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# Sequencing and Mutation Screening in Exon 1 of Camel Tyrosinase Gene

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**Abstract**

The tyrosinase (TYR) represents a decisive factor in the metabolic pathway leading to coat colour pigmentation as well as in hormone production. Mutations in the tyrosinase gene are responsible for the albino phenotype in the mammalian and they are also known to influence quantitative traits in mice. Based on the partial sequences of mouse and human it was possible to design a primer pair which could be used for the amplification of a 820 bp fragment in the exon 1 of the camel tyrosinase gene. The resulting camel tyrosinase sequence shows a high homology to the corresponding sequences of mouse (84.2 %), human (88.7 %), horse (89.3 %), cattle (90.1 %) and pig (91.9 %) respectively. By sequencing of 15 animals from different camel breeds a single nucleotide polymorphism (C/T) on position 200 after the ATG causing an amino acid substitution (Pro/Leu) was detected. A restriction site for Dde I provoked by the C-variant of this mutation could be used in a special restriction fragment length polymorphism analysis (PCR-RFLP) for genotyping of 157 animals from six different Pakistani camel breeds (Marecha, Dhatti, Larri, Kohi, Campbelpuri and Sakrai). Significant differences in the genotype frequency between the breeds were estimated. The Sakrai breed shows in comparison to Marecha, Dhatti, Larri and Kohi a distinctly higher frequency of the CC-genotype (CC = 0.40; CT = 0.56; TT = 0.04). Possible associations of these Dde I-genotypes with coat colour and special performance traits (like morphological characteristics or features for growth and production) will be elucidated and the results will be shown.

**Keywords:** Camel, genotyping, point mutation, sequencing, tyrosinase

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