

Species identification of the Anopheles fluviatilis complex using phylogenetic analysis PCR-sequencing in southwestern Iran

Gholamhossein Shahraki and Zeynab Barghamadi; Yasuj University of Medical Sciences, Iran



Introduction

Anopheles fluviatilis is transmission malaria disease in of cause mountainous areas in some parts of Iran. Some of malaria transmitter species in this country also are known as biological forms. The aim of this study was to identify An. fluviatilis complex species using phylogenetic analysis PCR-sequencing.

Methods

In this research Anopheles fluviatilis was caught from different areas of Boyer-Ahmad Kohgiluyeh and province at southwestern Iran at 2013. DNA was taken from 4 An. fluviatilis selected samples and PCR tests of 28S- D3 part was done on sample's DNA and then after sequence of obtained results were identified and were compared with similar samples of An. fluviatilis based on data's of gene word bank . Phylogenetic tree and individual sequences of samples were calculated.

Results

Obtained results of PCR product of 28S-D3 part of rDNA gene with the length of 333bp in An. fluviatilis of this province is shown in Figure 1.

All four samples of An. fluviatilis were sequenced which its results were recorded in Genbank with accession numbers of KJ396263, KJ396264, KJ396265 and KJ396266.

For verification of sequencings, species identification and phylogeny relationships of studied samples and existing samples in gene world bank, sequences were tested by Online BLAST software (available in Pubmed) and were compared with other sequences in gene world bank.

Figure 2 's findings shows that difference of U and T species of Anopheles fluviatilis is in number 78 nucleotide.

Obtained phylogeny tree of analysis of 28S-D3 part of rDNA gene, showed 4 samples of An. fluviatilis of Yasuj city. Sequence of other complex species (T-U) and also An. superpictus were as out group species.

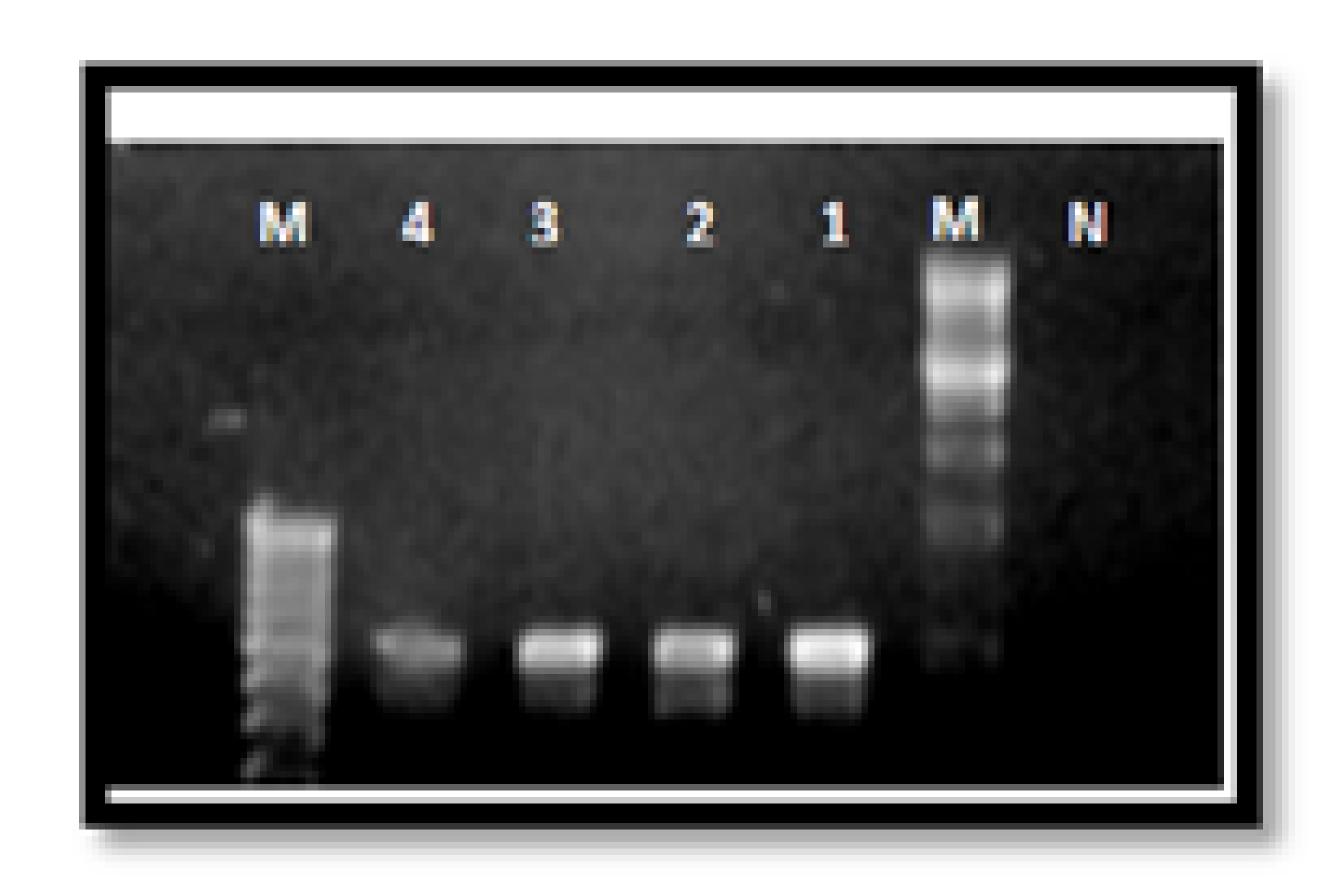


Figure 1: 1,2, 3 and 4 show samples of Anopheles fluviatilis; "M" shows marker size 100bp; "N" shows negative control

A2FLU.YASUI U GAAACCCACAGGCGAAGACAAATCGAGTGATGCGGGATTA CGGGTA 95 GQ864407southeasternfran_ T_{-} GAAACCCACAGGCGAAGACAAATCGAGTGGTGCGGGATTA CGGGTA 95

Figure 2: Difference between *Anopheles* fluviatilis U and T is in 78 nucleotide that is "A" in *An. fluviatilis* U and "G" in *An. fluviatilis* T

Conclusions

This study have been the first genetic diversity study of *An. fluviatilis* in **Boyer-Ahmad** Kohgiluyeh and province which four samples of An. fluviatilis selected were representative of this anopheles population in area and their DNA were extracted and were used in PCR reactions. it seems that T-U specie in rest of the country be as hybrid species.

This study showed that An. fluviatilis has species separate branch in southwestern Iran (with U genotype) which is different with branch of southeastern Iran (Hormozgan, Kerman and Sistaan & Baluchestaan provinces) with T genotype.

Further Research

recommend further research for the other vector species such as An. superpictus in this area and other infested areas.

References and cited literature

Mehravaran A, Oshaghi MA, Ebrahimzadeh A, Qureshi MI, Hasan Zahi A. Molecular identification of *Anopheles fluviatilis* complex in Sistan and Baluchestaan Province. J Hormozgan University Med Sciences. 2012; 15(4): 260-268 [in persian]. Vatandoost H, Oshaghi MA, Abaie MR, Shahi M, Yaaghoobi F, Baghaii M, et al. Bionomics of *Anopheles stephensi* Liston in the malarious area of Hormozgan province, southern Iran. Acta Trop. 2006; 97:196-203.



Yasuj University Medical Sciences



Published in ICUP 2017 Proceedings, available from QR code & www.icup.org.uk

