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ВТОРОЙ
МЕЖДУНАРОДНЫЙ СИМПОЗИУМ
ПО АГАМОВЫМ ЯЩЕРИЦАМ

2nd INTERNATIONAL SYMPOSIUM
ON AGAMID LIZARDS

По решению редколлегии журнала «Современная герпетология» в рубрике «Материалы конференции» публикуются тезисы докладов участников Второго Международного симпозиума по Агамовым ящерицам «DeAgamis2» – ведущих специалистов из научно-исследовательских организаций Бразилии, Германии, Египта, Канады, Китая, России, Сенегала, США, Украины, Франции и Японии.

Abstracts of the Second International Symposium on Agamid Lizards «DeAgamis2» are presented here by resolution of Editorial Board of the scientific journal «Current Studies in Herpetology». The authors are leading herpetologists from scientific centers of Brazil, Canada, China, France, Egypt, Japan, Germany, Senegal, USA, Russia and Ukraine.

AGAMID LIZARDS: RESULTS AND PERPECTIVES OF STUDY OF TAXONOMIC AND MORPHOLOGICAL DIVERSITY

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One of important aspect of integrative study of lizards of Agamidae family is an analysis of morphological diversity within this group of squamates according to recognizing compositional, structural and functional biodiversity (Noss, 1990). Agamidae is morphologically and ecologically diverse family belonging to Iguania that is a sister group to all the remaining squamates (Sukhanov, 1961; Moody, 1980; Estes, 1983, 1985). Agamid lizards are characterized by acro-pleurodont dentition, lack of the intravertebral autoto-my fracture plan existing in most other lizards and high structural diversity of integumental derivatives : scale sense organs, epidermal holocrine glands (femoral pores, callose scalation), and so on. There is a maximal diversity of attachment and replacement types in dentition within Iguania: pleurodont in Iguanidae, acrodont in Chamaeleonidae and pleuro-acrodont, or wholly acrodont (in *Uromastyx* and *Moloch*) in agamids. The study of structure and development of dentition revealed a special type of anlage of the eggteeth in Iguania in comparison with another squamates (Sergeyev, 1940; Ananjeva, Orlov, 1986).

Family of Agamidae includes about 350 species belonging to about 50 genera. During last 20 years some more new genera and species of agamids were described and new concept on the phylogeny and biogeography of agamids was established basing on the results of study of the mitochondrial genome (Macey et al., 2000) and revealing of cryptic diversity within many genera and species complexes (Ananjeva, Orlov, 2006; Ananjeva et al., 2008).

Agamids demonstrate a high diversity of epidermal holocrine glands (femoral/inguinal folllicular glands, or pores, and precloacal/abdominal callous glands (Maderson, Chiu, 1970; Moody, 1980; Sokolov et al., 1994). Femoral pores are typical for subfamilies Uromastycinae, Leiolepidinae, Hydrosaurinae, Amphibolurinae (except *Chelosania* and *Moloch*). They are absent only in two most diverse subfamilies: Agaminae and Draconinae that characterized by the lack of lense-like scale sense organs. In agamids of genera *Agama*, *Trapelus*, *Acanthocercus*, *Laudakia*, only of Agaminae subfamily, unique morphological structures (epidermal holocrine glands) are recorded (Duisebayeva, 1995). There are contraversal points of view if these structures are homologous (Smith, 1935) or nonhomologous (Moody, 1980).

Agamid lizards are interesting and perspective models to study speciation and taxonomic diversity of arid territories and tropical forest.

Study was supported by Grant RFBI 09-04-00132.

Key words: Squamata, Agamidae, morphology, taxonomic diversity, cryptic speciation.

PRELIMINARY DATA ON DNA BARCODING OF AGAMINAE WITH SOME TAXONOMICAL COMMENTS

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We studied more than 120 sequences (650 bp of COI-5P) of different forms of genera *Laudakia*, *Trapelus* and *Pseudotrapelus.*

a

b

Females of *Pseudotrapelus sp.* aff. *sinaitus* (Aqaba) (*a*) and *Pseudotrapelus sinaitus* (Wadi Rum) (*b*) (foto Daniel Melnikov)

There are three forms with presumably species-level genetic distances in *Pseudotrapelus*: south-east and central Jordan *P. s. sinaitus*, south-west Jordan – *P. s.* ssp., north Jordan and south Syria *P. s. werneri* (no molecular data).

Trapelus has two main groups – *Trapelus ruderatus* complex and *Trapelus agilis-sanguinolentus-persicus* complex. There are four main clades in *Trapelus ruderatus* complex. Specimen from westernmost locality – Konya (Turkey) – occupies the most basal position and is a sister clade to three other subclades – from Ham, Fars and Azerbaijan – Zanjan – Kermanshah provinces of Iran. There are five clades and numerous subclades within *Trapelus agilis-sanguinolentus-persicus* complex. Also there is a surprisingly deep phylogeographic structure with high divergence levels between clades which do not seem to correspond with known geographic barriers. Basal position occupies the specimen of *Trapelus persicus* from Ham (Dehloran).

Probably there are two sympatric forms in Khorasan. *Trapelus sanguinolentus* from Daghestan (Nogay) and Kazakhstan (Aral) forms a well supported clade which also includes one haplotype of *agilis* from Khorasan province.

Laudakia consists of two main clades – *L. tuberculata* and *L. nupta* complexes and *Laudakia stoliczkana-lehmanni-bochariensis-caucasia-microlepis-stellio. Laudakia caucasia* complex consists of numerous clades showing strong phylogeographic structure that corresponds well with orography of Caucasus – Elburz – Kopeth-Dagh, but surprisingly small genetic distances between them. *Laudakia microlepis* is sister to *Laudakia caucasia* complex. In *Laudakia stellio* complex – *L. brachydactyla* (Petra, Jordan) is a sister species to *L. stellio*, with subspecies *L. s. stellio* (Turkey) and the Middle East *Stellio*

(sensu Panov et Zykova) (Euphrates river, N Syria). *Laudakia nupta* complex consists of three forms of species level divergence: form from Khorasan – Esfahan, Hormozgan – Fars and Kermanshah – Khuzestan – Ham. *Laudakia tuberculata* is a sister species to *Laudakia nupta.*

Key words: DNA Barcoding, *Laudakia*, *Trapelus*, *Pseudotrapelus.*

AGAMID LIZARDS CROSSING THE WAY OF 60 YEARS OF HERPETOLOGY IN THE MUSEUM ALEXANDER KOENIG, BONN

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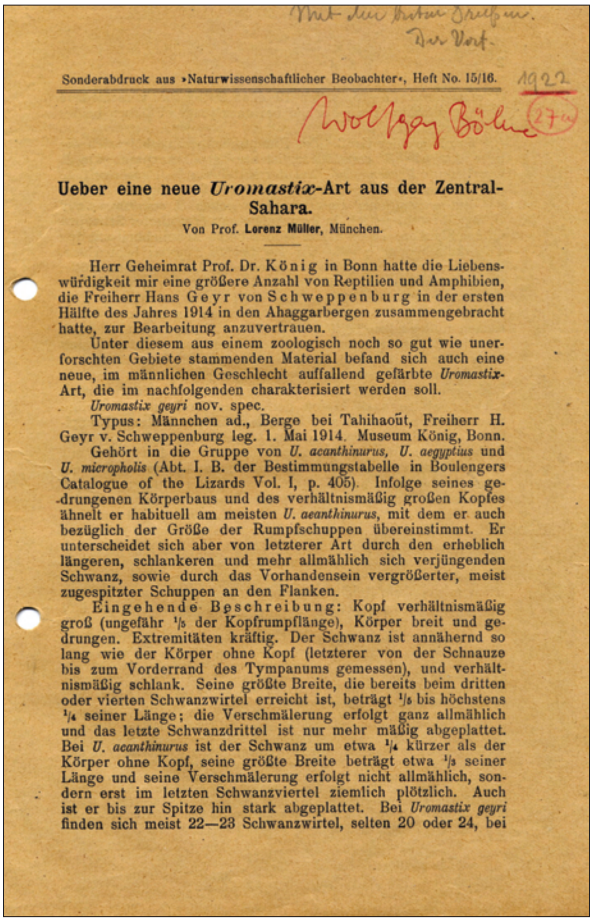
Brief historical sketch of Museum A. Koenig (ZFMK), Bonn. Founded by the St. Petersburg native Alexander Koenig (1858 – 1940) in 1900 as a purely ornithological research institution, it became a public museum in 1934 while the research part was extended to mammalogy and entomology. The herpetology department was founded only in 1951. It first housed merely few herps collected by Koenig and his assistants as by-catches during their mainly ornithological expeditions to North Africa. Remarkable is the Hoggar spiny tail lizard collected by Frhr. Hans Geyr von Schweppenburg and subsequently



Mit den besten Grüßen.
Der Verf.

Sonderabdruck aus »Naturwissenschaftlicher Beobachter«, Heft No. 15/16. 1922

Wolfgang Böhme (27a)

Ueber eine neue *Uromastix*-Art aus der Zentral-Sahara.

Von Prof. **Lorenz Müller**, München.

Herr Geheimrat Prof. Dr. König in Bonn hatte die Liebenswürdigkeit mir eine größere Anzahl von Reptilien und Amphibien, die Freiherr Hans Geyr von Schweppenburg in der ersten Hälfte des Jahres 1914 in den Ahaggarbergen zusammengebracht hatte, zur Bearbeitung anzuvertrauen.

Unter diesem aus einem zoologisch noch so gut wie unerforschten Gebiete stammenden Material befand sich auch eine neue, im männlichen Geschlecht auffallend gefärbte *Uromastix*-Art, die im nachfolgenden charakterisiert werden soll.

Uromastix geyri nov. spec.

Typus: Männchen ad., Berge bei Tahihaoût, Freiherr H. Geyr v. Schweppenburg leg. 1. Mai 1914. Museum König, Bonn.

Gehört in die Gruppe von *U. acanthinurus*, *U. aegyptius* und *U. micropholis* (Abt. I. B. der Bestimmungstabelle in Boulengers Catalogue of the Lizards Vol. I, p. 405). Infolge seines gedrungenen Körperbaus und des verhältnismäßig großen Kopfes ähnelt er habituell am meisten *U. acanthinurus*, mit dem er auch bezüglich der Größe der Rumpfschuppen übereinstimmt. Er unterscheidet sich aber von letzterer Art durch den erheblich längeren, schlankeren und mehr allmählich sich verjüngenden Schwanz, sowie durch das Vorhandensein vergrößerter, meist zugespitzter Schuppen an den Flanken.

Eingehende Beschreibung: Kopf verhältnismäßig groß (ungefähr $^1/_5$ der Kopfrumpflänge), Körper breit und gedrungen. Extremitäten kräftig. Der Schwanz ist annähernd so lang wie der Körper ohne Kopf (letzterer von der Schnauze bis zum Vorderrand des Tympanums gemessen), und verhältnismäßig schlank. Seine größte Breite, die bereits beim dritten oder vierten Schwanzwirtel erreicht ist, beträgt $^1/_6$ bis höchstens $^1/_4$ seiner Länge; die Verschmälerung erfolgt ganz allmählich und das letzte Schwanzdrittel ist nur mehr mäßig abgeplattet. Bei *U. acanthinurus* ist der Schwanz um etwa $^1/_4$ kürzer als der Körper ohne Kopf, seine größte Breite beträgt etwa $^1/_3$ seiner Länge und seine Verschmälerung erfolgt nicht allmählich, sondern erst im letzten Schwanzviertel ziemlich plötzlich. Auch ist er bis zur Spitze hin stark abgeplattet. Bei *Uromastix geyri* finden sich meist 22—23 Schwanzwirtel, selten 20 oder 24, bei

FORSCHUNGS museum KOENIG

Bonner zoologische Beiträge

On Agamid Lizards

Proceedings of 'DeAgamis – 1st International Symposium on Agamid Lizards' held in the Zoologisches Forschungsmuseum Alexander Koenig in Bonn, February 22–24, 2008

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First paper especially on ZFMK agamids (original descritpion of *Uromastyx geyri*) and the last comprehensive proceedings volume of DeAgamis I described by Lorenz Müller as *Uromastyx geyri* Müller, 1922, thereby becoming the first name-bearing herpetological type of ZFMK. Important acquisitions of agamids followed only 4 – 5 decades later: rich *Laudakia stellio* material from several Aegean islands (K.F. Buchholz); several rare and endemic *Laudakia* species from Afghanistan (Clas M. Naumann) and Pakistan (Khalid J. Baig); the Gottingen Museum collection with some historical agamid types; significant collections from West (Mauritania, Senegal) and East Africa (Kenya, Tanzania, Zambia) as well as from SE Asia (Thailand, Malaysia, Vietnam).

Research on agamid lizards at ZFMK was and is carried out in the course of several doctoral theses since the late 1970-ies: with the two DAAD fellows Scott M. Moody (from Ann Arbor, USA), Khalid J. Baig (from Islamabad), Thomas Wilms and Philipp Wagner, the work of the two latter being strongly supported by Andreas Schmitz (formerly also ZFMK, now Geneva). Agamid research in Bonn culminated by organizing the 1st international symposium «DeAgamis» which now finds its continuation in the present meeting «DeAgamis II» in St. Petersburg.

Key words: Squamata, Agamidae, Museum Alexander Koenig, Bonn.

PHYLOGENY, PHYLOGEOGRAPHY AND IDENTIFICATION OF ASIAN TOAD-HEADED AGAMAS *PHRYNOCEPHALUS* (SUPERSPECIES *VERSICOLOR*)

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We studied 16S and COI sequences of 42 specimens from 37 populations belonging to five taxa of *Phrynocephalus versicolor* species complex.

Most basal position in the NJ- and ML-trees occupies the clade comprising *Ph. hispida.* Within the remaining taxa, clearly separate position occupies the clade from Tuva and NW Mongolia – *Ph. kulagini* (*Ph. versicolor kulagini*) – this taxon is a sister clade to the group joining *Ph. versicolor* + (*Ph. frontalis* + *Ph. przewalskii*).

Modern range of *Ph. hispida* occupies Dzhungarian and Transaltai Gobi in Mongolia and from the eastern part of Xinjiang to Gansu province in China. This territory is regarded as a possible area of origin of *Ph.* (superspecies *versicolor*) and *Ph.* (superspecies *guttatus*) ancestors (Dunayev, 2009). Further dispersal of versicolor-group ancestor went in two basic directions: first lineage crossed Mongolian Altai and along the Great Lakes depression reached southern Tuva (Russia), where *Ph. kulagini* was formed. Another lineage moved to the east and gave rise to *Ph. przewalskii*, *Ph. frontalis* and *Ph. versicolor.* Further differentiation of this group seems to be a subject of adaptive radiation and morphological differentiation of taxa since several substrate races were formed.

Ph. przewalskii and *Ph. frontalis* are found in sandy areas in Ordos and Alashan deserts, whereas *Ph. versicolor* inhabit hammadas in Gobi desert. As a result of further dispersal of *Ph. versicolor* in southern Mongolia it formed narrow contact zones with two parapatrically distributed «cryptic» species (*Ph. hispida* and *Ph. kulagini*).

All taxa can be distinguished from each other on the basis of colouration. *Ph. frontalis* and *Ph. przewalskii* are distinct from other species in having bright-orange (aurantiacus) underside of tail in juvenile and young specimens, and from each other they can be distinguished by size or absence/presence of dark dorsomedial stripe. Other species of *Ph.* (superspecies *versicolor*) have yellow underside of tail in juveniles. *Ph. hispida* and *Ph. versicolor* are distinguished from *Ph. kulagini* in presence of pink (or orange) axillary spots, and from each other in white (in *Ph. hispida*) or black (in *Ph. versicolor*) end of tail undersurface in young and juveniles.

Part of molecular analysis was completed within the international program «Consortium for the Barcoding of Life (CBOL)».

Key words: *Phrynocephalus* (superspecies *versicolor*), *Ph. hispida*, *Ph. kulagini*, *Ph. przewalskii*, *Ph. frontalis*, «cryptic» species.

SEXUAL DIMORPHISM IN *TRAPELUS RUDERATUS RUDERATUS* (SAURIA: AGAMIDAE) WITH NOTES ON THE NATURAL HISTORY

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In agamid lizards, both sexual selection and natural selection influence the form of dimorphism in secondary sexual traits The genus *Trapelus* Cuvier, 1816 comprises four species on the Iranian Plateau as follows: *T. agilis* (Olivier, 1804), *T. lessonae* (De Filippi, 1865), *T. ruderatus* (Blanford, 1881) and *T. megalonyx* (Gunther, 1865). The distribution of *T. ruderatus* (=the formerly *T. persicus*) in Iran is limited to southern and southwestern regions of the Iranian Plateau.

Among the Iranian species of the genus *Trapelus* the study of sexual dimorphism has already been carried out in *Trapelus agilis.* In this relation, study of sexual dimorphism, coloration and color pattern, and natural history of the Persian agama (*Trapelus ruderatus*= the formerly *T. persicus*) is of interest and importance.

The patterns of sexual dimorphism in the Persian agama, *T. ruderatus*, in relation to environmental issues are discussed. We studied sexual dimorphism and some aspects of natural history and behavior of the Persian agama (*Trapelus ruderatus ruderatus*) from southwestern Iran. Uni-and multivariate statistical procedures were employed to explore the paptterns of sexual dimorphism in the Persian agama. Based on the statistical analyses, some characters show significant differences between males and females.

Key words: *Trapelus ruderatus*, sexual dimorphism, natural history, Ilam, Iran.

MALE-MEDIATED GENE FLOW IN THE TOAD-HEADED LIZARDS *PHRYNOCEPHALUS PRZEWALSKII*

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Using mitochondrial and microsatellite DNA data and a population genetic approach, we tested male-mediated gene flow in the toad-headed lizards *Phrynocephalus przewalskii.* The mitochondrial DNA (ND2 gene), on the one hand, revealed two major lineages and a strong population genetic structure (FST = 0.692; FST0 = 0.995). The pairwise differences between the two lineages ranged from 2.1% to 6.4% and the geographic division of the two lineages coincided with a mountain chain consisting of the Helan and Yin Mountains, suggesting a historical vicariant pattern. On the other hand, the nuclear microsatellite DNA revealed a significant but small population genetic structure (Fst = 0.017; Fst1 = 0.372). The pairwise Fst among the nine populations examined with seven microsatellite DNA loci ranged from 0.0062 to 0.0266; the assignment test failed to detect any naturally occurring population clusters. Furthermore, the populations demonstrated a weak isolation by distance and a northeast to southwest clinal variation, rather than a vicariant pattern. Morphological examination also corroborated the nuclear gene pattern. A historical vicariant event followed by male-mediated gene flow appears to be the best explanation for the observation. Approximately 2 – 5 Ma, climatic change may have created an uninhabitable zone along the Helan-Yin mountain chain and initiated the divergence between the two mitochondrial lineages. With further climatic changes, males were able to disperse across the mountain chain, causing sufficient gene flow that eventually erased the vicariant pattern and drastically reduced the population genetic structure, while females remained philopatric and maintained the mitochondrial DNA divergence. Although polygyny mating system and female philopatry may partially contribute to the reduced movement of females, other hypotheses, such as female intrasexual aggression, should also be explored.

Key words: male-mediated gene flow, microsatellite DNA, mtDNA, *Phrynocephalus,* population genetic structure, vicariance.

ASEXUALITY ON THE BEACH: PHYLOGENY, BIOGEOGRAPHY AND THE ORIGIN OF PARTHENOGENESIS IN *LEIOLEPIS*

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The Southeast Asian agamid lizard genus *Leiolepis* Cuvier, (1829) is an enigmatic, lineage, differing form other lizard groups in general morphology and ecology. Currently, *Leiolepis* contains nine species that collectively range throughout Indochina and the Malay Peninsula. Of these nine species, four are all female, parthenogenic species. Unlike their sexual congeners, these asexual species have pocketed distributions throughout Southeast Asia and are only found in secondary, or perpetually disturbed habitat. Using the mtDNA gene ND2, and two rapidly evolving nuclear genes we investigated the origins of these asexual species, and present a species level phylogeny for *Leiolepis.*

Key words: phylogeny, biogeography, agamid lizards, *Leiolepis*, parthenogenesis.

REMARKS ON THE TAXONOMY AND ECOLOGY OF SE ASIAN BUTTERFLY LIZARDS, GENUS *LEIOLEPIS* (AGAMIDAE: LEIOLEPIDINAE)

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We review recent taxonomic and ecological research on butterfly lizards (genus *Leiolepis* Cuvier, 1829) carried out at the Zoologisches Forschungsmuseum A. Koenig (ZFMK) in Bonn. The remarkable parthenogenetic forms («species») of *Leiolepis* are either diploid (L. *boehmei)* or triploid (*L. guentherpetersi*, *L. triploida).* In the case of *L. guentherpetersi,* a hybrid status has been proven, *L. guttata* providing the maternal line and *L. reevesii* being the paternal one. *L. triploida* is best explained as a hybrid of diploid parthenogenetic *boehmei* females and *L. belliana* males, the origin of the *L. boehmei* strain itself remaining unknown.

The taxon *rubritaeniata,* originally described as a subspecies of *L. belliana*, was later, after the raise of *L. b. reevesi* to full specific rank, referred to as *L. reevesii rubritaeniata.* Partly, a subspecific status was not even conceded. However, new morphological and molecular genetic data clearly demonstrate specific status also for *L. rubritaeniata*, an inland inhabiting butterfly lizard known from Thailand, Laos and a small part of Central Vietnam. During field surveys in the Phnom Kulen National Park in Cambodia, *L. rubritaeniata* was recorded for the first time also from this country.

Ecological data stem from an unpublished field study of a *L. belliana* population on Langkawi Id., West Malaysia. Apart from an unusual kind of locomotion during display, data were collected on spatial distribution, density, stomach contents, and social behaviour.

Key words: Agamidae, *Leiolepis,* review of *rubritaeniata*, *belliana*, taxonomic and natural history data.

SEXUAL DIMORPHISM OF BLACK ROCK AGAMA, *LAUDAKIA MELANURA LIRATA* (BLANFORD, 1874) (SAURIA: AGAMIDAE)

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The Black Rock Agama, *Laudakia melanura* (Blyth, 1854), is one of the representative faunal elements of the southeastern periphery of the Iranian plateau which extends from southern Iran east to northwestern Punjab. 9 females and 12 males were captured between September 2008 and February 2009 from different localities in Gando Protected Area located in Sistan and Baluchistan provinces which extends from 25°03' to 26°16' N and 61°09' to 61°53' E on the southeastern border of Iran and Pakistan.

Morphological analyses were performed using 14 metric and 9 meristic characters. T-test and principal component analysis (PCA) was performed on the log transformed matrix of metric and proportional characters. *T*-test shows significant differences in all metric characters with the exception of HL, HW and HH ($p < 0.05$). None of the meristic characters reached high enough probability to be used in discriminating between the two sexes. In this lizard, sexual dimorphism of head, in contrast to other congeneric species, is more due to the shape of head. In contrast to *L. caucasia* and *L. microlepis* in *L. m. lirata* patches of callous scales at abdomen and preanal regions usually occur independent to sex, nonetheless, in some females no callous scales was observed and others had some just in abdomen region.

Key words: *Laudakia melanura lirata*, sexual dimorphism, Gando Protected Area, Sistan and Baluchistan province, Southeastern Iran.

A STUDY OF BEHAVIOUR, HABITAT, DISTRIBUTION AND ECOLOGY ON *LYRIOCEPHALUS SCUTATUS* (LINNAEUS, 1758) IN SRI LANKA

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There are 18 species of agamid lizards distributed throughout Sri Lanka, 15 (83%) of them are endemic and the genera *Ceratophora* Gray, 1834, *Cophotis* Peters, 1861 and *Lyriocephalus* Merrem, 1820 are relic to the island. The genus *Lyriocephalus* Merrem, 1820 is monotypic and relict to Sri Lanka. *Lyriocephalus scutatus* is diurnal, sub-arboreal and slow moving agamid lizard. This colorful species is distributed in cool and shady forested areas with a dense canopy in wet & intermediate lowlands and mid hills up to elevations of 1600 m, snout-vent length (SVL) varies around 94 mm. Very little is known about the ecology, biology and behaviour of this species throughout its range, hence we have examined 52 localities (August 2004 to March 2007) throughout 11 districts. A total of 109 individuals (Males: 47, Females: 41 and Juveniles: 21) were observed in nature during dry and wet seasons. The analysis of habitat data has shown that species is widely spared within the well shading riverine forested areas and poorly in the home gardens. The results of this survey indicate *Lyriocephalus scutatus* lays eggs about 3 – 4 from March to May on shady, cool places nearly 1 foot away from the tree base. While laying eggs the females change their body color in to ground color. The eggs are 22.1 mm to 24.6 mm (mean 23.4 mm) long and 13.6 mm to 15.1 mm (mean 14.4.0 mm) wide. Mostly egg layings were recorded in mornings with high humidity. Hatchlings

Lyriocephalus scutatus (Linnaeus, 1758) from Sri Lanka come out from June to August after 65 – 71 days of incubation. The hemipenis of males is completely different comparative to the other agamid lizards in Sri Lanka. This species specially feed on earth worms, spiders, centipedes and other insects. These lizards' natural predators are Gray Hornbill, Blue Magpie, Shikra and other raptors, Cat snakes, Green Pitviper, Loris, Toque Monkeys and domestic cats. When a danger appears this lizard slowly climbs to the tree while moving around the stem. At night they sleep on the trees about 2.5 m to 4.5 m above ground level on branches diameter about 40 mm to 58 mm. *Calotes calotes*, *Calotes liolepis*, *Calotes liocephalus*, *Ceratophora aspera*, *Otocryptis nigristigma* and *Otocryptis wiegmanni* are recorded as other sympatric agamid lizards. The current habitat destruction shows a great warning to this species. The villagers inhabit in the forested areas believe several myths of this lizard. Therefore education awareness programs are needed to conserve this relict species.

Key words: Sri Lanka, *Lyriocephalus scutatus*, ecology.

PHYLOGEOGRAPHY OF *PHRYNOCEPHALUS VLANGALII* COMPLEX ON THE UPPER REACHES OF THE YELLOW RIVER INFERRED FROM mtDNA ND4-tRNAleu SEQUENCES

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A fragment of mtDNA ND4-tRNALeu from 189 samples in 26 populations was used to infer the phylogeographic structure of *Phrynocephalus vlangalii* complex on the upper reaches of the Yellow River. 703bp ND4-tRNALeu sequences defined 39 haplotypes. Both the Bayesian tree and MP tree comprised two Clades (A and B). Clade A included populations in Zoige Wetland (A1), populations in the west of Kuku-noor Lake (A2) and *P. theobaldi;* Clade B included populations in the south of Kuku-noor

a *b*

Male (*a*) and female (*b*) of *Phrynocephalus putjatai* from Haiyan and Tianzhu respectively

a *b*

Males of *Phrynocephalus vlangalii* from Suganhu (*a*) and Xiaman (*b*) respectively

Lake (B1) and those in the north of Kuku-noor Lake (B2). AMOVA showed that these five groups were distinctly different ($P < 0.01$), with 88.63% of the total genetic diversity being attributable to variation among groups. There might be recent population expansion in A1 and A2, which corresponded to the dry climate of the last interglacial period. The expansion times were estimated at about 0.189 – 0.105 Ma and 0.102 – 0.057 Ma, respectively. Molecular clock estimation indicated that Clade A and Clade B diverged at *ca.* 4.29 – 2.38 Ma, which fell within the timeframe of the A phase of Qingzang Movement. The divergence between B1 and B2 at *ca.* 1.73 – 0.96 Ma may be caused by the geological event in Huangshui valley. In early Pleistocene, populations in B1 may have strong gene flow because of geographic linkage, following with a few extinct haplotypes related to the uplift of Tibetan Plateau and the change of Yellow River route. The divergence triggered by A'nyemaqen Mountains between A1 and A2 was estimated at *ca.* 0.66 – 0.37 Ma, which may occurred at *ca.* 0.7 Ma glaciations.

Key words: *Phrynocephalus vlangalii* complex, mtDNA ND4, phylogeography.

WEST AFRICAN AGAMAS: SYSTEMATICS, GEOGRAPHIC DISTRIBUTION, ECOLOGY AND PHYLOGENY

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Few published data are available on West African Agamid lizards. From 2003 to 2009, we have collected 1,020 specimens from 11 countries (Senegal, Mauritania, Mali, Guinea, Liberia, Burkina Faso, Ghana, Togo, Benin, Niger, Nigeria) and investigated their systematics, geographic distribution, ecology and phylogeny. For molecular studies, we have used two separate portions of mitogenome, coding for 16S rRNA and for cytochrome B. DNA from 100 mg of homogenized muscular tissue conserved in ethanol, was extracted using the QIAGEN BioRobot MDx Workstation with customized extraction protocol and stored at 4°C until use in PCR amplifications. Primers were manufactured by Eurogentec, Seraing, Belgium. Polymerase chain reactions were performed in automated DNA thermal cyclers. PCR products were visualized by electrophoresis on a 1.5% agarose gel, stained with ethidium bromide and examined using an ultraviolet transilluminator. The PCR products were purified using a QIAquick Spin PCR Purification Kit (Qiagen) according to the manufacturer’s instructions. Sequencing of amplicons was performed using the BigDye Terminator Cycle Sequencing Kit with ABI automated sequencer. Obtained sequences were assembled, edited by BioEdit Sequence alignment editor v. 7.0.9.0 and compared with those available in GenBank by NCBI BLAST. Sequences of both mitochondrial genes from studied lizards were concatenated and aligned with CLUSTAL W program, and a neighbor-joining phylogenetic tree was constructed with Geneious 4.7.6 software.

Fourteen different species were recognized in the genus *Agama* in West Africa, excluding the easternmost part of Nigeria near the Cameroon border which was not included in our study: *Agama africana*, *A. agama*, *A. boueti*, *A. boulengeri*, *A. castroviejoi*, *A. cristata*, *A. doriae benueensis*, *A. gracilimembris*, *A. insularis*, *A. paragama*, *A. sankaranica*, *A. weidholzi*, and two undescribed species. According to biogeographic areas, four species were Sahelian, seven species were Sudanian, two species were Guinean, and one species was ubiquitous.

Key words: agama, systematics, geographic distribution, ecology and phylogeny, West Africa.

MOLECULAR STUDIES OF *PHRYNOCEPHALUS.* REVIEW

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From 2003 more than 18 molecular papers on *Phrynocephalus* were published (from 1 in 2003 to 9 in 2009). In some of them lizards were considered just as good model organisms for study population genetic processes (group of Prof. Fu Jinzhong), in other molecular methods were used to resolve taxonomic relationships in some groups of *Phrynocephalus* (our group and group of Dr. Evgeniy Dunayev). Many papers are focused on widely distributed species as *Ph. guttatus-versicolor* and *Ph. helioscopus-persicus* complexes or Tibetan forms of *Ph. vlangalii* group. Most popular marker is mtDNA ND2 sequence and there are only one work with nDNA sequence and just a few with microsattelites. Different used markers show in general a good congruence of results with each other and with morphology. Unique situation of *Ph. przewalskii* and *Ph. frontalis* (*Ph. guttatus-versicolor* complex) with great morphological differences and no genetic barriers is one of the most intriguing.

Males (upper photos) and females of *Ph. przewalskii* Strauch, 1876 (left photos) and *Ph. frontalis* Strauch, 1876. Scale is not equal – *Ph. przewalskii* is about twice bigger, 8 – 9 cm body length (foto Daniel Melnikov)

Key words: *Phrynocephalus*, molecular study, phylogeny, biogeography.

MITES OF THE FAMILY PTERYGOSOMATIDAE (ACARI: PROSTIGMATA) – PERMANENT PARASITES OF LIZARDS AND PERSPECTIVES OF THEIR IMPLICATION IN INFERENCE OF HOST PHYLOGENY

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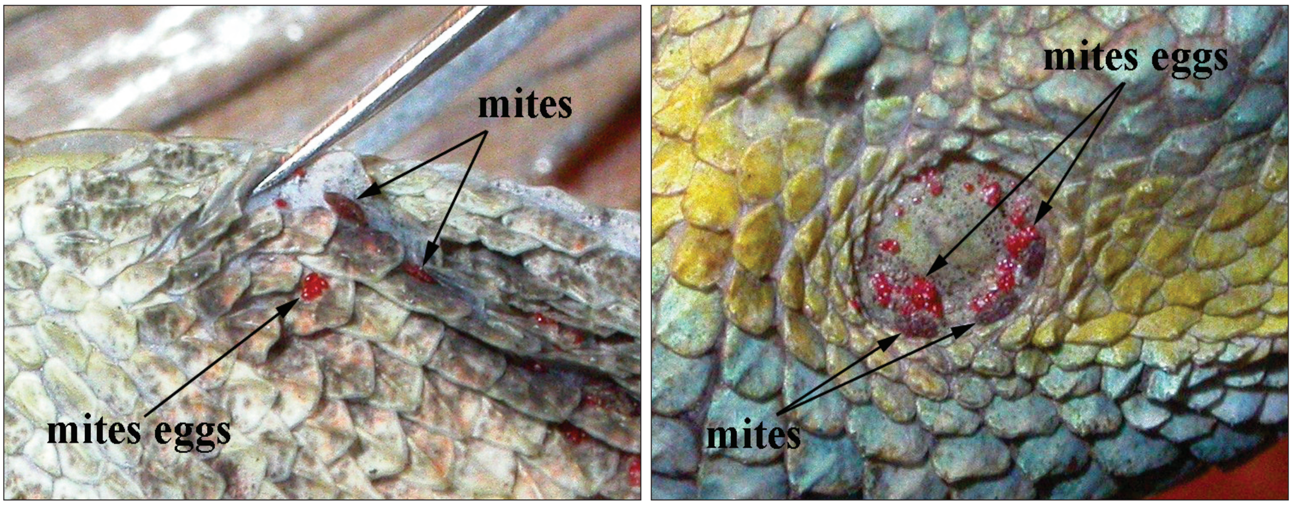
The mite family Pterygosomatidae is presented by permanent highly specialized ectoparasites. Most of them (about 200 species of 9 genera) are associated with lizards and live under or between host scales. Pterigosomatids are monoxenous parasites or associated with hosts belonging to the same genus; pterigosomatid genera or subgenera are limited in their diversity by particular lizard families. Hence, the pterygosomatid distribution on their hosts is generally highly non-random and the host-parasite associations of these mites may be used as a valuable data source to testify different host phylogenetic hypotheses. Parasitological data may also provide a unique window into the historical biogeography of lizards. Unfortunately the insufficient knowledge of pterygosomatid biodiversity and, as a result, the absence of their phylogenetic reconstructions prevents to the analysis of coevolutionary relationships between these mites and lizards. The hosts of the family Agamidae harbor mites of the subgenus *Pterygosoma* (about 50 species and subspecies). To date, these mites are known from hosts of 8 genera (from 48 known to date).Although several new species of *Pterygosoma* were recently described and many of them are under description two main problems impede to study the pterigisomatid biodiversity. (1) In agamid populations, the percentage of individuals infested by pterigisomatids is usually not so high. (2) In the herpetological expeditions, the dissection microscope which is necessary to find and accurately collect pterygosomatids is usually absent. Thus, the purposeful jointing efforts of herpetologists and acarologists are necessary for successful examination of pterygosomatid biodiversity and the following analysis of host-parasite relationships.



Undescribed pterygosomatids of *Calotes emma* Gray 1845 (left photo, throat region) and *Calotes mystaceus* Dumeril and Bibron, 1837 (right photo, ear region) (foto Daniel Melnikov)

Key words: Pterygosomatidae, Agamidae, phylogeny, host-parasite relationships.

BARCODING AGAMID LIZARDS OF VIETNAM

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The age of genomics has now arrived. It is feasible to gather the complete genomes of most vertebrate species. Because this effort requires a significant amount of both time and money, species identification is critical in order to avoid the innumerable errors present in online databases, such as GenBank. Agamid lizards, which are a major component of the Squamata, often form a dominant component of the herpetofauna throughout their range. Being diurnal, many species are commonly encountered by local residents. Some species are used as food and maintained as pets, yet others are rarely encountered owing to arboreality and crypsis.

We undertook a barcoding analysis of species and populations in Vietnam while using global representative taxa. We surveyed about 120 species representing seven genera, and multiple populations of species occurring in Vietnam. Intergeneric divergence was usually sufficient to unambiguously assign unknown samples to genera. Within genera containing multiple species, interspecific divergence allowed the correct identification of species. Intraspecific divergence was significant in some species indicating the possibility of multiple cryptic species. The analysis also detected misidentified specimens and museum cataloging errors, which would be critical to resolve before pursuing whole genome analyses.

The analysis indicated taxa requiring further investigation, while also finding those that exhibit very little genetic variation throughout the range of sampling.

Key words: Barcoding, Genome 10K, Vietnam; China.

SYSTEMATICS AND BIOGEOGRAPHY OF AGAMID GENUS *JAPALURA* IN THE EAST ASIAN ISLANDS

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The agamid genus *Japalura* consists of 27 species and occurs from tropical to warm temperate region in the eastern half of Asia, ranging from northern India, Nepal, southern China, northern Indochina, Taiwan, and Japan. From the subtropical islands of East Asia, five morphologically poorly diverged but chromosomally and genetically distinct endemic species have been recognized – *Japalura polygonata*, *J. swinhonis*, *J. brevipes*, *J. makii*, and *J. luei.* All these species occur in the mainland Taiwan, with partial syntopy in various combinations. Of these, only *J. polygonata* also occurs in the Ryukyu Archipelago of Japan and is polytypic, consisting of four subspecies – *J. p. xanthostoma* from northern Taiwan, *J. p. donan* from Yonagunijima Island of the Southern Ryukyus, *J. p. ishigakiensis* from some other islands of the Southern Ryukyus, and *J. p. polygonata* from the Central Ryukyus. The karyotype consisting of $2n = 46$ all telocentric chromosomes in a graded series is shared by all broadly ranging lowland (< 1,200 m asl.) populations of *J. polygonata* and *J. swinhonis.* In contrast, the remaining three species, all confined to montane habitats of mainland Taiwan (1,000 – 2,200 m asl.) exhibit remarkable karyotypic variations involving the chromosome number ($2n = 40$ in *J. makii*, and 36 in *J. brevipes* and *J. luei*), arm number ($NF = 70$ in *J. makii*, 46 in *J. brevipes*, and 52 in *J. luei*), and the number of size groups (two in *J. brevipes*, and three in *J. makii* and *J. luei*). Analyses of sequence variations in the mitochondrial 12S and 16S ribosome RNA genes supported monophyly of the three Taiwanese montane species with rather small genetic distances and their sister-group relationships to *J. polygonata*, leaving *J. swinhonis* outside. The result strongly suggests that the three montane species have recently originated through a series of speciations within Taiwan with driving forces from rapid chromosomal rearrangements. The analyses also strongly suggest an occurrence of initial divergence of *J. polygonata* in Taiwan and its subsequent, relatively rapid dispersals to most islands of the Ryukyu Archipelago, most likely via repetitive rafting. They further suggest that during the Late Pleistocene glacier period *J. swinhonis*, a species currently ranging almost throughout the lowland of Taiwan, entirely disappeared in its northern and western parts due to colder and more arid climate there, leaving surviving populations in only a few refuges of the southern and eastern parts. This also explains the absence of this quite adaptive lizard in eastern continent, which is separated from Taiwan only by fairly narrow (< 150 km) and shallow (< 100 m) Taiwan Strait. Current conservation status of the East Asian *Japalura* populations is also briefly reviewed with a discussion of desirable conservation measures.

Key words: dispersal, isolation, speciation, chromosomes, mitochondrial DNA, conservation.

MOLECULAR PHYLOGENY AND INTRASPECIFIC DIFFERENTIATION OF THE IRANIAN AND CENTRAL ASIAN SPECIES IN THE GENUS *TRAPELUS* (SAURIA: AGAMIDAE) INFERRED FROM MITOCHONDRIAL DNA SEQUENCES

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The steppe agamas of the genus *Trapelus* Cuvier, 1816, are an old clade of agamid lizards with an Afro-Arabian origin. The genus consists of about 14 – 15 species which are distributed from northwestern Africa, along the Saharan border, through the Near East to southwest and central Asia. They constitute one of the major components of the Iranian Plateau and central Asian fauna and are highly adapted to steppe, semi-deserts and desert environments. To date, published morphological and molecular phylogenetic hypotheses of *Trapelus* are only partially congruent, and the relationships within the genus are still far from clear. We investigated the phylogenetic relationships and intraspecific differentiation among the Iranian and Central Asian species of these lizards (69 individuals collected from 14 populations of four well-defined species and several unidentified specimens using two mitochondrial gene fragments (ND2 and cytochrome b)). The partition-homogeneity tests indicated that the combined dataset was homogeneous, and maximum-parsimony (MP), maximum-likelihood (ML) and Bayesian (BI) analyses were performed on this combined dataset. The trees reconstructed by different methods were generally very similar. Relationships among the examined species and populations were highly resolved. The basal position in the tree was always occupied by *Trapelus ruderatus* (= the formerly *T. persicus*) which in turn formed the sister taxon for populations of *T. lessonae.* The phylogenetic analysis together with genetic distances among the major clades suggested that, in the Iranian Plateau, *T. agilis*, genetically, represents a species complex containing at lease three well distinct taxonomic entities at the species level. The analyses also showed that, despite their vast distribution range, the Central Asian populations are genetically very homogenous, just representing a single taxonomic entity (i.e., *T. sanguinolentus*).

Key words: Agamidae, *Trapelus*, *T. agilis* complex, molecular phylogeny, intraspecific differentiation, mitochondrial DNA, Iranian Plateau, Central Asia.

NOMENCLATURAL DILEMMA OF *TRAPELUS RUDERATUS-LESSONAE-PERSICUS* (SAURIA: AGAMIDAE): SOLVING THE PUZZLE

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Based on extensive study and collecting material in the field and examining the relevant material in the museums and zoological collections, including the type specimens of *Trapelus ruderatus ruderatus* (Olivier), *T. megalonyx* Gunther, *T. lessonae* (De Filippi), *T. persicus* (Blanford) and *T. ruderatus baluchianus* (Smith), the taxonomic status of the ground agamids *Trapelus ruderatus ruderatus, T persicus* and *T. lessonae* has been re-evaluated.

Based on this study, it was found that the holotype of *Trapelus ruderatus ruderatus* is a subadult of the conventional *T. persicus* and that of *T. lessonae* is a typical form of the conventional *T. ruderatus ruderatus.* With regards to these remarkable mis-identifications by the original describers and in order to resolve the taxonomic and nomenclatural status of the three above-mentioned taxa, some major nomenclatural changes are proposed as follows: Since *T. lessonae* is the oldest available name, it is revived for all populations of the conventional *T. ruderatus ruderatus* and the specific name «*ruderatus*» is, in turn, assigned for all populations of the conventional *T. persicus* (due to priority rule). Therefore, the specific name «*persicus*» comes under the synonymy of «*ruderatus*» and is no longer available.

Key words: Agamidae, *Trapelus*, nomenclatural dilemma, taxonomic re-evaluation.

PREFERRED BODY TEMPERATURE OF FREE-RANGING STARRED AGAMA *LAUDAKIA STELLIO* (LINNAEUS, 1758) (AGAMIDAE) FROM EGYPT

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Preferred body temperature of Starred Agama *Laudakia stellio* collected from Western Coastal Desert of Egypt was monitored telemetrically in a temperature gradient. This species was found to be a good thermo regulator lizard. Behavior played the major role for body temperature regulation. Shuttling behavior between the hot and cold sides of the temperature gradient and voluntary hypothermia were found to be the main means of body temperature regulation. The mean selected body temperature was 35.9°C, 37.7°C at day and 32.9°C, 37.2°C at night in males and females respectively. Circadian rhythm was investigated under different light regime. At LD this species showed a well defined circadian rhythm with high selected body temperature during photophase and low value during scotophase. Under LL and DD the amplitude of the body temperature rhythm was greatly reduced. It was found that *Laudakia stellio* selected lower body temperature at night in spite of the availability of a wide range of temperatures in the temperature gradient which may prolong potential foraging time the following day.

Key words: preferred body temperature, Starred Agama, *Laudakia stellio*, circadian rhythm, Egypt.

HOW TO IDENTIFY SPECIMENS OF *UROMASTYX* LIZARDS WITHOUT MARKING

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Microchipping and other marking are always a bit risk procedures for animals, namely for endangered species. A set of photographs was created to identify confiscated *Uromastyx* specimens which were illegally imported from Morocco. A determination of subspecies was important for possible breeding.

Key words: *Uromastyx* lizards, marking, photography identification.

MOLECULAR DIFFERENTIATION AND DISTRIBUTION WITHIN THE SPECIES COMPLEX OF *PHRYNOCEPHALUS HELIOSCOPUS* (REPTILIA: AGAMIDAE)

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Phylogenetic inference was based on the analysis of 2 mtDNA fragments (1st subunit of the Cytochrome c-oxidase (COI) and 16S rRNA gene; 1156 bp in total) for 86 samples from 59 localities.

To provide a nuclear perspective on phylogenetic relationships between the revealed lineages we carried out the InterSINE-PCR analysis (for the first time for agamid lizards) using two independent primer systems. In addition we used demographic analysis of mtDNA data estimating mismatch distribution for the revealed lineages. Modern range of *Ph. helioscopus-complex* encompasses vast areas from Araks river valley in easternmost Turkey and southern Armenia in the west to Dzhungarian Gobi in western Mongolia in the east and from Altai territory of Russia (Kulunda) in the north to Fars province in central Iran in the south (Abadeh). We analyzed distribution data of the species complex and scrutinized locality information from 100 published literature sources and catalogues of 23 herpetological collections. Altogether 726 localities were revealed, for 627 of them we were able to identify exact geographic coordinates. After the locality information was plotted on the map, distribution of species and revealed lineages was analyzed using range modeling algorithm BIOCLIM using the software DIVA-GIS ver. 5.2.

Results of molecular survey show that at least 12 separate phylogenetic lineages (4 within *Ph. persicus* and 8 within *Ph. helioscopus)* within the species complex, all lineages are have high support values. Furthermore, analysis of InterSINE-PCR fingerprinting profiles confirmed deep genetic differentiation within the revealed lineages and resulted in highly congruent topology with high or moderate support values. Spatial analysis of distribution patterns within the species complex indicated significant structuring of the range in general coinciding with the revealed distributions of mtDNA lineages. Thus, presence of two isolated lineages of *Ph. helioscopus* in Turkmenistan is confirmed. Lineages of *Ph. persicus* have different altitude preferences and are isolated with mountain barriers.

Ecological range modeling proved to be useful for comparing potentially optimal habitats of different lineages. Peripheral areas surrounding the species complex range and central Turkmenistan deserts in the middle had the lowest suitability. The area of potentially unsuitable areas in central Kazakhstan separating subspecies *Ph. h. helioscopus* and *Ph. h. varius* is not well coinciding with revealed mtDNA pattern (according to molecular data this border is located further to the east). Spatial analysis of potential habitats indicated specific ecological preferences of each of the studied lineages. However, lineages restricted to isolated mountain valleys have much better model fits and their potential habitats are almost not overlapping, whereas optimal habitats of lineages inhabiting lowland and plain territories significantly overlap.

Part of the molecular analysis was completed within the international program «Consortium for the Barcoding of Life (CBOL)».

Key words: Agamidae, *Phrynocephalus*, InterSINE-PCR, COI, molecular systematics, phylogeography.

SPATIAL DISTRIBUTION AND ABUNDANCE TRENDS OF SPOTTED TOAD-HEADED AGAMA, *PHRYNOCEPHALUS GUTTATUS*, IN ITS NORTHERN HABITAT IN THE VOLGA REGION

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During our 1998 – 2008 field surveys in the Volgograd region and adjacent territories of the Astrakhan region and Republic Kalmykia, data on the distribution and abundance of *Phrynocephalus guttatus* (Gmelin, 1789) were collected. Now the population of *Ph. guttatus* in the Volgograd region is located on an isolated sandy massif on the left bank of the Don River within the Kalach-on-Don and Gorodishche districts. The abundance indices of *Ph. guttatus* substantially change within the limits of the peripheral population's habitat, which is caused by the high mosaicity of microstacies, the dynamics of projection vegetation covering parameters and its character, and some other factors. E.g., in the summer of 2005 and 2008 periods the abundance of *Ph. guttatus* varied from 3.6 and 4.1 ind/ha, respectively, on sites in inter-knoll depressions up to 34.7 and 32.9 on weakly-fixed barkhan-type hilly sands with rare motley-grass and shrubby vegetation.

The abundance of *Ph. guttatus* in Kalmykia was 15 – 25 ind/ha (Kireyev, 1982) and 5.9 – 99.1 ind/ha (Badmaeva, 1983). In 2000 and 2003, the abundance of *Ph. guttatus* in this territory varied from 1.2 to 27.8 ind/ha, with its maximum values being characteristic of the edges of semifixed hillock sands. Similar results were also obtained for small-hillock and hillock sands in the territory of Krasnyi Yar and Kharabali administrative districts of the Astrakhan region, where the abundance of *Ph. guttatus* varied from 13.6 to 38.5 ind/ha (1998) and from 5.3 to 35.4 ind/ha (2006). In May 2001, at similar sites of the isolated sandy massif Shkili (Akhtubinsk district, Astrakhan region) the abundance of the species was 9.7 ind/ha.

The revealed trend in the dynamics of quantitative indices is apparently due to the dynamics of abiotic factors. The indices of total solar radiation and annual precipitation level should be considered as determinants in this situation. E.g., A.A. Tishkov (1996) has shown that the modern warming in the steppe zone of the Russian Plain began at the end of the 19 century and reached its maximum within 1930 – 1940. Within 1940 – 1970, a cold spell was noted, and in the last decade of the 20 century the average annual temperatures were exceeded almost every year. Besides this gradual increase of the average annual temperatures, the climatic trend dynamics manifests itself as increased precipitation. It is enough to point out that in the territory under survey from late 1970s till mid-1990s, the annual precipitation exceeded its rate by 50 mm, in some years - by 120 – 190 mm. By F.R. Zaydelman et al.'s data (1998), the period from 1986 till 1995 was characterized by higher moisture than the 1975 – 1985 period. Moreover, in the 1990s these indices were synchronized with the reduction in the total head of livestock, which entailed the beginning of large-scale restoration of ecosystems and biodiversity reconstruction. In this period, mass invasion of turf-cereal communities towards past waste grounds and the formation of vast fallow lands in the place of agricultural fields (Neronov, 1998) were observed. Let us point out that, for *Ph. guttatus*, the humidization of living conditions is the determinant to limit its expansion north.

Thus, besides anthropogenic influence, climatogenic successions causing the mesophilization of steppe vegetation etc. have became a significant mechanism of transformation of natural ecosystems. To no small degree these changes affect spatially-separated local populations of animals. As to *Ph. guttatus*' populations, their isolated existence leads to a sharp increase of the specificity of their morphophisiological organization and gradual (sometimes sharp) contraction of the habitat. All these processes display most obviously in the conditions of the Lower-Volga region and adjacent territories, where the species' habitat has somewhat narrowed and the trend of abundance reduction of *Ph. guttatus* is obvious.

Key words: *Phrynocephalus guttatus*, biotopical distribution, abundance, Lower-Volga region.

PRELIMINARY STUDIES OF THE GENUS *ACANTHOCERCUS* (SAURIA: AGAMIDAE) IN THE CONTEXT OF THE ARID CORRIDOR IN AFRICA

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African lizards in the genus *Acanthocercus* are widespread in wooded savannahs from northeastern to southwestern Africa. Therefore, they are an ideal group for testing biogeographic hypotheses and evolutionary studies of arid corridor distributions and colonization events in Africa. However, to test these hypotheses a clear systematic and phylogenetic framework for the genus is needed but currently lacking. Constructing a phylogeny like this requires the solution of problems in different aspects of species determination, taxonomy and relationships.

In general, higher relationships in the genus *Acanthocercus* and its relationships to other Agaminae genera are poorly understood, but especially the understanding of the different species and subspecies of the *atricollis* species group should be reviewed for the understanding of the zoogeographic history of eastern Africa. A dense sampling within the genus and to related genera is lacking but necessary for testing monophyly, identifying sister taxa and distribution corridors. Herein a preliminary phylogeny is presented to show radiations within the genus, taxonomic problems on species level and results on distribution pattern in comparison with other arid species groups in Africa.

Key words: Agamidae, Agaminae, Acanthocercus, arid corridor, Africa.

ON THE THERMOBIOLOGY AND ACTIVITY PATTERN OF THE LARGE HERBIVOROUS DESERT LIZARD *UROMASTYX AEGYPTIA MICROLEPIS* BLANFORD, 1875 AT MAHAZAT AS-SAYD PROTECTED AREA, SAUDI ARABIA

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Field active body temperatures (*Tb*) and operative temperatures (*Te*) were assessed in a population of *Uromastyx aegyptia microlepis* at Mahazat as-Sayd Protected Area, Saudi Arabia to gain information on the extent and effectiveness of the thermoregulation in these animals. In summer *Tb* ranged between 23.2 and 47.2°C, in winter between 23.0 and 45.1°C and in spring between 25.5 and 45.9°C. There is a significant difference between respective *Tb* and *Te* distributions and all applied indices of thermoregulation suggest that *U. a. microlepis* is an active thermoregulator. Above ground activity, inferred from *Tb* data, is very variable between seasons, with the highest activity level in spring. In winter the animals showed a unimodal activity profile, with the highest activity between 11:00 and 15:00. In spring and summer the lizards exhibit bimodal activity profiles with afternoon activity being generally lower than morning activity levels. At midday activity is generally significantly lowered.

Key words: *Uromastyx aegyptia microlepis*, thermobiology, activity profiles, field active body temperatures.

A REVIEW ON THE TAXONOMY OF THE GENERA *UROMASTYX* AND *SAARA*

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The taxonomic relationships within the genus *Uromastyx* Merrem, 1820 were assessed using morphological and genetic methods, resulting in the resurrection of the genus *Saara* Gray, 1845 for *Saara hardwickii*, *S. asmussi* and *S. loricata.* A synopsis of all taxa considered to be valid within *Uromastyx* and *Saara* is provided.

Key words: *Uromastyx*, *Saara*, taxonomy.

BIOGEOGRAPHY AND SYSTEMATICS OF THE GENUS *ACANTHOSAURA* GRAY 1931 (SQUAMATA: AGAMIDAE) INFERRED FROM MITOCHONDRIAL AND NUCLEAR GENES

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The Southeast Asian lizard genus *Acanthosaura* is distributed throughout Myanmar, Thailand, Cambodia, Laos, China, Malaysia, and its offshore islands, Pulau Aur, Pulau Tioman, Pulau Penang, Pulau Perhentian, and Pulau Langkawi. I investigated the phylogenetic relationships of all nine of the currently recognized species of *Acanthosaura* using one mitochondrial gene (ND2 859bp) and three nuclear genes (KIF24 502bp; PRLR 583bp; MXRA5 860bp). Maximum parsimony, maximum likelihood, and Bayesian analyses of the mitochondrial DNA recover the wide-ranging *Acanthosaura lepidogaster* as a paraphyletic group. *Acanthosaura lepidogaster* from Vietnam, Laos, and China form a monophyletic group, but *A. lepidogaster* from Myanmar are sister to *A. crucigera* from Thailand and southern Myanmar and an undescribed species from Cambodia.

Acanthosaura bintangensis and *A. titiwangsaensis* form a monophyletic group with *A. armata.* There are two distinct clades within in the *A. armata* clade, one from the Seribuat Archipelago and the rest from Peninsular Malaysia and its other adjacent islands. The nuclear gene trees resolve the shallow nodes except that *A. crucigera* comes out paraphyletic with the undescribed species from Cambodia and *A. armata* from Peninsular Malaysia. This could be due to incomplete lineage sorting.

Key words: Agamidae, *Acanthosaura*, biogeography.