

The use of contemporary software in determining the population density of species of the Colubridae and Psammophiidae families

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Abstract. This research provides information on using contemporary software for assessing the density of Colubridae and Psammophiidae family representatives in the Kashkadarya region. TPS64until and TPS264Dig softwares were utilized for the mathematical modeling of molted skins of species of these families. Subsequently, the models underwent Principal Component Analysis (PCA) in Morpho J, enabling the classification of skin samples into their respective species. Recalculation of species population density was then conducted by aggregating the individuals of each species.

1 Introduction

Introduction: Determining the population density of reptile species poses considerable challenges due to their cryptic distribution in their habitats, resulting in unclear population estimates during research. The FMP method (Formozov, 1932, Malyshev, 1936, Pereleshin, 1950), which considers daily and seasonal movement patterns of species, partially addresses this issue. However, members of the Colubridae and psammophiidae families often conceal themselves in specific burrows and nests for extended periods without feeding, avoiding human and large animal activity, rendering the FMP method inadequate for precise numerical assessments of species composition and density. In such scenarios, researchers may resort to conducting separate stationary analyses in distribution areas to determine species composition based on their habits, yet the challenge of density remains unresolved [1-2].

In recent times, novel techniques have emerged for identifying and quantifying species, with a particular focus on understanding species distribution patterns through population characteristics. Indications of species presence can be discernible through traces such as molted skin. For instance, the species of snakes can be identified by analysing their molted skin [3-4].

In our study, we utilized specialized software tailored for analyzing morphological traits to enhance the accuracy of species counts based on the skin morphology of Colubridae and Psammophiidae families [3].

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2 Materials and methods

In the geometric-morphological analysis, samples were digitally represented using mathematical models in TPS64until and TPS264Dig softwares, aligning with the geometric features of specific landmarks. Subsequently, the mathematical model series underwent geometric-morphological analysis through the MorphoJ program, where species distinctions were assessed, leading to the differentiation of species from one another [5].

To conduct a geometric-morphological analysis on the skin of a snake, the Body of each species was divided into ten sections from the head to the tail. From each section, the dorsal-medial scale and five left and right dorsal-lateral scales were identified (refer to Figure 1A). First, landmarks were designated along the length of the scales and then a landmark was placed along only the width of the five left dorsal-lateral scales (refer to Figure 1B). Following the marking of all sections, a unified matrix pattern was established (refer to Figure 1C). Each species of matrix sample was then compared with the molted skin samples obtained during the study (refer to Figure 1D) [6-7].

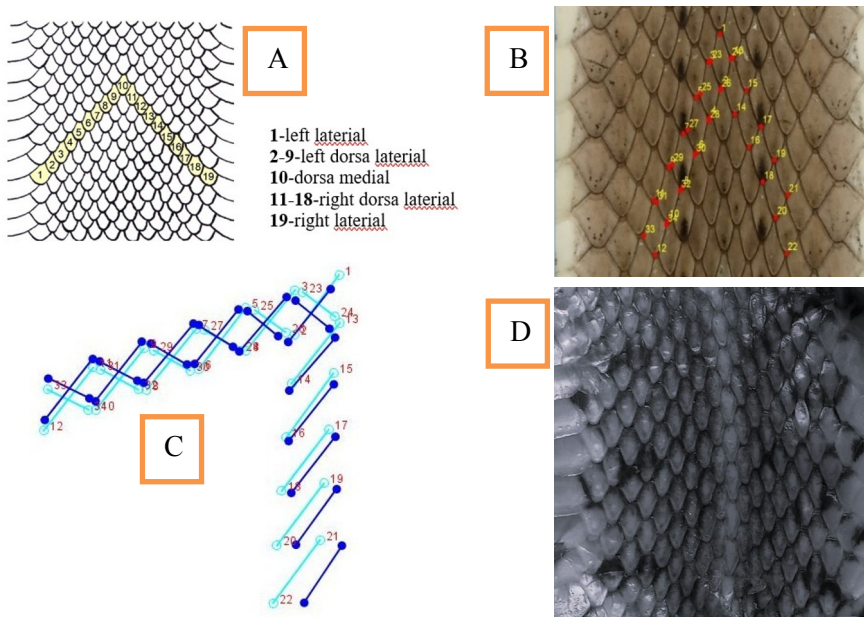


Fig. 1. Skin morphology models and examples: A) Location of scales B) skin sample used to create a matrix sample (Sample No. 11931 of herpetological collection of Institution of Zoology. Collector: Yangiboyev E.Ch.) C) variation matrix drawing obtained in the analysis D) molted skin sample collected in the study.

3 Results

From samples which collected in research conducted in the Kashkadarya region used to construct the matrix for geometric-morphological analysis. Skin matrix samples were obtained from various species including *Platyceps karelini* (Brandt, 1838), *Platyceps rhodorhachis* (Jean, 1865), *Hemorrhhois ravergieri* (Menetries, 1832), *Elaphe dione* (Pallas, 1773) belonging to the Colubridae family, and *Psammophis lineolatus* (Brandt, 1838) from the Psammophiidae family. Geometric-morphological matrix samples were then created for

morphological analysis. The field study spanned from 2021 to 2023, which 20 molted skin samples were collected over three years. These samples were compared with the matrix samples using Morpho J software, and subsequently categorized into their respective species (refer to Figure 2).

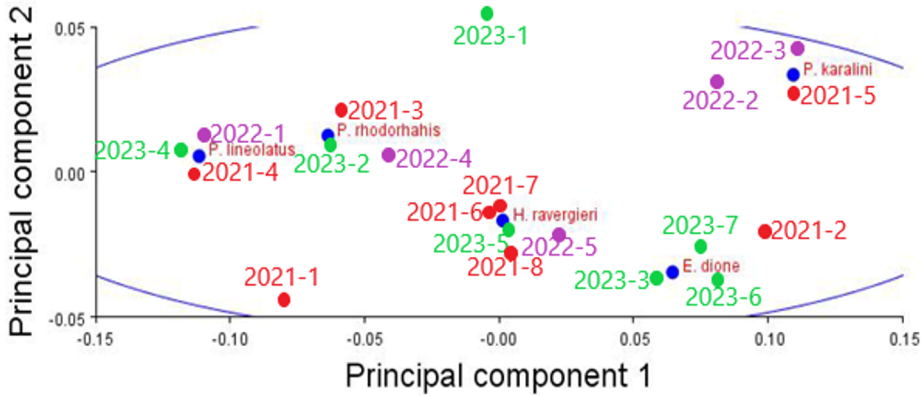


Fig. 2. Principal component analysis (PCA) of samples.

Following the identification of species, the population density of each was recalculated and compared with densities determined during field studies (refer to Table 1). Considering that the rise in the numerical value of the variations results in a higher standard error of the mean, discription statistical analysis was conducted on the mean densities derived from pre-morph-analysis and pre-morph-analysis (refer to Figure 3 Box plots).

Our study took place in the desert and hills of the Kashkadarya region, where species from the Colubradae and Psommophidae families are found, forming a single community. Hence, it's crucial for the population density mean post-morpho-analysis to be high in accuracy. As mentioned earlier, an elevation in species population density can elevate the mean value, potentially increasing standard error of the mean, thus potentially reducing the reliability of research findings. To ensure this scenario didn't occur in our study, we conducted an ANOVA test comparing two densities and examined their regression relationships (refer to Figure 3 reg. $yD_{(a)}-xD_{(b)}$).

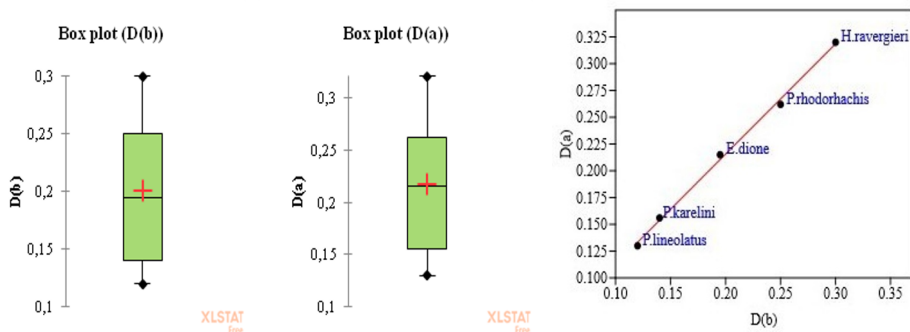


Fig. 3. ANOVA test results.

Table 1. Comparative analysis of population densities (M-mean, SD-standart divation, SEM-Standart error of the mean, C%-Variation coefficient, P%-Mean Relational Error, Pred-prediction from ANOVA test, Resd-residuals from ANOVA test).

Species	Density before morpho analysis (D _(b)) (Transect length-km)	Density after the morpho analysis (D _(a)) (Growth percentage) and (ANOVA)	Specific number of molted skin samples	Coordinate from which the molted skin samples were obtained
<i>P.karelini</i>	0.14±0,0013 (47 km)	0.156±0,0011 (111%) Pred(0.154) Resd(0.002)	2021-5 2022-2 2022-3	38.874813, 64.677280 39.331413, 65.546380 38.580731, 66.547868
<i>P.rhodorrhachis</i>	0.25±0.002 (62 km)	0.262±0.002 (104,8%) Pred(0.267) Resd(-0.005)	2021-3 2022-4 2023-2	38.671979, 65.577134 38.953915, 65.809305 38.856403, 67.100214
<i>H.ravergieri</i>	0.3±0.0045 (62 km)	0.32±0.0029 (106.7%) Pred(0.319) Resd(0.001)	2021-6 2021-7 2021-8 2022-5 2023-5	38.814129, 64.706350 38.649413, 66.729901 38.570003, 66.559613 38.951779, 65.879343 38.970872, 66.447106
<i>E.dione</i>	0.195±0.002 (51km)	0.215±0.001 (110%) Pred(0.210) Resd(0.005)	2021-2 2023-3 2023-6 2023-7	38.700736, 65.711777 38.828593, 67.093348 38.572869, 66.128597 38.546994, 66.128597
<i>P.lineolatus</i>	0.12±0.0051 (70 km)	0.13±0.004 (108.9%) Pred(0.133) Resd(-0.003)	2021-4 2022-1 2023-1	38.527886, 66.558302 39.337873, 65.650464 39.313616, 66.665420
M	0.201	0.217	-	-
SD	0.067	0.069	-	-
C%	0.334	0.319	-	-
SEM	0.034	0.035	-	-
P%	16.7%	15.9%	-	-

4 Discussion

It is important to highlight that, to prevent duplication of individual counts during the census due to daily and seasonal movements of the species, the population density was initially calculated using the FMP method. This measure ensures that each individual is counted only once. Based on the results, out of the skin samples collected during the field research, 3 were identified as belonging to the *P. karelini* species, resulting in an 11% increase in the species' average density. Additionally, 3 samples were classified *P. rhodorhachis* species, leading to a 4.8% rise in the average density of this species. Moreover, 5 samples were attributed to the *H. ravergieri* species, resulting in a 6.7% increase in its average density. Furthermore, 4 samples were identified as *E. dione* species, contributing to a 10% increase in its average density. The remaining 3 samples were assigned to the *P. lineolatus* species, showing an observed 8.9% increase in average density.

Descriptive and ANOVA analyses revealed that following, there was an increment of 0.016 ind/ha in population density compared to the pre-morpho-analysis density in the study (D(a)-D(b) 0.217 ind/ha – 0.201 ing/ha). Additionally, there was a noted increase in standard error of the mean (D(a)-0.034, D(b)-0.035). However, this observation isn't concerning as there was a decrease of 0.7% in Mean Relational Error. Consequently, there was a 0.7% reduction in average error rather than an increase. The regression analysis of average density after analysis shows an increase in the order of *P. lineolatus*, *P. karelini*, *E.*

dione, *P. rhodorhachis*, and *H. ravergeri*. It relates residuals and predicted density in ANOVA analysis.

5 Conclusion

In conclusion, our research considered the inclusion of molted skin samples when counting species from the Colubridae and Psammophiidae families. Utilizing the MorphoJ program for species classification based on molted skins resulted in an accuracy rate of 5-10% in determining the population density of the species. Moreover, the level of Mean Relational Error has been enhanced and sustained by 0.7%.

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