

The sand lizard (*Lacerta agilis*) in Poland; one or two subspecies ?
[POSTER]

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An investigation of the variability of the sand lizard (*Lacerta agilis*) in Poland was carried out using wide morphological and genetic analysis.

A total of 259 individuals of the sand lizard were analysed in morphological studies, 120 samples in allozyme electrophoresis and 12 samples in mtDNA sequencing (cytochrome b and D-loop region) were used. The samples coming from 8 populations.

Morphological studies included five qualitative features, 15 meristic features as well as 10 metric features used in traditional method and 27 distances used in “truss network” method.

Conclusions of this investigation there are: (1) Polish populations of the sand lizard are divided into two groups; one occurs in north-eastern and central-eastern part of Poland, the range of the other covers the majority of Poland area, the first group has many features of *Lacerta agilis chersonensis*, the second has features of *Lacerta agilis agilis* (or *L.a.argus* according to some researchers), (2) in populations in East of Poland were noticed some features typical for *Lacerta agilis exigua*, (3) the results of DNA sequencing allow to estimate that populations from the East of Poland and other parts of Poland separated about 300 000 years ago. A model of postglacial recolonisation of Central Europe which explain genetical impact of the eastern subspecies on Polish populations was suggested.

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**Nuclear DNA sequences confirm the basal phylogeny of the family Lacertidae,
as proposed by HARRIS, ARNOLD & THOMAS (1998)**
[POSTER]

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In total, roughly 1600 bp of the nuclear genes RAG-1 and c-mos were analyzed in representatives of 38 genera, respectively species groups, within the genus *Lacerta*. We aimed at testing the currently proposed phylogenies of the Family Lacertidae. The resulting data support basal split of the subfamily Gallotiinae (*Gallotia* and *Psammmodromus*). The remaining taxa segregate into two main groups, corresponding in general to the ‘primitive western palearctic assemblage’ and ‘Ethiopian and Saharo-Eurasian clade (ESE)’, as proposed by Harris et al. (1998). The genera of the latter clade (ESE) are further divided into two groups: the ‘Ethiopian’ and the ‘Saharo-Eurasian’ group. This suggests convergent adaptations to xeric conditions across these groups.

The genera of the first main clade could not be resolved with the marker used, the only exception being *Parvilacerta* and ‘*Lacerta danfordi*. All genera and species groups within *Lacerta* are represented by equivalent branches in the inferred maximum likelihood tree. This data therefore suggest an equivalent taxonomic ranking of the analyzed groups on generic level.