

# **STRUCTURAL PROPERTIES OF PARASITE - HOST INTERACTIONS NETWORKS**

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## INTRODUCTION

The last decade has been marked by a great revolution on understanding of a substantial variety of systems by the application of the complex networks approach. Inside modern ecology, applications range from epidemiology and spatial ecology to species interaction webs (Bascompte, 2003). Notably, by focusing on interaction patterns among species it is possible to describe communities properties more precisely, rather than simply its richness and abundance, thus allowing for a better understanding of the complex trophic relations or even coevolutionary patterns among them.

In these networks, each species can be treated as a single node and trophic or mutualistic interactions can be represented by links between nodes. This approach is particularly interesting because even simple characterizations of its structure allow us to retrieve a great deal of information about these systems. Therefore, more precise descriptions of the underlying networks allow more accurate predictions about environmental disturbance consequences, habitat loss, climatic changes and species invasions (Ings, 2009).

Coevolutionary networks are better represented as bipartite networks, a specific type of graph. In other worlds, they have two kinds of node, in which interactions occur exclusively among different nodes (Albert e Barabási, 2001). Each node will have an own number of degree (number of interactions with other nodes). An irregular distribution of these degrees characterizes such networks as complex ones. Basic network metrics can be retrieved from these systems, such as species richness, connectance and linkage density. Also, many coevolutionary networks share common characteristics as a free - scale topology. This topology is represented by a distinct degree distribution that fits in a power - law function (Barabási & Albert, 1999)

The most studied species networks so far involve predator prey, mutualistic and parasitoid - host webs. Only recently new efforts are being made to include parasites in food webs and network analysis (Lafferty, 2008a). This kind of investigation is of major importance, given that parasites play essential roles in communities functioning. Parasitism is also one of the most diffused consuming strategies among all organisms (Lafferty, 2008b). Their biomass is significantly high and may surpass that of top predators (Juris *et al.*, 2008). Through modifications of its host's physiology and behavior, they consequently alter the influence of these over the dynamic of communities (Wood *et al.*, 2007).

### **OBJECTIVES**

Given the importance of parasites in food - webs and the scarcity of studies concerning parasite - host interaction webs, the goal of the present study is to characterize the main properties of 15 parasite - host networks. The objective of our work can be addressed by the following questions: 1) does parasite - host webs of different environments, taxa and life strategies share general properties? 2) do they also share common properties in relation to other biotic and abiotic networks, such as a free - scale topology?

#### MATERIAL AND METHODS

For the description of the networks, fifteen parasite - host checklists were compiled from present literature. Each network was described as a bipartite graph represented by a matrix R of PxH size with *i* parasites in different lines and *j* hosts in different columns.  $A_{ij}$  represents a possible interaction between a pair of species. If it is 1, that means that this pair interacts, whereas if it is zero, that means they do not. Each parasite species has a sum of  $k_i$  elements that is the total number of interactions involving that species alone. The same is valid for a host species with  $k_j$  interactions.

The degree distribution is calculated by a histogram of all  $k_i$  species interactions for parasites, all  $k_j$  interactions for hosts and for both degree to the network as a whole. To investigate the presence of a free - scale topology, the degree frequency distribution is adjusted to a power - law regression and R<sup>2</sup> calculated. The cumulative distributions of P(k) therefore is fitted in the model P(k) k<sup>y</sup> were y is the fitted constant (degree exponent).

Networks with high R  $^2$  values were regarded as scale - free. Furthermore, the connectance of each network was calculated by the proportion of the real number of linkages of the network (L) divided by the total number of possible interactions (PxH).

#### **RESULTS AND DISCUSSION**

Many of the studied networks showed distinct characteristics related to the nature of their hosts, parasites and environment. Six of the networks were related to aquatic habitats, which were represented by fish hosts and a variety of parasite groups. Four networks included mammal hosts, four bird hosts, and one simultaneously amphibians and reptiles. Terrestrial parasites included both ecto and endoparasites, including groups such as helmiths and arthropods. The most rich host - parasite network had 718 different species, and the smaller one 56 species. In most communities (80%) the richness of parasites surpassed the number of host species.

Although those host - parasite networks are very heterogeneous in their composition, all of them displayed a free scale topology, as the degree distribution frequency decayed as a power - law. Means values of R <sup>2</sup> are 0,891  $\pm$  0,059. Free - scale topology in this case means that most species in the network have a low number of interactions with others species. However, a few of them dominate the number of interactions of the network, by being involved in a great number of interactions.

When parasites and hosts sets are analyzed separately, a similar pattern emerges. All parasite species share the same degree - distribution with mean R <sup>2</sup> value of 0.86  $\pm$  0.085. Fourteen of the 15 host species sets also have a scale - free degree topology, with mean R <sup>2</sup> of 0.85  $\pm$  0.079. Those results strengthen the arguments that a free - scale topology is independent of the network size, because it can be found at different scales of a same network. In fact, there was a weak correlation between network richness and power - law degree exponent (R <sup>2</sup>=0.135 for linear regression).

Assumptions of a free - scale model are that the network formation is not random, and rather have a self - organizing dynamic which includes preferential attachments according to node fitness. That causes inevitably the appearance of "hubs", nodes with a high number of interactions. These results are encountered in other coevolutionary networks as most plant - animal mutualistic networks, such as plant - polination and seed - dispersal (Jordano, 2003). Similar properties are encountered in a number of social and abiotic networks. As discussed in literature, we may hypothesize that all these networks may follow a common growing dynamic that inevitably leads to the same structural pattern. Adding to these models a evolutionary interpretation, the speciation of a previous parasite species and its attachment to the community network (specialist or generalist behavior) may also follow self - organizing laws. In a long - scale of coevolution between groups of parasite and hosts, a few parasite species emerges as great generalists and a few hosts are infected by a great number of parasites.

#### CONCLUSION

We thank for the authors for kindly providing the checklists of parasites for analysis. A special thanks for the support and encouragement from members of our research group. MRP was funded by CNPq (grant 571334/2008 - 3)

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