SEQUENCE ANALYSIS OF TOLL LIKE RECEPTOR 1 GENE OF CAMEL (Camelus dromedarius)

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ABSTRACT

In the present study complete mRNA sequence of camel TLR1 was analysed using various tools and softwares. The analysed sequence was made up of 2430 bp long contig with 2391 long open reading frame which translated into 796 aa. The sequence has been submitted in NCBI (Accession. No: MG655186). The Camel TLR1 sequence had 99% identity with the predicted TLR-1 protein of dromedary camel with two amino acid variation. The sequence alignment showed the highest similarity of camel TLR1 with pig, whereas lowest similarity was found with rabbit. The analysis of protein sequence revealed seven leucine rich repeats (LRR) domain in the extracellular region similar to that of goat. The 3D protein model showed a TLR 1 similar to that of other vertebrates.

Key words: Camel, mRNA, phylogenetic analysis, sequence analysis, toll like receptor 1