

# Strength of Phenotypic Selection in Two Populations of the Florida Scrub-Jay

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**Abstract.** Comparing populations of a species living in the wild with another living in a suburban environment can give us novel insights into the impact of human presence on the organism. This impact can be quantified by estimating phenotypic selection. A good model to estimate phenotypic selection is to regress components of fitness onto phenotypic values which yields the strength and direction of the selection. I propose to study this phenomenon in two populations of the Florida Scrub-Jay using detailed pedigree data and morphometric measurements collected for more than 20,000 phenotypes. After testing for temporal trends in the two populations' phenotypes, I will use components of fitness such as lifetime breeding success and total lifespan to estimate phenotypic selection. The strength and direction of this phenotypic selection can allow us to infer the impact of urbanisation on the jays and to check if they are being forced to adapt to new conditions. This study will increase our understanding of human impact on the jays and may aid in formulating conservation strategies for the endangered jay.

**Keywords:** Phenotypic Selection · Florida Scrub-Jay · Urbanization.

## 1 Introduction

Two populations of a species in different locations can elucidate the role of environment and other factors such as habitat suitability, human presence, and food availability on the populations' phenotypic adaptations. Observations that include the comparison of populations of the same species have been championed by population geneticists and have led to our basic understanding of phenotypic selection. These include iconic examples such as evolutionary changes in the beak sizes of Darwin's finches (Grant and Grant 1993). One method to estimate the strength of selection is to focus on a single generation and compare the success of different phenotypes at survival and reproduction (Linnen and Hoekstra 2009). Across generations the magnitude of the phenotypic response to selection depends on both heritability and strength of selection (Linnen and Hoekstra 2009). Since selection acts at a phenotypic level, it is possible to infer the strength and direction of selection despite having no genotypic data related to fitness traits. The direction and intensity of natural selection can be inferred by regressing relative fitness on phenotypic values. Fitness is usually broken down into components such as number of offspring produced or total lifespan (Linnen and Hoekstra 2009), as fitness itself is very hard to define. Directional selection results in a linear relationship between phenotype and relative fitness, wherein the gradient of the regression line is the strength of the selection (Lande 1979; Lande and Arnold 1983). Since phenotypes can be correlated with fitness directly or indirectly, it is important to calculate selection differentials and selection gradients to estimate the direct and indirect contributions of the phenotype on the fitness (Lande and Arnold 1983). Therefore a linear regression of change in phenotypic values on the overall fitness of a population can quantify phenotypic selection.

Phenotypic selection can differ among populations of the same species in different environments and thus can give us a better understanding of the population's adaptive responses to changes in the environment. Grant and Grant (1993) showed that on two occasions due to a disruption in the environment because of droughts, selection favored the populations of medium ground finch (*Geospiza fortis*) most adapted to the change in environment. This establishes that selection is a driving force in changing phenotypes over time. Thus it becomes important that we understand what changes in the environment constitute and contribute to this selection and whether or not

we are losing phenotypic diversity because of it. Reznick et al. (1997) showed that once guppies (*Poecilia reticulata*) were placed in a low-predation habitat, their size and age at reproductive maturity increased. There was also a strong direct selection for increased age at maturity, due to a change in the environment. These examples illustrate the importance of measuring multiple traits and estimating phenotypic selection from change in individual phenotypic value and fitness to gain an accurate picture of adaptation and evolutionary constraint in natural populations. Lastly, we can use the fact that a change in certain phenotypes confers greater fitness on a generation of organisms to further our analysis in predicting phenotypic selection. A number of previous studies have looked at selection on phenotypic traits to explain why a change in certain phenotypes may confer greater fitness on a generation of organisms. Fjerdingstad and Keller (2004) found that queen ants that were heavier at the time of mating were significantly more likely to mate with multiple males which led to them storing more sperm which ultimately led to a higher across-year survival. These results suggest that there is a link between variation in a quantitative trait such as weight and a change in fitness, which can be quantitatively established. These previous studies establish a need for studying a well-documented species with at least two populations in different environments which can be used to understand the dynamics between phenotypic selection and the environment. They also suggest that natural selection is a phenomenon that is happening all across the board, and has great impacts on fitness and overall health of a species. Moreover, there are only a few studies that have analyzed a wide range of data on phenotypic traits and fitness components of two populations of the same species, and even if they have they have had sample sizes less than 135 individuals resulting in low statistical power to detect selection (Kingsolver et al. 2001). Lastly, human impact and our rapid urbanization of non-human animal's habitat can be examined closely through using techniques like phenotypic selection on two populations of the same species.

Here, I propose to investigate and elucidate a potential relationship between variations in morphometric phenotypes and the overall mean fitness of two populations of the Florida Scrub-Jay (*Aphelocoma coerulescens*, hereafter FLSJ). This analysis will allow me to closely monitor the selection on various phenotypes of the study population along with its strength. The FLSJ, a species categorized as Vulnerable by the IUCN, is endemic to Florida and remains native to the scrub ecosystem which is fire-maintained and xeric, (Woelfenden and Fitzpatrick 1984). Two populations of this

non-migratory and monogamous bird have been studied closely at the Archbold Biological Station in Florida (hereafter Archbold population), and near the Lake Wales Ridge Wildlife and Environmental Area (hereafter PLE population). An important caveat here is that Archbold is a relatively undisturbed population living in the wild, while the PLE population is rapidly losing its habitat because of urban development. These populations have been extensively pedigreed, every individual is uniquely banded, and censused every month since 1969. This is in addition to documenting morphometrics of every individual (such as bill length and bill depth), body condition (such as weight), and life history (such as lifespan, fecundity, and clutch size). This provides a wealth of information on mostly every individual of the Archbold and PLE populations and allows for an investigation between morphometric phenotypes and fitness (Chen et al. 2016). The two population's relative fitness will be the response variable to the selection on a phenotype (Lande and Arnold 1983; Arnold and Wade 1984). Relative fitness can then be expressed in units of phenotypic standard deviation of the phenotype, which can then allow for a comparison between phenotypes and fitness components (Kingsolver et al. 2001), allowing for an effective comparison between the two populations. The pivotal question is whether or not the PLE population is facing phenotypic selection as a response to human encroachment and urbanization. We are well-poised to answer this question since the Archbold population will serve as a control as it can establish a baseline phenotypic selection, allowing us to pinpoint deviance's from it in the PLE population. Moreover, due to phenotypic selection being expressed as a function of variation in phenotypes and fitness in both of the populations, we have the measurements in comparable units to examine the effects of urbanization.

This project will be using an extensively pedigreed population with a large sample size (10,442 Archbold jays) and large number of measurements (Archbold: 19,237; see Table 1) to fill in the gaps of our current knowledge on selection on phenotypes and phenotypic selection. As mentioned before, most of published studies on natural population's selection have had low sample sizes and we are hoping to mitigate that bias by using rich data from all the phenotypes of interests. Therefore, the wealth of demographic, genetic, and phenotypic data along with a large sample size poises us for a very significant and detailed dive into looking at selection on FLSJ's traits, as a function of its environment.

**Table 1.** Full count of phenotypic measurements in Archbold.

	Nestlings	Fledgling	Juvenile	Yearling	Row Total
Weight	2825	685	1766	2270	7546
Bill Depth	0	419	1217	419	2055
Bill Width	0	417	1216	419	2052
Tail Length	946	471	1181	282	2880
Culmen	0	409	1180	437	2026
Head Length	0	418	1219	442	2079
Head Breadth	0	1	456	142	599
Column Total	3771	2820	8235	4411	<b>19237</b>

## 2 Objectives and Hypotheses

### 2.1 Objectives

I aim to:

*Aim 1:* Test for significant temporal trends in the mean phenotypic values in the Archbold and PLE Populations by using the Mann-Kendall Statistical test.

*Aim 2:* Elucidate any evidence of selection on individual phenotypes by looking for significant correlations between individual phenotypes and components of fitness.

*Aim 3:* Compare selection on the two population's individual phenotypes and attempt to explain any deviation through literature or field studies.

### 2.2 Hypotheses

This project has two guiding hypotheses:

1. I predict that there will be no presence of significant temporal trends (monotonic trends) in the Archbold population. This is based on the fact that this is a natural population with high levels

of conservation and remains relatively undisturbed from urban development and other problems. This population will have no selection pressure to adapt to because the environment is not changing drastically. Conversely, there will be a significant temporal trend associated with the phenotypes in the PLE population. This is based on the fact that the PLE population is facing habitat loss at an unprecedented rate leading to a plummeting population and food shortage, increasing selection pressures.

2. I predict that here will be no evidence of selection on the phenotypes of the Archbold population. This is, again, due to its relatively undisturbed environment which gives it little to no reasons to adapt. However, I would hypothesize that the PLE population will be experiencing directional selection, due to its immediate need to adapt to urbanization and human presence.

### 3 Methods

This project will be divided into three phases, corresponding with our three aims. The first phase is looking at temporal trends. The second phase is running regression on individual phenotypes after identifying fitness components and then inferring the significance, directionality, and strength of the selection. The third phase is the comparison stage and would require us to go through the individual phenotypes from each population to look for discrepancies in selection values and attempt to explain the reasons behind the discrepancy or the absence thereof.

#### 3.1 Phase 1: Temporal Trends

I will run the Mann-Kendall test on the mean values of the phenotypes based on the natal year of the jays, and this will allow us to infer whether or not there is a temporal trend in the phenotypic values. Table 1 was made after a filtration attempt wherein all birds with pertinent phenotypes measured were counted in the Archbold population, and serves to show the sheer richness of the data available. There are certain parameters which must be kept in mind as data analysis begins: for example I will only be analyzing jays born after 1990 because that is when the tracts which they habitat stabilized in size. This is important because now we have limited our jays to a certain area thus ensuring that they either belong to the central PLE or Archbold population effectively controlling for any

peripheral territories. Moreover, we only included jays whose birthdate was known to ensure we know its age since these morphometrics change with time, and allow us to control for the age effect. All jays below the age of 11 days were excluded from the project because their morphometrics were usually not measured due to their small size. Jays measured at 11 days post-birth are categorized as Nestlings, 12-70 days post-birth as Fledglings, 71-365 days post-birth as Juveniles, and 365 days and onwards as Yearlings.

### **3.2 Phase 2: Regression and other calculations**

This phase will begin with choosing suitable fitness components for phenotypes to be regressed against. These fitness components include but are not limited to lifetime reproductive success, clutch size, and lifespan. Regression, much like everything else in this project, will be done in R-Studio and will include significance, directionality, and strength of the selection. Since phenotypes can be correlated with fitness directly or indirectly, it is important to also calculate selection gradients and selection differentials to estimate the direct and indirect contributions of the phenotype on the fitness. Selection gradients are calculated using multiple regressions to control for indirect selection and while selection differentials are the slope of the phenotype-fitness regression, when phenotypic values are standardized by subtracting population mean and dividing by the population standard deviation (Linnen and Hoekstra 2009). If our selection gradient and differential estimates are similar then we can be confident that our phenotypes of interests are mostly under direct selection relative to indirect selection.

### **3.3 Phase 3: Comparisons**

This phase will commence after all data analyses has been done and will require significant effort to investigate whether or not there was selection on the phenotypes of the two populations and how did they differ from each other. This phase will require a considerable amount of literature and field studies review to elucidate why such presence or absence of selection in different phenotypes across the two population could be taking place.

## 4 Predicted Results

I predict that we will see a temporal decline in all of the morphometric traits for example: the mean weight of jays across years will decrease etc. in the PLE tract. This will mostly be due to the fact that there is stress on the jays due to habitat loss and fragmentation leading to a decrease in potential food sources. However, I think that there will not be a temporal change in the morphometric phenotypes of the jays in the Archbold population since there are aggressive conservation strategies at work there, and because it is not being urbanized like PLE. I also predict that the overall fitness (the sum of many components of fitness) will be increasing in PLE, leading to a directional selection on all the morphometric phenotypes in the population. The reason for this is again that the PLE population is under stress from a decreased habitat size to diminished access to food. The overall fitness in Archbold will remain stable showing phenotypic selection is not at work due to this population being well-conserved and free from detrimental human intervention. Morphometric traits and the overall fitness of the Archbold population will remain stable. Data analyses may prove our predicted results to be wrong: and may suggest that there is stability in all morphometric traits in both of the populations, suggesting that natural selection is not actively acting upon the phenotypes. This could be because the birds could robustly be dealing with the changes in their environments. It could, conversely, show that the overall fitness is decreasing in both of the populations which could be explained by the lack of immigration in the Archbold population from PLE leading to inbreeding (Chen et al. 2016). The decrease in fitness of the PLE population could be due to the plummeting number of birds leading to genetic drift.

## 5 Significance of Work

We have a rich database of a large number of genotyped jays, with measured phenotypes and extensive pedigrees, allowing us to gain an insight into the selection pressures on these populations of the FLSJ. At this point we only require substantial data analyses to analyse these results, as we have all the data and understand the theory. Furthermore, as mentioned before, these two populations of the FLSJ are living in drastically different environments and while not all differences in their fitness and phenotypic makeup can be attributed to the environments, it can at least start to explain how



the presence of urban development in PLE is impacting the jays. In addition, this project will not only be informative about the changes in the morphometric phenotypes but also about the strength and directionality of those changes, and may move us to reconsider our conservation policies. Lastly, this project has impact upon greater conservation strategies as habitat loss is not unique to the jays but rather is being experienced by a multitude of species worldwide.

## 6 References

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