Supplementary information





Supplementary information 1. Dry body weight plotted against body length of three-spined sticklebacks, before (upper figure) and after (lower figure) dry weight was power-transformed (x0.25) to achieve approximate linearity (and hence homoscedasticity when run in a GLM, see Grafen and Hails (2000). The *R2*-value of a GLM of the x0.25 transformed dry weight over body length was 0.909. This *R2*-value is higher (and hence gives a better approximation to linearity) compared to *R2*-value from other transformations like x1/3, ln(x), lg(x), x2, x0.5, and 1/x. Filled and open triangles are from Lake Nedre Vollvatn and Lake Storvatnet, respectively.

Supplementary information 2.

Body length of stickleback host as the response variable in a GLM Type III (adjusted) sums of squares (SS). The predictors are ‘year’ of sampling 1996 and 1997 from Lake Nedre Vollvatn and 2012 and 2014 from Lake Storvatnet, and ‘single-multiple infection’ by tapeworm(s) were added as fixed factors. Adjusted *R*2 = 0.476.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Source | SS | df | *F* | *P*-value |
| Analysis of variance |  |  |  |  |
| Single-multiple infections | 4.828 | 1 | 5.806 | 0.017 |
| Year | 2.651 | 3 | 1.063 | 0.366 |
| Error | 142.177 | 170 |  |  |
| Total | 3547.700 | 175 |  |  |
|  |  |  |  |  |

Supplementary information 3a.

This model is similar to the model presented in Table 2a, except that here wet fish weight (instead of dry fish weight) is used when calculating the response variable ‘Host condition’ (residuals of x0.25- transformed fish wet weight adjusted for fish body length) and the predictor ‘Parasite-index’. The model explained 56.1% of the variation (*R*2 = 0.561).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Source | | SS | df | *F* | | *P*-value |
| Analysis of variance | |  |  |  | |  |
| Single-multiple infection | | 7.431 | 1 | 17.842 | | < 0.001 |
| Parasite index | | 42.783 | 1 | 102.726 | | < 0.001 |
| Year | | 38.102 | 3 | 30.496 | | < 0.001 |
| Error | | 70.800 | 170 |  | |  |
| Total | | 27.982 | 176 |  | |  |
| Term | |  |  |  | |  |
| Coefficients | Coeff. | | S.E. Coeff. | | *t* | *P*-value |
| Constant | 1.637 | | 0.1346 | | 12.16 | < 0.001 |
| Single-multiple infection | -0.4662 | | 0.1104 | | -4.22 | < 0.001 |
| Parasite index | -4.7337 | | 0.4670 | | -10.14 | < 0.001 |



Supplementary information S3b.

This table and the figure show that condition of hosts measured as by wet weight is lower for hosts infected by 1 tapeworm (open circles) compared to tapeworms infected by ≥ 2 tapeworms (filled circles), after adjusting for weight of the parasite (Parasite index). “Host condition” and “Parasite index” are calculated using wet host weight in this figure, otherwise the data are the same as in Fig. 1a (where host dry weight are used). The lower linear regression line shows hosts infected by 1 tapeworm, whereas the upper regression line shows hosts infected by ≥ 2 tapeworms.

Supplementary information S4. Statistics from Lake Nedre Vollvatn in (a) 1996, and (b) 1996 and 1997 pooled. “Condition” (residuals of power-transformed dry body weight adjusted for length) as response variable in a GLM Type III (adjusted) sums of squares (SS). The predictor ‘single-multiple infection’ is whether the stickleback host was parasitized by one or multiple tapeworms (*Schistocephalus solidus)* (non-parasitized hosts are not included), and ‘parasite index’ is wet weight of all tapeworms, as percentage of the sum of fish dry body weight (after removing weight of parasites) plus wet weight of all tapeworms.

a)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Source | | SS | df | *F* | | *P*-value |
| Analysis of variance | |  |  |  | |  |
| Single-multiple infection | | 0.171 | 1 | 4.091 | | 0.047 |
| Parasite index | | 0.250 | 1 | 5.995 | | 0.017 |
| Error | | 2.918 | 70 |  | |  |
| Total | | 12.031 | 73 |  | |  |
| Term | |  |  |  | |  |
| Coefficients | | Coeff. | S.E. Coeff. | *t* | | *P*-value |
| Constant | 0.620 | | 0.1087 | | 5.70 | <0.001 |
| Single-multiple infection | -0.115 | | 0.0570 | | -2.02 | 0.047 |
| Parasite index | -0.00415 | | 0.001694 | | -2.45 | 0.017 |
| Adjusted *R*2 = 0.061 |  | |  | |  |  |

b)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Source | | SS | df | *F* | | *P*-value |
| Analysis of variance | |  |  |  | |  |
| Single-multiple infection | | 0.166 | 1 | 4.227 | | 0.043 |
| Parasite index | | 0.374 | 1 | 9.524 | | 0.003 |
| Year | | 0.225 | 1 | 6.494 | | 0.012 |
| Error | | 3.688 | 94 |  | |  |
| Total | | 13.767 | 98 |  | |  |
| Term | |  |  |  | |  |
| Coefficients | Coeff. | | S.E. Coeff. | | *t* | *P*-value |
| Constant | 0.496 | | 0.1064 | | 4.66 | < 0.001 |
| Single-multiple infection | -0.0954 | | 0.0464 | | -2.06 | 0.043 |
| Parasite index | -0.004301 | | 0.001394 | | -3.09 | 0.003 |

Adjusted *R*2 = 0.169.