PARTIAL CLONING OF c-MET cDNA AND ITS TISSUE DISTRIBUTION IN ARABIAN CAMEL (Camelus dromedarius)

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ABSTRACT

The present study was, aimed to clone Hepatic growth factors receptor (c-Met). Arabian camels RT-PCR was conducted using liver tissue RNA and primers designed based on data from different animal species published in gene bank. The PCR product was sequenced and analysed using different bioinformatics programs. The results confirmed that the obtained sequence is related to c-Met gene family. The nucleotides sequence was deposited in the DDJB with accession number KC794957. Furthermore, the data showed base frequencies of A = 27.5%, C = 23.9%, G = 20.6% and T = 28.00%. Of the 600 nucleotides used for tree analyses, 454 were constant and 146 were variables. The neighbourjoining tree showed clustering of the species of family Camelidae with each other with strong bootstrapping (100 BP for MP and NJ methods). The deduced amino acids showed two non-synonymous substitutions discriminating *C. dormedarius* from other camelids; aspartic acid (D94) into histidine (H94) in other camelids at G281 \rightarrow C281 and glutamine (Q144) into histidine (H144) at A430 \rightarrow C430. The results exhibited ubiquitous expression of c-Met mRNA in the tested tissues; kidney, liver, skeletal muscle, spleen, testis and heart. The obtained results are expected to be important for addressing the genetic diversity of the Afro-Arabian camel and clarifying the relationships among its available breeds.

Key words: Arabian camel, cloning, c-Met, distribution