

# Conserved and Non-Conserved Loci of the Glucagon Gene in Old World Ruminating Ungulates

Mohamad Warda\*, Eman M. Gouda, Adel M. El-Behairy, and Said Z. Mousa

Department of Biochemistry, Faculty of Veterinary Medicine, Cairo University, Cairo, Egypt.  
Fax: 025 725240. E-mail: Maawarda@mail.eun.eg

\* Author for correspondence and reprint requests

Z. Naturforsch. **61c**, 135–141 (2006); received May 24/July 16, 2005

The homology and diversification of genomic sequence encoding glucagon gene among native Egyptian buffalos, camel and sheep were tested using cattle as model. Oligodeoxynucleotide primers designed from the available GenBank data were used for PCR probing of the glucagon gene encoding sequence at different loci. The DNA oligomer probes were constructed to flank either the whole gene encoding sequence or different intra-gene encoding sequences. The PCR products were visualized using agarose gel electrophoresis. All species showed a same size band of prepro-glucagon when PCR was used to amplify the whole gene encoding sequence. In contrary, amplifications of different intra-gene loci failed to give the same results. The results indicated variable degrees of diversity among old world ruminating ungulates in the glucagon gene encoding sequence. Compared with other ruminants, the variation appears predominantly in camel. Surprisingly, the similarity in size between both amplification products of whole gene encoding sequence and the proposed size of glucagon cDNA definitely excludes the possibility of large intervening introns spanning the genomic sequence of the glucagon gene in these species. This indicates that, in contrast to other tested mammals, the glucagon gene includes an essentially full-length copy of glucagon mRNA. The study revealed a possible new aspect of glucagon gene evolution in order to correlate its corresponding protein function among different ruminant species.

*Key words:* Glucagon, PCR, Ruminants