead larvae that could not be diagnosed visually, we inspected smears under a light microscope at 400× for the presence of occlusion bodies. To see how the area of virus disc consumed affected infection risk, we analyzed the data using a mixed-effects logit model, and again used AIC analysis to choose between different models. As Table shows, the best model for feral larvae included only effects of full-sib family, but this model could not be distinguished from a model that included an effect of area consumed. The model with a family by area interaction in contrast received very little support. Meanwhile, for the laboratory larvae, the best model included only an area effect, and the other two models received very little support. As we describe in the main text, we suspect that the lack of an interaction between family and area was due to a combination of variability in physiological susceptibility, at least among feral larvae, and variability in how close larvae got to cadavers before they stopped feeding.

References

Dwyer G., Elkinton J.S., & Buonaccorsi J.P. (1997) Host heterogeneity in susceptibility and disease dynamics: Tests of a mathematical model. *The American Naturalist*, **150**, 685–707.

Table S1: AIC analysis of infection rate data.

	Feral Larvae		Laboratory Larvae	
Model	Δ AIC	AIC wt.	Δ AIC	AIC wt.
Family Effect	0	68.4	13.5	0.1
Area Effect	1.8	27.8	0	81.7
Family by Area	5.8	3.8	3.0	18.2