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Evolutionary and Ecological Determinism of Host Specificity in Arthropod Parasites

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Supported by UCARE

Introduction

Understanding why some parasites infect more species than others is crucial for predicting where and when disease will spread, which can inform the management of wildlife, agriculture, and human health. By analyzing available genetic data, conclusions can be drawn about the risk for potential emerging disease risk caused by parasites.

A comprehensive database of parasites for mammals has already been created (GMPD) and contains host numbers for many parasites that can be used in conjunction with genetic information to inform evolutionary models as a trait.

Arthropods are a phylum with a large amount of available genetic data and diversity and can thus serve as a model group for testing evolutionary models against the trait of generalism. The results of this evaluation can then be used to quantify the nature, whether environmentally or evolutionarily, of parasite generalism.

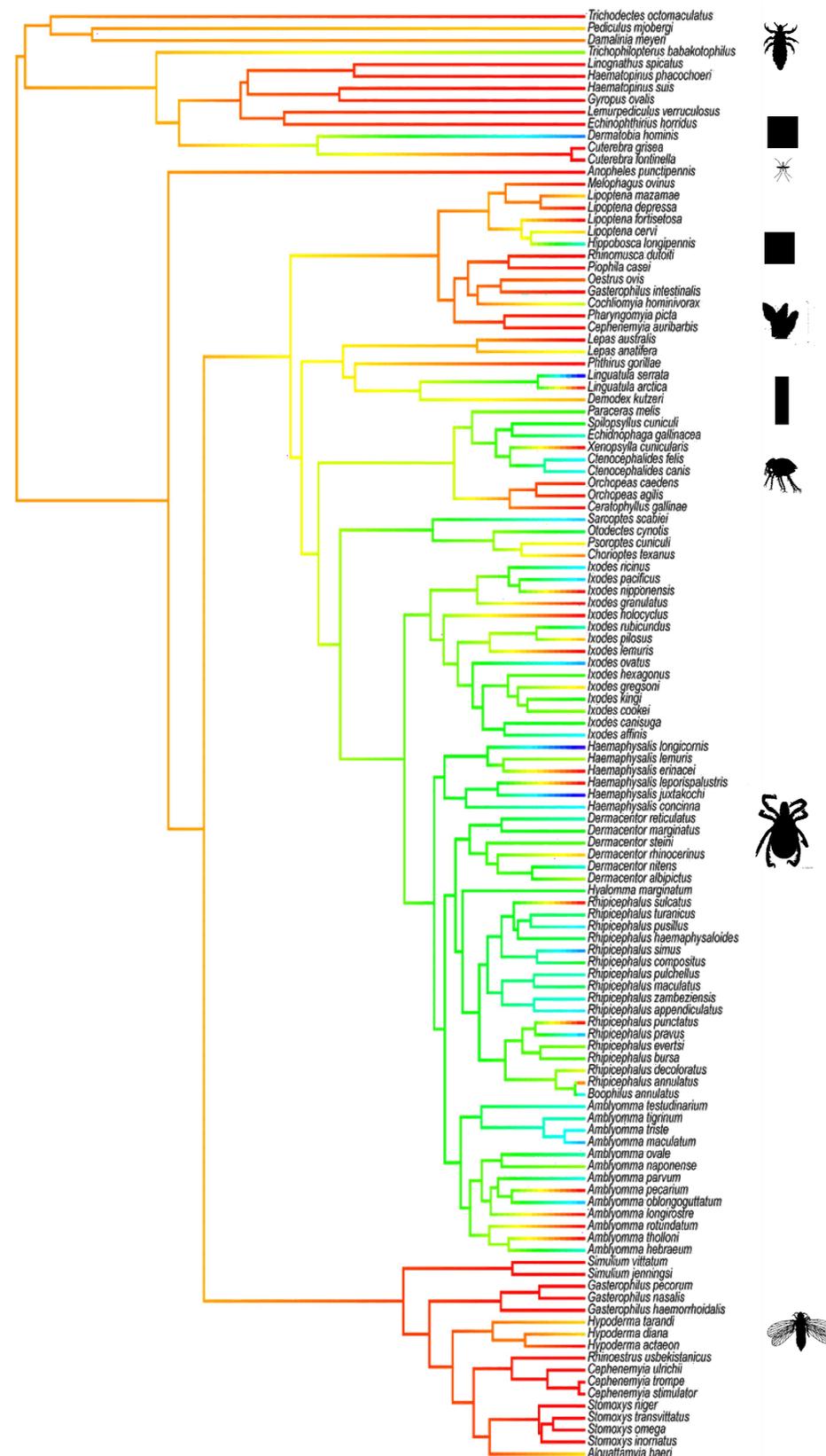
Methods

121 Parasitic Arthropod species were selected based on available genetic information. Cytochrome Oxidase 1, 12S and 16S sequences were collected from NCBI GenBank to create a matrix with all genetic data and parasite names. Genetic data was then parsed and aligned using a Muscle Alignment in Geneious Prime. Following the alignment partitions were found using PartitionFinder, then the data was input into BEAUti to set the parameters for finding the consensus phylogeny. BEAST, TRACER, and TreeAnnotator were then used to find a consensus phylogeny for the Arthropods.

Following creation of the phylogeny, R was used for statistical analysis. The number of hosts for each parasite was acquired from the Global Mammal Parasite Database (GMPD) and from this a generalism score was calculated for each parasite and mapped onto the tree. Phylogenetic signal was then analyzed from the tree to determine the evolutionary model that best explains the observed patterns of generalism

Generalism Mapped Tree for Arthropods

(Red: Lowest Generalism, Blue: Highest Generalism)



Results

Overall Phylogeny

- Phylogenetic analysis for the complete phylogeny indicated 'Lambda' was the most accurate model, with a value of 0.3359 indicating that **generalism is only weakly signalled by phylogeny.**

Outgroups Removed

- Removing outgroups (top clade) and groups with low posterior probability from the overall tree resulted in a determined best model of 'Lambda' with a value of 0.2878 again indicating that **generalism is more weakly signalled by phylogeny** compared to the overall tree.

Tick Only Tree

- Pruning the tree to contain only the tick clade (central large clade) resulted in a most accurate model for generalism being 'White Noise' (non-phylogenetic). This result indicates that the observed pattern of **generalism is best explained by a normal distribution** and not the phylogeny.

Discussion

In the overall phylogeny it was observed that the 'tick' clade had a pattern of generalism noticeably different than that of the other groups in the phylogeny. This was investigated further by pruning the tree progressively to see if the best model would change. It was found that the phylogeny weakly signalled generalism in both the overall and pruned tree. In the tick only tree, generalism was shown to best explained by normal distribution.

These results indicate that for ticks especially, it is likely the ecology and/or environmental factors play a larger role than evolution in determining host generalism. For all arthropod parasites, it is shown that generalism is likely only minimally constrained by phylogeny. More research is needed to determine the mechanisms that inform parasite host generalism however the results of this analysis indicate that phylogeny alone minimally explains patterns of host generalism in the arthropods tested.