## Genetic Variations of Two Casein Genes among Maghrabi Camels Reared in Egypt

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Abstract : Camels play an important socio-economic role within the pastoral and agricultural system in the dry and semidry zones of Asia and Africa. Camels are economically important animals in Egypt where they are dual purpose animals (meat and milk). The analysis of chemical composition of camel milk showed that the total protein contents ranged from 2.4% to 5.3% and it is divided into casein and whey proteins. The casein fraction constitutes 52% to 89% of total camel milk protein and it divided into 4 fractions namely  $\alpha$ s1,  $\alpha$ s2,  $\beta$  and  $\kappa$ -caseins which are encoded by four tightly genes. In spite of the important role of casein genes and the effects of their genetic polymorphisms on quantitative traits and technological properties of milk, the studies for the detection of genetic polymorphism of camel milk genes are still limited. Due to this fact, this work focused using PCR-RFP and sequencing analysis - on the identification of genetic polymorphisms and SNPs of two casein genes in Maghrabi camel breed which is a dual purpose camel breed in Egypt. The amplified fragments at 488-bp of the camel ĸ-CN gene were digested with AluI endonuclease. The results showed the appearance of three different genotypes in the tested animals; CC with three digested fragments at 203-, 127- and 120-bp, TT with three digested fragments at 203-, 158- and 127-bp and CT with four digested fragments at 203-, 158-, 127- and 120-bp. The frequencies of three detected genotypes were 11.0% for CC, 48.0% for TT and 41.0% for CT genotypes. The sequencing analysis of the two different alleles declared the presence of a single nucleotide polymorphism (C $\rightarrow$ T) at position 121 in the amplified fragments which is responsible for the destruction of a restriction site (AG/CT) in allele T and resulted in the presence of two different alleles C and T in tested animals. The nucleotide sequences of K-CN alleles C and T were submitted to GenBank with the accession numbers; KU055605 and KU055606, respectively. The primers used in this study amplified 942-bp fragments spanning from exon 4 to exon 6 of camel aS1-Casein gene. The amplified fragments were digested with two different restriction enzymes; SmlI and AluI. The results of SmlI digestion did not show any restriction site whereas the digestion with AluI endonuclease revealed the presence of two restriction sites AG^CT at positions 68^69 and 631^632 yielding the presence of three digested fragments with sizes 68-, 563and 293-bp.The nucleotide sequences of this fragment from camel aS1-Casein gene were submitted to GenBank with the accession number KU145820. In conclusion, the genetic characterization of quantitative traits genes which are associated with the production traits like milk yield and composition is considered an important step towards the genetic improvement of livestock species through the selection of superior animals depending on the favorable alleles and genotypes; marker assisted selection (MAS).

**Keywords** : genetic polymorphism, SNP polymorphism, Maghrabi camels, κ-Casein gene, αS1-Casein gene **Conference Title** : ICASVM 2016 : International Conference on Animal Science and Veterinary Medicine **Conference Location** : London, United Kingdom **Conference Dates** : August 25-26, 2016

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