

Modeling and Allometric Analysis of two Butterfly Species of the Genus *Colotis*

Ali Elkarmi^{1,*} and Lina Shaheen²

¹ Biology and Biotechnology Department, Faculty of Science, Hashemite University, Zarqa, Jordan; ² Physical and Life Sciences Department, King's Academy, Madaba-Manja, Jordan

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Abstract

A sample (282) of two butterfly species *Colotis phisadia* (144) and *Colotis chrysonome* (138) was collected and allometric analysis in addition to growth models were used to analyze the morphology and growth of these two species. The objective of this study is to find out if it is feasible to use allometry and growth models as tools to differentiate between these two species. Butterflies were randomly collected and measured for maximum body length, body width, wing length, wing width and head diameter. Two growth models were used: the Von Bertalanffy growth model and Gompertz. The results indicate that the two butterfly species have different allometric parameters indicating significant differences in morphology and the feasibility of using allometry for this purpose while the growth models showed large similarities in the growth of these two species.

Keywords: Modeling, Allometry, Growth Models, *Colotis* Spp.,

1. Introduction

Colotis phisadiaphisadia (GODART 1819) belongs to family Pieridae sub-family Pieridae (Katbeh-Bader *et al.*, 2004); it is common in Jordan and in tropical Africa and Arabia but limited to the Dead Sea area in Jordan. It is characterized by an intermediate size, white, yellow or orange wing ground color with black or greenish markings. *Colotis chrysonome* (KLUG 1829) belongs to family Pieridae sub-family Pieridae (Katbeh-Bader *et al.*, 2004), an Afrotropical species and known as the Golden Arab. Tropical oases in southern part of the Dead Sea are typical localities for this butterfly (Larsen and Nakamura, 1983). *Maeruacrassifouas* is a food source (Katbeh-Bader *et al.*, 2004), and fluctuation in the number of this butterfly is dependent on this food source (Walker and Bittaway, 1987). The legs are equally developed (Korshunov and Gorbunov, 1995), and the larvae are Green in color, with markings and stripes.

Palmer *et al.* (2019) conducted a study of the scaling and allometry of butterfly wing patterns. Their results indicated that the color patterns showed that the positions and size of the pattern elements scaled isometrically with wing size. Mirth *et al.* (2016) carried out a study on the allometry and size control to analyze the evolution of morphological scaling relationships. They indicated that allometric studies and population genetics provide a mechanism for the understanding of evolution and allometry. Wolfe *et al.* (2010) showed that limb evolution in butterfly members of the families Nymphalidae and Riodinidae are likely evolved reduced forelimbs in parallel. Kunte (2007) analyzed the allometry of proboscis

lengths using Costa Rican butterflies. He stated that a strong positive relationship exists between proboscis length in relation to body size and handling time per flower on nectar plants. Garcia-Barros (2006) showed that the evidence for intra-specific allometry between the traits investigated and egg weight varied among the species, indicating that the slope of such relationship may be a specific feature. Stepan (2000) calculates the allometric relationships of dried forewings of ten butterfly species to the butterflies' gross morphological parameters. He concluded that the distal regions of the wings are stiffer against forces applied to the ventral side. Akand *et al.* (2017) examined the morphometric variations in the species of two sub-families of butterflies of the family Lycaenid. They stated that there were differences between the two subfamilies and can be used as good indicators to identify the species more correctly. Bai *et al.* (2015) carried out a geometric morphometric study of the wing shapes of the butterfly *Pieris rapae*. They concluded that there are significant differences in the forewings and hindwings of the butterfly.

The purpose of this study which is the first in Jordan is to examine the feasibility of using growth models and allometric parameters to differentiate between two butterfly species and to examine the differences in the growth and allometry of two species belonging to the same genus.

2. Method

2.1. Study area and species

The two species are found in the area of the Dead Sea, Wadi Arabah and sometimes Aqaba (Katbeh-Bader *et al.*,

* Corresponding author. e-mail: karmi@hu.edu.jo.

2004), and the male is characterized by a pale salmon-pink ground color on the upper side of the forewing. Its base is spotted with bluish-grey scales that extend outwards and are merged with a black patch that occupies the apex of the cell (Borroret *al.*, 1981). Its hindwing is white with a base dotted with bluish-grey. The female is very variable, but resembles the male in markings (Borroret *al.*, 1981).

2.2. Collection and analyses

A total of (282) butterflies (*Colotis phisadia* (144) and *Colotis chrysonome*(138) were collected and the maximum body length (BL), body width (BW), wing length (WL), wing width (WW) and head diameter (HD) were measured using a digital caliper accurate to 10 μ m (E-Base, MC 02050282-I, China). The following figure shows the locations of the above measurements.

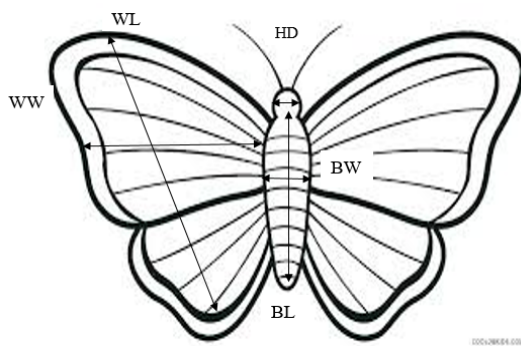


Figure 1. Locations of the measurements carried out on the butterfly

Allometric analyses was carried out using nonlinear regression analysis of the parameters BL and BW; WL and WW; BL and HD; BW and HD; BL and WL; BW and WW. All measured parameters were analyzed using the equation:

$$Y = A * X^b$$

Where b is the allometric coefficient and A reflects the ratio of Y/X.

All calculations were carried out using STATISTICA software for windows (StatSoft, USA).

Utilizing body length as a measure of growth the Von Bertalanffy's growth model:

$$BL(t) = L_{max}(1 - A * e^{(-kt)})$$

and the Gompertz growth model:

$$BL(t) = L_{max}e^{(-A * e^{(-kt)})}$$

were used, where BL is the body length, L_{max} is the theoretical maximum body length, A is a constant that indicates the ratio between the maximum body length and minimum body length, and k is the growth coefficient. The variables L_{max} , A and K were calculated using the Quasi-Newton method for nonlinear estimates (Ostle and Mensing, 1975) and STATISTICA software for windows version 10 (StatSoft, USA).

3. Results

There are significant differences between the allometric results of *Colotis phisadia* from *Colotis chrysonome*. The allometric results between body length and body width of *Colotis phisadia* showed that the constants $A=17.1335$ and

$b=0.4779$ while those of *Colotis chrysonome* were $A=6.0028$ and $b=0.8684$. Moreover, the results between body length and head diameter of *Colotis phisadia* were $A=17.1583$ and $b=0.5811$ while those for *Colotis chrysonome* were $A=5.6481$ and $b=1.0333$. Table (1) shows the results of all the allometric analyses between all parameters. Furthermore, the results indicated that there is no allometric relationship between body width and wing length; and body width and wing width of *Colotis phisadia* while there was a clear allometric relationship between these parameters for *Colotis chrysonome* (table 1).

Figures (2-7) show the results (in mm) between body length and body width, wing length and length width; and body length and head diameter of both butterfly species.

There is almost always a difference in the results of the allometric measurements between both species, and in some cases the allometric coefficient (b) is less than one in the case of *Colotis phisadia* and slightly more than one in the case of *Colotis chrysonome*.

The results of the growth models although show slight differences between both species as in the growth coefficient k calculated by the Von Bertalanffy's model ($k=0.1463$ for *Colotis phisadia* and $k=0.0933$ for *Colotis chrysonome*) and by Gompertz model ($k=0.1879$ for *Colotis phisadia* and $k=0.1109$ for *Colotis chrysonome*) (table 2); these slight differences indicate that the growth of both species is similar but not identical. The other parameters shown in table (2) are for the theoretical maximum length of the butterfly and the relationship between the minimum and maximum length (constant A).

Table 1. Allometric results of *Colotis phisadia* and *Colotis chrysonome*

	<i>Colotis phisadia</i>	<i>Colotis chrysonome</i>
Body Length–Body Width	$A=17.1336$ $b=0.478$	$A=6.0028$ $b=0.8684$
Wing Length–Wing Width	$A=1.0481$ $b=0.9239$	$A=0.6498$ $b=0.9872$
Body Length–Wing Width	$A=0.3273$ $b=1.2461$	$A=0.4050$ $b=1.2049$
Body Length–Wing Length	$A=0.3333$ $b=1.3227$	$A=0.7457$ $b=1.1898$
Body Width–Wing Length	$A=0.0006$ $b=2.5138$	$A=0.1909$ $b=1.0972$
Body Width–Wing Width	$A=0.0001$ $b=2.4835$	$A=0.10633$ $b=1.1181$
Body Length–Head Diameter	$A=17.1583$ $b=0.5811$	$A=5.6482$ $b=1.0333$
Wing Length–Head Diameter	$A=19.7542$ $b=0.4283$	$A=5.8906$ $b=0.8086$

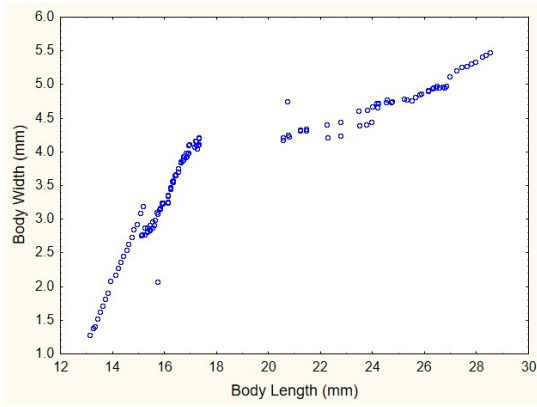


Figure 2: Measurements of body length and width of *Colotis phisadia*

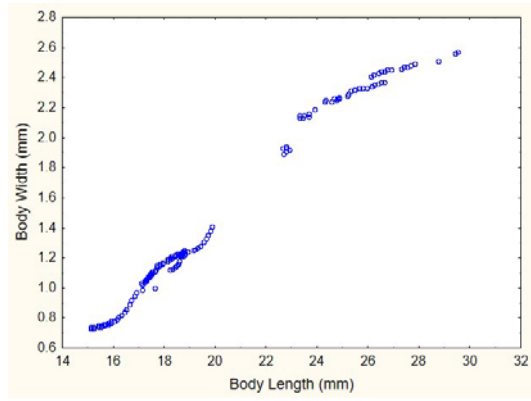


Figure 5: Measurements of body length and width of *Colotis chrysonome*

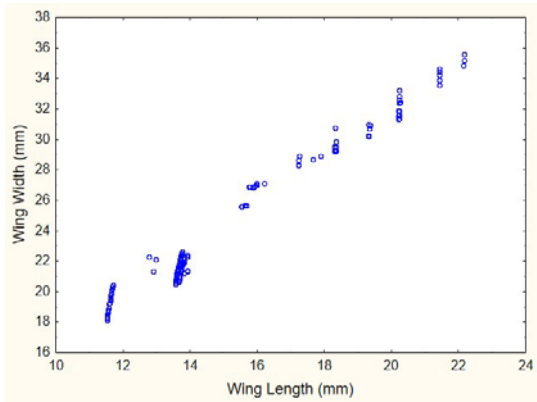


Figure 3: Measurements of wing length and width of *Colotis phisadia*

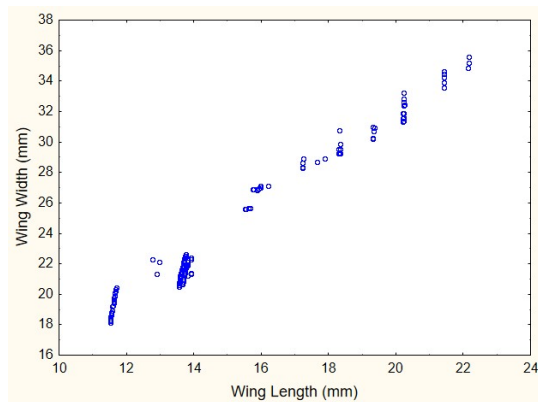


Figure 6: Measurements of wing length and width of *Colotis chrysonome*

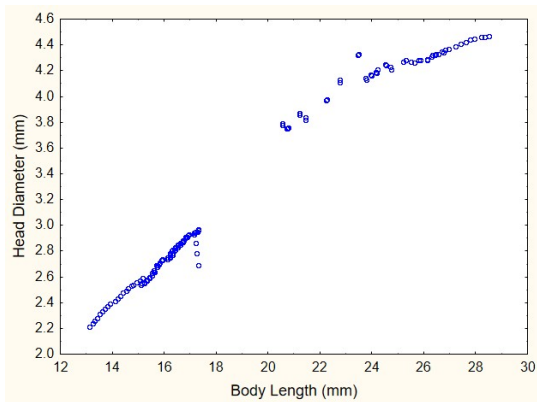


Figure 4: Measurements of body length and head diameter of *Colotis phisadia*

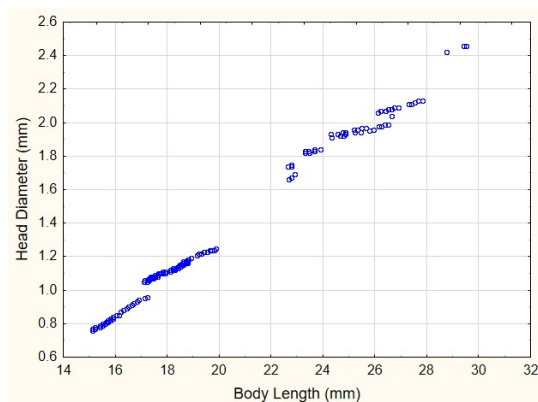


Figure 7: Measurements of body length and head diameter of *Colotis chrysonome*

Table 2. Results of the Von Bertalanffy's and Gompertz models

	Colotis phisadia	Colotis chrysonome
Von Bertalanffy's		
L _{max}	29.5	30.1
A	0.6047	0.5478
k	0.1463	0.0933
Gompertz		
L _{max}	29.3	30.3
A	0.8711	0.7601
k	0.1879	0.1109

4. Discussion

There are clear differences in the allometry of the two species of the butterflies. This can be attributed to differences in the genetic material of both species. These differences were enough to result in different allometric coefficients. Benitez *et al.* (2013) conducted an allometric research and concluded that the differences in sexual dimorphism of wing shape may be influenced by natural selection demonstrating the occurrence of two clearly different genetic materials. Ramirez-Ponce *et al.* (2017) showed that allometry can be explained within a framework of natural or sexual selection. Akand *et al.* (2017) results confirm the findings of this research. They showed that it is possible to differentiate between species since significant differences in forewing length, hind wing length, body length and antenna length. Morphometry existed in the species of the subfamilies Polyommatainae and Theclinae. The results of Chazot *et al.* (2015) showed that microhabitat has determined wing shape evolution, and a common selective force connects sexual dimorphism of forewing shape and color pattern. According to Owen (2012), morphometric analysis can be useful for species identification and classification. He stated that a strong method is to combine morphometric genetic methods, especially to in the areas of systematic and taxonomy.

Kunte (2007) examined proboscis length in butterflies using allometric approach showing a strong positive relationship between relative proboscis length and handling time per flower. Elkarmi and Ismail (2007) stated that allometry can be used to differentiate between two populations of the same species of *Melanoides tuberculata* living in hot and in cold waters.

The two models used showed similar but not identical results indicating that there are similarities in the growth patterns of the two butterfly species even though the morphology and allometric parameters differ. This can be explained by the closeness of the genetic material between the two species.

The limited number of studies using growth models to examine the difference between two species makes it difficult to assess our results. From these few studies, Tschinke *et al.*, (2003) concluded that growth models can be used to study the changes in body size and shape occurring during the course of evolution. Palmer (1983) research indicated that models can be used to study the relationship between body growth and predator size, prey size and prey species. Elkarmi and Ismail (2006a, 2006b and 2007) used Bertalanffy's and Richards' growth models to study the growth of the gastropods and limpets.

In conclusion, our results indicated that allometric analyses proved to be a useful tool to study the morphology of two species belonging to the same genus. Models of growth, however, can be used to show the closeness of the species in the growth patterns not the differences between them. Both methods are useful in the areas of environmental and taxonomy studies.

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