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Appendix 1

Details of literature search and inclusion criteria

We searched *Web of Science* for published studies on stable isotope measurements of metazoan parasites and their respective hosts using the search string (parasit* AND stable isotop*) and a topic search across all years up to 9 March 2016. All 265 papers retrieved were initially checked for their potential suitability by their title and abstract. In addition, we screened the reference sections of all potentially suitable studies for additional published studies not found by *Web of Science*. From all potentially suitable studies, we only retained those that reported $\delta^{13}C$ and/or $\delta^{15}N$ measurements for both parasites and their respective hosts, i.e. we omitted studies that measured only host or parasite tissue. In addition, to be included in our analysis, isotope ratio measurements had to be based on at least two replicate parasite and host samples. Finally, parasites had to be clearly associated with the respective host, i.e. parasitic organisms such as lampreys which were collected free-living without a specific association to a host were excluded.

Appendix 2

Details of protocols to retrieve $\delta^{13}C$ and $\delta^{15}N$ stable isotopes from the literature

We used the following higher taxonomic affiliations for host species: arthropods, birds, cnidarians, echinoderms, fish, lophotrochozoans (polychaetes & bivalves), and mammals; and for parasite species: *major taxa*: arthropods, helminths, lophotrochozoans (polychaetes & bivalves), vertebrates; *within arthropods*: arachnids, copepods, dipterans, siphonapterans (fleas), hymenopterans, hyperiid amphipods, isopods, phthirapterans (lice); *within helminths*: cestodes, nematodes, trematodes.

While for parasites whole body samples were usually used, host isotope measurements were usually based on specific host tissues (in 26 of the 35 studies). In most cases, particularly for fish hosts, this was muscle tissue. However, some studies reported isotope values from several alternative host tissues. In the case of fish hosts, we followed the general choice of authors to use (white) muscle tissue as the reference for analyses in all but a few cases where other specific tissues were used by authors reflecting the location of a parasite on its host and its known feeding

mechanism (e.g. heart instead of white muscle as reference for blood feeding gnathiid isopods). We followed the same procedure for all other host types where several tissues were investigated and used the putative host tissues utilised by a parasite based on the information given by the respective authors.

$\delta^{13}C$ and $\delta^{15}N$ data from parasites or hosts were taken from the text or tables of the respective publications. If data were only available in the form of graphs, we used the software *ImageJ* (<https://imagej.nih.gov/ij>) to extract the data (average of two readings). In cases where sampling took place in several seasons or at several localities, we used average values for each parasite–host combination. In addition, we noted the number of replicate measurements per parasite and host. While host replicates were always based on single individuals, parasite individuals from a host were pooled in some studies to generate enough material for isotope measurements (in 33 of the 101 parasite–host pairs included in our study). Thus, a parasite 'replicate' included multiple parasite individuals in those studies.

For the entire data acquisition process, we used a validation procedure as follows: DWT, MAG and TK developed the data base configuration and inclusion criteria. DWT conducted the initial data compilation which was independently validated by MAG. Any inconsistencies were discussed among DWT, MAG and TK.

Appendix 3

Construction of parasite and host trees

In multi-species ecological studies, species share a different amount of evolutionary history with one another. To correct for such non-independence, the expected co-variation between species can be modelled, as a random factor, using a covariation matrix derived from a phylogeny under an assumed model of evolution (Hadfield and Nakagawa 2010; Nakagawa and Santos 2012). Both host and parasite trees were generated using an online phylogenetic tree generator, phyloT (<http://phylot.biobyte.de>), which constructed a composite tree based on data from the National Centre for Biotechnology Information (NCBI) taxonomy database and, where possible, polytomies were resolved using the studies of Parmentier et al. 2016, Olson et al. 2003, Logan et al. 2004, Waeschenbach et al. 2012, Benz 1993, Whiting 2002, Peters et al. 2017, and Munro et al. 2011. Three polytomies in our parasite tree, namely within Order Cyclopoida, Genus *Anilocra* and Genus *Hyperia,* were unresolvable with information available in the literature. In addition, the species identity of some nematodes was not reported in a number of studies, and hence we were unable to obtain the position of those nematodes in the phylogenetic tree. For these four cases, polytomies were randomly transformed into dichotomies. The phylogenetic trees were constructed without branch lengths and then converted to an ultrametric tree following Hadfield and Nakagawa (2010).

The estimated covariance among related species was then estimated assuming a Brownian-motion model of evolution. Using MCMCglmm (Hadfield 2010), generalised linear mixed models were fitted using a Markov chain Monte Carlo (MCMC) algorithm with a weakly informative prior (V = 1, nu = 0.002; where V is variance and nu is the degree of belief parameter). This method samples from a posterior distribution and provides the mean and credible intervals of that distribution. In any case where the 95% credible interval does not cross zero the difference is considered significant.

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Appendix 4

Testing for 'spurious correlations' between δ and Δ quantities

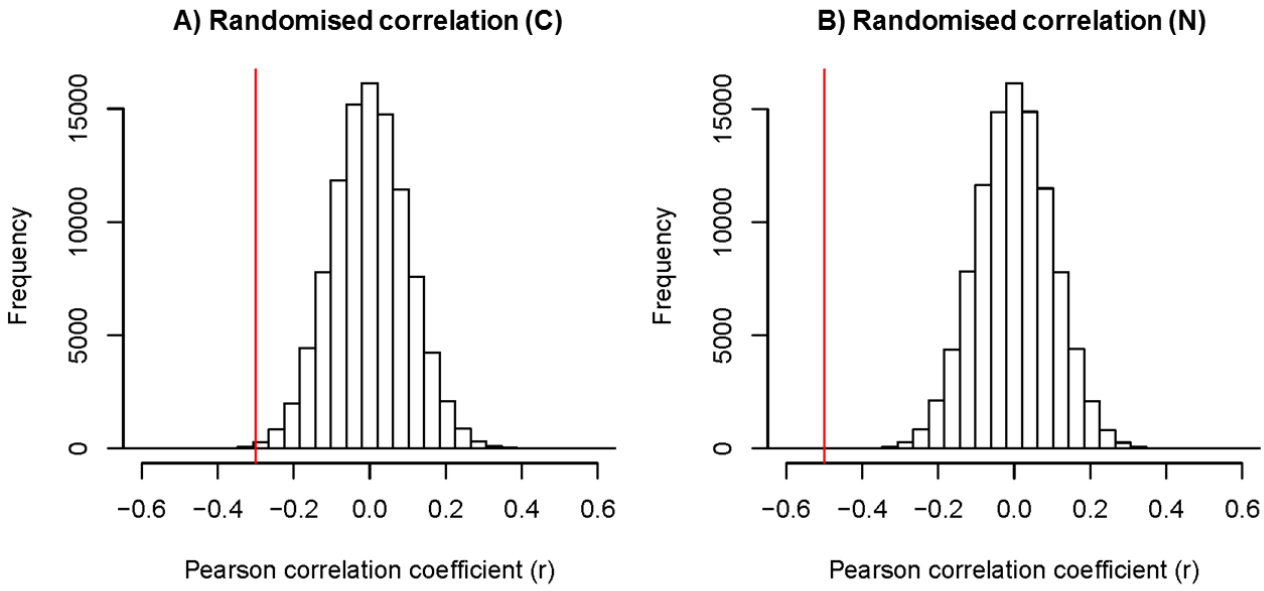

Figure A1. Randomisation tests reveal that the negative associations between $\delta^{13}C$ and $\Delta^{13}C$, $\delta^{15}N$ and $\Delta^{15}N$, respectively are not due to spurious correlations. The histograms (A for carbon and B for nitrogen, respectively) show the correlations between the δ and Δ quantities from 100 000 randomised samples. The red vertical bars indicate the actual observed correlations with significant difference from the mean of the randomized correlations (p-value = 0.001 and <0.001, respectively for carbon and nitrogen).

Appendix 5

DIC-based model selection of predictors & random effects variance in the null and consensus models

Table A1. DIC-based model selection of predictors for carbon discriminant factors. Ten best models were chosen based on DIC values through an exhaustive search of all fixed factor combinations. An information theoretic approach was applied to compare the contribution of the moderators and the 'consensus model' was chosen based on the moderators that appeared in the majority of the 10 selected models with the lowest DIC values. Therefore, the consensus model comprised of (intercept) + Host isotopic value + Host sample size + Parasite habitat + Parasite sample size.

Model	Host habitat	Host isotopic value	Host sample size	Parasite habitat	Parasite feeding type	Parasite sample size	Lipid extraction	DIC
(Intercept) +	FALSE	TRUE	TRUE	FALSE	FALSE	TRUE	FALSE	385.82
(Intercept) +	FALSE	TRUE	TRUE	TRUE	FALSE	TRUE	FALSE	386.06
(Intercept) +	FALSE	TRUE	TRUE	FALSE	FALSE	TRUE	FALSE	386.21
(Intercept) +	FALSE	TRUE	TRUE	TRUE	FALSE	TRUE	FALSE	386.26
(Intercept) +	FALSE	TRUE	TRUE	FALSE	FALSE	TRUE	FALSE	386.31
(Intercept) +	FALSE	TRUE	TRUE	TRUE	FALSE	TRUE	FALSE	386.39
(Intercept) +	FALSE	TRUE	TRUE	FALSE	FALSE	TRUE	FALSE	386.70
(Intercept) +	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE	FALSE	386.79
(Intercept) +	FALSE	TRUE	TRUE	TRUE	FALSE	TRUE	FALSE	386.93
(Intercept) +	FALSE	TRUE	TRUE	TRUE	FALSE	TRUE	FALSE	386.97

The predictors included are as follows with the sample size indicated in parentheses for categorical variables: Host habitat – freshwater (20), marine (61), terrestrial (20); Host isotopic value ($\delta^{13}C$); Host sample size; Parasite habitat – ecoparasites (31), endoparasites (60), gills (10); Parasite feeding type – blood feeding (26), other (75); Parasite sample size; Lipid extraction–yes (7), no (94).

Table A2. DIC-based model selection of predictors for nitrogen discriminant factors. Ten best models were chosen based on DIC values through an exhaustive search of all fixed factor combinations. An information theoretic approach was applied to compare the contribution of the moderators and the 'consensus model' was chosen based on the moderators that appeared in the majority of the 10 selected models with the lowest DIC values. Therefore, the consensus model comprised of (intercept) + Host habitat + Host isotopic value + Host sample size + Parasite sample size.

Model	Host habitat	Host isotopic value	Host sample size	Parasite habitat	Parasite feeding type	Parasite sample size	Lipid extraction	DIC
(Intercept) +	TRUE	TRUE	TRUE	FALSE	FALSE	TRUE	FALSE	366.46
(Intercept) +	TRUE	TRUE	TRUE	FALSE	TRUE	TRUE	FALSE	366.89
(Intercept) +	FALSE	TRUE	TRUE	FALSE	FALSE	TRUE	FALSE	366.93
(Intercept) +	TRUE	TRUE	TRUE	FALSE	FALSE	TRUE	FALSE	367.51
(Intercept) +	TRUE	TRUE	TRUE	FALSE	FALSE	TRUE	TRUE	367.58
(Intercept) +	TRUE	TRUE	TRUE	FALSE	TRUE	TRUE	FALSE	367.74
(Intercept) +	FALSE	TRUE	TRUE	FALSE	TRUE	TRUE	FALSE	367.83
(Intercept) +	FALSE	TRUE	TRUE	FALSE	FALSE	TRUE	FALSE	367.96
(Intercept) +	TRUE	TRUE	TRUE	FALSE	TRUE	TRUE	TRUE	368.19
(Intercept) +	TRUE	TRUE	TRUE	FALSE	FALSE	TRUE	TRUE	368.23

The predictors included are as follows with the sample size indicated in parentheses for categorical variables: Host habitat – freshwater (20), marine (61), terrestrial (20); Host isotopic value ($\delta^{15}N$); Host sample size; Parasite habitat – ecoparasites (31), endoparasites (60), gills (10); Parasite feeding type – blood feeding (26), other (75); Parasite sample size; Lipid extraction– yes (7), no (94).

Table A3. Random effects variance in the null and consensus models for carbon and nitrogen isotope discrimination factors of parasites. 95% credibility intervals are shown in parentheses.

		Carbon		Nitrogen	
	Effects	Null model	Consensus model	Null model	Consensus model
Random	Parasite species name	1.49 (0.0003 - 3.35)	1.13 (0.0003 - 3.01)	0.27 (0.0002 - 1.24)	0.24 (0.0002 - 1.09)
	Parasite phylogeny	0.17 (0.0002 - 0.78)	0.22 (0.0002 - 0.96)	10.45 (1.08 - 24.80)	10.71 (1.48 - 22.43)
	Host species name	0.31 (0.0003 - 1.12)	0.37 (0.0002 - 1.30)	1.08 (0.0005 - 2.09)	0.86 (0.02 - 1.75)
	Host phylogeny	0.57 (0.0003 - 2.53)	0.42 (0.0002 - 2.02)	1.17 (0.0003 - 4.64)	0.33 (0.0003 - 1.56)
	Study ID	0.39 (0.0003 - 1.32)	0.27 (0.0002 - 1.10)	0.82 (0.0003 - 2.27)	0.57 (0.0003 - 1.75)
	Residual variance	1.91 (0.72 - 3.32)	2.05 (0.79 - 3.48)	1.61 (0.78 - 2.52)	1.40 (0.69 - 2.17)