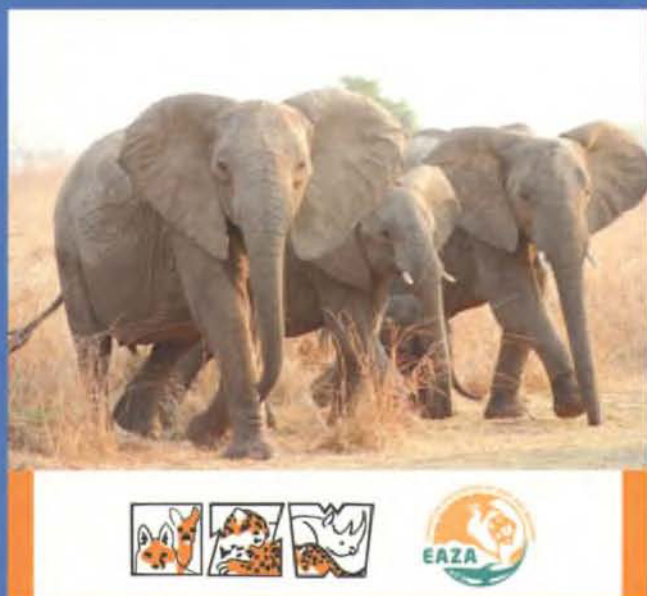


9th International Conference on Behaviour, Physiology and Genetics of Wildlife

18th – 21st September 2013
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Edited by

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Population structures in two closely related seabirds – crested and whiskered auklets (*Aethia cristatella* and *A. pygmaea*)

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Crested auklets (CA) and whiskered auklets (WA) are small seabirds with bright plumage and complex social behaviour that breed in the North Pacific. Out of the breeding season, auklets spend time at sea, and it is still known nothing about the dispersion of young birds. Here we tested morphometric, acoustic and genetic variability in both species. We collected data for CA and WA at eight and three sites, respectively, around the Bering and the Okhotsk seas. We measured body weight and lengths of wing, tarsus, bill, crest and auricular plume (totally 309 CA from four sites and 108 WA from three sites). We also analysed two main call types, the Bark and the Trumpet call of CA (200 and 100 calls from four sites, respectively), and the Mew and the Beedoo call of WA (300 and 90 calls from three sites, respectively). Also for CA we analysed the control region's fragment (408 b.p.) of mitochondrial DNA (totally 128 samples from five sites) and four microsatellite loci (totally 183 samples from five sites). ANOVA post-hoc Tukey test shows a negligible effect of "site" on morphometric variables of CA ($p > 0.05$ for most of comparisons) and a highly significant effect on morphometric variables of WA ($p < 0.001$ for all comparisons). The differences between colonies of WA were large, so we did not find an overlap in two parameters from six. We also found a little effect of "site" on temporal-frequency variables of the Bark ($p < 0.001$) and no significant effect on those of the Trumpet call ($p > 0.05$) in CA, but in WA the effect of "site" on acoustic variables was again much more evident for both call types ($p < 0.001$ for all comparisons). Also, for CA no genetic differentiation between colonies was found. A high haplotypic ($H = 0.994 \pm 0.002$) and a relatively low nucleotide diversity (0.013 ± 0.007) were noted for all sites. We suppose that the gene flow is very intense between CA' colonies, but it is restricted between WA' colonies. This difference could reflect the ecology of the species: WA prefers to feed close to colonies during the whole year, whereas CA leaves them in winter and spends this time in the sea. So, we show that the relation to the colonies could be an important factor for the population structure formation in colonial seabirds. We suggest that gene flow in CA could be provided mostly by young birds' dispersion, because of the high level of adult nest fidelity.