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Evolution of Bartonella across different host

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Bacteria of the genus Bartonella are fastidious, Gram-negative and aerobic bacilli. The genus currently consists of 19 species, including three subspecies of Bartonella vinsonii, and some subtypes of Bartonella quintana and Bartonella henselae. Recently, Bartonella spp. seroprevalence is pretty high more than 30% in HIV positive patients, blood donors or injecting drug users in west countries. Throughout the climate changes, the increasing vector positive rate increasing the infectious risk in human. Therefore, the purpose of this study will try to understand the evolution situation in this one of the famous zoonotic agent Bartonella spp. This study used systematic review and downloaded the Bartonella spp. sequences from different host in the GenBank. Phylogenetic analysis of gltA gene was approached for understanding the evolution relationship among host. The bootstrap value represented in 1000 for branch robustness statistical examination. The Neighbor-joining tree of 28 gltA sequences with 245 bps length presented 4 clusters with mixed host species. The first clusters correlated with human only. The second clusters correlated with deer and cattle. The 3rd and 4th clusters were both mixed with different animal and human. These two zoonotic clusters would become the most important species for further investigation. These works will help a lot for the zoonotic disease control, treatment and prevention systems and especially for the vaccine development.

Title: Evolution of Bartonella across different host

Program: Veterinary Public Health

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Learning Objectives: To demonstrate the role Bartonella species transmission among different species.

Learning Areas:

Public health biology

Primary geographic focus of the program or study: Taiwan

Session 4273.3: Emerging Infections: perspectives on zoonotic diseases in the near past and on the horizon to include unique zoonoses, MRSA in animals, hemorrhagic fevers, vector borne disease. etc (ID=35386)

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Qualified on the content I am responsible for because: I am PI in this study.

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