Figure S1. A histogram of the 50,000 simulated values for the proportion of diploid males for a single female with id=M-7 using parameters $n_{loci} = 1$; $s = 0.19$. The grey line depicts the smoothened density function f_{M-7} obtained by `approxfun()`. The actual datapoint of the proportion of diploid males for female M-7 is 0 out of 7 diploid offspring (dashed vertical line). The likelihood for the current parameters is $f_{M-7}(0 \mid 1, 0.19) = 0.295$.
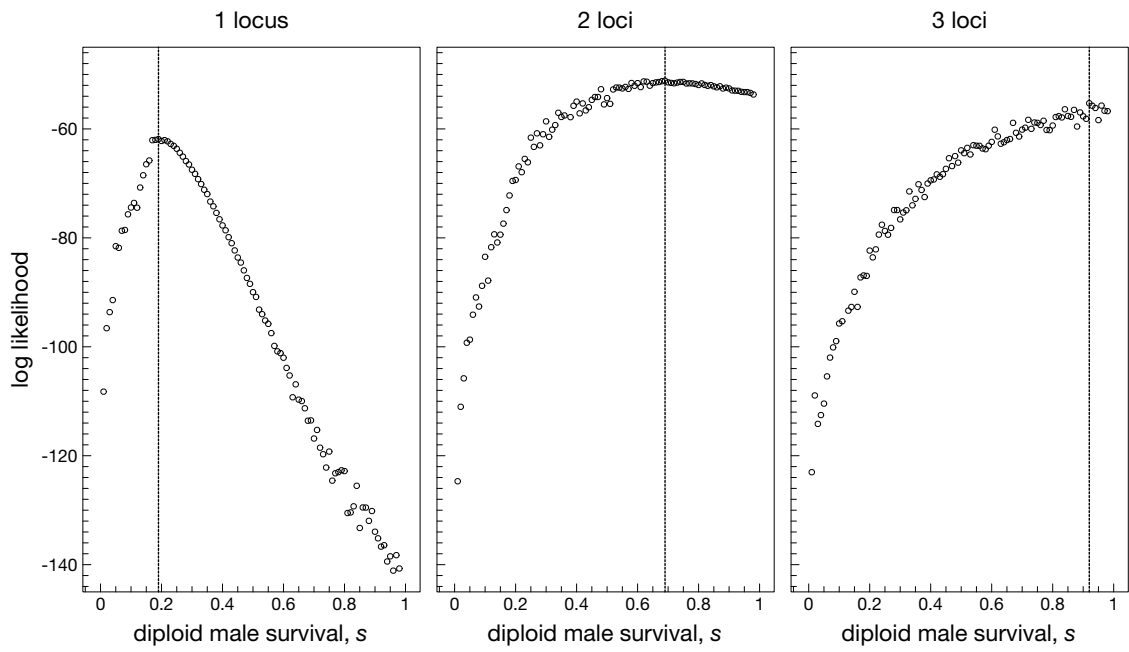
Figure S2. Total likelihood value for different values of diploid male survival *s* and the number of CSD loci, n_{loci}. Likelihood is maximized for *s*=0.69 and n_{loci}=2.
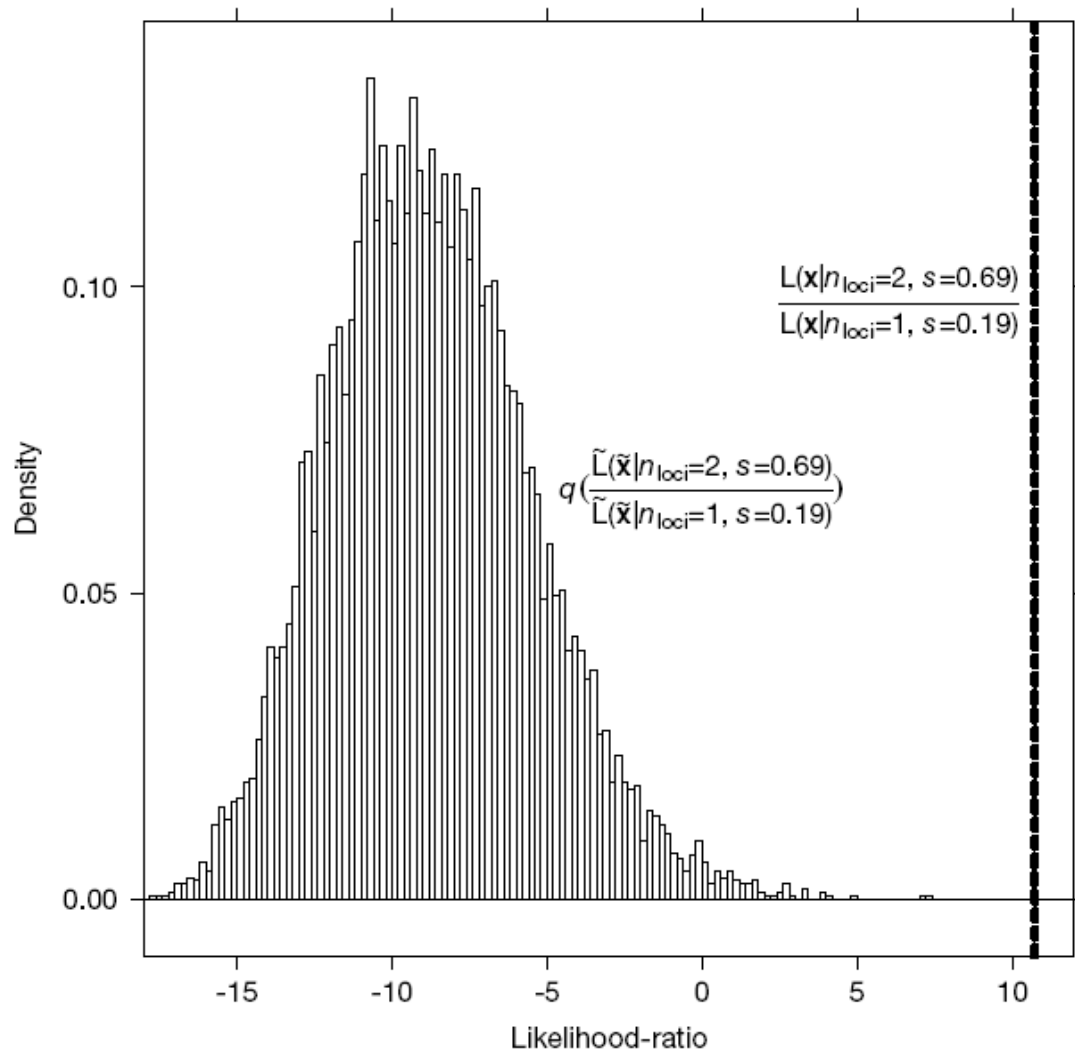
Figure S3. The histogram depicts the distribution q of 5,000 likelihood ratio test values for simulated data $\tilde{\mathbf{x}}$, when the null hypothesis $n_{loci}=1, s=0.19$ holds true. This is compared to the actual likelihood ratio for the experimentally observed dataset $\mathbf{x}$, which amounts to a value beyond the distribution q. As such, the likelihood ratio test in Table 3 in the main text results in a significance value $p=0.000$
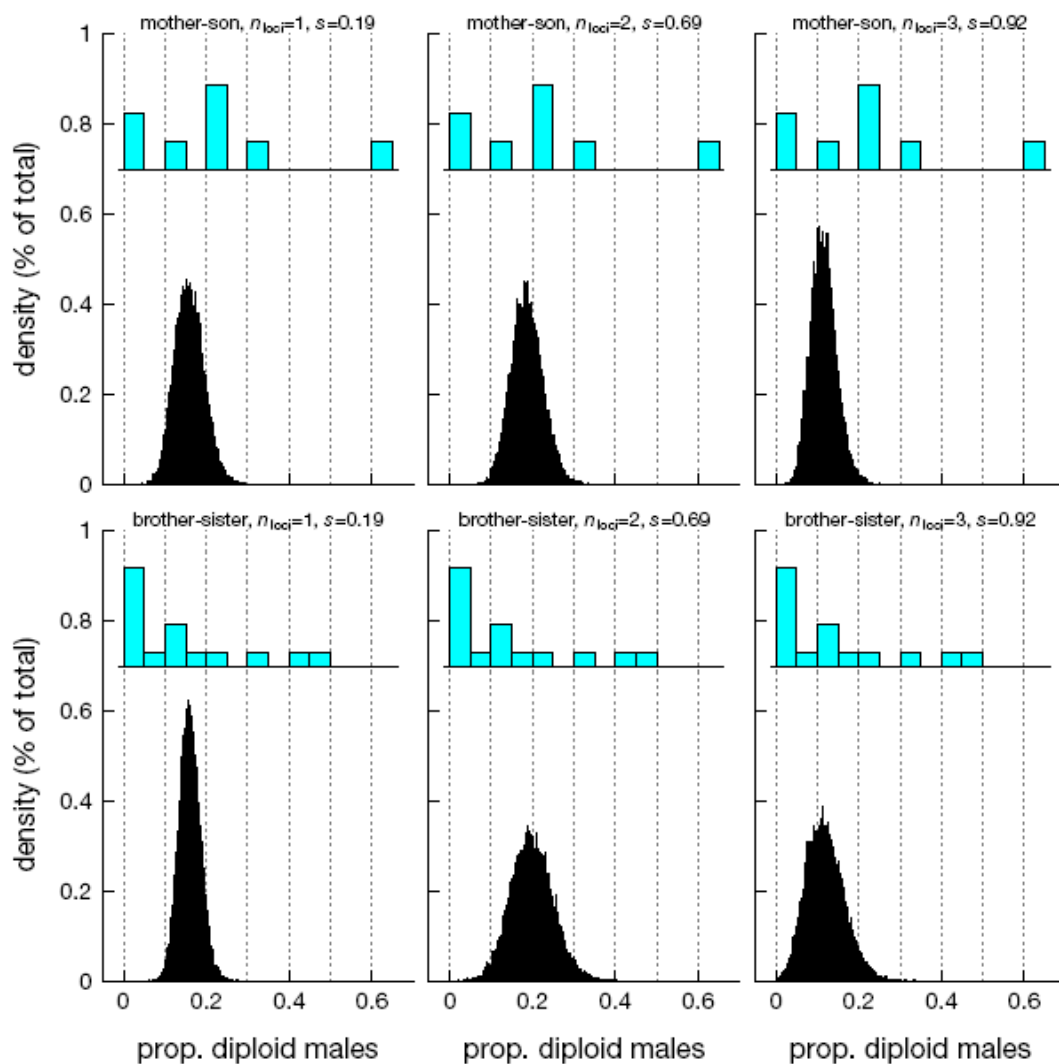
Figure S4. Predicted (black histogram) and observed (green histogram) proportions of diploid males per generation for each of the three models that had the highest likelihoods in Figure S2. Distributions with multiple loci are predicted to be wider in generation two, which matches the data. In contrast, the single locus distribution becomes narrower, as the proportion of diploid males is always 0.5 for each individual mother, whereas the proportion of diploid males is more variable in a multilocus model due to more possibilities of segregation of different CSD alleles in different mothers during the BS generation. MS: mother-son (generation 1), BS: brother-sister (generation 2).
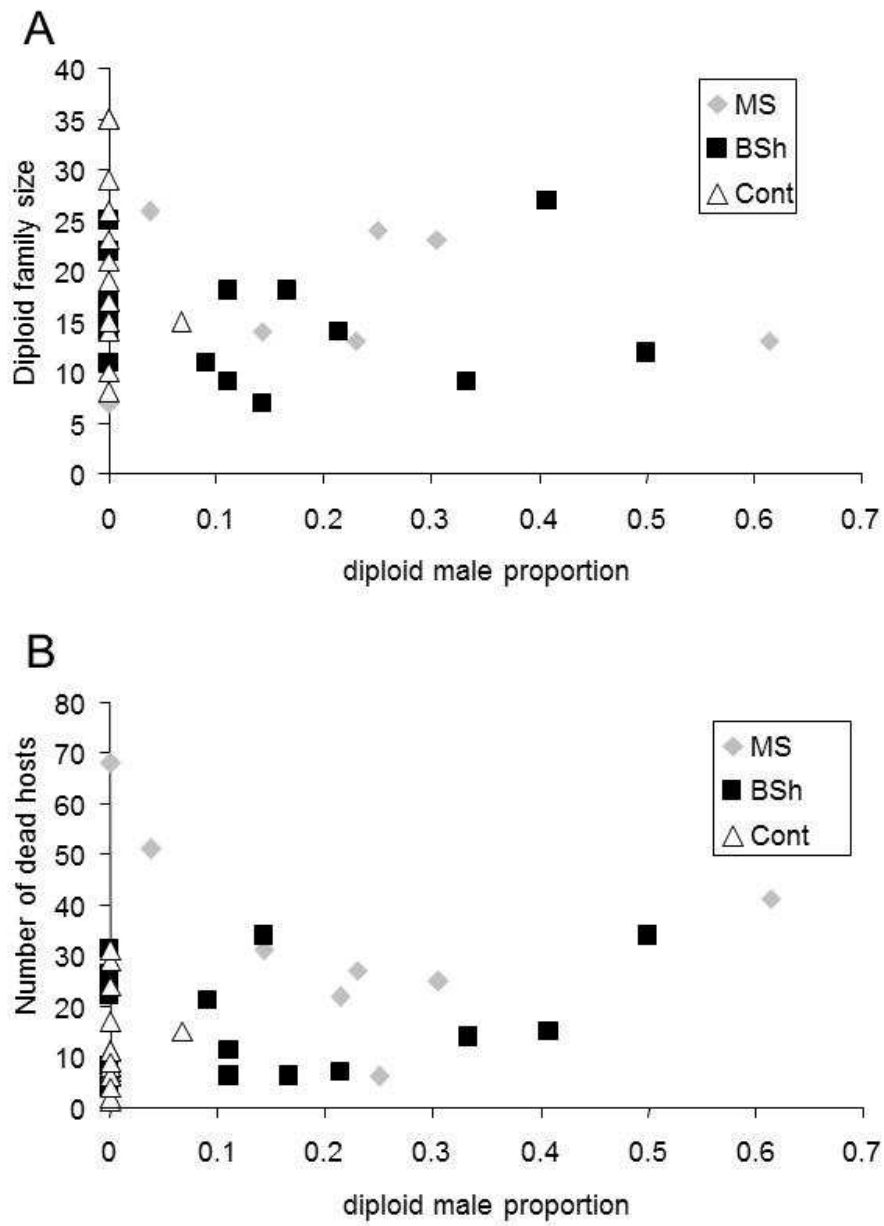
Figure S5. Scatter plots showing the absence of a relationship between the proportion of diploid males and (A) diploid family size, and (B) the number of dead hosts.