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RIBOSOMAL DNA-ITS2 GENOTYPES OF THE MALARIA VECTOR ANOPHELES SUPERPICTUS (DIPTERA: CULICIDAE) FROM IRAN

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Abstract:

Recent advances in DNA based technology have made available a wide range of molecular characteristics for taxonomic and systematic studies of malaria vectors. One region of the anopheline mosquito genome that has received particular attention is the ribosomal DNA. In this study, mosquitoes of the *Anopheles superpictus* collected from a wide geographical distribution of Iran were investigated for sequence variation within the ribosomal DNA ITS2. Two morphological forms of this species were identified based on adult female palpi and compared to genotypes identified by the rDNA ITS2 sequences. Sequence analysis of the ITS2 within and between populations identified three genotypes designated as X, Y, and Z. Genotype X occurred in north, west, south, and central regions whereas genotypes Y and Z were found sympatric in Baluchistan in southeast corner of the country. Totally 127 mutations occurred in the 518 bp region sequenced. The rate of genetic variation was 24.52% in which respectively 0.2%, 0.77% and 23.55% corresponded to 28S, 5.8S, and ITS2 regions. The length of ITS2 region was varied between populations; one group had 357 and other one 378 bp. These genotypes appeared to be evolving independently suggesting the possibility of cryptic species within taxon. This study is the first comparative study on morphological and genetic characteristics of *An. superpictus* and for the first time in the world reporting this taxon as a species complex.

Keywords:

rDNA-ITS2 . Genetic population

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