There are two datasets and processing scripts, organized into Experiment 1 and Experiment 2. Before running any of the scripts, ensure that 1) the data folders and scripts folders are all located in the same directory (e.g., put all folders on the Desktop) and 2) All references to setwd("~/Desktop/") in the script you are running have replaced "~/Desktop/" with the name of that directory (if it's the Desktop, you don't need to change these). Otherwise, attempts of stats or figure scripts to access data will fail. Statistics scripts will also source scripts from the general stats scripts folder, so make sure this folder is in the same directory.

In Experiment 1, juvenile soapberry bugs were raised on seeds of three host plants (nathost=Cardiospermum corindum, Koelreuteria elegans, and Koelreuteria paniculata) that were either intact or had experienced prior feeding by adult soapberry bugs (Treatment: "Y"=prior feeding, "N"=intact). Before being given to juveniles, holes created by adults were counted for seeds in the prior feeding treatment. Once they reached adulthood, all bugs were measured for morphology.

In Exp.1.data.survival.csv, the data is recorded as follows: ID (identifying number), Family (parent ID number), Population (collection location), pophost (host species from which the parents were collected), nathost (developmental host), Trmt (prior feeding or intact treatment), hatch.date (date the nymph hatched), S1.cones, S2.cones, and S3.cones (holes created by adults in seeds 1, 2, and 3), death.date (day the juvenile died, if it did not reach adulthood; otherwise NA), eclosion.date (date the juvenile reached adulthood; otherwise NA), sex (sex, if it reached adulthood), feeding1 (number of hours seed 1 was in the incubator; for prior feeding treatment, the number of hours it was exposed to adult feeding); lifespan (lifespan for bugs that died before reaching adulthood; otherwise #VALUE!), Dvpt.time (time from hatch to adulthood, for bugs that reached adulthood; otherwise #VALUE!).

In Exp1.data.morphology.csv, morphological measures for the same experiments for individuals that reached adulthood. Columns are as follows: ID (same as in Exp.1.data.survival.csv), sex, thorax (width of pronotum at widest point), beak (length of rostrum), wing (length of forewing), and wmorph (wing morph, short or long).

For all scripts, setwd() calls should be updated at the top of each section to the location of the unzipped dryad folder. Scripts call each other and data files using the organization of the whole file structure, so do not rearrange folders within these! Scripts analyzing these two Experiment 1 datasets are in the "Experiment 1 stats" folder, for comparing C. corindum and K. elegans. “1-load\_survival” contains functions for loading and organizing the data files into a format that works for the analyses; these are loaded and called within the other scripts. “1a-facilitation.survival.R” analyzes survival in Experiment 1. “1b-facilitation.survival.by.holes” analyzes survival split in early and late, and as a function of the number of holes drilled in each seed within the prior feeding treatment alone. “1c-development.time.R” analyzes development time, both as a function of treatment and as a function of hole number within the prior feeding treatment. “1d-body size.R” analyzes thorax width, both as a function of treatment and as a function of hole number within the prior feeding treatment. Statistics scripts are in R and commented.

Appendix A stats and Appendix B stats deal with cases including K. paniculata as a collection host and natal host, respectively. Statistics scripts are in R and commented to explain what's going on at each stage.

In Experiment 2, juvenile soapberry bugs were raised on seeds of two host plant (C. corindum and K. elegans) that were either intact or cracked manually with pliers. Once they reached adulthood, morphology was measured for each individual.

In Exp2.data.survival.csv, the data is recorded as follows: Number (identifying number), Parents (parent ID number), bugpop (collection location), natpop (collection location of rearing host seeds), hatch date (date the nymph hatched), eclosion date (date the juvenile reached adulthood; otherwise NA), death date (day the juvenile died, if it did not reach adulthood; otherwise NA), sex (sex, if it reached adulthood), cracked (seed treatment: n=intact, y=cracked), lifespan (lifespan for bugs that died before reaching adulthood; otherwise gigantic negative number), Dvpt.time (time from hatch to adulthood, for bugs that reached adulthood; otherwise #VALUE!), mathost (host the mother was reared on).

In Exp2.data.morphology.csv, columns are as above, with the addition of beak (length of rostrum), thorax (width of the pronotum at the widest point), wing (length of forewing), and wing2 (wing morph, short or long)

For all scripts, setwd() calls should be updated at the top of each section to the location of the unzipped dryad folder. Scripts call each other and data files using the organization of the whole file structure, so do not rearrange folders within these! Scripts analyzing these two Experiment 2 datasets are in the “Experiment 2 stats” folder. “2-load\_survival.R” loads and organizes the Exp2.data.survival csv file into a format that works for the analyses. “2a-Cracked.vs.intact.survival.R” analyzes survival in Experiment 2. “2b-Crackedvsintact.survival.day7.R” analyzes survival split in early and late. “2c-Cracked.vs.intact.dvpt.time.R” analyzes development time. “2d-Crackedvsintact.body.size.R” analyzes thorax width. Statistics scripts are in R and commented.

The “Figures” folder contains 3 scripts. Figure code.R generates the figures from the body of the paper. FigsAA.R generates the figures from Appendix A. FigsAB.R generates the figures from Appendix B.

The “general stats scripts” sub-folder contains scripts for running multiple model comparisons that are used for multiple analyses.