

MOLECULAR CHARACTERISATION AND *in silico* ANALYSIS OF NOD-LIKE RECEPTOR P12 (NLRP12) IN DROMEDARY CAMEL

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ABSTRACT

In the present study, complete coding sequence of camel Nod-like receptors P12 (NLRP12) was sequenced and analysed using various tools and softwares. The coding sequence had 3454 bp long contig and 3281 nucleotide long open reading frame (ORF) which translated into 1093 amino acid long protein sequence. The Camel NLRP12 protein sequence had maximum similarity with that of Pig (87.37%) while minimum similarity was found with mouse (80.20%). The protein domain prediction of camel NLRP12 showed the characteristic N-terminal PYRIN domain, a central NACHT domain associated with FISNA domain and eleven C-terminal LRR domain which was found conserved in all studied species. However, one LRR domain was found missing in cattle NLRP12. The NLRP12 of camel was phylogenetically closely related to pig and distantly related to mouse NLRP12. The equal numbers of LRR domain, compared to other species except cattle, may suggest similar ligand binding capacity in camel NLRP12 in order to activate immune responses.

Key words: Camel, domain architecture, innate immunity, NLRP12, phylogeny, sequence analysis