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## Sexual dimorphism, plumage variability and species determination in nightjars: the need for further examination of the Nechisar Nightjar *Caprimulgus solala*

Nightjars are widely distributed all over the world, and there are some 200 species (Sibley & Monroe 1990). However, most aspects of their biology and life histories are poorly known. In African species, the lack of knowledge is so marked that even the ranges of the species remain controversial. The small number of individuals examined and the unusual difficulties of identification, even in the hand, are the principal causes of this problem (Fry & Harwin 1988). In fact, these and other authors (Sibley & Monroe 1990) grouped 12 out of their 21 recognized African nightjar species into four superspecies, using plumage, song and breeding ranges as classification criteria. Recently, a new species, the Nechisar Nightjar *Caprimulgus solala* has been determined through the examination of a unique wing found on a road in Ethiopia (Safford *et al.* 1995). The wing size and relative position of wing patches compared with those from other species were used to reach this conclusion. Here, we wish to emphasize the importance of ascertaining the intraspecific variability in morphometric data of nightjars as a basis of any accurate comparison between species and individuals.

Almost all nightjar species have wing and tail patches. Variability of these characters has been rarely considered (Ingels & Ribot 1982, Jackson 1984, Cramp 1985), and no in-depth studies have been made. We studied biometric and plumage variability between 1988 and 1995 in a Spanish population of the Red-necked Nightjar *Caprimulgus ruficollis*, a migratory North African and southern European species (Fry & Harwin 1988). Our results showed an age-related development of sexual dimorphism in nightjars for the first time (Forero *et al.* 1995). Sex differences were found in all primary and rectrix white spot sizes and were more pronounced than in body measurements. Wing spots of males became significantly larger with age, thus increasing the age-related sexual dimorphism. Since this and other nightjar species perform territorial and courtship flight displays during which these patches are prominently exhibited (Mengel 1972, Cramp 1985), we suggest that the high patch-size variability could be related to sexual selection processes. Secondary sexual characters, probably those particularly important in sexual selection, are known to show high coefficients of variation (coeff. var.), sometimes larger than 10%. However, ordinary morphologic characters usually have coeff. var. between 2% and 3% (Møller 1994a, Evans & Barnard 1995). After analysing new data, we found coeff. var. for each patch measurement (coeff. var. = 11–52) more than five times higher than for other biometric characters (coeff. var. = 1.7–8.6, Mann-Whitney *U*-tests,  $P < 0.02$  for all comparisons within sex and age categories; Table 1). Moreover, both ranges and coeff. var. markedly increased when we pooled age classes and sexes. Although data are not available from nightjars, fluctuating asymmetry is known to be accentuated in secondary sexual characters (Møller 1994b), and, in general, both sexual characters (Hill 1994, Møller 1995) and body size (Zink & Remsen 1986, Slotow & Goodfriend 1996) are strongly subjected to geographic variation. Furthermore, male traits are frequently shown by females of some species (Muma & Weatherhead 1989, Potti 1993, Tella *et al.*

**Table 1.** Coefficients of variation (coeff. var.), ranges and sample sizes of body measurements and patch sizes from Red-necked Nightjars

Measure- ment <sup>a</sup>	Age <sup>b</sup>	Males			Females			Pooled		
		Coeff. var.	Range	n	Coeff. var.	Range	n	Coeff. var.	Range	n
Wing	J	1.7	202–220	56	1.9	188–219	368	2.0	188–240	619
	FY	2.1	199–217	26						
	AFY	2.6	200–240	56						
Tail	J	4.7	130–163	24	4.3	139–162	24	3.9	130–171	379
	FY	2.6	155–171	21	2.8	150–164	15			
	AFY	3.9	145–171	34	2.7	147–163	64			
Tarsus		4.6	20–24.5	65	5.2	19.4–24.9	60	4.8	19.4–24.9	128
Bill		6.8	21.9–32	77	8.5	22.3–33.5	72	7.8	21.9–33.5	152
P10	J	16.2	7–22	35	19.8	6–20	68	22.8	6–27	142
	AFY	10.8	17–27	34						
P9	J	15.9	9–24	33	15.3	9.5–22	70	20.7	9–29	144
	AFY	11.0	16–29	35						
P8	J	18.6	8–27	28	17.2	9–21	70	24.2	8–29	140
	AFY	16.1	8–29	37						
T5		14.7	15–38	121	36.6	3–32	156	40.3	3–38.5	284
T4		20.6	11–34.5	69	52.1	0–28	71	53.1	0–34.5	142

<sup>a</sup> P refers to patch size in wing primaries 10, 9 and 8 and T to patch sizes on tail rectrices 5 and 4.

<sup>b</sup> Age was determined through capture–recapture data ( $n = 1060$ ) and moult patterns (Gargallo 1994, Forero *et al.* 1995). To avoid pseudoreplication, we took a measurement only from birds that were caught more than once in the same year. J: juvenile; FY: first year; AFY: after first year: when there were not significant age differences (Forero *et al.* 1995), data were pooled without abbreviation.

1996, in press), and characters of ancestral species could appear in old birds of some species, even leading to incorrect species identification (Potti & Merino 1995). Any of these factors could possibly increase the phenotypic variability in nightjars even more than is already recognized.

None of these sources of variability could be reliably detected by examining small samples. Safford *et al.* (1995:table 3) compared the only available wing with wing biometry from 23 African species of nightjars (Jackson 1984). Two species, Black-shouldered Nightjar *Caprimulgus nigriscapularis* and Rwenzori Nightjar *Caprimulgus ruwenzorii*, were not considered in this comparison, and another species, Slender-tailed Nightjar *Caprimulgus clarus*, was pooled with Long-tailed Nightjar *Caprimulgus climacurus* (see Fry & Harwin 1988). Furthermore, 16 species were represented by data from 1–20 individuals (Jackson 1984, Louette 1990). In only 4 of the 23 contrasted species, separated data of male and female were given. In addition, in two of the species, the females and immatures were pooled. Because of the small samples, the statistical power was low to detect sex and age differences.

Jackson (1984) pointed out that plumage variability within a nightjar species often exceeds that between species and that his identification key could be used only with adequate sample sizes of each species, again stressing the dangers of the use of this key for nightjar identification. Nevertheless, the comparison between wing biometry from other African species and from the new one is made with only eight wing characters of the 22 body characters proposed by Jackson (1984). In the comparisons made by Safford *et al.* (1995: table 3), 17 of these species overlapped with the new one in at least one comparison, and six overlapped in at least half of the eight

comparisons. The overlaps could have been more numerous if larger sample sizes were available. In another case, a particular bird with extreme measurements was excluded from the specific range of its own species. This possibility can be illustrated by the Red-necked Nightjar. Jackson (1984) collected biometric data of only three males and two females of this species, and these were used by Safford *et al.* (1995). After obtaining a much increased sample size, we found 98% of birds ( $n = 619$ ) were outside of the previously known wing extremes, and 80% ( $n = 284$ ) were outside of the previous ranges of tail patch sizes.

We have not measured the position of patch on the ninth primary (P9) in relation to the extension of the emargination on this feather (a ratio that Safford *et al.* considered conclusive). However, the very high variability in the size of this patch (coeff. var. = 20.7) in the Red-necked Nightjar and the relatively constant wing-length (coeff. var. = 2.0) make it difficult to believe that the value of this ratio remains nearly constant. In a hypothetical case, if we compared a bird of extreme measurements with a small sample of the same species biased, perhaps, towards one sex, one age class or one geographic area, we could consider that this bird was a new species. In fact, Safford *et al.* (1995) clearly illustrated this risk in their figure 3. An “exceptionally large individual” of the Plain Nightjar *Caprimulgus inornatus* was previously considered a new species, *Caprimulgus ludovicianus*. This individual was placed in their figure 3 in relation to the relative position of the P9 patch as distant from its own species as *C. solala* is from five other species. The incorrect placement of this individual could have been a result either of its large size or of the methodological procedure. Safford *et al.* (1995) calculated the ratios between wing measurements using the means

of each species rather than the means of the ratios from each individual. With the use of this method, unique values were obtained and the variance that defines the limits of the species was neglected. Most individual birds will present ratios different from those obtained for the means of their own species. This same methodological problem has been recently highlighted by Collister and Wicklum (1996): up to two-thirds of Loggerhead Shrikes *Lanius ludovicianus* were incorrectly classified into the subspecies previously defined through calculating ratios from mean measurements.

As Safford *et al.* (1995) pointed out, the Nechisar Nightjar wing could not be assigned to any known species. We agree with this conclusion, but we think it could be because data on intraspecific variability were not available for most of the species compared and because the methodology used failed to consider variability. The need for voucher specimens has been recently recommended to facilitate DNA phylogenetic analyses (Winker *et al.* 1996), and we encourage further research using molecular techniques to reaffirm the determination of this new species, as has been suggested in other cases (Ellis 1995). High-quality DNA has been extracted from both skins and feathers of long-dead bird specimens (Ellegren 1991, Leeton *et al.* 1993). Although possible geographic variation in DNA within a species could make the interspecific discrimination difficult using small samples, these DNA analyses are more likely to be conclusive than are phenotypic comparisons. In fact, the DNA from a unique shrike successfully allowed the recent determination of a new species (Smith *et al.* 1991).

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MANUELA G. FORERO & JOSE L. TELLA *Estación Biológica de Doñana, CSIC, Avda. M<sup>a</sup> Luisa s/n, Pabellón del Perú, 41013 Sevilla, Spain*

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