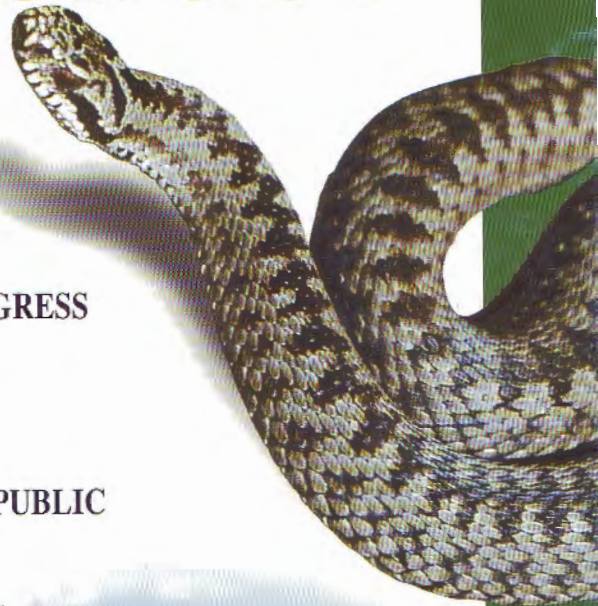


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STABILITY OF A *BOMBINA* HYBRID ZONE

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KEY WORDS: Anura, Discoglossidae, *Bombina*, hybrid zones

The hybrid zone between *Bombina bombina* and *B. variegata* is maintained by a balance between dispersal of parental types into the zone and selection against hybrids. In the Cracow transect, variation in morphology (i.e. the spotting pattern of the ventral side) is highly correlated with clines of six unlinked allozyme loci, mtDNA and mating call. Morphology is thus a good indicator of a population's genetic composition. A thousand dried skins of *Bombina* collected from over 100 sites in the Cracow area by Michalowski (1958) was re-scored for diagnostic spots. Comparison of the present and earlier patterns allows inferences about position, width and stability of the hybrid zone.

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VERTEBRAL MORPHOLOGY OF NON-COLUBROID SNAKES

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KEY WORDS: Reptilia, Serpentes, osteology, vertebrae

The occurrence of paired haemapophyses is characteristic for the caudal portion of the vertebral column of almost all snakes. Haemapophyses are also present in sacral vertebrae of the colubroids, but in the remaining snakes they are replaced by other structures. The sacral vertebrae (at least anterior sacral vertebrae) of most non-colubroids (most boines and pythonines, *Loxocemus*, *Xenopeltis*, *Bolyeria*) possess a single hypapophysis; these are followed by the caudal vertebrae provided with haemapophyses. In the caudal vertebrae of *Acrantophis*, *Sanzinia*, and tropidophiines the haemapophyses are vestigial or replaced by a haemal keel; in *Calabaria*, the haemapophyses are entirely reduced. Cyliodrophines are unique in possessing hypapophyses throughout both sacral and caudal portions of the column. In contrast, in scolecophidians and *Anilius* and *Cylindrophis* (which are characterized by simple vertebral morphology throughout the column), the sacral and caudal vertebrae are devoid of any subcentral structures.

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OLDEST FOSSIL VIPERS FROM THE OLD WORLD

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KEY WORDS: Viperidae, Africa, Asia, Europe, Miocene

Fossil Viperidae do not afford useful information dealing with the phylogeny of the group. However, they provide the latest possible dates for the appearance of various viperid lineages. The oldest Old World Viperidae come from the earliest Miocene (ca 23.5/22 million years). They are represented by vertebrae and fangs; the latter are already typical fangs of vipers. In the Americas the oldest Viperidae is approximately coeval, but perhaps slightly younger (latest Arikarcean). In Europe, the '*Vipera aspis*' complex first appears in the earliest Miocene (MN 1) of France and Germany. The '*Vipera berus*' complex is first known in the earliest Miocene (MN 1 or 2) of France. The earliest representatives of the 'oriental vipers' complex come from the latest lower Miocene (MN 4) of France, Germany, and the Czech Republic. In Africa, the Viperidae are first known from the middle Miocene (ca. 15 m.y.); they belong to the '*Vipera aspis*' complex. In Asia, the earliest viperid is an indeterminate form from the early Miocene of Thailand; it is slightly younger than the earliest European one. All these Viperidae from the Miocene appear to be of modern type, most of them may even be referred to *Vipera*. This shows that the origin of Viperidae certainly markedly antedates the Miocene. (To be published in *Kaupia*, Darmstadt)

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PREY-HANDLING BEHAVIOUR OF THE SAND VIPER *VIPERA AMMODYTES AMMODYTES* (SERPENTES: VIPERIDAE)

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KEY WORDS: Serpentes, Viperidae, *Vipera*, behaviour

In this work, we studied the prey-handling behaviour of the sand viper (*Vipera ammodytes ammodytes*) feeding on mice and lizards. The snakes were placed in an experimental arena and allowed to settle down, after which prey animals were introduced. The prey animals were adult wall lizards (*Podarcis muralis*) and adult and juvenile laboratory mice. We observed two methods of prey catching: grab-and-hold and strike-and-relocate. The grab-and-hold method was predominant when snakes were given lizards and small mice, while strike-and-relocate was the main method of immobilization when adult mice were presented. We also measured some other parameters; e.g. time of prey death, direction of swallowing (head first, tail

first) and duration of swallowing. The differences shown may have adaptive significance in foraging, and increasing hunting efficiency while simultaneously decreasing the risk of snake injury by larger prey animals.

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HEMATOLOGY OF THE SAND VIPER *VIPERA AMMODYTES AMMODYTES* (SERPENTES: VIPERIDAE)

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KEY WORDS: Serpentes, Viperidae, *Vipera*, hematology, blood cells

We studied the morphology of the circulating blood cells as well as the hematological parameters of the sand viper (*Vipera ammodytes ammodytes*). White blood cell counts, erythrocyte counts and indices (hemoglobin content, hematocrit, MCV, MCH, MCHC), size of morphotic elements and morphology and percentage of various leukocyte populations will be presented. These results are compared with hematology data obtained on other viperids as well as in the light of seasonal changes of hematological parameters.

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WHY THE COBRA IS RESISTANT TO ITS OWN NEUROTOXIN

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KEY WORDS: *Naja*, α -bungarotoxin, acetylcholine receptor, natural resistance, convergent evolution

Evolution of animal toxins required a mechanism preventing their actions in the organism producing them. To date, only one resistance strategy has been demonstrated, where components of Crotalinae venoms are neutralized by conspecific blood plasma. Venoms of the Elapidae snakes contain α -neurotoxins, like α -bungarotoxin (α -BTX), targeted against the acetylcholine receptor (nAChR). To identify the resistance mechanism in Elapidae, we cloned the homologue of the Chordata α -BTX binding site from the *Naja haje* nAChR α subunit, and constructed a *Naja/Mus* chimeric α subunit. Co-injection of this chimeric α subunit and the wild type *Mus* β , γ and δ cRNAs into *Xenopus* oocytes expressed an α -BTX resistant nAChR, as assayed by two microelectrode voltage-clamp (TEVC). Further TEVC and Western blot analysis of several sub-chimeric and point mutated versions of the *Naja/Mus* nAChR, demonstrated that the unique *N*-glycosylation at N¹⁸⁹-Y¹⁹⁰-S¹⁹¹ in the *N. haje* nAChR is responsible for α -BTX resistance.

However, the oligosaccharide attachment in *N. haje* does not inhibit the acetylcholine-induced responses. The analog occurrence of *N*-glycosylation at N¹⁸⁷-V¹⁸⁸-T¹⁸⁹ in the Elapidae venom resistant *Herpestes ichneumon*, Herpestidae, Carnivora nAChR α subunit is a striking example of convergent evolution at the molecular level. The approach described here can be used to identify the resistance mechanism against other neurotoxins of animal origin, as well as to characterize their binding sites.

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PROBLEMS CONCERNING SYSTEMATICS OF *RANA CHENSINENSIS*

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KEY WORDS: Amphibia, Ranidae, *Rana temporaria*, taxonomy, phylogeny, cytochrome b gene

The brown frogs of the *Rana temporaria* group with distinct reddish body color are distributed widely in the Palearctic region. They are notoriously difficult to classify because of morphological similarities. Especially, brown frogs with 2N=24 chromosomes, distributed in East Asia, are the most complex taxonomically, and several populations from within and around China have long been identified as *R. chensinensis*, which was originally reported from Shaanxi Province, western China in 1875 by David. However, recent studies have made clear that populations of so-called *R. chensinensis* include several distinct taxa. Actually, *R. chensinensis* from Shaanxi is morphologically different from Japanese relatives. Moreover, *R. chensinensis* has long been pointed out to be highly polymorphic and assuredly includes several taxa within China. Consequently, it is indispensable to study both intra- and interpopulational genetic relationships for understanding relationships and constructing more appropriate taxonomy of frogs now called *R. chensinensis*. In this study, we investigated genetic variations found among populations of so-called *R. chensinensis* and its relatives based on mitochondrial cytochrome b gene sequence. It was made clear that topotypic *R. chensinensis* from Shaanxi is genetically different from members of Japanese brown frogs with 24 chromosomes, and this result coincided with that obtained from morphological study. The topotypic population is also found to be differentiated from other Chinese populations.

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