



A NOTE ON THE VALIDITY AND DISTRIBUTION
OF *ZOOTOCA VIVIPARA SACHALINENSIS*

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Currently, four subspecies of *Zootoca vivipara* are recognized: the nominotypic form in the major part of the vast distribution area of the species, *Z. v. pannonica* from the Pannonian lowlands, and *Z. v. sachalinensis* from the Far East (Sakhalin and Hokkaido Ids., Amur/Ussuri region) (Böhme 1997). Recently, the oviparous populations of SE Central Europe (Carinthia, Slovenia, NE Italy) have been added as *Z. v. carniolica* (Mayer et al. 2000).

In contrast to the uniformity of morphological features such as scalation and colour pattern which makes the subspecies difficult to diagnose, there is variation in the reproductive mode, karyotypes and mitochondrial DNA sequences. In southern Europe two oviparous groups of populations of this otherwise strictly viviparous species have been proven to occur. Four different karyotypes are currently known (Kupriyanova et Böhme 1997, Odierna et al. 2000); and the numerous haplotypes found (Heulin et al. 1999, Mayer et al. 2000) can be assigned to 8 haplotype groups (= haplotypes with minor differences).

Recently we have sequenced parts of the mitochondrial 12S- and 16S-rRNA genes (together 951 bp) of a specimen from Sakhalin Island (for the methods applied see Mayer et al. 2000). This sequence (Genbank Acc. No. AF316169 and AF316170) is almost identical with the sequence of a specimen from the vicinity of St. Petersburg published by Fu (2000; Genbank Acc. No. AF206594). The Sakhalin specimen shows only one inversion at the positions 741/742 of the St. Petersburg sequence.

This striking genetic uniformity across an area with a West-East extension of more than 8000 km

is paralleled by karyological characters: All samples investigated so far from an area between the Eastern Carpathians, the Polish-Belarus border and the Baltic area to Karelia in the West on the one hand, and Sakhalin Island in the East on the other, possess an acrocentric female sex chromosome (Kupriyanova et Rudi 1990, Odierna et al. 1993, Kupriyanova et al. 1995, Orlova et Kozlovskii 1996, Kupriyanova 1997, Kupriyanova et Böhme 1997).

Although it has been impossible, so far, to trace morphological differences between Central European populations and those from Eastern Europe and Asia, we conclude that the karyologically and genetically uniform lizards of the latter area represent a distinct evolutionary lineage or entity within the species *Zootoca vivipara* which is clearly definable by its karyotype (type A according to Kupriyanova 1990) in combination with its mitochondrial haplotype. The name *Z. v. sachalinensis* is applicable. However, in spite of earlier concepts (see Dely et Böhme 1984), this subspecies must be considered as ranging throughout the Asian part of the species' range including the adjacent part of eastern Europe.

The existence of two oviparous groups of populations and of several different mitochondrial haplotypes in Western and Central Europe makes it likely that the colonisation of the Asian part of the species' range was a recent, post-Pleistocene event. Other vertebrates with similar distribution patterns (e.g. the *Bufo bufo*, *Hyla arborea* and *Rana arvalis* groups, the striped field mouse *Apodemus agrarius*: see Dely et Böhme 1984; the Eurasian *Vipera berus* group) offer interesting examples for comparisons. Those groups with

own speciation centers in the Far East (the amphibians cited above) must certainly be considered to have diverged much earlier from their European relatives. The nominal Far East endemic *Vipera berus sachalinensis*, however, should be reconsidered accordingly (see Nilson et al. 1994).

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