

The taxonomy of the bustards is poorly understood phylogenetically and has not been extensively evaluated using molecular methods. We sequenced part of the mitochondrial cytochrome *b* gene, the control region (central domain II), and an intro-exon crossing fragment of the nuclear chromo-helicase-DNA binding gene (*CHDI*) in 27 bustard taxa (including multiple subspecies) representing 11 genera and four gruiform outgroup species. Molecular datings suggest a Miocene origin for the family. Inferred phylogenetic relationships include (i) the basal polytomy consists of ten branches (mostly consistent with traditional genera) suggesting a rapid early radiation, (ii) sister relationships between several couplets of genera are: *Ardeotis* with *Neotis*, *Afrotis* with *Eupodotis* (excluding *E. rueppellii*), *Otis* with *Chlamydotis*, and *Houbaropsis* with *Sypheotides*, (iii) the genus *Eupodotis* may be polyphyletic, and (iv) the currently delimited genera *Ardeotis* and *Neotis* do not form independent monophyletic lineages. Molecular evidence for the Afro-tropical origin of the Otididae is provided.

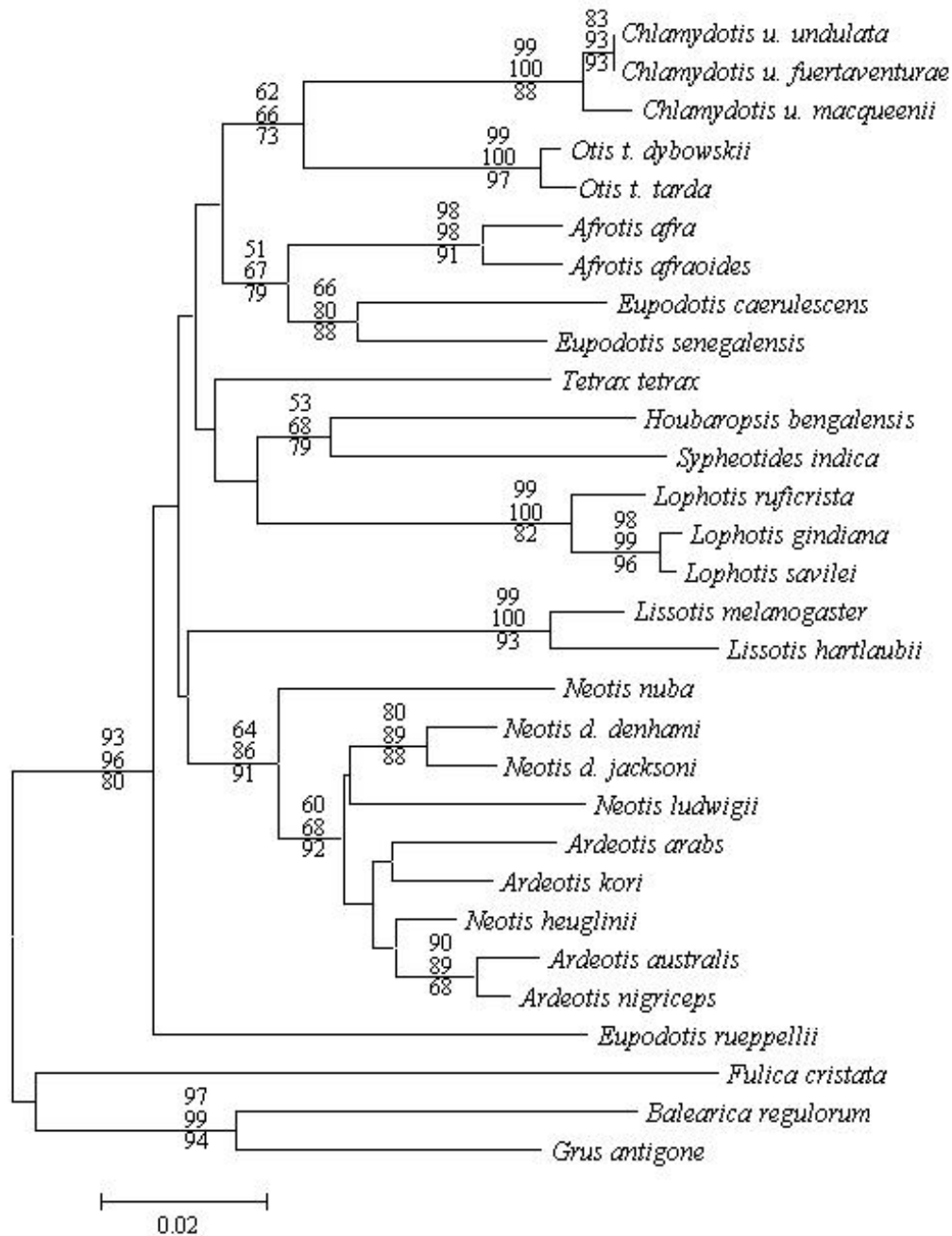


Fig. 1 Phylogenetic relationships among the Otididae based on mitochondrial cytochrome *b* sequences using neighbor-joining of Kimura 2-parameter distances. The tree was rooted using gruiform taxa. Identical branching patterns were determined by both maximum parsimony ( $L = 400$ ,  $CI = 0.513$ ) and maximum-likelihood ( $\log L = -3063.6$ ) analyses. Numbers indicate per cent bootstrap support for maximum parsimony (top), neighbor-joining (middle), and maximum likelihood (bottom), based on 1,000 iterations. Only nodes supported with >50% in all three analyses are indicated.

### Ancestral Area Analysis

The distribution history of the bustards was analyzed in terms of ten main distribution areas listed in Table 1. Each area was treated as a single character, which was optimized onto the neighbor-joining *cyt b* tree (Fig. 1) by using either forward or reverse Camin-Sokal parsimony. Comparing the number of necessary gains and losses under the two optimizations, respectively, the order of areas from where the modern bustards most likely originated, as indicated by the *G/L* and *AA* values listed in Table 1, is (1) South Africa, (2) East Africa, (3) North Africa or Middle East, followed by the others. Using both procedures to overcome polytomies, we obtained essentially the same results. Thus, South and East Africa, represent most likely the ancestral area, given the assumption that the ancestral area was smaller than the present distribution of the family. There would be many more intercontinental migrations which had to be minimized if the ancestral area would be assigned to either Europe, Asia or Australia, rather than to Africa.

Table 1 Estimation of Ancestral Area for the Otididae Based on the Cladogram Depicted in Figure 3 by the Method of Bremer (1992)

Area	Gain (G)	Loss (L)	G/L	AA
Southern Africa	7	11	0.64	1.00
East Africa	6	11	0.55	0.86
Northern Africa	3	6	0.50	0.78
Middle East	3	6	0.50	0.78
Sahelian Africa	6	13	0.46	0.72
Near East	2	6	0.33	0.52
Far East	2	6	0.33	0.52
India	3	9	0.33	0.52
Australia	2	7	0.29	0.45
Europe	3	11	0.27	0.42

*Notes* G = number of necessary gains under forward Camin-Sokal parsimony.  
L = number of necessary losses under reverse Camin-Sokal parsimony.  
AA = G/L quotients rescaled to a maximum value of 1 by dividing with the largest G/L value.