

3-4-10. Molecular phylogenetic analysis of *Haemaphysalis longicornis* (Acari: Ixodidae) based on tropomyosin

In Yong Lee¹, Kyoung Yong Jeong¹, Joo Hwan Kim²,
Won Ja Lee³ and Won Ku Lee⁴

¹*Dept. of Parasitology, Yonsei University;* ²*Dept. of Biology Daejeon University;*
³*Dept. of Medical Zoology, National Institute of Health;* ⁴*Faculty of Biological Sciences, Chonbuk National University*

The complementary DNA encoding tropomyosin of the hard tick, *Haemaphysalis longicornis* (Acari: Ixodidae), was amplified by reverse transcriptase polymerase chain reaction with degenerate primers designed on the basis of known tropomyosins of arthropods and thereafter cloned in plasmid vectors.

The cDNA clone thus obtained, with an insert of 1042 bp, contained an open reading frame of 855 bp encoding tropomyosin with 285 amino acid residues flanked 3' - non coding region.

The deduced amino acid composition is rich in glutamate (57 residues), leucine (28 residues), alanine (34 residues), and arginine (23 residues). Interestingly, this protein does not have any cysteine, tryptophan, and proline. The BLAST search of the GenBank showed that *H. longicornis* tropomyosin has the homology with 30 species. Platyhelminthes, Nematoda, Mollusca, Arthropoda, and Chordata showed the percentage of identity in amino acid sequence varied with 60.0%, 73.2%, 80.5%, and 56.3%, respectively. Even though they are in phylogenetically very distantly related species, the degree of homology and functional similarity is in general high.

The feasibility of using tropomyosin gene segments for phylogenetic study of animals should be explored further. Applying this sequence primer approach to many other lineages will surely improve our understanding of eukaryotic evolution.