

## Application of 16S rRNA, cytochrome b and control region sequences for understanding the phylogenetic relationships in *Oryx* species

H.A. Khan, I.A. Arif, A.A. Al Homaidan and A.H. Al Farhan

Molecular Fingerprinting and Biodiversity Unit,  
Prince Sultan Research Chair Program for Environment and Wildlife,  
College of Science, King Saud University, Riyadh, Saudi Arabia

Corresponding author: H.A. Khan  
E-mail: khan\_haseeb@yahoo.com

Genet. Mol. Res. 7 (4): 1392-1397 (2008)  
Received September 29, 2008  
Accepted October 9, 2008  
Published December 16, 2008

**ABSTRACT.** The present study reports the application of mitochondrial markers for the molecular phylogeny of *Oryx* species, including the Arabian oryx (AO), scimitar-horned oryx (SHO) and plains oryx (PO), using the *Addax* as an outgroup. Sequences of three molecular markers, 16S rRNA, cytochrome b and a control region, for the above four taxa were aligned and the topologies of respective phylogenetic trees were compared. All these markers clearly differentiated the genus *Addax* from *Oryx*. However, for species-level grouping, while 16S rRNA and cytochrome b produced similar phylogeny (SHO grouped with PO), the control region grouped SHO with AO. Further studies are warranted to generate more sequencing data, apply multiple bioinformatics tools and to include relevant nuclear markers for phylogenetic analysis of *Oryx* species.

**Key words:** *Oryx*; Endangered species; Conservation; Mitochondrial DNA; Phylogenetic relationship