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Razi University
Faculty of Science
Department of Biology

M.Sc. Thesis

Systematics and biogeography of the Family Gekkonidae with special reference to the Genus *Cyrtopodion* in Iranian plateau

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بیوسیستماتیک و بیوجغرافی خانواده جکونیده با تاکید بر جنس *Cyrtopodion* در فلات ایران

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Abstract

In these study more than 150 specimens of Iranian house gecko, *Cyrtopodion scabrum* was collected from 30 distinct localities in different part of Iranian Plateau. Then this specimen was examined base on more than 40 metric and meristic characters.t-test and Post-ANOVA pair wise analysis and two multivariate analyses including Principal Component Analysis (PCA) and Cluster analysis were carried out based on 30 metric and 12 meristic characters across all groups. Results of these analyses, suggest that there is sexual dimorphism in *C.scabrum* but there is not any geographic Pattern between various regions of Iran.

In another study systematics and biogeography of the Genus *Tropiocolotes* was discussed. based on extensive study and research in various regions of the Iranian Plateau, and museum material examined the validity of postmental character in *Tropiocolotes sp* are questioned especially for separate *T.helenea* from *T.latifi* by Founding of two specimens of *Tropiocolotes latifi* with one species of *Tropiocolotes helenae* in sympatric manner in central Iran Plateau (Esfahan Province) invigoration our hypothesis.

In another study systematics and distribution of the *Cyrtopodion heterocercum* was discussed. Based on extensive study and field work in various regions of the central Iranian Plateau, eight specimens of the geckonid lizard, *Cyrtopodion heterocercum,* were collected from Khansar, Kashan and Semirom in Isfahan Province, central Iran. Based on our hypothesis after collecting this species in the Central Iranian Plateau, it is obvious that the Zagroos Mountains have not played a limiting role in its distribution.

In another study the ectoparasites of Geckonid lizards of the western and southwestern regions of Iranian Plateaue with regards to their respective parasite loads, especially in *Cyrtopodion scabrum*, was examined .The Unknown species of mites which were collected on four different species of geckonid lizards including *Cyrtopodion scabrum*, *Cyrtopodion heterocercum* , *Asaccus elisae* , *Asaccus grisreonotus* was reported for first time. The taxonomic status of this unknown mite and its host preferences are discussed.

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This thesis is dedicated to

Our

Grand Grandfather

Charles Darwin

Chapter 1

Introduction

1-1- Aims of the study

The aim of this study is to gather information of the family Gekkonidae and to organize this information into a hypothesis of relationships (e.g. Systematics of Gekkonidae) and analysis of geographic variation in Most distributed Gecko of Iran (*Cyrtopodion scabrum*), for this Examination ,we supply material from various part of Iran to test our hypothesis about this taxon. The area selected for this study was Most regions of Iran and sampling performed in the Kermanshah , Ilam, Lorestan, Isfahan, Khuzestan ,Tehran, Fars, Boshehr, Kerman, Sistan & Balochestan provinces on most part of Iranian Plateau .Museum material, mainly from Tehran University Zoological Museum (TUZM), Muze-ye Melli-e Tarikh-e Tabii, Tehran (MMTT), Razi University Zoological Museum (RUZM). In order to recognize the types of characters that can use in morphology based, analysis, different types of characters have evaluated. Other aims of this study are investigation about Systematic and biogeography of *Cyrtopodion heterocercum* and *Tropiocolotes sp*, we also try to find various parasites of the Gekkonidae family in Iran (such as Ectoparasits and Endoparasites) and finally Scientific contribution to the science of systematic in the Iranian Plateau and Middle East and increasing the knowledge about the lizard fauna in the Iranian Plateau by finding new taxa of lizards.

1-2- Amniotes and their Phylogeny

Amniotes include most of the land-dwelling vertebrates alive today, namely, mammals, turtles, Sphenodon, lizards, crocodylians and birds. It is a diverse clade with over 20000 living species. Amniotes include nearly all of the large plant- and flesh-eating vertebrates on land today, and they live all over the planet in virtually every habitat. They also sport disparate shapes - chameleons, bats, walruses, Homo sapiens, soft-shelled turtles, ostriches and snakes are but a few examples - and they include some of the smallest (sphaerodactyline geckoes) and largest (mysticete whales) vertebrates. Although Amniotes was fundamentally land dwellers, several clades such as ichthyosaurs, plesiosaurs, pinnipeds and cetaceans have returned to the sea. A few forms are gliders - the Flying

Dragon lizards, Honey Creepers, and Flying Squirrels - and powered aerial flight has originated three separate times, first in pterosaurs, then in birds, and later still in bats.

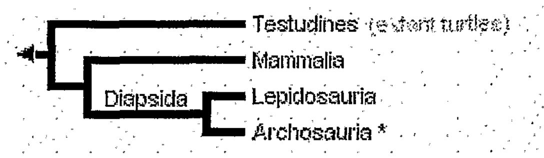
An extensive fossil record documents the origin and early evolution of Amniota, and that record has played a key role in understanding phylogenetic relationships among the living amniotes (Gauthier et al., 1988b). The oldest amniotes currently known date from the Middle Pennsylvanian locality known as Joggins, in Nova Scotia (Carroll, 1964). The relationships of these fossils indicate that amniotes first diverged into two lines, one line (Synapsida) that culminated in living mammals, and another line (Sauropsida) that embraces all the living reptiles (including birds). One Joggins fossil, the "protorothyridid" Hylonomus, appears to be a very early member of the line leading to Sauria (Crown-clade diapsids), the clade encompassing all living diapsids. This suggests that the more inclusive clade of which turtles (Testudines) are part (Anapsida) in most morphological phylogenies had diverged as well, even though its current record extends back only to the Lower Permian (Laurin & Reisz, 1995).

An older amniote (from the Lower Carboniferous) was reported (Smithson, 1989). However, more recent studies suggested that it was only a close relative of amniotes (Smithson et al., 1994), and the latest study even suggested that it was more likely to be a stem-tetrapod or an early amphibian than a relative of amniotes (Laurin & Reisz, 1999).

1-3- Discussion of phylogenetic relationships

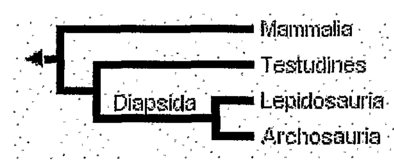
Generations of systematists have studied amniote phylogeny at diverse genealogical levels, and until a few years ago, its broad outlines were thought to be reasonably well understood. Indeed, recognition of the major living clades, such as mammals, turtles and birds, antedates the Theory of Descent. Relations among these taxa, and especially the connections of various fossils to them, have been contentious in post-Darwinian times. Much of that controversy can, however, be attributed to the fact that during the first two-thirds of this century, there was little thought given to what constituted evidence for phylogenetic relationships. The origins of the major extant lines of Amniota have become clearer in the post-Hennigian era. Nevertheless, the precise relations of a number of clades, most notably the turtles among extant forms and the aquatic and highly divergent ichthyosaurs and sauropterygians among extinct forms, remain contentious.

Early phylogenetic analyses placed turtles outside of the remaining amniotes (only crown-clade names are listed to simplify the trees):



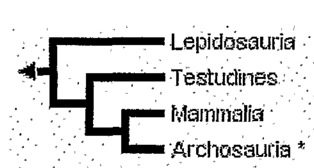
Major living amniote clades after Gaffney (1980).

Gauthier et al. (1988a, b, and c) later placed turtles as the sister clade to Sauria (crown-diapsids), and this topology has now gained wide acceptance, at least among morphologists and paleontologists:



However, Rieppel (1994, 1995), Rieppel & deBraga (1996) and deBraga & Rieppel (1997) have suggested that turtles may be the sister clade to lepidosaurs. This requires that turtles are saurians who have lost both the upper and lower temporal fenestrae (holes in the skull associated with jaw muscles) so diagnostic of diapsid reptiles:

The three trees presented above include only extant taxa, and many phylogenetic analyses of amniotes have ignored extinct taxa. However, it is important to bear in mind that discovering the globally most parsimonious tree requires the inclusion of extinct taxa in a phylogenetic analysis (Gauthier et al., 1988b). Without fossils, the best-supported tree for amniotes inferred from morphological data is the following (although only one more step is required to switch the positions of lepidosaurs and turtles):

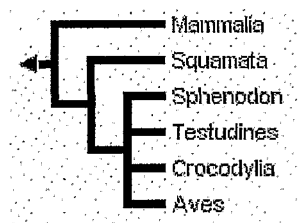


Tree based on living amniotes only (after Gauthier et al., 1988b).

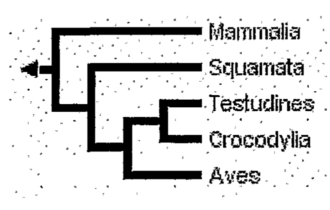
Recent molecular evidence for amniote relationships conflicts with paleontological and morphological evidence. Initially, some gene sequences suggested a close relationship between birds and mammals, although never with strong statistical support (e.g., Bishop & Friday, 1987; Goodman et al., 1987; Hedges et al., 1990). More recently, a study of the molecular evidence for the origin of birds (15 genes; 5280 nucleotides, 1461 amino acids) discovered strong support (100% bootstrap P value, BP) for a close relationship between birds and crocodilians (Hedges, 1994). A smaller data set of 11 transfer RNA genes (686 sites) also resulted in a bird-crocodilian grouping (Kumazawa & Nishida, 1995). A basal position for mammals was supported (99% BP) by analysis of a 3 kilobase portion of the mitochondrial genome containing the two ribosomal RNA genes (Hedges, 1994). In the same study, a Sphenodon-squamate relationship also was found, but support for that grouping and for the position of turtles was not very strong.

The most recent molecular phylogenies have generally placed turtles among archosauromorphs, and often within archosaurs (Mannen et al., 1997; Mannen & Li, 1999; Hedges & Poling, 1999). The latter placement is the least compatible with the morphological evidence, and no convincing explanation has been found so far to explain this discrepancy.

Many gene sequences of birds and mammals exist, but the relatively small number of sequences from representatives of other amniote lineages, especially tuataras (Sphenodon) and turtles, has hindered the estimation of a robust molecular phylogeny for all major groups of living amniotes. This is reflected by the low resolution of the molecular phylogeny obtained by Hedges & Poling (1999) when Sphenodon (using only sequences of genes available in sphenodon) was included:



Without Sphenodon and using the greater number of sequences available for other taxa, Hedges & Poling obtained the following fully resolved phylogeny, in which turtles are the sister-group of crocodilans:



If extinct amniotes are considered, the phylogeny is much more complex and controversial. Formerly, captorhinids were believed to be closely related to turtles

(Gauthier et al., 1988b, c), but more recently, procolophonids (Reisz & Laurin, 1991; Laurin & Reisz, 1995), pareiasaurs (Lee, 1993, 1994, 1995, and 1996), and even sauropterygians (a group of Mesozoic diapsids) have been suggested to represent early relatives of turtles (Rieppel, 1994, 1995; Rieppel & deBraga, 1996; deBraga & Rieppel, 1997).

1-4- Evolution of reptiles

The class reptilia are no longer recognized by phylogenetic systematists, because it is not a monophyletic group. Traditionally, the class Reptilia included the turtles, tuatara, lizards, snakes, and crocodilians. Birds, which descend from the most recent common ancestor of reptiles, have traditionally been classified by themselves in the class Aves. Reptiles, therefore, are a paraphyletic group unless birds are included. Furthermore, based on shared derived characteristics, crocodilians and birds are more recently descended from a common ancestor than either is from any living reptilian lineage; thus, they are sister groups. In phylogenetic systematics (cladistics), turtles, tuataras, lizards, snakes, crocodilians, and birds are placed in the monophyletic group Sauropsida. The Sauropsida include three groups: turtles (Testudomorpha); tuataras, lizards, and snakes (Lepidosauromorpha); and the crocodilians and birds (Archosauromorpha). In this method of classification, turtles are placed at the base of the tree. New evidence from 2 nuclear genes and analyses of mitochondrial DNA and 22 additional nuclear genes join crocodilians with turtles and place squamates at the base of the tree (Hedges and Poling, 1999; Rieppel, 1999). Morphological and paleontological evidence for this phylogeny are unclear at the present time.

Considerable disagreement continues between proponents of evolutionary (traditional) taxonomy and cladistics. The classification used in this text, for the most part, will follow the cladistic method. Comparisons between the two classification methods will be presented at appropriate points.

The fossil record for reptiles is much more complete than the one for amphibians. Based on current evidence, all lineages of modern reptiles can be traced back to the Triassic period (Fig 1-1). Disagreement, however, exists concerning origins and relationships prior to the Triassic and whether reptiles had a monophyletic, diphyletic, or even a polyphyletic origin. Molecular investigations, including comparative protein sequence studies of amniote (sauropsids and mammals) myoglobins and hemoglobins

(Bishop and Friday, 1988), are shedding new light on reptilian relationships. A cladogram giving one interpretation of the relationships among the amniotes is presented in Fig. 1-1. Molecular geneticists are attempting to extract intact DNA from dinosaur bones and from vertebrate blood in the gut of amber-preserved biting insects whose last meal might have been taken from a dinosaur (Morrell, 1993a). Although a report exists of DNA being extracted from 80-millionyear- old dinosaur bones (Woodward, 1994), most molecular evolutionists feel that the DNA came instead from human genes that contaminated the sample (Stewart and Collura, 1995; Zischler, et al., 1995).

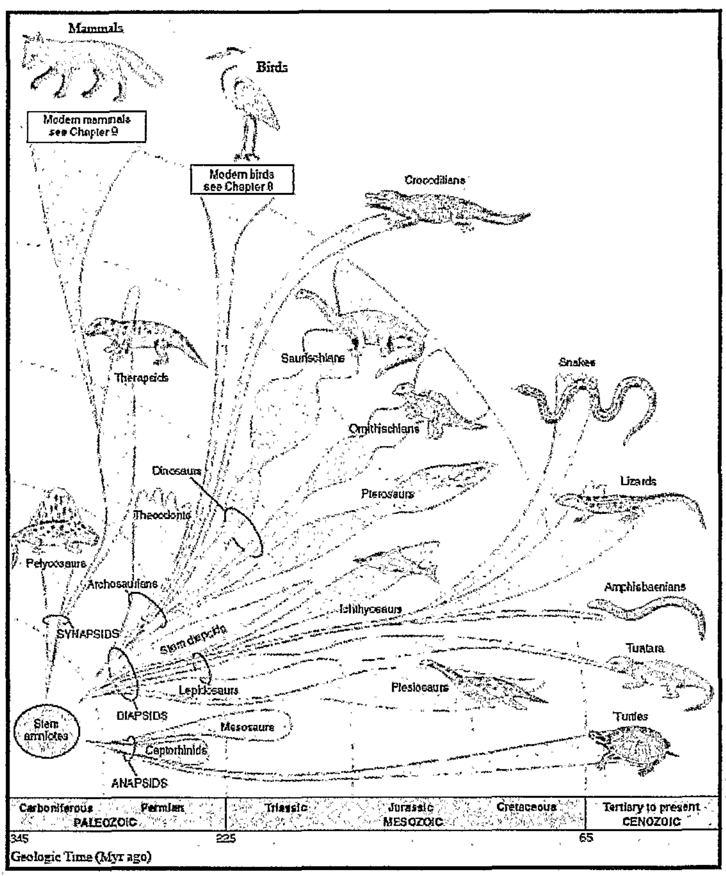


Figure 1-1: The evolutionary origin of amniotes. The evolution of an amniotic egg made reproduction on land possible. As was shown all lineages of modern reptiles can be traced back to the Triassic period

1-4-1-Ancestral reptiles

The earliest amniote skeleton comes from the Lower Carboniferous of Scotland, approximately 338 million years ago (Smithson, 1989). More recently, the same site yielded another Lower Carboniferous tetrapod, *Eucritta melanolimnetes*, which Exhibits characters from three different types of primitive tetrapods: temnospondyls (relatives of living amphibians), anthracosaurs (amniotes and their close relatives), and baphetids (crocodile-like body with a unique keyhole-shaped orbit) (Clack, 1998). Since temnospondyls and anthracosaurs have previously been found at this site between Glasgow and Edinburgh, it has been hypothesized that at least three different lineages of early tetrapod may have independently evolved into medium-sized fish-eating animals. This is but one of numerous examples of parallel evolution in vertebrates. Most recently, the smallest of all known Lower Carboniferous tetrapods, *Casineria kiddi* with an estimated snoutvent length of 85 mm, was reported from East Lothian, Scotland (Paton et al., 1999). *Casineria* shows a variety of adaptations to terrestrial life. For example, vertebrae are connected to each other to form a relatively stiff backbone, which would have served as a suspension bridge to hold up the animal's body. *Casineria* also possessed the earliest pentadactyl limb, which is clearly terrestrially adapted. The humerus had a constricted shaft and exhibited torsion between proximal and distal articulations, features associated with the maintenance of postural support and strong evidence of locomotion on land. All limbs described from earlier Late Devonian animals, such as *Ichthyostega* and *Acanthostega*, possessed more than five digits and belonged to arguably aquatic forms (Paton et al., 1999). The authors note that the degree of terrestriality exhibited by *Casineria* indicates that the transition to land-dwelling may have taken place within a period of about 20 million years. By the end of the Carboniferous (about 286 million years ago), at least two phylogenetic lines of reptiles existed: the pelycosaurs (order Pelycosauria) and the more primitive captorhinids (suborder Captorhinomorpha of the order Cotylosauria). Both of these forms have been found together in deposits approximately 300 million years old in Nova Scotia. Because of their similarity, some investigators believe that they probably evolved from a common ancestor in the Early Carboniferous (Carroll, 1988). Romer's (1966) observation, that the development of the amniote egg was so complex and so uniform among reptiles that it is not likely it could have evolved independently in two or more different groups of amphibians, lends additional weight to the belief that the origin of reptiles was monophyletic. Carroll (1988) noted that by the Upper Carboniferous, amniotes had diverged into three major lineages: synapsids gave rise to mammals, anapsids to turtles, and diapsids to all of the other reptilian groups including birds.

Members of the order Anthracosauria (subclass Labyrinthodontia) most closely resemble the primitive captorhinomorphs. One group of these amphibians, the seymouriamorphs (suborder Seymouriamorpha), possessed a combination of amphibian