DOI: 10.46991/JISEES.2025.SI1.084

Origin and Diversity of Parthenogenetic *Darevskia* Lizards and Their Parental Species through Microsatellite Marker Analysis

Irena A. Martirosyan[1*], Dmitrii O. Odegov[1], Eduard A. Galoyan[2], Marine S. Arakelyan[3], Andrey A. Vergun[1], Anastasiya E. Girnyk[1], Vitaly I. Korchagin[1], Alexey P. Ryskov[1]

[1] Institute of Gene Biology, RAS, Moscow, Russia
[2] Institute of Ecology and Evolution A.N. Severtsov, RAS, Moscow, Russia
[3] Faculty of Biology, Yerevan State University, Yerevan, Armenia

ABSTRACT

The Caucasian rock lizards of the genus *Darevskia* include approximately 40 species, of which seven are parthenogenetic. These parthenogenetic species originated through a reticulate speciation process in which all female species arise from hybridization events between sexual parental forms. Remarkably, all seven parthenogenetic *Darevskia* species were formed through various combinations of just four sexual species: *D. raddei* and *D. mixta* served as maternal parents, while *D. portschinskii* and *D. valentini* acted as paternal contributors. All parthenogenetic lizards are diploids, and the mechanism of restoration of ploidy is premeiotic endoreplication. This makes the complex intraspecific structure of the parental species especially relevant, as these species are represented by diverse subspecies and populations that have participated in multiple independent hybridization events. To address such complexity, we successfully used molecular methods based on the microsatellite locus polymorphism of the nuclear genome. These methods allow us to explore the genetic characteristics of complexes of bisexual species, species identification, characteristics of triploid hybrids arising in zones of sympatry of parthenogenetic and parental bisexual species, as well as to understand the sources of intraspecific polymorphism in unisexual lizards. We demonstrated deep differentiation within the *D. raddei* complex and revealed molecular differences between subspecies of the *D. portschinskii subspecies* for the first time. It was also used for the identification of lizard samples from previously unstudied populations in Armenia. The family analysis of the parthenogenetic species revealed that the main sources of intraspecific polymorphism in these clonal lineages are either post-origin mutations or the involvement of multiple founder individuals. However, the molecular mechanisms underlying the origin and diversity of parthenogenetic species remain unresolved. To address this, whole-genome sequencing of parthenogenetic species, along with their parental sexual species, can provide new insights and hypotheses regarding their origin and persistence.

Keywords: *Darevskia* lizards, parthenogenesis, species identification, reticulate speciation

References:

1. Spangenberg, V.; Arakelyan, M.; Simanovsky, S.A.; et al. Tendency towards clonality: deviations of meiosis in parthenogenetic Caucasian rock lizards. *Biol. Reprod.* **2025,** *113*, 387–396. DOI:10.1093/biolre/ioaf091
2. Tarkhnishvili, D.; Yanchukov, A.; Şahin, M.K.; et al. Genotypic similarities among the parthenogenetic *Darevskia* rock lizards with different hybrid origins. *BMC Evol. Biol.* **2020,** *20*, 122. DOI:10.1186/s12862-020-01690-9

[*]Corresponding Author:

Irena Martirosyan, Ph.D., Institute of Gene Biology, RAS, 34/5 Vavilova str., 119334, Moscow, Russia. Email: irena-m@yandex.ru