Appendix C

Host genetic distances

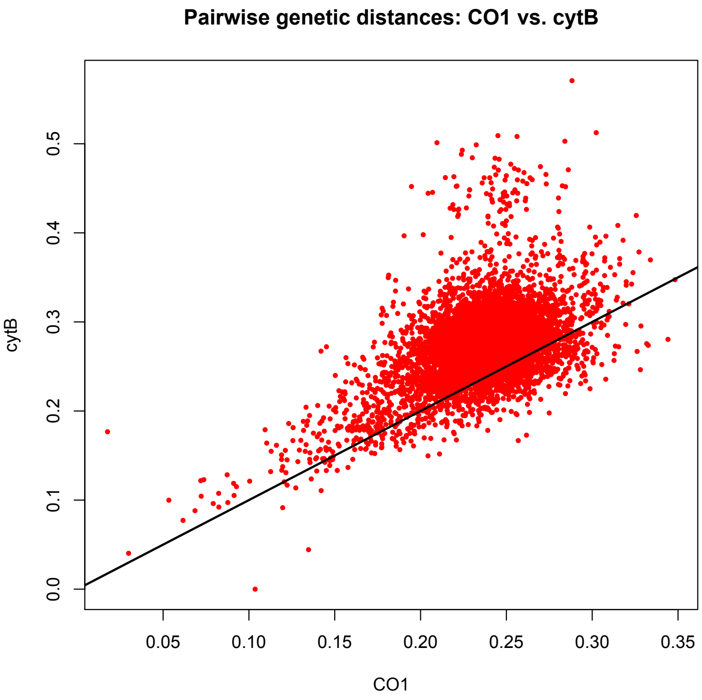
Methods

Host mitochondrial DNA sequences (complete mitochondrial genomes and full or partial sequences from mitochondrial loci) were downloaded in fasta format from the NCBI nucleotide database using an Entrez Direct query. Sequences were discarded if the sequence header did not contain the species name (either full or abbreviated scientific name). They were then sorted by locus (limited to cytochrome oxidase 1, cytochrome B, 12s and 16s) based on regular expression matches to the sequence header and the assignment to loci checked by local BLASTN [1] searches (default settings, version 2.2.29) to databases of representative sequences from the relevant locus. When multiple sequences were available for a given locus and host, a consensus sequence was generated using the EMBOSS program *cons* [2]. The consensus sequence was used in downstream analyses except in cases when just two sequences had contributed to the consensus and the result contained more than 1% of variable positions. In such cases the first sequence was used instead of the consensus if a megaBLAST [1] search against the NCBI nucleotide database hit a member of the same genus with percentage identity greater than 90%, and the second sequence used otherwise. For hosts without sequence data for a particular locus, sequences were extracted from mitochondrial complete genomes when available using BLASTN. Consensus sequences for all available host species were combined and aligned - adjusting for direction - using MAFFT for each locus. Alignments were then trimmed with trimAl [3] to include only those columns where less than 50% of taxa had a gap and those taxa where 50% of the nucleotide positions had the same 'element' (e.g. a gap or a residue) as more than half of the other taxa in the alignment.

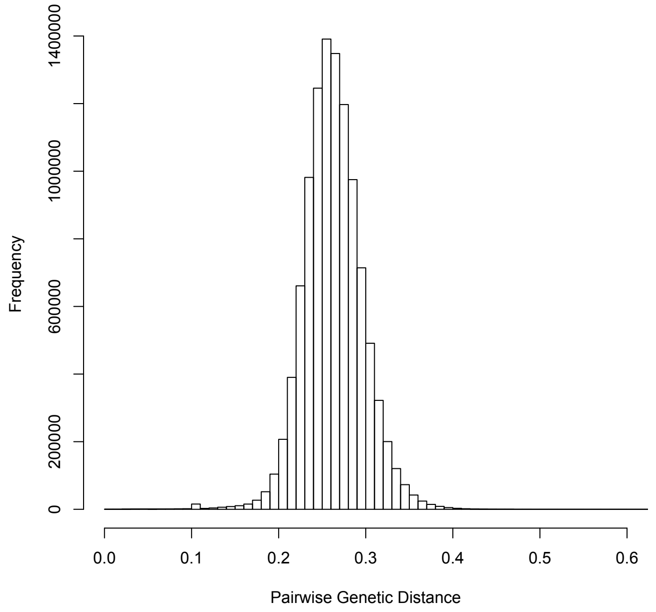
Trimmed alignments were used to compute pairwise genetic distances using the dist.dna function and the K80 model of DNA evolution [4] in the R package *ape* [5]. Since different taxa were represented among loci, the consistency of pairwise distances among loci across a range of divergence times was assessed. The pairwise genetic distances between those host taxa with sequences for all loci were extracted. For each locus these pairwise genetic distances were plotted against their corresponding pairwise distance generated from cytochrome oxidase 1 sequences. The point patterns were compared to the one-to-one line (complete correspondence), and correspondence to this line used to select the loci to be concatenated using *ape*. Pairwise genetic distances were recalculated on this final concatenated alignment. Missing pairs were imputed using a custom R script by averaging according to the following relationships between taxa: 1) pairs from different genera – the mean of the genetic distances of one member of the pair (determined by the data available) to congeners of the remaining pair member was calculated, 2) pairs from the same genera – the mean genetic distance of all the other pairwise comparisons within that genus was calculated. Where no data were available for any member of a genus, the mean within genus average for all genera was used. If suitable data were unavailable the same principals were applied at increasing taxonomic levels (family, order, class) until values were obtained for all pairwise comparisons.

A UPGMA tree was calculated from the full distance matrix using *phangorn* in R [6] and the tree reordered from root to tip so that edges from the root node were listed first ('cladewise' reordering).

The total number of host species in our dataset was 4,621, but sequence data from a single gene were not available for all hosts. The pairwise genetic distances calculated using data from the cytochrome oxidase 1 gene corresponded to those from cytochrome B (Fig. S1) and these loci were selected for concatenation and subsequent calculation of pairwise genetic distances. Overall, 3,253 host species were represented by cytochrome oxidase 1 sequences and 2,193 host species by cytochrome B, 1,915 host species had sequences from both loci whilst a total of 3,531 host species had representative sequences from one or both loci. The mean pairwise genetic distance between hosts was 0.263 (standard deviation=0.034; Fig. S2).

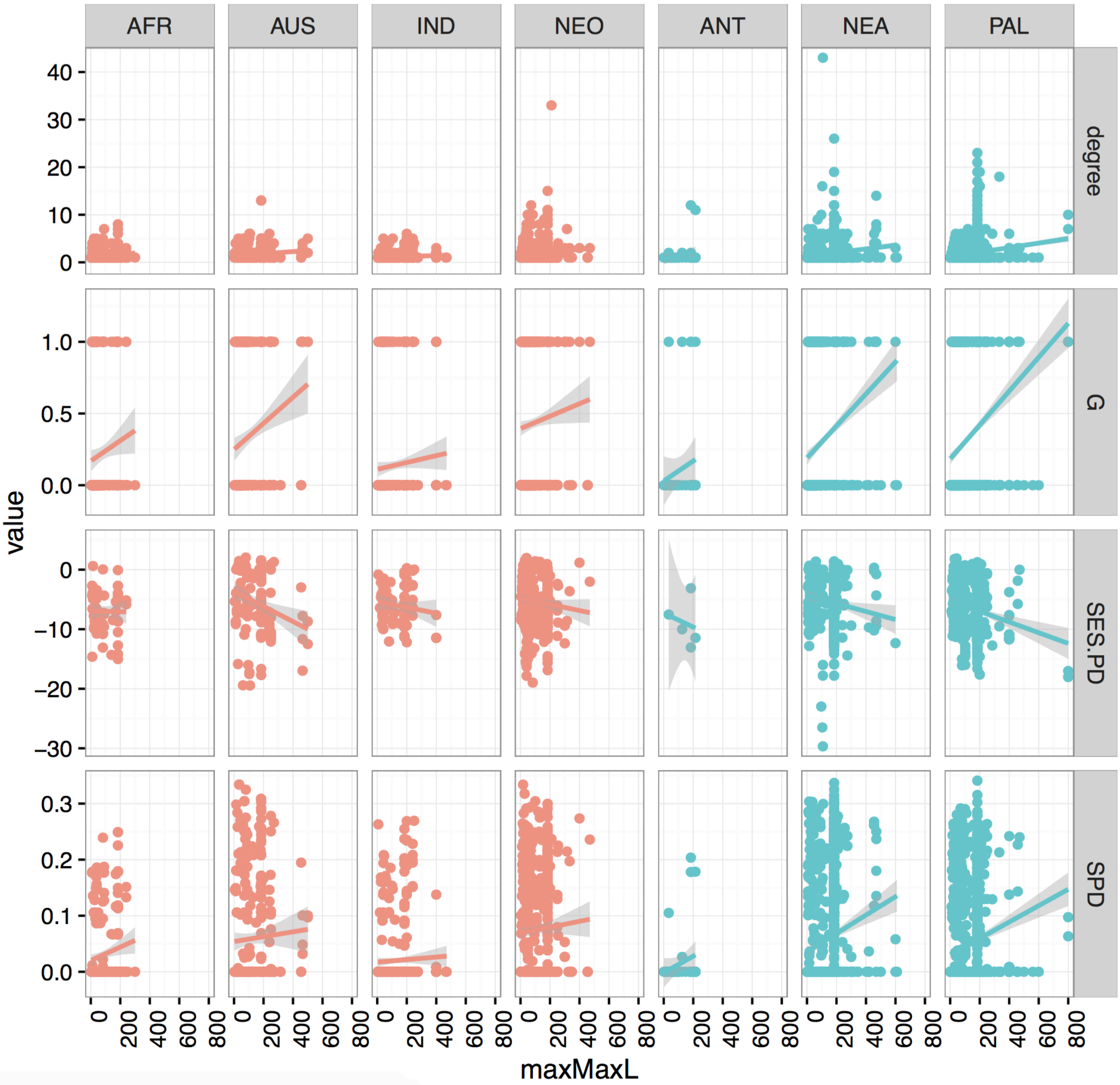


Supplementary Figure 1: Comparison of pairwise genetic distances between hosts generated from cytochrome oxidase 1 (CO1) sequences and cytochrome B (cytB) sequences plotted against one to one line.

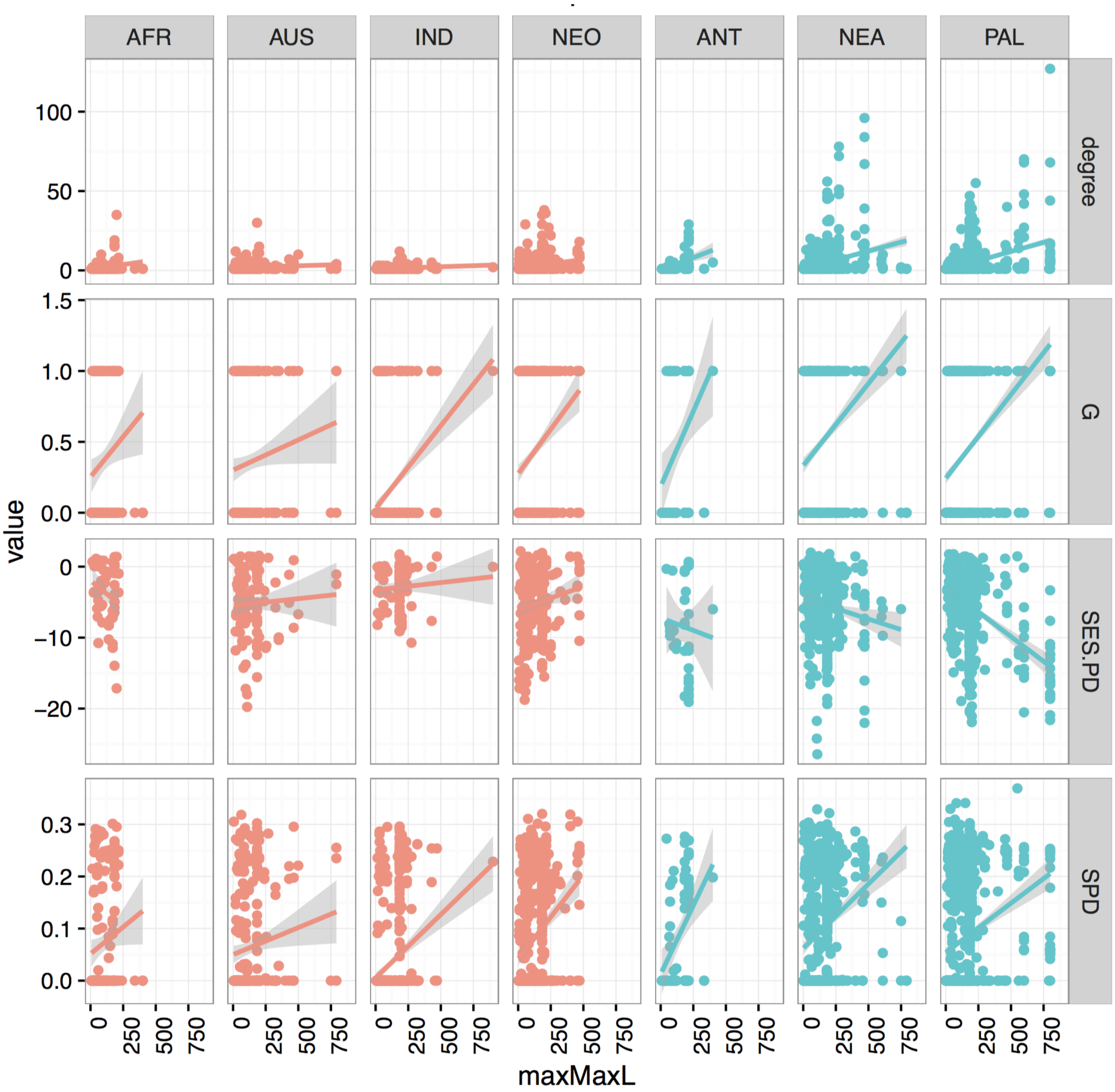


Supplementary Figure 2: Distribution of genetic distances from all pairwise comparisons of hosts.

Supplementary material for [Author], [Year], [Title], *Phil. Trans. R. Soc. B.* doi: 10.1098/rstb.[paper ID in form xxxx.xxxx e.g. 10.1098/rstb.2014.0049]



Supplementary Figure 3: Correlation between generalism metrics and maximum host length for directly transmitted parasites in each geographic region, with warm regions in red and cool regions in blue. Lines are linear models with grey 95% confidence bounds.



Supplementary Figure 4: Correlation between generalism metrics and maximum host length for trophically transmitted parasites in each geographic region, with warm regions in red and cool regions in blue. Lines are linear models with grey 95% confidence bounds.

Supplementary Table 1: Results of multivariate negative binomial regression (degree ~ Length * Transmission * GeoGroup), with each of three measures of length (mean, max, CV) separately. For mean and max length the scale of the coefficient is unit change in log degree per SD increase in length measure, for CV length the scale is unit change in log degree per cm increase in CV.

Predictor	Coefficient	Confidence Interval		Z-score	Residual degrees of freedom
Intercept	0.462	0.415	0.509	19.314	
Mean length	-0.102	-0.152	-0.052	-4.011	
Trophic transmission (ref = direct)	0.239	0.171	0.306	6.946	
Geo group cool (ref = warm)	0.106	0.045	0.167	3.414	
Length*trophic	-0.068	-0.141	0.004	-1.868	
Length*cool	0.092	0.028	0.158	2.848	
Trophic*cool	0.576	0.49	0.663	13.098	
Length*trophic*cool	-0.066	-0.16	0.029	-1.416	8595
Intercept	0.493	0.448	0.538	21.52	
Max length	0.086	0.034	0.139	3.276	
Trophic transmission (ref = direct)	0.208	0.143	0.272	6.321	
Geo group cool (ref = warm)	0.055	-0.003	0.114	1.855	
Length*trophic	0.178	0.106	0.249	5.154	
Length*cool	0.154	0.087	0.221	4.632	
Trophic*cool	0.355	0.271	0.439	8.318	
Length*trophic*cool	0.065	-0.025	0.154	1.531	8595
Intercept	0.971	0.855	1.087	16.714	
CV length	0.192	0.02	0.365	2.25	
Trophic transmission (ref = direct)	-0.025	-0.201	0.151	-0.29	
Geo group cool (ref = warm)	0.085	-0.059	0.23	1.178	
Length*trophic	0.638	0.384	0.893	5.1	
Length*cool	0.118	-0.102	0.338	1.083	
Trophic*cool	0.126	-0.096	0.349	1.153	
Length*trophic*cool	0.322	-0.001	0.645	2.065	3028

Supplementary Table 2: Results of multivariate logistic regression (G ~ Length * Transmission * GeoGroup), with each of two measures of length (mean, max) separately. For both length measures the scale of the coefficient is unit change in log odds ratio per SD increase in length measure.

Predictor	Coefficient	Confidence Interval		Z-score	Residual degrees of freedom
Intercept	-0.826	-0.925	-0.73	-16.625	
Mean length	-0.329	-0.438	-0.222	-5.976	
Trophic transmission (ref = direct)	0.048	-0.095	0.19	0.657	
Geo group cool (ref = warm)	0.092	-0.033	0.218	1.44	
Length*trophic	0.146	-0.009	0.301	1.856	
Length*cool	0.34	0.206	0.476	4.935	
Trophic*cool	0.507	0.322	0.691	5.382	
Length*trophic*cool	-0.255	-0.45	-0.06	-2.57	8595
Intercept	-0.742	-0.837	-0.648	-15.352	
Max length	0.148	0.039	0.258	2.656	
Trophic transmission (ref = direct)	-0.028	-0.169	0.114	-0.382	
Geo group cool (ref = warm)	-0.017	-0.142	0.109	-0.263	
Length*trophic	0.311	0.154	0.47	3.856	
Length*cool	0.402	0.256	0.549	5.374	
Trophic*cool	0.485	0.298	0.672	5.074	
Length*trophic*cool	-0.193	-0.408	0.021	-1.771	8595

Supplementary Table 3: Results of multivariate linear regression (SPD~ Length * Transmission * GeoGroup), with each of three measures of length (mean, max, CV) separately. For mean and max length the scale of the coefficient is unit change in SPD per SD increase in length measure, for CV length the scale is unit change in SPD per cm increase in CV.

Predictor	Coefficient	Confidence Interval		Z-score	Residual degrees of freedom
Intercept	0.049	0.045	0.054	23.781	
Mean length	-0.014	-0.019	-0.01	-6.679	
Trophic transmission (ref = direct)	0.01	0.004	0.017	3.388	
Geo group cool (ref = warm)	0.002	-0.004	0.007	0.637	
Length*trophic	0.008	0.002	0.014	2.454	
Length*cool	0.011	0.006	0.017	4.035	
Trophic*cool	0.028	0.02	0.036	6.74	8595
Length*trophic*cool	-0.015	-0.023	-0.007	-3.644	
Intercept	0.052	0.047	0.056	24.726	
Max length	0.002	-0.003	0.007	0.776	
Trophic transmission (ref = direct)	0.01	0.004	0.016	3.129	
Geo group cool (ref = warm)	0	-0.006	0.005	-0.127	
Length*trophic	0.021	0.014	0.028	6.179	
Length*cool	0.014	0.008	0.02	4.498	
Trophic*cool	0.023	0.015	0.031	5.669	8595
Length*trophic*cool	-0.015	-0.023	-0.007	-3.561	
Intercept	0.126	0.117	0.135	26.634	
CV length	0.065	0.051	0.079	9.188	
Trophic transmission (ref = direct)	0.029	0.015	0.043	3.967	
Geo group cool (ref = warm)	0.017	0.006	0.029	2.933	
Length*trophic	-0.005	-0.026	0.017	-0.438	
Length*cool	-0.036	-0.054	-0.018	-3.941	
Trophic*cool	-0.014	-0.032	0.005	-1.469	3028
Length*trophic*cool	0.035	0.008	0.062	2.539	

Supplementary Table 4: Results of multivariate linear regression (SES.PD ~ Length * Transmission * GeoGroup), with each of three measures of length (mean, max, CV) separately. For mean and max length the scale of the coefficient is unit change in SES.PD per SD increase in length measure, for CV length the scale is unit change in SES.PD per cm increase in CV.

Predictor	Coefficient	Confidence Interval		Z-score	Residual degrees of freedom
Intercept	-5.816	-6.194	-5.439	-30.226	
Mean length	-0.72	-1.158	-0.282	-3.221	
Trophic transmission (ref = direct)	1.336	0.788	1.883	4.785	
Geo group cool (ref = warm)	-0.156	-0.637	0.326	-0.634	
Length*trophic	1.412	0.752	2.071	4.197	
Length*cool	0.039	-0.542	0.62	0.133	
Trophic*cool	-1.033	-1.721	-0.345	-2.943	3028
Length*trophic*cool	-1.94	-2.789	-1.091	-4.478	
Intercept	-5.674	-6.025	-5.324	-31.733	
Max length	-0.693	-1.1	-0.286	-3.338	
Trophic transmission (ref = direct)	0.994	0.466	1.522	3.692	
Geo group cool (ref = warm)	-0.133	-0.6	0.334	-0.556	
Length*trophic	1.08	0.532	1.628	3.864	
Length*cool	-0.096	-0.629	0.437	-0.354	
Trophic*cool	-0.126	-0.814	0.562	-0.36	3028
Length*trophic*cool	-1.48	-2.162	-0.799	-4.261	
Intercept	-7.007	-7.617	-6.398	-22.547	
CV length	2.6	1.687	3.512	5.586	
Trophic transmission (ref = direct)	1.662	0.72	2.604	3.458	
Geo group cool (ref = warm)	0.722	-0.044	1.488	1.848	
Length*trophic	-1.267	-2.663	0.13	-1.779	
Length*cool	-2.034	-3.215	-0.853	-3.376	
Trophic*cool	-1.306	-2.502	-0.111	-2.142	3028
Length*trophic*cool	1.118	-0.655	2.892	1.236	

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