Braz. J. vet. Res. anim. Sci.
São Paulo, v.33, n.4, p.203-206, 1996.

Importance of phylogenetic systematics and its potential use in Veterinary studies

Importância e potencial utilização da sistemática filogenética em estudos de Veterinária

Antonio Carlos MARQUES[1]; Dalton de Souza AMORIM[2]

CORRESPONDENCE TO:
Antonio Carlos Marques
Departamento de Zoologia
Instituto de Biociências da USP
Caixa Postal 11294
05422-970 - São Paulo - SP - Brasil
e-mail: acmarque@usp.br

1 - Departamento de Zoologia Instituto de Biociências da USP - SP
2 - Departamento de Biologia Faculdade de Filosofia, Ciências e Letras da USP - Ribeirão Preto - SP

SUMMARY

The basic principles of phylogenetic systematics are presented, focusing on how the knowledge of phylogenetic relationships among species of a given group of wild animals is heuristically important to resolve veterinary cases, from treatments to the anatomic knowledge of this group and its representatives.

UNITERMS: Phylogeny; Cladism; Case-control studies; Wild animals; Veterinary.

INTRODUCTION

Veterinary science basically deals with comparative studies on some animal groups. In this sense, the veterinary field is closely related to or even dependent on the field of Biology called systematics. Nevertheless, there is a gap of knowledge between the "basic science" of systematics and the "technological field" of Veterinary.

Phylogenetic systematics, also known as cladistics, the most recent paradigm in systematics, was developed by the German entomologist Willi Hennig[4,5,6]. More recently, several companion studies[1,3,9,13] have made this approach in Biology and its underlying principles the chief field of evolutionary and comparative studies.

The aim of this paper is to delineate the basic knowledge of the phylogenetic systematics and to show how this can be usefully employed in the veterinary sciences (for example, clinical procedures applied to wild animals or the knowledge on the anatomy of groups). Similar studies already exist for immunology and parasitology[2], as well as in a more general sense[1,3].

The basic knowledge about phylogenetic systematics

The central goals of phylogenetic systematics are: (a) to reconstruct the phylogeny of groups of organisms and (b) to propose an information system in the form of a classification, which precisely reflects the knowledge about the evolutionary history of a given group.

From a methodological point of view, one of the central contributions of Hennig was to demonstrate that there are three different kinds of similarities to justify a taxon: plesiomorphic, apomorphic, and homoplastic similarities. The first of these two terms refers to different stages in the history of modification of a structure. Plesiomorphic is the name given to a preexisting condition from which a modified, apomorphic condition arose. For example, the epidermic scales of lizards are homologous to the epidermic feathers of birds. In the time scale sense, we can hypothesize that the "scales" are the preexisting form, the plesiomorphy, from which the apomorphy "feathers" arose.

To provide a hypothesis for the phylogeny of a given taxon, it is necessary first to distinguish, among different homologous structures which are the plesiomorphic and which are the apomorphic. When we gather the whole set of species that share an apomorphic similarity, we are able to construct a monophyletic group, that is a group which includes an ancestral species, in which such similarity arose, and all its descendant species. Any apomorphic similarity must have originated at some level in the evolution of a group, being inherited by its descendants. Hence, for each shared apomorphy or group of apomorphies we have a correspondent monophyletic group. A set of species gathered only by plesiomorphic similarities does not necessarily correspond to a monophyletic group.

Phylogenies, also known as cladograms, synthesize the genealogical information of a taxon. Given a set of information about any kind of structure in a given species belonging to a group, the evolution of any structure can be readily understood under the light of the phylogeny of that group. Hence, if a classification reflects the phylogeny of a group, instead of merely depicting general similarity, such classification can be much more useful to readers of any area because the whole group had the same evolution, from its DNA to its metabolic rates.

It is a goal of phylogenetic systematics that phylogenetic classifications themselves should allow any reader to recover the phylogeny of any group. Such kind of classification can be obtained through a fundamental principle: to accept only monophyletic taxa. In the example above, birds are a valid group based in the apomorphic feathers. On the other hand, to group the set of animals with scales in a taxon named "Reptiles" results in a taxon based on a plesiomorphy, and this group should be abandoned in phylogenetic classifications, since it is not a monophyletic group.

The third kind of similarity, called homoplasy, consists of similar features which arose independently more than once in the evolutionary history of a group, being convergent structures. One classical example of homoplastic condition is the endothermic control of temperature seen in mammals and birds. These controls presumably arose independent of each other, being incorrect to propose a taxon based on the character "endothermy", in which mammals and birds constitute a monophyletic group.

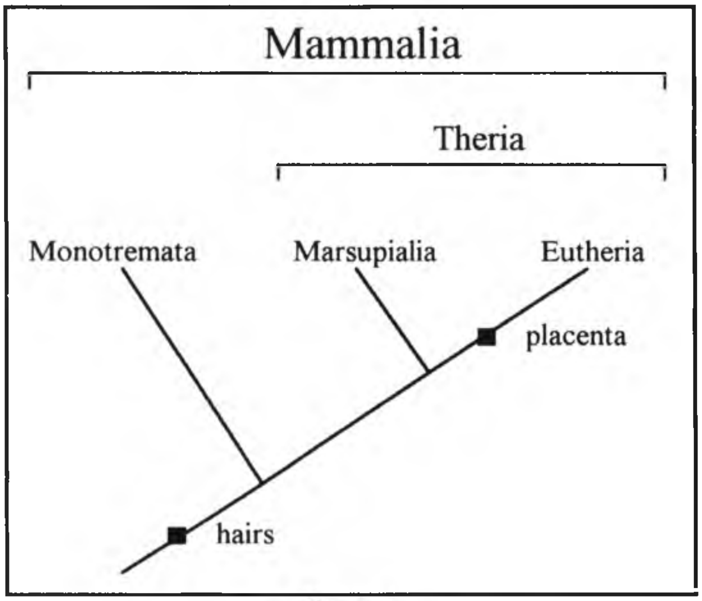

Figure 1
Phylogenetic hypothesis of relationships within the mammals (adapted from Novacek[10], 1992).

The use of phylogenetic content in the veterinary sciences

Phylogenies also allow heuristic generalizations about the distribution of characters, even for species or groups on which we have no direct information. The basic algorithm for this predictive power has been extensively described elsewhere[7]. The recovering of the evolution of structures and the predictability of the phylogenies are powerful tools which now begin to be used by many applied areas, including veterinary studies.

Just as introduction, in Fig. 1, it is shown that the presence of hairs is a synapomorphy, i.e., an apomorphy shared by various groups, of the taxon Mammalia; also, the presence of a placenta is synapomorphic for the Eutheria. It is not necessary to say that each eutherian or marsupial species present hairs, because it is shown the presence of hairs is a synapomorphy of Mammalia. Similary, it is not necessary to say that ornithorhyncans do not present placenta, because this structure arose at a level from which they are not descendants. It is also not necessary to enumerate the presence of amniotic eggs because it is a plesiomorphy, since this character appeared in the evolutionary history in the ancestor of "reptiles".

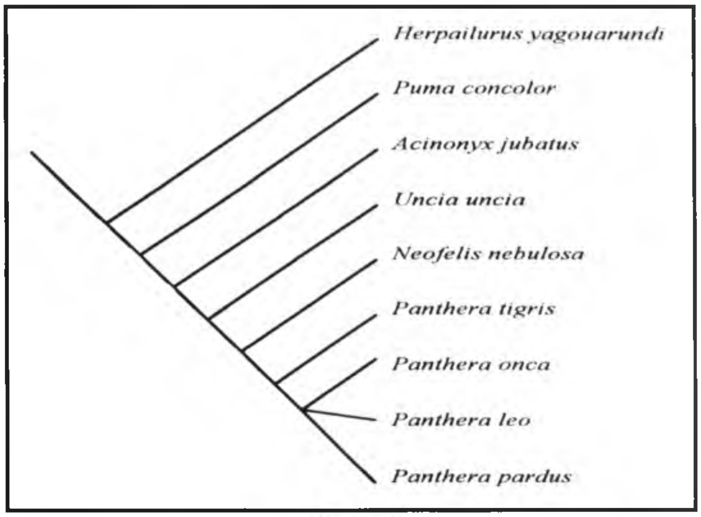

Figure 2
Phylogenetic hypothesis for the relationships among species of a monophyletic subgroup of Felidae (Salles[11], 1992).

Another example can illustrate the anatomic predictability of phylogenies. Salles[11] (1992) furnishes a phylogeny of the extant Felidae of the world, including species frequently found in zoological gardens and wild species. Consider the phylogeny in Fig. 2. Suppose - as a hypothetical example - one faces a dentary problem on the roots of the upper fourth premolar of a tiger (*Panthera tigris*), but has no handy available information for that species about the teeth structure on tigers. Having information about the roots of that tooth for lions (*Panthera leo*) and mountain cougars (*Puma concolor*) - both presenting the pair of roots fused (Fig. 3) -, it would be possible to make a generalization for the tiger, which would most certainly present the same fusion. If one knows that most genera of Felidae present separate roots, as well as *Herpailurus yagouarundi*, in face of the phylogeny it would be possible to conclude that the apomorphic condition of this character (fused roots) is restricted to the genera *Puma*, *Acinonyx*, *Uncia*, *Neofelis*, and *Panthera* - actually one of Salles[11] (1992) conclusions. The same algorithm could be applied to any condition desired. For example, one needs to anesthetize a tiger, so it is necessary a model species for allometric calculations of the most appropriate dosage of the anesthethic substance - cf. Sedgwick[12] (1993). If there is available information of "in vitro" studies in anesthetic procedures only for mountain cougars, lions and domestic cats, the most appropriate models for the calculations are the mountain cougars and lions, since they are more related to the tiger than the domestic cat. Concluding, any feature shared by *Puma concolor* and *Panthera leo* is present in the same condition in *Panthera tigris*, with the very few exceptions of the features which suffered modifications in the very stem of *Panthera tigris*.

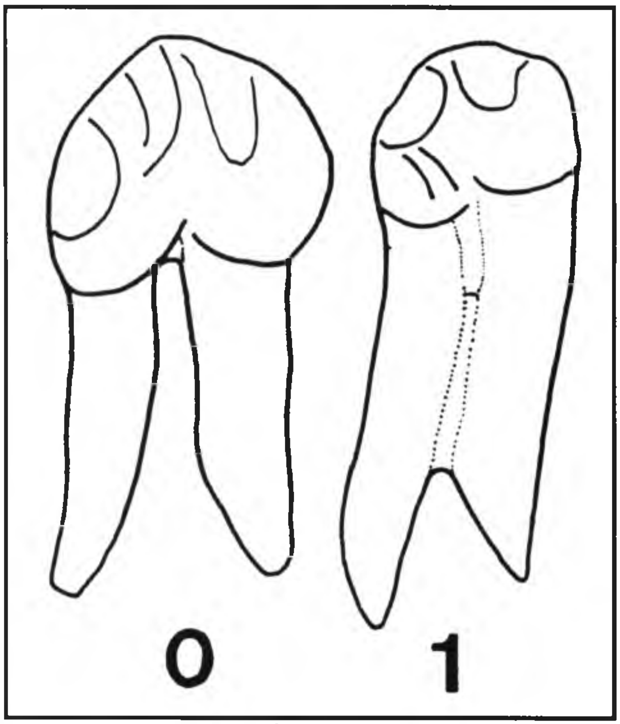

Figure 3
Upper fourth decidous premolar of two different species of Felidae, showing a transformation series for the number of roots of the tooth. Condition O in *Lynx rufus*; condition 1 in *Panthera onca* (modified from Salles[11], 1992).

It is important to note that a taxonomic name does not guarantee the monophyly of a given taxon, unless this name is based on a cladogram. In Fig. 4, the two classical groups of retrovirus, human immunodeficiency virus (HIV) and simian immunodeficiency virus (SIV), are not monophyletic both. In the figure, some strains of HIV, called HIV1 are closer to chimpanzee virus, instead the strains of HIV2 are related to other simians. So, to treat a chimpanzee (*Pan troglodytes*) infected by SIV, it is better to start with the basic amount of knowledge collected for the HIV1 (e.g., its membrane anatomy, nucleic acid codification, potential vaccines, *etc.*), since they have the same ancestors, instead of comparing with other SIVs or with HIV2.

The application of phylogenetic reasoning is very important for groups on which there is few or no information available. To make generalizations about features regarding a wild animal that must be treated, a veterinary clinician should choose phylogenetically close taxa on which there is available information and proceed using a set of reasonings as those applied in the examples above.

Certainly, people try to do this intuitively. However, the development of the phylogenetic method has demonstrated that the intuitive argumentation on evolution very frequently fails, since plesiomorphic, homoplastic and apomorphic similarities are not discerned. Animals with similar "ecological" conditions, for example, mammals inhabiting the water environment such as sirenians and cetaceans, do not necessarily have a close phylogenetic relationship. A taxonomic name, even being traditional and widespread like the "Reptilia", does not necessarily justify a monophyletic taxon.

ACKNOWLEDGEMENTS

We acknowledge the kindness of Dr. José Eduardo P.W. Bicudo, Dr. Benjamin Eurico Malucelli, Dr. Marco Antonio Gioso, Dr. Pedro Primo Bombonato, Dr. Wagner Intelizano, Lilian R. Marques de Sá, and Maria Eugenia L. Summa, and an anonymous referee, who read an earlier version of the manuscript, offering valuable suggestions.

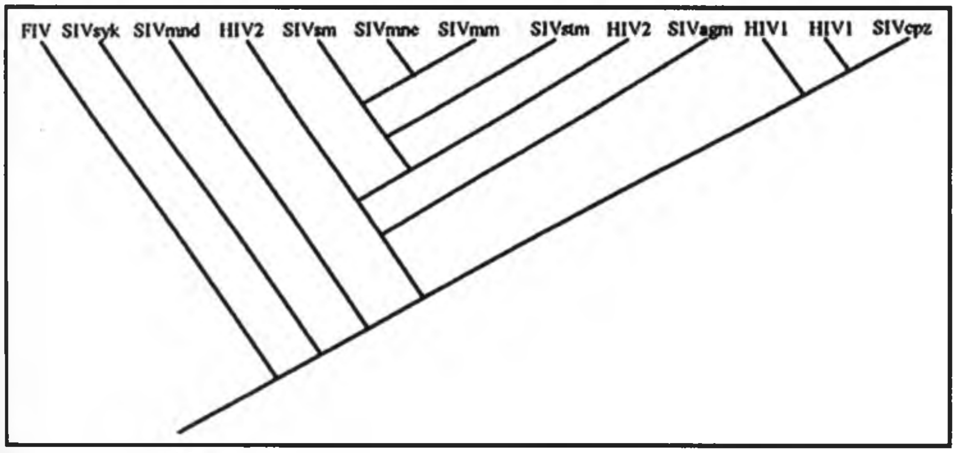

Figure 4
Phylogenetic hypothesis of relationships among immunodeficiency retroviruses of felids (FIV), Sykes'monkey (SIVsyk), mandril (SIVmnd), human (HIV1 and HIV2, more than one, strain, sooty mangabey (SIVsm) pig-tailed macaque (SIVmne), rhesus macaque (SIVmm), stump-tailedmacaque (SIVstm), African green monkey (SIVagm), and chimpanzee (SIVcpz) (adapted from Mindel *et al.*[8], 1995.

MARQUES, A.C.; AMORIM, D.S. Importance of phylogenetic systematics and its potential use in Veterinary studies. **Braz. J. vet. Res. anim. Sci.** São Paulo, v.33, n.4, p.203-206, 1996.

RESUMO

São apresentados princípios básicos de sistemática filogenética, enfocando como o conhecimento das relações filogenéticas de um dado grupo de animais silvestres é heuristicamente importante para resolver casos veterinários, desde tratamentos até conhecimento da anatomia dos grupos e seus constituintes.

UNITERMOS: Filogenia; Cladismo; Estudos de casos e controles; Animais silvestres; Veterinária.

REFERENCES

1-AMORIM, D.S. **Elementos básicos de sistemática filogenética**. São Paulo, Sociedade Brasileira de Entomologia, 1994. 314p.

2-AMORIM, D.S.; AMORIM, D.S. Phylogenetic approaches to the study of immunology and parasitology: some comments on potential research programs. **Brazilian Journal of Medical and Biological Research**, v.25, n.10, p.967-71, 1992.

3-AX, P. **The phylogenetic system**: a systematization of organisms on the basis of their phylogenesis. Chichester, John Wiley & Sons, 1987. 340p.

4-HENNIG, W. **Grunozüge einer Theorie der phylogenetischen Systematik**. Berlin, Deutscher Zentralverlag, 1950.

5-HENNIG, W. Phylogenetic systematics. **Annual Review of Ecology and Systematics**, v.10, p.97-116, 1965.

6-HENNIG, W. **Phylogenetic systematics**, New York, University of Illinois Press, 1966. 236p.

7-MADDISON, W.P.; DONOGHUE, M.J.; MADDISON, D.R. Outgroup analysis and parsimony. **Systematic Zoology**, v. 33, p.83-103, 1984.

8-MINDEL, D.P.; SCHULTZ, J.W.; EWALD, P.W. The AIDS pandemic is new, but is HIV new? **Systematic Biology**, v. 44, p.77-92, 1995.

9-NELSON, G.; PLATINICK, N.I. **Systematics and biogeography**: cladistics and vicariance. New York, Columbia University Press, 1981. 567p.

10-NOVACEK, M.J. Fossils topologies, missing data, and the higher level phylogeny of eutherian mammals. **Systematic Biology**, v.41, p.58-73, 1992.

11-SALLES, L.O. Felid phylogenetics: extant taxa and skull morphology (Felidae, Aeluroidea). **American Museum Novitates**, v.3047, n.1, p.1-67, 1992.

12-SEDGWICK, C.J. Allometric scaling and emergency care: the importance of body size. In: FOWLER, M.E., ed. **Zoo & wildlife therapy**. Philadelphia, W.B. Saunders, 1993.

13-WILEY, E.O. **Phylogenetics**: the theory and practics of phylogenetic systematics. New York, John Wiley & Sons, 1981. 439p.

Recebido para publicação: 15/08/94
Aprovado para publicação: 08/11/95