Evolutionary Correlation Between Wing and Bill Length of Barn Owls

Evolution (BIO 461)

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Introduction

Avian species have been used for hundreds of years for evolutionary biology research, because of their diversification of traits and their ability to adapt and thrive in different environments in many different parts of the world. Evolutionary processes in birds have sculpted their plumage color, song, bill size, wing size, feet shape, and many other phenotypic traits in order to survive in their environments (Wynns 2016). Some of these traits are correlated to one another and can be traced back by observing evolutionary relationships amongst the species in phylogenetic trees.

Evolutionary correlation, as defined in scientific literature, is when two or more phenotypic traits evolve together due to evolutionary processes such as genetic drift, mutation, migration, natural selection, and some environmental factors. By observing evolutionary correlation, we are able to predict specific changes about the species and their environments through time (Harmon 2021). Pearson's correlation test allows us to measure the linear correlated relationship between two variables, as positive correlations tend to be closer to 1, no correlations reside at 0, and negative correlations tend to be closer to -1 (Gonzalez et al. 2019).

In order to build on this research, data was collected from three different species of barn owls, *Tyto furcata* (American barn owl), *Tyto javanica* (Eastern barn owl), and *Tyto alba* (Western barn owl). The American barn owl can be found in the tropics and subtropics of South American forests, and they hunt for rats, mice, other aviator species, and insects (Lewis 2022). The Eastern barn owl can be found in the woodlands and semi-deserts of China, Indonesia, Australia, and offshore islands, and they hunt things like voles, bats, reptiles, frogs, and shrews (Lewis 2022). The Western barn owl can be found in the wooded forests of Britain, Europe, Africa, and in the Middle East, and they hunt small rodents, pocket gophers, lizards, rabbits, and insects (Lewis 2022).

Larger bill size will add some weight to the owl, resulting in it being heavier. The heavier the animal, the larger the wings it must have to sufficiently fly through the air (Science Learning Hub). This analysis will explore if overall wing length and bill length are evolutionary correlated to one another in all three species of barn owls. With that being said, it could be expected that as bill length increases, overall wing length will also increase across the species. It is hypothesized that bill and wing length are evolutionarily positively correlated and will have a positive linear Pearson's correlation coefficient.

Materials and Methods

Data Collection

To test this hypothesis, data was collected and obtained from the paper "Geographical variation in bill size provides evidence for Allen's rule in a cosmopolitan raptor." Data was collected through random sampling. Latitude, longitude, bill length, sex, island, and wing length were all taken in 7,619 museum specimens across the three barn owl species from 1809-2017 in 140 museums and private citizens (Romano et al. 2019). The total sample included 3,902 Western barn owls, 2,525 American barn owls, and 1192 Eastern barn owls. 3,054 of the sample were male, 3,270 were female, and 1,295 individuals were unsexed (Romano et al. 2019). For the purpose of this experiment, only species type, bill length, and wing length were used for the analysis. All sexes were included in the study to ensure there was not a bias against either sex. Wing length was taken in millimeters and bill length was measured in centimeters (mm*10). Bill and wing were measured in different units in order to compare the ratio between them as dependent variables.

Phylogeny

The second phylogeny, Figure 1, was also created by the *Biological Journal of the Linnean Society* for the paper "Phylogeny, biogeography, and diversification of barn owls (Aves: Strigiformes)" in April of 2016. This phylogeny estimates divergence in time at each node for each of the species. Their analysis was based on 2838 bp of three mitochondrial markers (16s, Cox1, and Cytb) and one nuclear marker (Rag1). Mitochondrial markers are the structural or functional properties of the mitochondria (Bioblast). Nuclear markers are antibodies of the nucleus and its structure (Thermo Fisher Scientific). The probability value was based on the Bayesian analysis. For the purpose of this study, only time divergence is notable, because it is recognized that the data is not independent. Divergence was calculated through fossil calibrations and reconstructed ancestral ranges.

Wing and Bill Length Plot

A plot was created by R studio, each species was placed on the graph in different colors to differentiate the species (Figure 2). The y-axis measured wing length (mm) and the x-axis measured bill length (mm*10). The log of the x and y values were used to show exactly how much wing length increases as each bill length is increased. A legend was also added to clarify the species.

Data Analysis

A Pearson's correlation test was used to determine how significantly correlated wing and bill length are to each other using R studios (Figure 3). This analytical test is measured from -1 to 1. Pearson correlation coefficients closer to -1 signifies a negatively correlated relationship, a Pearson correlation coefficient at 0 signifies that there is little to no relationship between the variables, and a Pearson correlation coefficient closer to 1 signifies a positively correlated relationship.

Results

Figure 1 shows the divergence in time between the clades. The T. *alba* clade evolved first around 11 million years ago. The T. *furcata* and T. *javanica* split from one another about 8 million years ago. The T. *furcata* clade diverged approximately 4 million years ago, and the T. *javanica* clade diverged about 3 million years ago (Romano et al. 2019).

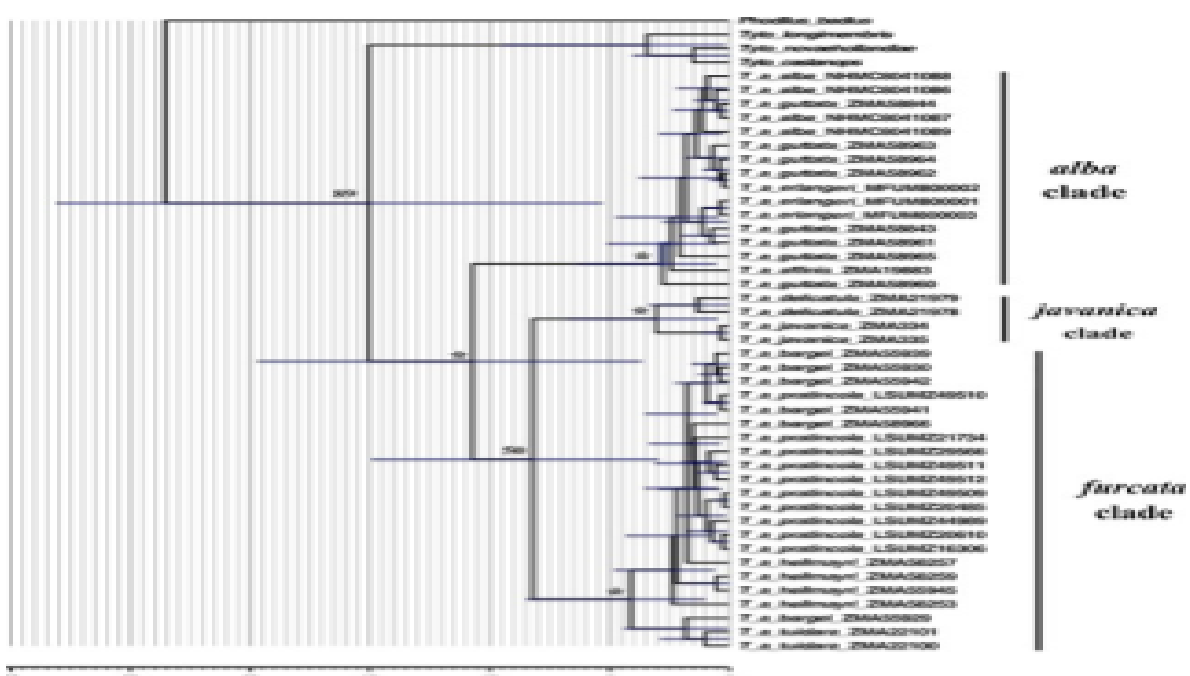

Figure 1: The phylogeny of the divergence in time between the three species of barn owls created by the *Biological Journal of the Linnean Society* in 2016.

Figure 2 displays the species on a scatter plot. It shows the relationship between bill length and wing length. The data point points for *Tyto alba* (Western barn owl) are mainly grouped together with only a few outliers, indicating that there is less variation in wing and bill size amongst this species. In the bottom left section of the graph, *Tyto alba* has the shortest bill and wing length compared to the other species, while in the upper right section of the graph, *Tyto furcata* has the largest bill and wing length. *Tyto javanica* mainly resides somewhere in the middle for both bill and wing length. All three species show a positively linear relationship on the scatter plot.

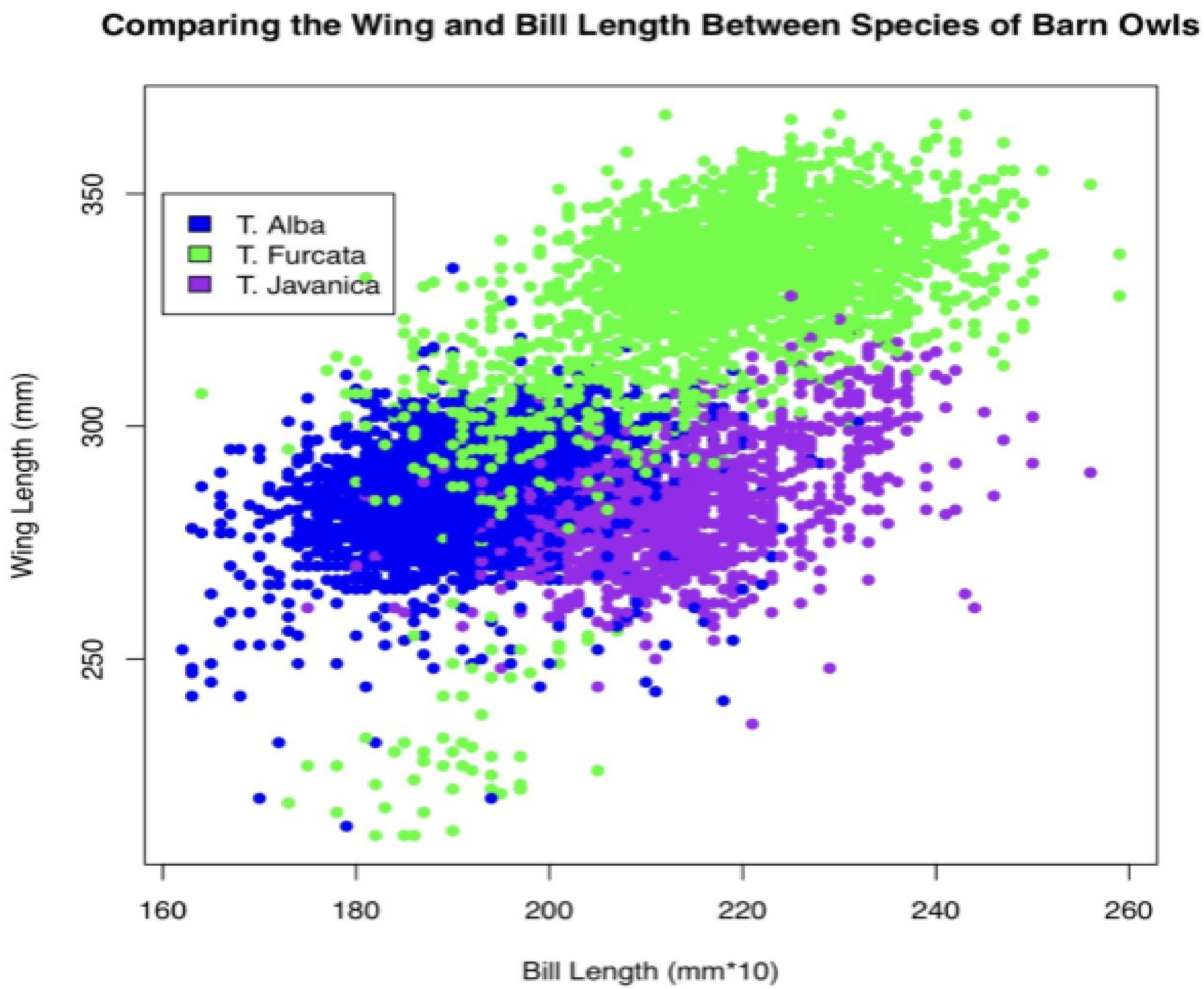

Figure 2: Wing and Bill length plot for three species of barn owls, *Tyto alba, Tyto furcata, and Tyto Javanica.*

Figure 3 shows the results of the Pearson correlation test. The T-value is shown to be 73.3. The degrees of freedom are shown to be 7617. The p-value was found to be less than 2.2e-16. The correlation coefficient is found to be 0.643135.

Pearson correlation coefficient	0.643135
T-value	73.3
Degrees of freedom	7617
P-value	2.2e-16
95% confidence interval	0.6297750, 0.6561146

Figure 3: The Pearson correlation analysis test for wing and bill length.

Discussion

The results of the Pearson correlation coefficient was shown to be 0.643135 (Figure 3). This analysis ranges from -1 to +1. When the correlation coefficient value is closer to 1, it shows a positively linear relationship between the two traits. The coefficient value found in this study shows that there is a positively linear correlation between bill and wing length amongst the species. This result was supported by the p-value of 2.2e-16, because it is less than 0.05, meaning that the test is statistically significant and that there was a very small chance that the result was due to a random sampling error (Beers 2023) and (Figure 3). With this finding, we are able to reject the null hypothesis that there is no correlation between wing and bill length in barn owls species and support the alternative hypothesis that there is an evolutionary correlation between the traits.

The plot of the three barn owl species also supported the hypothesis, because smaller wing length correlated to smaller bill length and larger wing length resulted in larger bill length, with a few exceptions as outliers (Figure 2). Interestingly in Figure 3, each species tends to group themselves closely together while also having some overlap between the clades. *Tyto javanica* is shown to be the most positively linear (Figure 2). This figure was able to support the hypothesis that there is an evolutionary correlation between the two traits, as one trait increases so does the other trait.

Results from this experiment could possibly be explained by species divergence in time. The cause of this divergence could weigh heavily on natural selection. Natural selection through evolution could have selected for these correlations between wing and bill size, in order for the owls to adapt and survive in their environments. Smaller bill size is typically used for catching, gripping, and tearing prey (Barn Owl Centre). The *Tyto alba* species were found to have the smallest bill and wing size (Figure 3). Their bill size is most likely due to the fact that their diets consist of things that may be hard to catch without a bill that is able to tightly grip the prey (Lewis 2022). Their smaller wing size is beneficial to them, because smaller wings are energy efficient, especially in their warm climates, because they require less flapping and rely more on gliding (RSPB). The *Tyto furcata* barn owl species was found to have the largest bill and wing length. Their bill length can be beneficial to catching prey. Larger wingspans can be helpful to barn owls to fly quickly and can be used for swift and silent hunting (Optic Mag 2023). Each species has specific bill and wing length sizes, which are likely to be the most beneficial to their habitat, creating an evolutionary correlation between them.

As mentioned earlier, the data was not entirely independent of each other, creating some bias in the study. This study could be repeated in the future to show more independence between the data using the phyl.RMA function in R and incorporating a phylogeny that can be read into R studio. Future studies will allow us to look further into trait correlations between different species of barn owls and determine a genetic linkage amongst the traits. However, many other biases in this study were prevented by obtaining random samples of each of the species, considering all genders, collecting specimens from different locations around the world, and having a large sample size of 7,619 in total. The correlation in this study is ultimately significant and supports the hypothesis, because it enables predictions about selection between the traits amongst the species living in different environments, and provides insight about their environmental adaptations.

Work Cited

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