

Genetic variation in parthenogenetic Caucasian rock lizards of genus *Darevskia*

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Studying the genetic variation in unisexual species is very important for understanding the molecular basis of their diversity. Different methods of genome analyses were used to study the genetic variation in parthenogenetic lizard species of genus *Darevskia*. Multilocus DNA-fingerprinting shows that *Darevskia* lizards possess species-specific patterns and display some level of intrapopulation variation with different microsatellite probes. Mutant fingerprint phenotypes were revealed in families and tissues of *D.unisexualis* and *D.armeniaca*.

DNA-fingerprinting RAPD and mitochondrial DNA analysis were used to study intraspecies structure of *D.rostombekovi* lizards. This data suggests that *D.rostombekovi* have a more complex intraspecies structure, than was previously supposed.

To understand the molecular basis of microsatellite variability it is important to know the detailed structure of microsatellite containing loci. Earlier we cloned and sequenced a number of polymorphic microsatellite containing loci of *D.unisexualis*. PCR amplification and the sequence analysis of population samples of related species of genus *Darevskia* showed that allelic differences of these loci were caused by variation in a number of tandem repeats in microsatellites clusters and point mutations in the flanking regions. This information is significant for understanding the basis of genetic variability of parthenogenetic lizards, which arises partly from mutations in microsatellite loci, and for studying relationships between species of genus *Darevskia*.

