

**Abstract:**

Genus *Trapelus* (Cuvier, 1816) consists of 13 species. The *Trapelus agilis* is one of the members of the genus *Trapelus* that distributed in Iran, Afghanistan, Pakistan, India and Central Asian countries. A total number of 16 specimens from *T. agilis* were collected belong to Sistan and central plateau of Iran. Eighteen morphological traits were analyzed by SPSS.v16 software. In order to compare the populations, a partial sequence of the 16SrRNA mitochondrial gene was amplified by Polymerase Chain Reaction and send to Macrogen south Korea for sequencing. To investigate the phylogeny relationships between populations, the uncorrected distance genetic was take in the MEGA.6 software. Haplotype network was designed to examine the genetic divergence in Popart software. The phylogenetic trees, the Maximum likelihood, Maximum Parsimony, and Bayesian inference. The molecular results indicate that genetic diversity is high among populations.

Key worda: Agamidae, Genetic distance, Phylogeny, Morphologic



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**Comparing Population of *Trapelus agilis*
(Olivier, 1804) in Sistan with other Population
of this Species in Central Plateau of Iran.**

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