

Phylogeny – an overview



Introduction

Phylogenetics is concerned with the study of evolutionary relatedness between species, populations and groups of organisms. The essential idea in phylogenetics is that all of the organisms on earth are derived from one single common ancestor. Phylogenetics is also involved in the production of a phylogenetic tree, or dendrogram. A dendrogram visually depicts the evolutionary and ancestral relationships between various organisms. They show where different species shared a common ancestor in the past (see figure 1).

As can be seen from figure 1, a phylogenetic tree can show where each group or species once shared a common ancestor, and also how closely related each group or species is. For example, it can be seen in the diagram above that groups B and C are more closely related, as they share a more recent common ancestor (time 1), than they are with group A (time 2). Each node on the diagram where the lines diverge represents the point at which a species split (or branched). The process through which a species splits in to one or more new species is known as speciation. Speciation can arise when a species becomes split by means of geographical isolation. The four modes being allopatric, parapatric, peripatric and sympatric (Baker, 2005) However, the extent to which genetic drift is involved in this process is still a matter of current discussion (Venditti et al, 2010).

However, there are a number of different ways that species can be related depending upon which characteristics are used to differentiate or characterise them. The two main characteristics used are concerned with

either morphological or molecular data. Morphological characteristics include warm-blooded (endothermic) or cold-blooded (ectothermic), possession of a notochord, unicellular or multicellular etc. Molecular characteristics include the investigation of cellular DNA, RNA and other types of genetic data (DeSalle et al, 2002).

Before the advent of modern genetic techniques that are necessary to study molecular information, morphological data was solely used in the classification of organisms. In the mid 1800s the first widely accepted genealogical tree was produced by Ernst Haeckel (see figure 2).

Figure 2 - Monophyletic tree of organisms produced by Ernst Haeckel in 1866, identifying 3 main groups of organism; Plantae, Protista and Animalia.

Along with the monophyletic tree, Haeckel also proposed the theory that ontogeny recapitulates phylogeny. That is, an organism's development mirrors the evolutionary development of its species (Breidbach, 2002). Although this theory has been superseded by modern science, there are still scientists that give credit to Haeckel's theory. For example, Williamson (2006) posits that certain embryos and larvae represent adult forms of other taxa that have been transferred by means of hybridisation. This is known as the 'Larval Transfer Theory'.

However, it should be noted that the views expressed by Williamson (2006) do not fit in with the current views in molecular biology, and there is much evidence to the contrary of the larval transfer theory, as outlined by Timmer (2009) and Hart et al (2009).

As previously mentioned, the arrival of technology capable of analysing organisms to the molecular level has given rise to a wide range of differences between the morphological and molecular relationships between species.

One area of continued research is that of the Hammerhead Shark (family, Sphyrnidae). As their name would suggest, the hammerhead shark family is distinguished from other shark families by the distinct shape of their head (see figure 3). That is, the shape of the head is dorsal-ventrally compressed and laterally expanded. This structure is known as the cephalofoil (Lim et al, 2010). Ecologically, sharks are a very diverse group encompassing an array of the ocean's most fierce predators, many of which face over-exploitation and extinction. Phylogenetic relationships within the shark family are, to date, still poorly understood, and phylogenetic estimations of risk priority is still of utmost importance considering their dwindling numbers (Zuavo et al, 2011).

Within the family Sphyrnidae each species is morphologically different based on the size and shape of the cephalofoil and also the size of the body in ways that significantly affect each species' specific functionalities (see figure 5). Cephalofoil morphology can vary quite greatly; for example the bonnethead shark (*Sphyrna tiburo*) has an evenly rounded cephalofoil whereas the winghead shark (*Eusphyra blochii*) has a very narrow and widened cephalofoil (Cavalcanti, 2005)

Figure 3 - An example of the Scalloped Hammerhead Shark showing the flattened and elongated cephalofoil

In the past, many studies have been conducted in to categorising the hammerhead shark family based up on their morphological features, and different studies have yielded different conclusions (see figure 4).

Figure 4 - Comparison of the morphological arrangements of the hammerhead shark family by two separate studies.

Considering that the studies of Gilbert (1967) and Compagno (1988) were both based on morphology they differ quite greatly in their conclusions. Almost all assumed relationships vary within the two studies with the exceptions of *Carcharhinus*, which both studies agree to be the oldest member of the family and. Reasons for these incongruities could be due to a lack of character development at branching points, uncertainties in character polarity or poor differentiation of character states (Arnold, 1990).

Figure 5 - Ultrametric tree displaying the diversification with in the Sphyrnidae family derived form nuclear gene data. The time scale displayed assumes a divergence point between forty and fifty million years

The non-consensus encountered in morphologically relating hammerhead sharks could also be, in part, due to the on going debate as to how the morphology of the cephalofoil came about. Nakaya (1995) suggests that the current hammer shaped head has evolved from other *Carcharhinid* sharks that have slightly flattened heads, and that a flattened shape provides hydrodynamic lift thus increasing their manoeuvrability (see figure 5).

Figure 6 - Different morphologies of the hammerhead shark's cephalofoil

However, it appears that for smaller members of the hammerhead family the cephalofoil doesn't infer any manoeuvrable advantages. Therefore another hypothesis for the cephalofoil's evolution involves the potential advantages of positioning sensory structures (eyes and nostrils) at the lateral ends of the head, or across the head's surface with specific note to the ampullae of Lorenzini (Kajiura, 2001). However, it should be noted that very few of the hypotheses regarding the evolution of the cephalofoil have been empirically tested (Cavalcanti, 2005). Furthermore, a more recent study by Kajiura et al (2002) found no significant difference in electrosensory reception between hammerhead sharks and other shark families.

Modern technology has recently been able to explore and compare the Sphyrnidae family at a molecular level. This allows the scientific community to further understand the relationships within the family, and between its species. These scientific methods employ techniques that are able to closely investigate the subtle differences in genetic material that allows a deeper understanding of how closely (or distantly) certain species are related within a family.

Genetic analysis of the hammerhead phylogeny can yield a new and insightful exploration of how the family are related, and to the extent of their intraspecific relatedness.

To investigate this area in greater detail, one must consult the scientific literature to elucidate this matter further. It is possible to differentiate each species (and therefore each individual) according to certain genetic data. For

Example, a recent study conducted by Lim et al (2010) used mitochondrial and nuclear genes to infer the phylogeny of the hammerhead shark family.

The study was based on mitochondrial and nuclear gene analysis amounting to 6, 292 base pairs. Bayesian analysis of their data along with Bayesian estimation of the species tree (BEST) (Liu, 2008) revealed the same topology of relationships within the shark family. Further, they conducted Shimodaira-Hasegawa tests that gave results that they believe can refute previous hypotheses of the hammerhead phylogeny. They reveal that their new hypothesis suggests that ancestors of all extant sharks were large, that is of a body size of 200cm or greater. It is also suggested by Lim et al that the small body size is likely to have evolved twice at separate times and places. They also hypothesize that once the cephalofoil evolved it went through divergent evolution in separate lineages. Their hypothesis on the divergent evolution of the cephalofoil is mirrored by that outlined by The New Scientist (2009).

The genes studied in the report were 3 nuclear genes (Dlx1, Dlx2 and ITS ND2) and mitochondrial genes denoted as D-loop and Cyb + COI (see figure 6).

Figure 7 - Maximum likelihood trees showing the relationships within and between the genus *Sphyrna*, *Eusphyra* and *Carcharhinus*

Again, the results here seem to vary quite a lot with each gene analysis. However, the tests on all the genes seem to agree, to a certain degree, that *tiburo*, *corona*, *tudes* and *media* all appear to be the most recent additions to

the Sphyrna family, and all tests also conclude that Carcharhinus is the most closely related to the family's common ancestor.

Firstly, the suggestion that Carcharhinus is the oldest member of the hammerhead family compares favourably with the morphological studies carried out by Gilbert (1967) and Compagno (1988). Secondly, the suggestion that tiburo is the most recent edition compares favourably with Gilbert (1967) but not with the more recent study by Compagno (1988).

As can be seen from the previous discussions the molecular data does not seem to compare very favourably with the results of the morphological data. Considering that the two methods of classification are very quite considerably, it comes as no great surprise that they are capable of yielding significantly different results. To press this point further, a report by Pisani et al (2007) statistically analysed incongruence in, and between, 181 molecular trees and 49 morphological trees. The study was undertaken to challenge the widely-held view that molecular phylogeny should take precedence over morphological phylogeny. As would be expected, incongruence was found to be greater between (as opposed to within) morphological and molecular trees and this was proven to be statistically significantly different. Molecular trees did, however, show a higher average congruence but the difference wasn't statistically shown to be significant.

Their results seem to indicate that it would be particularly useful to compare both molecular and morphological trees to detect areas of incongruence. Furthermore, the report highlights the fact that one form of phylogenetic

analysis should not automatically be considered to be more useful (or indeed correct) than another.

However, there are certain exceptions where one form of phylogenetic analysis should be considered a priori. For example, it can be extremely difficult to morphologically study the phylogeny of microscopic organisms such as bacteria. Although bacteria do leave fossils (such as in certain stromatalites) they tend to lack the distinctive morphological features that are present in larger organisms. As a result, molecular data is a far more effective way of reconstructing their phylogeny (DeLong et al, 2001).

Another group of organisms that don't leave a good fossil record are the Elasmobranchs (sharks, skates and rays). This is due to the fact that they are cartilaginous fish and therefore it is rare to find a full fossil in good condition. It is more common, however, to find the fossilised remains of their teeth. It is possible to explore the evolutionary past of an animal just by examining tooth fossils as shown by Nyberg et al (2006).

Overall, it would seem that in some cases the morphological data does compare favourably with the molecular data, but in many cases this is just not the case. In most cases using both methods together seems to be the most beneficial way for the continuation of phylogenetic studies.

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Figure 1: <http://archive.peabody.yale.edu/exhibits/treeoflife/phylo.html> (01/04/11)

Figure 2: <http://plus.maths.org/content/reconstructing-tree-life> (03/04/11)

Figure 3: <http://www.guardian.co.uk/environment/gallery/2008/jun/12/wildlife.endangeredspecies> (01/04/11)

Figures 4, 5 and 7: http://www.sciencedirect.com/science?_ob=MiamiCaptionURL&_method=retrieve&_udi=B6WNH-4Y9SVTC-5&_image=fig1&_ba=1&_user=7351886&_coverDate=05%2F31%2F2010&_alid=1706627755&_rdoc=1&_fmt=full&_orig=search&_cdi=6963&_issn=https://assignbuster.com/phylogeny-an-overview/

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Figure 6: [http://deepseanews.](http://deepseanews.com/wpcontent/uploads/2009/12/screenshot_01.jpg)

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