

عنوان مقاله:

New findings on the molecular systematics of ticks (Argasidae & Ixodidae) and the detection of tick related microbial pathogens in Iran

محل انتشار:

دومین کنگره بین المللی بیماریهای منتقله بوسیله ناقلین و تغییرات آب و هوایی و چهارمین کنگره ملی حشره شناسی پزشکی ایران (سال: 1398)

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خلاصه مقاله:

Background: Ticks are obligatory blood-feeding arthropods that vectors of microbial pathogens that cause disease in humans and animals. Ticks are considered to be second worldwide to mosquitoes as vectors of human diseases. Our understanding of ticks and tick-borne diseases is changing on many levels due to the application of significant technological advances. Objectives: We aimed to study the systematics of ticks collected on domestic and wild animals as well as tick harbored microbial (bacterial and protozoan) agents during the several years of continuous study in different areas of Iran. Materials and Methods: Various hard and soft tick species of the genera Hyalomma, Haemaphysalis, Rhipicephalus, Argas, Alveonassus, Ornithodoros, Otobius and the agents including Aegyptianella, Anaplasma, Borrelia, Theileria, Mycoplasma, Coxiella, Francisella, Brucella and Rickettsia in ticks were studied using molecular methods. The sequence data were submitted to GenBank. Results: The taxonomic status and new records of tick species using nuclear (ITS2) and mitochondrial genes (COI and 16S rRNA) were studied. Sequences of six different genes for Rickettsia (16- & 23- S rRNA, gltA, ompA, ompB, sca4) along with a new Rickettsia species for Iran (R. hoogstraalii), five gene fragments for Coxiella (16S rRNA, IS1111, com1, htpB and icd), and various genes of remaining microbial agents were obtained. Conclusion: This study is a prospected window for further studies to study .of ticks and related microbial pathogens in Iran

کلمات کلیدی:

Tick, Systematics, PCR, Sanger sequencing, Phylogenetic tree, Iran

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