

عنوان مقاله:

Investigation of molecular evolution and epidemiological links related to circulating Avian Avulavirus 1 isolates between 1995 and 2016 in Iran

محل انتشار:

سومین کنگره بین المللی و پانزدهمین کنگره ملی ژنتیک ایران (سال: 1397)

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خلاصه مقاله:

Evolution of Avian Avulavirus 1 isolates and emergence of genetic variants are related to different agents i.e., host adaptation, immune response evasion and selective pressures. Hence, investigation of epidemiological links between circulating viruses in different regions and their evolutionary relatedness are of the major issues for biosecurity strategies, yet many bottlenecks remain unsolved. In this study, we have conducted molecular investigation of circulating Avian Avulavirus 1 isolates in Iran (1995-2016) based on virus classification methods. On the basis of evolutionary divergences, sub-genotype VIg, VIj, VIIj, VIId, XIIIa and XIId isolates have been circulated in the Iran during 21-year period. Data analysis revealed that VIg isolates shared highest similarity to VIg sub-genotype isolates (i.e., Russian and Polish viruses). While, the lowest difference of VIj sub-genotype isolates (2012) was from a virus isolated in 2015 in India. Furthermore, evolutionary divergences indicated that Chinese and Ukrainian viruses may have played crucial role in emergence of VIIj isolates. Our study also showed that XIIIa isolates circulating in Iran may have resulted in the emergence of adapted variants known as XIId sub-genotype isolates. Here, we suggest the evolutionary and epidemiological study of virulent Avian Avulavirus 1 isolates could help providing accurate molecular data in the region, and result in designing more efficient recombinant vaccines.

کلمات کلیدی:

Avian Avulavirus 1, Epidemiology, Newcastle disease virus, Fusion protein, Classification, Evolution

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