**A broadscale test of host-symbiont cophylogeny reveals widespread phylogenetic congruence**

**Symbioses are prolonged and intimate associations between organisms of different species1, typically defined in terms of an interaction between a larger host organism and a smaller symbiont2. Symbiotic relationships may be mutualistic, where both partners benefit from the interaction, parasitic, where one partner benefits and the other suffers a cost, or commensalistic, where one partner benefits while the other neither benefits nor suffers a loss3. Symbioses are extremely common and exert substantial biological influence, with great evolutionary and ecological relevance for disease4,5, driving major evolutionary transitions6-8, and affecting the structure and function of ecological communities9,10. Symbioses are also of considerable applied importance, due to the benefits provided by ecosystem services such as pollination and biocontrol, and the costs associated with harmful pests and pathogens11,12. Yet, much remains unknown about the patterns and processes that characterise symbioses. A major unanswered question is the degree to which symbiont phylogenies track those of their hosts. Currently, it is unclear whether symbiont evolutionary trees are typically congruent with those of their hosts, or if patterns differ for parasites and mutualists. Here, we perform a meta-analysis of host-symbiont phylogenetic congruence considering mode of symbiosis, host-symbiont taxonomy, and life-history, encompassing 232 host-symbiont cophylogenetic analyses from the primary literature. Our analysis represents an advancement from qualitative studies, toward a systematic and quantitative framework to investigate host-symbiont cophylogeny. We show that symbiont phylogeny reflects host phylogeny, and that the signature of congruence extends across host and symbiont diversity and life-history, demonstrating a general tendency of symbionts to track host phylogeny over evolutionary time. We identify two aspects of symbiont life-history that appear to promote closer ties between host and symbiont: vertical transmission and mutualism. We find that mode of symbiosis and mode of transmission are intimately interlinked, but we demonstrate that vertical transmission is the dominant factor in promoting host-symbiont phylogenetic congruence. Given the pervasiveness of symbioses across ecosystems and the tree of life, these findings provide fundamental insights into the processes responsible for generating the Earth’s rich biodiversity.**

**Main**

Symbiosis exists across all taxonomic levels and is a common feature of life (Fig. 1). A key unanswered question in the study of symbiosis is the extent to which symbiont phylogenies track those of their hosts. Given an ancestral host-symbiont association, multiple rounds of strict cospeciation will result in a symbiont phylogeny that perfectly mirrors host phylogeny, and thus phylogenetic congruence (Fig. 2a). In practice, perfect congruence is considered to be rare, due to the influence of disruptive events such as host switching (Fig. 2b), extinction (Fig. 2c), independent speciation (Fig. 2d), or failure to speciate (Fig. 2e), which lead to incongruence in host-symbiont phylogenies13 (Fig. 2f). The idea that symbionts track their hosts over evolutionary timescales, cospeciating in synchrony, is encapsulated by ‘Fahrenholz’s Rule’, which states that parasite phylogeny reflects host phylogeny14,15. Fahrenholz’s Rule was formulated over one hundred years ago, yet a persistent assumption of host-specialization and accompanying host-parasite phylogenetic congruence remains within the field of host-symbiont interactions16, despite apparently limited support from the literature17. Given the availability of statistical methods to quantify host-symbiont phylogenetic congruence (e.g.18,19), and a recent accumulation of studies that apply these approaches, opportunities now exist to examine the generality of Fahrenholz’s Rule within a formal quantitative framework.

We apply meta-analytical methods to analyse a large body of published studies that quantify phylogenetic congruence for particular symbioses. We consider reported test statistics from the two most widely applied approaches for estimating host-symbiont phylogenetic congruence: one based on estimations of shared discrete macroevolutionary events (i.e. 'TreeMap'20), and one based on branch-length comparisons to estimate overall similarity (i.e. 'Parafit'21). Firstly, we examine the extent to which symbiont phylogeny tracks host phylogeny, providing a broadscale analysis of cophylogeny. We then test the validity of Fahrenholz’s Rule specifically, by testing the generality of the prediction that parasite phylogeny mirrors host phylogeny across multiple host and parasite taxa. If parasites are specialized and tightly coevolved to single host species22, we expect a strong signal of phylogenetic congruence between host and parasite phylogenies. Alternatively, if parasites commonly shift to new host species, either with parasite speciation following host-switching events23,24, or without speciation25, we expect a weak or absent signal of phylogenetic congruence. Next, we compare the findings for parasites to those for mutually beneficial symbiotic interactions *sensu* Bronstein26. Mutualism can be viewed within the framework of ‘reciprocal exploitation’27. Within this framework, the incentive to cheat28,29 may destabilise the longevity of mutualisms over protracted evolutionary timescales, resulting in no greater overall phylogenetic congruence between hosts and mutualists than that observed for parasites. Conversely, mutualisms may be robust to such challenges and thus be evolutionarily persistent30,31, which would result in a pattern of tight host-mutualist phylogenetic congruence. To distinguish between these alternatives, we test host-mutualist phylogenetic congruence across host and mutualist taxonomic diversity, while simultaneously providing a general comparison of host-symbiont phylogenetic congruence between mutualism and parasitism.

Given the paucity of formal testing of the drivers of host-symbiont phylogenetic congruence, we extend our analyses beyond considering the type of symbiosis only, to examine the influence of several classic traits of relevance for host-symbiont interactions. Host specificity is a central aspect of symbiont life history with widespread ecological and evolutionary implications9,32, and may exert an independent effect on host-symbiont phylogenetic congruence beyond the mutualist-parasite divide. If specialist symbionts are evolutionarily or ecologically ‘tied-in’ to their host associations, undergoing few or no host shifts33-35, they are expected to display high phylogenetic congruence with their hosts. However, if specialists possess an ability to make host-shifts of varying frequency and magnitude (while remaining associated with one or few hosts)36,37, congruence may be low. Meanwhile, truly generalist symbionts are expected to show low phylogenetic congruence with their hosts, unless dominant interactions occur within a subset of total host range38. We also consider the influence of endosymbiosis versus ectosymbiosis. Endosymbionts are fully enclosed within the host, and are considered to have a more intimate interaction with host physiology, biochemistry and immunity than ectosymbionts5,32, which may translate into tighter associations, and greater host-symbiont phylogenetic congruence. Lastly, we examine the relevance of mode of transmission, to test the general expectation that vertical transmission promotes greater phylogenetic congruence39-41. If a symbiont is vertically transmitted (whether it has positive, neutral, or negative effects on the host), this should automatically decrease the likelihood of host-switching, and increase the likelihood of cospeciation. Therefore, cophylogenetic congruence should emerge as a consequence. In contrast, horizontal transmission should facilitate exposure to novel hosts, potentially leading to host-switching, and decreased host-symbiont phylogenetic congruence.

Considering 232 published host-symbiont cophylogeny studies (Extended Data Tab. 1), spanning a wide spectrum of host and symbiont taxa, we found support that host and symbiont phylogeny show a tendency to reflect one another, with only moderate variation in the strength of phylogenetic congruence among studies (STATS; Fig. 3a). Furthermore, the strength of the association identified is likely to be a considerable underestimate of the true pattern, given the limits of current approaches to quantify congruence between host and symbiont phylogenies (see Methods, ‘Estimates of effect size’). Next, we examined parasitism and mutualism separately. Our results show that host and parasite phylogenies display greater similarity than expected by chance, with parasite phylogeny tending to mirror host phylogeny, consistent with a broad interpretation of Fahrenholz’s Rule (STATS; Fig. 3b). However, host and mutualist phylogenies show greater congruence than that observed between host and parasite phylogenies, suggesting a stronger tendency of mutualists to track host phylogeny (STATS; Fig. 3b). A potential explanation for this pattern is that reciprocal benefits provide a more cohesive force to unite host and symbiont evolutionary trajectories, than the antagonistic interactions involved in parasitism.

To further dissect cophylogenetic patterns between symbiont and host phylogenies, we examined whether taxonomy exerted an effect by partitioning studies according to broad taxonomic groups for hosts and symbionts. We found that effect size was positive across all host taxonomic groupings considered, with host-symbiont associations involving microbial hosts showing greatest congruence, followed by invertebrate hosts, vertebrate hosts, and lastly plant hosts (STATS; Fig. 3c). For symbiont taxa, effect size was also positive across all taxonomic groups, but variation in phylogenetic congruence was lower (STATS; Fig. 3d). Host-symbiont cophylogenies involving plant symbionts displayed markedly higher congruence, primarily driven by results for mutualistic algal symbionts and their lichen hosts, but sample size for this category was small, reflecting the scarcity of studies focussing on these associations in relevant cophylogenetic literature.

Splitting host taxonomy by mode of symbiosis revealed that the observed higher phylogenetic congruence of host-symbiont cophylogenies involving a microbial host is driven primarily by greater congruence between microbial hosts and mutualist symbionts (Fig. 3d). Congruence is also relatively high for invertebrate hosts that harbour a mutualistic symbiont, while congruence appears to be lowest for plant hosts that harbour a parasitic symbiont (Fig. 3d). Splitting symbiont taxonomy by mode of symbiosis revealed much less variation, except for higher congruence exhibited by cophylogenies involving a plant symbiont (which are relatively rare), and the finding that cophylogenies involving a microbial mutualist symbiont are slightly more congruent than the remaining categories (Fig. 3e).

We examined if host specificity is associated with host-symbiont phylogenetic congruence using two estimators: (i) host range (mean number of links between hosts and symbionts per symbiont within a cophylogeny), and, (ii) host taxonomic breadth (an index of the number of higher host taxonomic ranks associated with each symbiont within a cophylogeny). No significant association was identified for either measure of host specificity (STATS; Fig. 3f and Fig. 3g), suggesting that host specificity, at least, the range of which observed in our data set, is not an important general determinant of host-symbiont cophylogeny.

We also tested the obvious hypothesis that the more intimate relationship associated with endosymbiosis may translate into greater congruence between host and symbiont phylogenies. However, contrary to this hypothesis, we find that the distinction between endosymbiosis and ectosymbiosis has no influence on the degree of phylogenetic congruence observed between hosts and their symbionts (STATS; Fig. 3h).

A major prediction for host-symbiont cophylogeny is that vertical transmission (i.e. ‘intergenerational transmission’, as opposed to horizontal ‘infectious transmission’) should promote phylogenetic congruence39-41. In line with this prediction, we found that mode of transmission was a highly significant correlate of host-symbiont phylogenetic congruence, with the strongest effect observed for vertical transmission, followed by the effect observed for mixed modes of transmission (symbionts are transferred via either route), and with horizontal transmission showing the lowest effect size (STATS; Fig. 3i). An issue affecting our data is that all of the vertically transmitted symbionts included in our analysis are classified as mutualists. However, many of the parasitic symbionts included show a mixed mode of transmission, and splitting by mode of symbiosis reveals that parasites with mixed modes of transmission show greater phylogenetic congruence with their hosts than horizontally transmitted parasites (STATS; Fig. 3j). Similarly, mutualistic symbionts show a stepwise increase in phylogenetic congruence with hosts, from horizontal to mixed, and from mixed to vertical transmission, with vertically transmitted mutualists displaying considerably greater phylogenetic congruence than horizontally transmitted mutualists (STATS; Fig. 3j). No significant interactions were present among modes of symbiosis and modes of transmission, highlighting that vertical transmission is the variable that explains the effect on phylogenetic congruence.

Employing a large quantitative and systematic review of the cophylogeny literature, we tested major hypotheses regarding the drivers of host-symbiont phylogenetic congruence. We found support for a general pattern of congruence between host and symbiont phylogenies, in line with a liberal interpretation of Fahrenholtz’s Rule. Significant congruence was observed both for hosts and their parasites and for hosts and their mutualists, but it is was significantly stronger in the latter case. We also identified an effect of mode of transmission on host-symbiont phylogenetic congruence, with vertical transmission correlated with greater congruence. Thus, we suggest that: (i) mutualism promotes greater host-symbiont phylogenetic congruence, and, (ii) this is driven primarily by a predominance of vertical transmission among mutualists, as opposed to parasites.

The observation that strict vertical transmission is uncommon in parasites fits with predictions that vertical transmission should favour decreased virulence, since reducing host fitness ultimately reduces a symbiont’s own opportunities for transmission42,43. Accordingly, parasite lineages forced to express strict vertical transmission have been demonstrated to shift along the parasitism-mutualism continuum towards greater host benevolence, both empirically44,45, and comparatively46,47. Meanwhile, a key question remains whether mutualism facilitates the evolution of vertical transmission, or if the process typically proceeds as argued above. A study of bacterial symbionts concluded that horizontal transmission was the most primitive mode, and that vertical transmission is an inescapable evolutionary end point, given the mutational processes that impact a symbiont as a consequence of adopting strict vertical transmission48. However, these conclusions may be taxon-specific, and need to be examined across host-symbiont taxonomic diversity.

Elucidating the processes that drive symbiont diversification is fundamental to understanding the factors responsible for generating the Earth’s biodiversity, given that symbionts represent a considerable proportion of total species diversity49,50. Meanwhile, unravelling the factors that influence host-symbiont phylogenetic congruence is crucial for improving knowledge of host-switching, a major research focus in host-parasite interactions, with direct implications for the prediction and mitigation of zoonoses, emerging infections, and the control of agricultural pests51-53. To our knowledge, this study represents the first quantitative appraisal of host-symbiont cophylogeny, a central aspect of host-symbiont evolution. With this study, we hope to initiate a new direction in the study of symbiosis, towards formal quantitative and systematic analyses that seek to address fundamental questions regarding the nature of host-symbiotic evolutionary relationships. Importantly, considerable variation in congruence exists among host phylogenies and both parasite and mutualist phylogenies. Therefore, a core challenge is to identify which factors are of importance in fostering close cophylogeny. As the number of individual cophylogenetic studies increases, the power of these analyses will increase, permitting more detailed approaches to tease apart patterns and underlying mechanisms. Crucially, meta-analyses are only as good as the studies upon which they are based. A continued accumulation of taxonomically well-sampled, multi-locus host and symbiont phylogenies, ideally taking phylogenetic uncertainty into account, will provide a powerful platform on which to base further analyses.

**Methods**

**Measures of host-symbiont phylogenetic congruence**

-More detailed description of how the tests for phylogenetic congruence work.

**Data collection**

-How the literature was searched systematically. At the macroevolutionary scale (i.e. discounting within-species studies)

-How data were categorised e.g. classification of the mode of symbioses was taken from the authors. In cases where this was not mentioned, the literature was consulted.

**Meta-analysis**

We used *p* values obtained from randomaization tests that are implemented in ‘TreeMap’ and ‘Parafit’ as measures of incongrace. These *p* values were converted into *r* and its transformation *Zr*. We can caculate *requivalent* via *t* values with *df* = *N* - 2 values from *p* values (one-tailed) (Rosenthal and Rubin 2003) and then, also obtain *Zr*equivalent from *r*equivalent, as follows:

where *N* is sample size and, in our case, the sum of the numbers of host and symobiont species included in a randomaixation test.

All statstical analyses were conducted using R versino 3.5.2 (R Core Team 2018). We used multilevel (random-effects) meta-analytic and meta-regression models (Nakagawa and Santos 2012) becuase multiple effect sizes were obtained from some studies (i.e., study IDs were included as a random factor in the models to account for non-indepedence). All meta-analytic models were implemented using the function, *rma.mv* in the R pacakge, *metafor* version 2.0-0 (Viechtbauer 2010). All model specifications and model selection procedures are found in our elecotronic supplmentary materials (ESM)

-How done, how bias avoided, etc.

**Publication bias and sensitivity analysis**

* egger regression with the full model - say reason why
* truncations due to the number of simulations……
* boundaries due to N (randomization tests) is creating
* sensitivity analysis - two jusntificaitons
  1. why we put TreeMap and Parafit data
  2. Trancation are not biasing our main results!!!
  + simulation numbers are not different between parasites and mutualists

**Data availability**

A copy of the dataset analysed in this study is included in the supplementary information.

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**Author contributions**

RP conceived the study, all authors designed the study. SN performed the analyses. AH collected the data and drafted the manuscript. RP and SN provided comments and contributed to the final manuscript.

**Competing interests**

The authors declare no competing interests.

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**Supplementary Information**

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