The Inter-SINE-PCR (IS-PCR) method for the study of molecular systematics of Caucasian lacertid lizard (Sauria: Lacertidae)

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IS-PCR method reveals a set of DNA sequences separating copies of short interspersed repeats (SINE) [Buntjer, 1997]. The resulting electrophoretic patterns possess taxon-specific features at a intra-generic level. Degrees of molecular genetic diversities have been tested by the values of DNL coefficients and roughly range between 0.0 - 0.20 for intrapopulational levels, 0.3 - 0.5 for intersubspecies of one species, and about 0.6 - 0.9 for known good species. These values were obtained in our study of populations of *Darevskia raddei* complex and their two systematic subspecies in comparison with some other species of *Darevskia* group (*D. rudis*, *D. chlorogaster* and "*D. tristis*"). On the basis of these features for 17 *D. raddei* populations we show that the difference of south-western Azerbaijan (Talysh) population from other populations by DNL (0.4) is similar to that between *D. r. raddei* and *D. r. nairensis*. This observation supports the subspecies status for Talysh sample. The same values of molecular genetic diversity were found for *D. rudis obscura* and "*D. tristis*" from North-Pontic Ridge of Turkey that could argue for the subspecies level for "*D. tristis*" within the *D. rudis* complex, as was suggested by Bohme and Bischoff [1984]. Both groups mentioned differ from *D. raddei* by the values of DNL of 0.6 - 0.7. Nearly the same correlations were obtained when some populations of *D. praticola* and *D. derjugini* were studied. Some of the known systematic subspecies of these species were supported by IS-PCR markers, the others were not: the data will be presented. In another species complex studied by IS-PCR – *Lacerta* s. str. – 12 populations inhabitating a vast territory (from Baltic States and Ural Mountains to Caucasus) differed by DNL ranging from 0.02 to 0.2 apparently belong to *L. agilis exigua* subspecies as was deduced by morphology. The same DNL values characterize intrapopulational similarity in the *L. a. chersonensis*, but the differences between these two systematic subspecies reach the values of around 0.6. The samples from Munchen (presumably *L. a. argus*) also differs from the first two by 0.6 - 0.7. The most important is that the molecular differences between each of these subspecies and *L. strigata* and *L. media* were characterized also by the same order of values. In other words, the genetic distances between *L. strigata*, *L. media*, and three subspecies of *L. agilis* have the same level and all of them could be considered either as subspecies of *L. agilis*, or the three subspecies of this species could be evaluated as a separate species.

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