## Title

Ecomorphology of Body Shape and Life History in two Poeciliids (Gambusia spp. and Poecilia reticulata)

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## UNIVERSITY OF CALIFORNIA <br> RIVERSIDE

Ecomorphology of Body Shape and Life History in Females of the Genus Gambusia (Poeciliidae) and in Guppies (Poecilia reticulata, Poeciliidae)

A Dissertation submitted in partial satisfaction of the requirements for the degree of

Doctor of Philosophy
in
Evolution, Ecology, and Organismal Biology
by
Rafael Mauricio Torres-Mejia
December 2012

Dissertation Committee:
Dr. David Reznick, Chairperson
Dr. Kurt Anderson
Dr. Theodore Garland, Jr.
Dr. Derek Roff

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The Dissertation of Rafael Mauricio Torres-Mejia is approved:
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Committee Chairperson

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This is dedicated to Rosa and José, who showed me the beauty of nature and were always part of it

## ABSTRACT OF THE DISSERTATION

Ecomorphology of Body Shape and Life History in Females of the Genus Gambusia (Poeciliidae) and in Guppies (Poecilia reticulata, Poeciliidae)
by

Rafael Mauricio Torres-Mejia<br>Doctor in Philosophy, Graduate Program in Evolution, Ecology, and Organismal Biology<br>University of California, Riverside, December 2012<br>Dr. David N. Reznick, Chairperson

Multiple, potentially interacting features of the environment and the phenotype shape the way organisms evolve through adaptation. Ecomorphology aims to understand such intricate relationships between and within environmental and phenotypic variables. In this dissertation I made an integrative analysis of the combined effects of current velocity and predation on the evolution of body shape and life history of fishes.

In the first chapter I made an interspecific analysis of body shape in Gambusia females. As predicted, they showed larger caudal areas in highpredation sites. In contrast, flow had a small influence on shape. Pregnancy reduced the magnitude of phenotypic divergence between females from contrasting predation and flow regimes. These results indicate that adaptation to predation, and to a lesser extent flow, is key to body shape evolution in females of the genus Gambusia.

In the second chapter I analyzed the macroevolutionary pattern of life history in female Gambusia and its relationship with predation, flow, and latitude. Gambusia females showed a large range of variation in reproductive allocation, number of embryos, and size of embryos. One species of Gambusia showed incipient levels of maternal provisioning. Female body size was the best predictor of interspecific life history variation. Life history was not related with flow, or latitude, but females in high predation sites increase in ovary size at greater rates as they grow than females in low predation sites.

In the third chapter I explored more in depth the relationship between flow regime and body shape, comparing populations of Trinidarian guppies from sites with contrasting hydrologies. We tested the correlation between guppy shape, geomorphological features correlated with flow regime (watershed area, relief, and shape), and other environmental characteristics potentially interacting with guppy shape (pool volume, canopy cover, flow velocity, and the abundance of prawns and Rivulus hartii). We observed a correlation between body shape and geomorphological features of the watersheds. However, these results varied between sexes. We found gradients of prawn and Rivulus abundances that explained some of the body shape variation. Additionally, we found that pregnancy dissipated the correlations between environmental variables and shape.

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## Introduction

Multiple, potentially interacting features of the environment and the phenotype shape the way organisms evolve through adaptation (Reznick and Travis 1996). Ecomorphology aims to understand such intricate relationships between and within environmental and phenotypic variables (Arnold 1983; Garland and Losos 1994). Even though a multidimensional understanding of adaptation has been advocated (Ricklefs and Miles 1994), such integrative approaches are still rare (Walker 1997). Here we embrace complexity by analyzing how multiple correlated phenotypic characteristics are determined by multiple environmental factors.

A general concept in evolutionary biology is that adaptation within species can explain patterns of adaptive variation among higher taxa (Darwin 1872: 49; Watson et al. 1936: 58; Charlesworth et al. 1982; Arnold et al. 2001). However, an alternative view is that divergence within species cannot always explain divergence at the macroevolutionary scale (Goldschmidt 1940; Van Valen 1974; Stanley 1979; Eldredge and Cracraft 1980) because the direction of phenotypic divergence can be modified by other evolutionary processes (e.g. random genetic drift). A useful approach to test the evolutionary continuum among scales intra- and interspecific scales is to produce models of divergence from microevolutionary patterns to predict patterns at the macroevolutionary level (Arnold et al. 2001; Losos and Ricklefs 2009). In the first two chapters of the
dissertation I used this strategy to explain the interspecific patterns of body shape and life history in female Gambusia in response to predation and flow, testing predictions derived from models that were developed to assess microevolutionary processes.

Predation is a crucial biotic factor in nature. Organisms have evolved diverse strategies to avoid or escape from predators, from behavioral (e.g. activity patterns, habitat preferences, faking death, vigilance), to morphological (e.g. horns and spikes, camouflage, aposematic colorations), to biochemical (e.g. chemical defense), and the list continues (Langerhans 2006). One mechanism to escape from predators is to move away from them. To do so organisms may evolve shapes that improve an escape response (Langerhans 2009). Biomechanical theory states that in fishes the hydrodynamic efficiency is proportional to streamlining of anterior area of body and to depth of caudal region (Walker 1997). As predicted by biomechanical theory, fishes living in highpredation environments have an increased caudal area.

Life history theory predicts that high mortality risk in adults (e.g. due to predation) favors increased reproductive effort (Gadgil and Bossert 1970; Law 1979). Empirical studies have confirmed such predictions. In independent studies it has been observed that in habitats with high predation risk Poeciliid fishes have smaller embryos, higher fecundities, and mature younger (Reznick and Endler 1982; Reznick et al. 1996; Johnson and Belk 2001; Jennions and Telford 2002; Reznick et al. 2002). For example, females of fishes living in sites with predatory
fishes have higher reproductive allotments in Poecilia reticulata (Reznick and Endler 1982) and Gambusia hubbsi (Downhower et al. 2000).

The dynamics of medium (i.e. air, water) may exert a powerful effect on phenotypes. Such effects are apparent in terrestrial habitats, where strong winds uproot trees (Ennos 1999) and restrict bird migration (Erni et al. 2005). However they are more evident in aquatic systems, where up to $95 \%$ of fish in a stream may be washed-out by flash floods (Chapman and Kramer 1991). Fishes evolve characteristics morphologies to avoid being flushed-out by strong currents. As expected by biomechanical theory, high water velocity is related with larger caudal areas. It has been hypothesized that high body depth is related with slow water velocities (Gatz 1979), but in general the effect of water velocity on streamlining, abdomen distention, or head size is not clear.

The relationship between water velocity and life history of fishes has received little attention. It is unknown how the mortality schedule is influenced by water velocity. There is some evidence that swimming performance is lower at young ages (Humphries et al. 1999), which may decrease the chances of surviving after floods. Therefore even exploratory information about life history variation in response to current is needed.

Body shape and life history are interrelated. Data from 23 lizard species indicated that morphology was a good predictor of relative clutch mass (Vitt and Congdon 1978). Such morphology was related with foraging ("sit and wait" vs "wide foraging") and with escape responses. More streamlined lizards (the wide
foragers) have relatively smaller clutch masses, what was explained as the effect of a limited abdomen volume to invest in reproductive functions. Further studies have supported such hypothesis (Vitt 1981; Griffith 1994; Forsman and Shine 1995; Pizzatto et al. 2007), but there is some disagreement (Ballinger et al. 2000). Conversely, reproduction may impair performance, likely through a modification of body shape. Theoretical and empirical studies have shown that body shape determines swimming performance (Domenici 2003; Langerhans et al. 2004). To have an extended abdomen may increase drag, and therefore reduce swimming performance (Plaut 2002). Ghalambor et al (2004) found that embryos of livebearing fish (Poecilia reticulata) increase in volume as development progressed. At the same time the locomotor performance of mothers declined. The rate of decline was faster in guppies from high predation localities. The high predation guppies had higher rates of acceleration when they were not gravid or when the young were early in development, but they lost this performance advantage when the young were approaching the end of development. The carrying of embryos or eggs has been proposed to reduce locomotor performance abilities also in lizards (Husak 2006), salamanders (Finkler et al. 2003), and snakes (Shine 2003).

Separate analyses of body shape, and life history in response to water velocity and predation would forfeit the opportunity to understand how all of these factors might interact in shaping the phenotype of fishes. For that reason a multidimensional analysis is desirable. However, it is hard to find a biological
system that offers clear gradients of the environmental variables in question (predation and current). Even in that case, it is preferable that variation through such gradients were due to multiple rather than unique evolutionary invasions to alternative environments, what permits formal comparative analyses. In this dissertation I will show why Poeciliids of the genus Gambusia and guppies (Poecilia reticulata) are such desirable systems.

## The Gambusia system: an opportunity to study the the effect of predation and flow on body shape and life history at the interespecific level

The more than 44 current species that compose the genus Gambusia are naturally distributed from North America to Colombia, and in the Caribbean islands (Rosen and Bailey 1963; Lucinda 2003). Their habitats range from mountain streams to brackish waters. Populations of several species of Gambusia have colonized multiple times, naturally or by deliberate introduction, a diversity of habitats with a large range of predation and water velocity regimes. On the other hand, some species have a characteristic habitat, which can be readily classified as low- or high-predation or water current regimes. The current phylogenetic hypotheses for Gambusia (B. Langerhans, unpub.) show that such invasion of different habitats may have been independent. Therefore Gambusia could be viewed as a natural evolutionary experiment with replicates and performed at intra- and interspecific levels.

Gambusia has a large variation in body shape and life history. Body shapes vary from blunt- to stylized looking species. Even among populations, there are patterns of shape variation clear the naked eye, like the two morphs of G. yucatana reported for low- and high-current habitats (Greenfield et al. 1983). The sparse life history data for species of Gambusia show a two-fold variation in size at maturity, a four-fold variation in embryo size, a ten-fold variation in reproductive allocation, and an astonishing 50-fold variation in fecundity within the genus (Krumholz 1963; Reznick and Miles 1989; Daniels and Felley 1992; Downhower et al. 2000; Abney and Rakocinski 2004; Pyke 2005). This range of variation is outstanding for a genus with only a two-fold range of body size.

In the first chapter of my dissertation I perform an interspecific analysis in females of 22 species of Gambusia, while taking into account the effect of phylogeny, pregnancy, and size. I use several commonly methods to quantify shape and discuss the differences among them. I show that female Gambusia have larger caudal areas in high-predation sites, in agreement to biomechanical theory. In contrast, flow regime is not related to body shape, against theoretical predictions, although an interaction between flow and predation was detected. We also observe that pregnancy reduced the magnitude of phenotypic divergence between females from contrasting predation and flow regimes. Most models showed high levels of phylogenetic signal. These results indicate that adaptation to predation, and to a lesser extent flow, is key to body shape
evolution in the genus Gambusia. Additionally, the importance of phylogenetic history and the role of pregnancy in explaining shape are discussed.

In the second chapter I analyze the effect of predation, flow, and latitude in life history of Gambusia. Surprisingly, despite there is a large range of life history variation in Gambusia, and predation and flow explain some of the body shape variation, life history was not related with predation or flow. We explored the correlation of life history with latitude, another factor associated with reproduction, and life history still remained unexplained.

## Guppies as an ideal system to study the the effect flow regime on body shape and life history at the intraspecific level

In the third chapter of the dissertation I focus on flow, analyzing flow regime as a disturbance. Disturbances are ubiquitous phenomena (e.g. fires, floods, earthquakes) well recognized in ecological literature as agents that can disrupt ecosystem, community, or population structure. Even though disturbances can be seen as selective factors characterized by intensity, frequency, timing, and predictability (Lytle and Poff 2004), the adaptive evolution of organisms in response to disturbances has rarely been addressed (Lytle 2001). Flash floods in mountain streams are ideal phenomena to understand the evolutionary implications of disturbances. Flash floods are short-lived but severe (Swanson et al. 1998), causing high mortalities to aquatic fauna. Moreover, it is possible to
quantify and analyze the hydrological regime of mountain rivers using tools developed by engineers and geologists (Gordon et al. 2004). By contrasting the hydrology of mountain rivers against the natural history of their biota one can observe the evolutionary implications of these disturbances.

I study the evolutionary consequences of flash floods on body shape and life history of Trinidadian guppies. Biomechanical theory predicts that fishes may reduce costly swimming in turbulent flows, like those created by floods (Liao 2007), by optimizing unsteady (non-constant velocity) swimming useful for acceleration. Since guppies use their tails for propulsion during unsteady swimming, it is expected that guppies from flood-prone sites will have larger caudal areas. Life history theory predicts that a differential mortality among age classes would cause a change in optimal reproductive effort. Empirical studies have confirmed such predictions regarding predation. It is known that flash floods cause higher mortality in smaller fish (Chapman and Kramer 1991). Therefore guppies living under contrasting flow regimes should vary in life history traits, such as reproductive allocation. That was exactly what we found, although the variation was in the opposite direction, perhaps because of density dependence. We conducted a comparative survey across natural populations with contrasting flow regimes in order to determine if the hydrological variation was related with the phenotypic variation of interest.

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## Chapter 1

## Body shape macroevolution in female Gambusia (Poeciliidae): a phylogenetic approach with a comparison of morphometric methods

Abstract: Whether micro-and macroevolutionary processes form a continuum has been contentious. Here we analyze the macroevolutionary pattern of shape variation using a theory that has been largely tested at the microevolutionary level. Biomechanical theory of fish swimming predicts that locomotor cost is reduced with streamlined bodies. However, organisms can deviate from optimal streamlining with respect to reducing costs by having larger caudal regions, a morphology that generates more thrust and should allow for increased burstswimming performance. Predation and flow are crucial environmental factors for fish, and theory predicts that fish in high-predation sites will have larger caudal areas, and fish in high-flow sites will have more streamlined bodies. Most tests of these predictions have been at the intraspecific level, either with oviparous species or with males of viviparous species (to avoid the complications of pregnancy). Here we perform an interspecific analysis in females of 20 species of Gambusia, while taking into account the effect of pregnancy. Several commonly used methods to quantify shape were compared. The effect of pregnancy was analyzed using life history traits gathered through dissections. Phylogenetic relatedness was accounted for by testing our adaptive models using phylogenetically informed statistical methods. As predicted by biomechanical
theory and in agreement with microevolutionary studies, female Gambusia showed relatively larger caudal regions in high-predation sites. In contrast to predictions from theory and previous observations, flow had a relatively small influence on shape, only significant for some shape variables and under some models of character evolution. Pregnancy reduced the magnitude of phenotypic divergence between females from contrasting predation and flow regimes. Size and shape, in general, showed strong effect of phylogenetic signal. These results indicate that adaptation to predation, and to a lesser extent flow, is key to body shape evolution in the genus Gambusia. Additionally, the importance of phylogenetic history and the role of pregnancy in explaining shape are discussed.

## Introduction

The conceptual bridge between micro- and macroevolution has been a contentious topic in evolutionary biology (Arnold et al. 2001). Microevolution refers to evolutionary processes that occur within populations and among conspecific populations, whereas macroevolution refers to larger-scale events among higher taxa (Travis and Reznick 2009). It has been suggested that adaptation at the microevolutionary level can explain macroevolutionary patterns of variation (Darwin 1872: 49; Watson et al. 1936: 58; Charlesworth et al. 1982; Arnold et al. 2001). Under this view, macroevolution is an extension of microevolution (Charlesworth et al. 1982). The support of this view is that a given selective factor would tend to drive phenotypes of different species to similar directions in morphospace (Charlesworth et al. 1982). However, it has been highlighted that alternative evolutionary processes (e.g. random genetic drift, hybridization) can switch the direction of divergence, adding random noise to macroevolutionary patterns (Stanley 1979: 189). This supports the alternative view that microevolutionary divergence cannot be extrapolated to explain all macroevolutionary patterns and processes (Goldschmidt 1940; Van Valen 1974; Eldredge and Cracraft 1980). One strategy to determine the connection between micro- and macroevolution is to use models obtained at the microevolutionary level to predict macroevolutionary patterns (Arnold et al. 2001; Losos and Ricklefs 2009). Here we use that strategy, predicting fish shape at a
macroevolutionary level by using adaptive models largely tested at the microevolutionary level.

According to biomechanical theory, streamlined shapes (forms similar to foils that present little resistance to flow of fluid) minimize drag and thus reduce costs during steady swimming (cruising at constant velocity; McHenry and Lauder 2006). At the other end of the spectrum, bodies with deeper caudal regions generate more thrust by displacing more water during unsteady swimming (motion with linear or angular acceleration; Lighthill 1971; Webb 1982; Walker 1997). (The caudal area is the region where most of thurst is generated in the majority of fishes [Lauder and Tytell, 2006]). A negative correlation between sprint and endurance performance has been observed in fish (Langerhans 2006, 2009b; Oufiero et al. 2011b). Correspondingly, fishes seems to show an inherent morphological trade-off. Fish with larger caudal regions generate more thrust but show reduced streamlining, while fish with tapering caudal areas may increase streamlining but produce less thrust (Langerhans and Reznick 2010). Evidence gathered mostly among populations within species indicates that fish shape aligns along this trade-off in relation to variation among populations in predation and flow, two crucial factors in freshwaters. Fish in high-predation habitats have deeper caudal areas than fish from low-predation sites (Walker 1997; Langerhans and DeWitt 2004; Andersson et al. 2006; Hendry et al. 2006). This is because fish use bursts of unsteady swimming (i.e., rapid production of thrust mostly by the caudal area) to escape from predator strikes (Domenici 2003). Fish
in high-flow sites have more streamlined bodies that those living in low-flow habitats (Langerhans 2008; Langerhans and Reznick 2010), as a way to minimize drag, thereby decreasing the energetic cost of swimming in flow (Aleev 1977). Here we study the effect of both predation and flow on shape at the macroevolutionary level using a comparative approach. We predict that fish from high-predation sites have larger caudal areas, whereas fish from low-predation or high-flow sites have more streamlined bodies. Furthermore, we implement the two most common methods to measure streamlining (Streamlining and Fineness indexes, see Methods) to determine whether or not our results are sensitive to the methods used.

Gambusia is an excellent system to test our ecomorphological hypotheses. The genus currently contains 44 species of small, viviparous, and typically omnivorous fishes, naturally distributed from North America to Northern Colombia, and in the Caribbean west of Puerto Rico (Rosen and Bailey 1963; Lucinda 2003). Gambusia have repeatedly colonized a diversity of habitats with distinct predation and flow regimes (Langerhans et al. 2007). Therefore, Gambusia can be used as a natural, replicated evolutionary experiment to test the effect of predation and flow at the micro- and macroevolutionary levels. For example, at the interspecific level, Langerhans and Reznick (2010) studied the effect of flow on shape in 12 species of Gambusia, observing that males from high-flow sites are more slender and have a lower drag coefficient, characteristics that make them more apt for steady swimming. Here we take a
complimentary approach and study the functional morphology of female Gambusia in different flow and predation regimes.

The association between environmental factors and body shape may be more pronounced in females than in males because females bear the extra burden of carrying offspring, and this has been shown to reduce locomotor performance in fishes (James and Johnston 1998; Plaut 2002; Ghalambor et al. 2004), salamanders (Finkler et al. 2003), lizards (Garland 1985; Husak 2006), snakes (Shine 2003; Webb and Lannoo 2004), and mammals (Gittleman and Thompson 1988). This reduction in locomotor performance could be caused by interacting physiological and biomechanical mechanisms. Physiologically, pregnancy can increase the demand for nutrients and oxygen (Plaut 2002), or interfere with physiological functions such as digestion (Weeks 1996). Mechanically, pregnancy can decrease performance during unsteady swimming (an increase of mass reduces the ability to accelerate during burst-starts; Webb 1982) or during steady swimming (an alteration of body shape can increase drag; McHenry and Lauder 2006). It has been suggested that pregnancy can also increase frictional drag by increasing surface area (Ghalambor et al. 2003). We test this idea including surface area as one of the dependent variables analyzed. Previous studies on the functional basis of fish shape have not accounted for the effect of pregnancy of females, or have avoided the issue by analyzing only males. Here we analyze pregnancy by using the difference in shape between females early and late in pregnancy as dependent variables in the analyses.

Accounting for pregnancy is particularly important in this study because the genus Gambusia shows remarkable life history variation (e.g. brood size ranges from one to hundreds of embryos per female; Pires et al. 2011). Therefore we predict that pregnancy has an effect on body shape variation associated with swimming performance, by increasing abdominal area and reducing streamlining.

## Methods

## Source of specimens

Specimens were obtained from museum and personal collections (Table 1, Appendix 1.1). Institutional abbreviation in collection name follows Sabaj-Perez (2010). Among Gambusia museum collections we focused on those with a large number of individuals, where habitat could be characterized using field notes (see below), from localities with the least anthropogenic alteration, and obtained during summer (to avoid seasonal effects). A subsample of females was chosen from each collection with the criteria of including the full range of body size and avoiding females with bent or twisted bodies. A total of 46 collections and 20 species were analyzed (Table 1.1). From the total 967 individuals used to calculate minimum size at maturity (see below), 875 fish were retained in further shape analyses after excluding juveniles and bent specimens. The number of collections was reduced to 26 after merging the data of some collections (all from
the respective same species ) with similar environmental characteristics. This was done to increase the respective sample size (Table 1.1).

## Habitat characterization

We determined predation and flow regimes of each locality (Figure 1.1) by analyzing original field notes, following Reznick et al. (1994). Field notes of each collection were obtained from the online databases of AMNH, NEODAT II, NMNH, and UMMZ. Localities were plotted in Google Earth to obtain geographic coordinates. Flow regime was categorized as low (LF, lakes and ponds) or high (HF, streams). Predation regime of each locality was estimated in three steps. First, the fish community of each site was characterized from field notes (i.e. the list of all other fish collected in that site, Appendix 1.2). Second, the diet of each member of the fish community was obtained from a literature review (Appendix 1.3). Third, localities were classified into two predation regimes, depending on the diet of the highest trophic level of any fish reported for that site. Sites were classified as either low- (LP) or high-predation (HP), depending on the presence of piscivorous fish (Appendix 1.3).

## Photographs and Dissections

Prior to dissections, lateral and ventral photographs of specimens were taken following the indications in Zelditch et al. (2004). During dissections we measured standard length of females (SL) using calipers (to the nearest 0.1
mm ), fecundity (number of embryos), and stage of development of embryos (see below). Additionally, ovarian tissue dry weight (to the nearest 0.01 mg ), and mean embryo weight for each female (dry weight of batch of embryos/fecundity, to the nearest 0.01 mg ) were measured for a parallel study on the life history of the genus (Torres-Mejia, unpub.). Stage of development of embryos was quantified using the scale of Haynes (1995), as modified by Pires et al. (2007); these stages range from egg (stage 0) to fully-formed embryo ready for birth (stage 50 ). Minimum size at maturity was estimated for each collection as the SL of the smallest female with stage of development of embryos $\geq 2$.

## Geometric Morphometrics

Shape variation was analyzed with two-dimensional, landmark-based geometric morphometrics (GMM; Zeldtich et al. 2004). GMM is a quantitative method to analyze shape variation using coordinates of points located in distinct positions along the body. Coordinates of multiple specimens are superimposed to extract shape variation independent of location, scale, and rotation of the specimens in the images. TpsDig2 2.12 (Rohlf 2008) was used on lateral pictures to digitize 10 landmarks and 3 semilandmarks (Figure 1.2 B). Semilandmarks (landmarks that define non-homologous positions along the outline) were slid to minimize the bending energy criterion, using methods outlined in Zelditch et al (2004), and Rcode adapted from Morpho (Stefan Schlager, unpub). Procrustes superimposition was performed using R-code adapted from Claude (2008).

The effect of intraspecific variation in female size and pregnancy condition (within each sample) was accounted for by estimating shape configuration at two stages: early in pregnancy (when embryos were at developmental stage 0 ) and late in pregnancy (embryos at stage 50). In both cases, body size was equal to the average centroid size (the square root of the sum of distances between each landmark and their centroid; Zeldtich et al. 2004). These two extreme morphologies were estimated with a multiple regression model (Monteiro 1999; Berner 2011) for each collection, having projected landmark positions as dependent variables, and centroid size and stage of development of embryos as the predictors. The resulting size- and pregnancy-standardized geometric morphometric configurations were used for further analyses. The effect of pregnancy condition on shape and the interaction of that effect with size, predation, and flow was quantified by substracting superimposed configurations early in pregnancy from those late in pregnancy. The resulting differential configurations were used in further analyses. These differences were visualized by adding them onto the average female configuration.

Each of the three geometric morphometric configuration sets (early in pregnancy, late in pregnancy, and their difference) was analyzed with a Principal Components Analyses (PCA) to reduce dimensionality. Principal Components (PC) that accumulated more than $99 \%$ percent of variation were retained in further analyses. Differences in shape were visualized using vectors with length,
thickness and darkness that indicate the magnitude of variation between superimposed shapes with R-code derived from Claude (2008).

## Streamlining and Areas

We measured streamlining using the streamlining Index (SI, McHenry and Lauder 2006), and the fineness index (FI; Langerhans and Reznick 2010). SI indicates the similarity in the distribution of mass of a fish in comparison with the optimal distribution of mass of a streamlined foil of the same maximal length, width, and depth (McHenry and Lauder 2006). A SI value of one indicates an optimal distribution of body mass along the longitudinal axis of the fish.

Deviations from optimal mass distribution may come from having more mass towards the head $(\mathrm{SI}<1)$ or more mass towards the tail $(\mathrm{SI}>1)$. FI quantifies the body elongation of a fish, ranging from the asymptotic value of 0 (a infinitely elongated body) to one (an optimally elongated body, its length 4.5 times its depth). A custom code was implemented to calculate SI and FI using Matlab 7.5 with Image Processing Toolbox 6.0 (MathWorks, Natick, MA). The 3D surface area of each fish (SA) was calculated digitally in the same Matlab code. The relative size of the caudal peduncle was calculated as the 2D caudal peduncle area (CP, Figure 1.2B) over 2D lateral body area. These areas were measured by taking advantage of the landmarks digitized for GMM analysis. Each area was estimated as the sum of the areas of triangles whose vertices were the
respective enclosing landmarks. See further details about estimation of streamlining variables in Appendix 1.4.

The effect of intraspecific variation in female size and pregnancy condition was accounted for using multiple regression models, as was done in the GMM analysis. In this case SI, FI, SA, and CP were the dependent variables, and female size was quantified as log-transformed SL. The resulting size- and pregnancy-standardized variables were used for further analyses. The effect of pregnancy on these morphological variables was tested by using the difference between the values early and late in pregnancy, as was done in the GMM analysis. Therefore, in the adaptive models explained below, we analyzed three values for each morphological variable: early in pregnancy, late in pregnancy, and their difference.

## Statistical analysis: testing the independence of predation and flow

The independence of predation and flow was evaluated prior to shape analyses, using phylogenetic independent contrasts (PIC; Felsenstein 1985; Garland et al. 1992). Accounting for phylogenetic relatedness when analyzing correlation of environmental regimes is justified because closely related species tend to live in similar ecological environments (Losos 2008), an argument made before (Garland et al. 1992; Oufiero et al. 2011a).

## Statistical analysis: adaptive models

We first analyzed size as a dependent variable of predation and flow, using the models:

$$
\begin{gathered}
\text { size }=\text { predation }+\varepsilon \\
\text { size }=\text { flow }+\varepsilon \\
\text { size }=\text { predation }+ \text { flow }+\varepsilon \\
\text { size }=\text { predation }+ \text { flow }+ \text { predation }{ }^{\star} \text { flow }+\varepsilon
\end{gathered}
$$

where predation and flow are the predictor variables, $\varepsilon$ is the error term, and size was measured in two ways, as the mean centroid size and as log-SL. Similarly, for each morphological variable we tested five adaptive hypotheses:

$$
\begin{gathered}
\text { morphology }=\text { size }+\varepsilon \\
\text { morphology }=\text { size }+ \text { predation }+\varepsilon \\
\text { morphology }=\text { size }+ \text { flow }+\varepsilon \\
\text { morphology }=\text { size }+ \text { predation }+ \text { flow }+\varepsilon \\
\text { morphology }=\text { size }+ \text { predation }+ \text { flow }+ \text { predation*flow }+\varepsilon
\end{gathered}
$$

where morphology represents each morphological variable (SI, FI, SA, CP, and each of the three PC scores), size was a covariate (centroid size when the dependent variables were GMM variables, and log-SL in other cases), predation and flow are the predictor variables, and $\varepsilon$ is the error term.

Adaptive models were evaluated using a phylogenetic framework to account for the potentially hierarchical structure of the data. We fulfilled this with two different methods, depending on whether the dependent variables were

GMM variables or not. In the first case, we used phylogenetic MANCOVAs (Garland et al. 1993; Revell et al. 2007) because they can handle multiple dependent variables (in this case PC scores), while accounting for covariates (body size), when factors are tested (in this case predation and flow). Two models of character evolution were tested, Ordinary Least Squares (OLS, equivalent to a standard, non-phylogenetic MANOVA that assumes all samples are equally related in a star-phylogeny; Garland et al. 2005), and Brownian Motion (BM, random divergence). For the BM model, the probability of the F statistics obtained from OLS was calculated using empirical null distributions. These distributions were calculated from Monte Carlo simulations of tip data (1,000 simulations), using the original topology as the phylogenetic structure, and observed root values as starting values. P-values were the proportion of times that the observed F-statistic was larger than the simulated F-values.

Shape variation explained by MANCOVA predictors was visualized using a canonical analysis as explained in Langerhans (2009b). This method of visualization of group differences avoids the distortion of shape space that would occur if canonical values from MANCOVA were directly analyzed (Langerhans 2009b; Mitteroecker and Bookstein 2011). First, we extracted the Sum of Squares and Cross-Products matrix (SSCP) for each predictor (size, predation, flow, and predation*flow) from MANCOVA. Second, an eigenanalysis of the SSPC produces $n-1$ eigenvectors, where $n$ is the number of levels of the respective factor. Third, eigenvector values were multiplied by the matrix of PC
scores to produce a divergence vector, which is a linear combination of the PC scores that has the highest correlation with the respective factor in Euclidean space. Fourth, shapes associated with the mean divergence vector values for each factor level were calculated by regressing divergence vector values against PC scores. The phylogenetic signal (K; Blomberg et al. 2003) of each canonical vector, and the probability that each K was larger than the null hypothesis of no signal $(\mathrm{K}=0)$ were calculated using phylosignal in the R package picante (Kembel et al. 2010). This probability is calculated as the frequency that the observed phylogenetically correct mean (MSE) was larger than $n$ randomized MSE. In this study $n=9,999$.

When dependent variables were non-GMM variables, we accounted for phylogeny using phylogenetic Generalized Least Squares (GLS; Grafen 1989). This method is a linear model that structures the error term as a multiple of the variance-covariance matrix of phylogenetic relatedness (Martins and Hansen 1997; Garland and Ives 2000; Rezende and Diniz-Filho 2012). Before running GLS, we plotted PIC of each trait to detect the presence of potentially influential points, which were never observed. Three models of character evolution (i.e. structure of the error) were evaluated for each GLS adaptive model. The first model of character evolution was OLS (non-phylogenetic, assuming phylogenetic signal in the residuals is null). The second model (RegPagel) is a regression model that assumes Brownian motion (Pagel 1999; Garland et al. 2005), and simultaneously estimates the parameter coefficients and $\lambda$, a measurement of
phylogenetic signal (i. e. the effect of shared evolutionary history in phenotypic variation; Blomberg et al. 2003). Algebraically, $\lambda$ is a factor that multiplies the offdiagonal elements of the variance-covariance matrix of relatedness (Freckleton et al. 2002). The value $\lambda$ ranges from zero, indicating phylogenetic independence equivalent to a star phylogeny, to one, indicating covariation of traits fully proportional to shared phylogenetic history. The third model was the OrnsteinUhlenbeck process (RegOU), which assumes Brownian motion that tends to drift towards an optimum determined by selection (Hansen 1997; Butler and King 2004). As in RegPagel, RegOU also allows the simultaneous estimation of regression coefficients and a measure of phylogenetic signal, in this case the parameter $d$ (Lavin et al. 2008). The value of $d$ also indicates the optimal stretching of the branch lengths. When $d$ is less than one the tree is less hierarchical and more like a star-phylogeny (i.e. nodes pulled towards the root). When $d$ is larger than one the tree is more hierarchical than the original (i.e. nodes pulled towards the tips).

To select among the multiple models for each dependent variable we used model selection with model averaging (Burnham and Anderson 2002). First, small sample corrected Akaike information criterion (AICc; Anderson and Burnham 2002; Hansen et al. 2008) was calculated for each set of models for each GLS. AIC $C_{c}$ differences $\left(\Delta_{i}\right)$, the difference in AICc values between each model and the best supported one (the one with the lowest AICc), were used to estimate the Akaike weights $(w)$ :

$$
w_{i}=\frac{\exp \left(-0.5 \Delta_{i}\right)}{\sum_{j=1}^{J} \exp \left(-0.5 \Delta_{j}\right)}
$$

where $J$ is the total number of models. Akaike weights are Bayesian posterior probabilities (i.e. model probabilities) that indicate the amount of evidence explained by each model (Anderson 2008), ranging from zero (model not explaining variation) to one (model fully explaining variation). Evidence Ratios, the number of times the best model is were estimated Evidence Ratio (ER) equals the $w$ the most-supported model of the set over each model's w. It indicates the number of times the best model has more evidence than each model (Anderson 2008). Average coefficients and their standard errors were calculated as the values obtained from each model, weighted with their respective $w_{i}$. Model averaging was performed with unconditional estimation (using all models instead of only those including each parameter; Anderson 2008), which is a better alternative when the objective is to determine the strength of the response variable predictors (Grueber et al. 2011). There is some debate about the use of unconditional estimation as opposed to conditional estimation (considering only the models that included a parameter to calculate its average coefficient; Grueber et al. 2011). We performed estimation with both methods and found few substantial differences; therefore we show here only unconditional estimations. We did not attempt to include more models in our
model sets because of our small sample size. A rule of thumb in model selection procedures is that the number of models should not exceed the sample size (Anderson 2008). In this study, the sample size was 26, and for each dependent variable we tested 25 models.

## Statistical analysis: phylogeny of Gambusia

The Gambusia phylogeny used in these analysis (B. Langerhans, unpub.) is available in Appendix 1.5. The phylogeny was constructed using majority (50\%) consensus, and is based upon two mitochondrial (ND2, Cyt b) and one nuclear (S7) gene. Branches were transformed using two methods. In the first method the phylogeny had branch lengths proportional to the units of inferred nucleotide substitution (Appendix 1.6). When we had data for multiple populations per species, we added new branches with length 0.00461 , which was chosen because this was the average distance between pairs of conspecific Gambusia populations (B. Langerhans, unpub.). Modeling error covariance with a tree that has branch lengths proportional to nucleotide substitution assumes that the variance of evolutionary change is proportional to the amount of divergence in the genes used to reconstruct the phylogeny (Oufiero et al. 2011a). This method contrasts with the common recommendation of using a tree where tips are contemporaneous for extant species or populations (i.e. ultrametric), which assumes that the expected variance of evolutionary change is proportional to time. We repeated all analyses using the ultrametric tree obtained by stretching
the branches with a penalized likelihood algorithm, using function chronopl (with lambda set to one) in the R package ape (Paradis et al. 2004). The results were qualitatively the same as the results with the original branch lengths; therefore, here we only show the latter results.

In the second phylogenetic transformation, branch lengths were set to a constant value of one (Appendix 1.7). This reduces magnification of phenotypic differences between populations of the same species. Magnification occur because phylogenetic distance is used to weight phenotypic differences; such magnification could be exaggerated when comparing closely related taxa, the case of populations of the same species. However, this branch length transformation implicitly assumes that phenotypic divergence occurs at speciation events and/or as populations split from each other.

Soft-polytomies (multifurcations resulting from lack of resolution at a given node) in the available phylogeny were resolved prior to analysis by making the tree dichotomous using the function multi2di in the package ape (Paradis et al. 2004). These newly resolved branches were manually set to zero length. Type I error produced by soft polytomies was corrected by reducing the degrees of freedom of the denominator when calculating the significance of F-values for each coefficient of phylogenetic regression models. The reduced degrees of freedom were equal to $N-k-1-z$, where $N$ are the number of tips in the phylogeny, $k$ the number of parameters estimated for the respective model, and $z$ are the
number of branches that were set to zero length (Garland and Díaz-Uriarte 1999), in this study $z=5$.

Except for GLS regressions, which were performed using the Matlab program RegressionV2.m (A. R. Ives and T. Garland Jr.; Lavin et al. 2008), all analyses were executed using code written in $R$ ( $R$ Development Core Team 2011).

## Results

Predation and flow showed low but significant phylogenetic signal (predation: K= $0.179, p=0.036$; flow: $K=0.195, p=0.008)$. PIC of predation and flow were negatively correlated ( $\mathrm{r}=-0.75, \mathrm{p}<0.001$ ).

## GMM variables

PCs from GMM indicated a considerable range of body-shape variation among Gambusia females (Appendix 1.8-1.10). As expected, the main effect of pregnancy on shape was a distension of the abdominal area (Appendix 1.8). Size partially explained shape of females early in pregnancy; females of larger species have deeper bodies posterior to the opercle and shorter caudal peduncles (Figure 1.3, first row). This effect dissapears late in pregnancy because there is a tendency for smaller females to have a more extended abdomen when pregnant (Table 1.3). The pregnancy-size interaction effect was
correlated with SI , suggesting that larger species have relatively less abdominal mass late in pregnancy.

The effect of predation on shape was correlated with streamlining: highpredation species showed a displacement of lateral area from the dorsal profile towards the caudal area (Table 1.3; Figure 1.3, second row). This effect was correlated with SI , corroborating that there is a displacement of mass towards the caudal area. The effect of predation was statistically significant under the three phylogenetic scenarios. There was a tendency for an interaction between predation and pregnancy: high-predation species tend to have more distended abdomens late in pregnancy.

Flow regime explained very little of the variation in shape, with only a tendency for high-flow species to be more elongated (Table 1.3; Figure 1.3, third row). This tendency was significant only in females early in pregnancy when accounting for phylogeny (under the BM model with original branch legnths, $\mathrm{p}=0.016$ ). There was an interaction between flow and pregnancy, with high-flow species having slightly more distended abdomens. This interaction was significant only when accounting for phylogeny (under BM with original branch lenghts, $\mathrm{p}=0.018$ ). There was also an interaction between predation and flow, with LP species being more elongated in LF sites, and vice versa in HF sites (Table 1.3; Figure 1.3, fourth row). This interaction was not influenced by pregnancy, but it was significant only when accounting for phylogeny (under BM model with original branch lenghts).

## Non-GMM variables

None of the GLS models for each dependent variable had a distinctly high AICc value (Appendix 1.5), or accounted for a high proportion of evidence (Table 1.3, $w$ values). However, average models are qualitatively similar models to the bestsupported model for each dependent variable (Table 1.3). The best-supported phylogenetic models were most often the ones with branch lengths proportional to molecular distance, rather than constant branch lengths (Table 1.3).

Variation in body size showed high levels of phylogenetic signal and was not related with predation or flow, neither when size was measured as log SL or as CS (Table 1.3). SI early in pregnancy was independent of body size, but related to predation (Tables 1.3 and Appendix 1.11). This effect of predation dissapeared late in pregnancy because HP species showed a greater reduction in streamling with pregnancy, indicating that they had a larger abdominal distension when pregnant (Figure 1.4). LP species had SI values lower than the optimal, whereas the range of SI values in HP species included optimal values during intermediate stages of pregnancy (Figure 1.4). Most SI models showed high levels of phylogenetic signal, including the interaction between pregnancy and predation effect (Table 1.3 and Appendix 1.11).

FI showed a tendency to be negatively related with body size, implying that larger females diverge from the optimal fineness by having deeper bodies. There was a clear interaction between size and pregnancy, with larger species being more optimally elongated when pregnant as compared with smaller
species. FI was not related to predation, flow, or their interaction. In general, models that have FI as the dependent variable showed relatively low levels of phylogenetic signal (Table 1.3 and Appendix 1.11).

Both SA and CP were strongly related to body size but not to predation or flow (Table 3). Not surprisingly, SA was related to pregnancy (reflecting the abdominal distension late in pregnancy), and CP was not (caudal peduncle area does not change with pregnancy). Regressions with SA and CP showed moderate levels of phylogenetic signal in the residuals (Table 3 and Appendix 1.11).

## Discussion

This study is one of only a handful that have tested the ecomorphological predictions of biomechanical theory in female fishes while accounting for pregnancy, and the first to do so at the interspecific level using phylogenetically informed statistical methods. Furthermore, this study is unique in simultaneously analyzing the effects of predation and flow, two main selective factors in freshwaters. We found that predation, and to a lesser extent flow, were related to body shape of Gambusia females in a manner predicted by biomechanical theory. Some of the shape variation was explained by an interaction between predation and flow. Pregnancy interacted with predation, reducing the divergence among predation regimes when females are late pregnancy.

Our results at the macroevolutionary level largely match the previous observations at the microevolutionary level, suggestings a continuum from microto macroevolution. However the proportion of shape variation explained by our adaptive hypothesis was relatively small compared to the large range of morphological variation observed. This may be indicative that divergence is not necessarly larger at the macroevolutionary level, as suggested before (Bell 1995). This phenotypic stabilization could represent a peak in the adaptive landscape, reached by either micro- or macroevolutionary divergence.

This study's conclusions have two main limitations. First, we analyzed field-caugh specimens, which may be showing variation that is correlated with unmeasured environmental factors. This could be seen as a positive quality, that despide the possible noise coming from unmeasured factors we still found a significant effect of predation, and in less extend flow. But it also brings the question of whether these differences would remain if the fish had been maintained in a common garden (i.e., whether the phenotypic differences have a plastic or a genetic basis; Garland and Adolph 1991). Previous studies on Gambusia lead us to consider that the body shape differences observed have a considerable genetic basis. In G. affinis (Langerhans et al. 2004) and G. hubbsi (Langerhans 2009a), differences in shape among wild populations of each species were still observed in common garden experiments. However, a common garden study would clarify this question for body shape of female Gambusia.

A second limitation of this study is that we are assuming that the body shape observed is a good proxy of locomotor ability. Moreover, we assumed that the locomotor traits presumably correlated to shape are related with performance. Measuring performance is important because it the direct subject for the action of selection (Arnold 1983). However, there is evidence that our observations on body shape is the kind that have repercusions on performance and fitness. Previous studies in fish evidence the correlation between caudal region area and thrust ( Langerhans et al. 2004; Langerhans 2009a), and between optimal streamlining and higher endurance (Langerhans and Reznick 2010), and lower inertial drag coefficients (McHenry and Lauder 2006). Moreover, acceleration ability causes high survivorship during predatory strikes in G. hubbi (Langerhans 2009a). Anyhow, a study of shape, performance (e.g., Langerhans 2009a), and fitness in female Gambusia would shed light on this issue.

## Body size effect on shape

Females of Gambusia species show a relatively narrow range of body sizes (mean collection body size: 22.48-43.17 mm SL; Chapter 2). Nevertheless, body size was a good predictor of most body shape variables. The main allometric effect on shape was that larger species had deeper bodies posterior to the opercle, and shorter caudal peduncles. This effect was not correlated with SI, indicating that body size in Gambusia varies without affecting streamlining (a
proxy of minimization of drag). Furthermore, larger bodies showed less shape change with pregnancy, possibly because larger females have more abdominal space available for a given gonadal mass. If the change in shape produced by pregnancy increases drag when swimming, then having larger bodies may minimize this particular aspect of the cost of pregnancy in this genus.

## Correlation of predation and shape

Here we provide interspecific evidence that fish shape responds evolutionarily to predation as predicted by biomechanical theory - that is, fish exposed to HP environments have relatively larger caudal regions than their LP counterparts. However, Gambusia females attained this morphology in an unexpected manner. Whereas most fish living in HP sites have smaller heads and larger caudal peduncles (Walker 1997; Langerhans and DeWitt 2004; Langerhans et al. 2004; Hendry et al. 2006), HP Gambusia did not have larger caudal peduncles and instead showed a displacement of dorsal mass toward the postero-ventral direction. The direct measurement of caudal peduncle area from lateral pictures did not match the SI results, indicating that estimating relative caudal peduncle area is not necessarily a good proxy for estimating caudal peduncle mass, a variable directly linked to swimming power output (Altringham and Ellerby 1999). Theoretically, fish with deeper caudal peduncles displace more water when undulating, and therefore generate more thrust (Lighthill 1971; Lauder and Tytell 2006). At the same time, a larger mass requires larger power thrust to produce
displacement (Lauder and Tytell 2006). Therefore, a net gain in power thrust could be obtained by an increase in caudal peduncle depth or by a reduction in the anterior mass, the latter being the case of Gambusia females. Future studies will be required to determine if these populations and species actually differ in swimming performance, as would be expected from the differences in body shape.

Unexpectedly, LP females were not more streamlined. Early in pregnancy, both LP and HP females deviated from the optimal SI values, the former because of their bulkier abdomens, the latter because of their relatively large caudal region. Pregnancy displaced LP females even more from optimality, whereas HP females passed through optimal streamlining at intermediate stages of pregnancy. This may indicate that shape of LP species could be responding to other selective pressures that require larger abdomens. Perhaps LP species may have larger digestive systems because of a more herbivorous diet as occurs in guppies (Zandonà et al. 2011). In pregnant HP females, it is unclear whether their more streamlined bodies are an incidental by-product of pregnancy or an adaptation to minimize locomotion costs in their demanding environments. It would be worthwhile testing whether the enhanced streamlining of pregnant HP females allows for better steady-swimming performance since the only study that has compared the effect of pregnancy on fish swimming performance focused on unsteady swimming (Ghalambor et al. 2004).

## Weak correlation between flow and body shape

A recent review on the association between flow regime and body shape (Langerhans 2008) found that in about 75\% of studies fish from HF habitats are more streamlined. That result was consistent across phylogeny and at both intraand interspecific levels. We found the same trend in our GMM analysis of Gambusia females, but the effect was rather weak (HF females were more elongated, but the effect was not significant). We can rule out our lack of a highly significant result being due to a lack of phenotypic variation in body depth because such variation was observed (Appendix 1.8-1.10). Instead, this difference in magnitude could be an outcome of two factors. Firstly, predation and flow were negatively correlated, and correlation of predictor variables in a linear model reduces their estimated effect size (Tabachnick and Fidell 2001). It is possible that the effect of predation and flow were partially overlapping, given that the biomechanical predictions were opposite for the two regimes (i.e. HF and LP females were expected to be more streamlined, and HF fequently had LP regimes). However, our GLS results indicate that this correlation did not obscure the effect of flow because model selection showed that the models where size and flow were the only predictors had considerably less support (Appendix 1.11).

Secondly, the classification of flow regimes was a rather rough description of flow. Most studies, including this one, contrast lotic (streams) vs. lentic (lacustrine) habitats. The problem with this straightforward contrast is that rivers and lakes also differ, in addition to water velocity, in many other aspects, such as
benthic biota and structure, physical and chemical parameters, and productivity (Wetzel and Likens 2000). Moreover, neither lentic nor lotic habitats are homogeneous. Lentic habitats may have complex benthic areas where the key factor is maneuverability (Domenici 2003), which is higher in fish with deeper bodies (Webb 1984). Lotic habitats vary spatially in flow regime, from mountain streams structured as series of step-pool and pool-riffle patterns (Wohl and Merritt 2008) to lowland rivers with sinuous streambeds and lateral flooplain expansions (Church 2002). Lotic habitats also vary temporally, from streams whose flow rarely changes to the more typical streams that periodically flood (Sabo and Post 2008). These changes in flow can be characterized by their frequency, magnitude, seasonality, and timing, among other factors (Poff et al. 1997; Sabo and Post 2008). It would have been ideal for our study to have characterized flow in this way; however, those methods are very data-demanding (e.g., the recommended length of daily flow time series is 20 years; Sabo and Post 2008), and such flow data were not available.

We show that female Gambusia have a different evolutionary shape response to flow-regime than male Gambusia (Langerhans and Reznick 2010). Whereas we observed that flow explained a modest amount of shape variation, Langerhans and Reznick (2010) observed that male Gambusia living in HF regimes were clearly more elongated. The differences between these two studies could lie in intersexual differences in divergence patterns or in methodological differences between the studies. Regarding the first option, sexes may (Gilchrist
et al. 2004; Berner et al. 2008; Blob et al. 2008) or may not (Butler et al. 2000; McGuigan et al. 2003; Hendry et al. 2006) respond in parallel to a given type of selection (Garland et al. 2011). A joint analysis using both sexes while accounting for pregnancy could be fruitful. Regarding methodology, there are three main differences between our study and that of Langerhans and Reznick (2010). First, there was only partial overlap in the species sampled. Second, the phylogeny used here was a more updated version of the one used in the previous study, although this effect is expected to be small because comparative methods are relatively robust to minor changes in phylogenetic topologies (Díaz-Uriarte and Garland 1998). And third, predation regime was not included as a factor in the previous study. Analyzing predation and flow simultaneously proved particularly important in this study because these factors were correlated, as was discussed above.

## Importance of pregnancy

We found that pregnancy generally had the effect of increasing abdominal size in Gambusia females. This is not surprising because species of Gambusia produce large batches of embryos that increase in wet mass through development (Chapter 2). More interestingly, pregnancy had the effect of reducing the presumably adaptive differences in shape across the gradient of predation. Early in pregnancy, HP females clearly had relatively larger caudal peduncles. Pregnancy increased the mass in the anterior portion of the body (the abdomen).

However, the increase was estimated to be larger for HP females, reducing the differences in shape between LP and HP. Two previous studies at the intraspecific level found that pregnancy reduces adaptive divergence, the same result we found at the interspefic level. Early in pregnancy, guppies from HP localities have faster burst-starts than LP guppies, a pattern reversed late in pregnancy (Ghalambor et al. 2004). Brachyrhaphis rhabdophora (Poeciliidae) from HP sites have larger caudal peduncles and more elongated bodies than those from LP sites, but only early in pregnancy, as late in pregnancy those differences disappeared (Wesner et al. 2011). Therefore, there seems to be a widespread phenomenon of pregnancy reducing adaptive divergence in body shape in response to predation.

## Phylogenetic effect on evolution of shape in female Gambusia

The two main environmental variables analyzed here, predation and flow, showed phylogenetic signal and were negatively correlated. This indicates niche conservatism in this genus (i.e., related species tend to live in similar habitats). Similarly, a fair amount of size and shape variation was explained by phylogenetic relatedness ( d and $\lambda$ in Table 1.3 and Appendix 1.11), another example of the ubiquity of phylogenetic signal and its high levels in morphological characters (Blomberg et al. 2003). Significant levels of phylogenetic signal were found when analyzing both GMM and functional variables for shapes early and late in maturity. In contrast, the difference between shapes early and late in
pregnancy generally showed low phylogenetic signal, implying that the way female shape changes throughout pregnancy is independent of phylogeny. The exception was the effect of pregnancy on SI , which was better explained by RegPagel models with high phlogenetic signal. Therefore, the manner in which females vary in the distribution of their mass with pregnancy in response to predation has a strong phylogenetic component in Gambusia.

## Sensitivity of results to methods used to measure shape

Here we measured SI, FI, relative caudal peduncle area, and PCs from geometric morphometrics. Most papers on ecomorphology of fish shape typically implement one of these methods. By including all of these measures in the same study we demonstrate that these methods are not interchangeable. Streamlining is commonly measured with FI (or a similar body-to-depth proportion index), perhaps because of its simplicity. FI has some support in biomechanical theory in that the most-streamlined shapes are 4.5 times deep as long (Blake 1983). However, that optimum is not a critical value (i.e., does not have a narrow peak), as fish with a wide range of body proportions (from two to six times deep as long) have very similar drag coefficients (Blake 1983). Moreover, a fish could have an optimal body-to-depth ratio but still have a shape far from streamlined because FI does not take into account the location of the maximal depth. An object as blunt as a mallet could still show the optimal fineness proportion of 4.5. McHenry and Lauder's (2006) SI is a better alternative to meause streamlining because it is
based on the comparison of a body with empirically tested foils. Additionally, the expected correlation between SI and swimming performance has been supported empirically, as optimal SI values were related to higher endurance in Gambusua affinis (Langerhans and Reznick 2010), and with lower inertial drag coefficients in Danio rerio (McHenry and Lauder 2006).

Geometric morphometrics is very good at estimating axes of morphological variation (Zeldtich et al. 2004) but may not necessarily extract variation that is most closely related to biomechanical function. Configuration in shape space is typically used to calculate axes of correlated variation (equivalent to Principal Components). The resulting vectors of variation may or may not be related to streamlining. Most studies on fish ecomorphology typically inspect thinplate splines of PCs looking for shapes similar to the morphology of interest. However, such qualitative inspections are poor estimations of how close the fish matches a shape that optimizes a functional trait. Regarding streamlining in particular, a body may look streamlined in one perspective (e.g. lateral view), but reveal mass distributions that depart from streamlining in other perspectives. In this study, we were able to visualize difference in shape using GMM, and at the same time we found their functional significance by correlating GMM variables with SI (Table 1.2). We suggest that geometric morphometrics can be complementary to direct calculation of streamlining, and that both methods should be performed in conjuction when studying body shape in fishes.

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Table 1.1. Overview of collections analyzed. Predation levels: low (LP) and high (HP). Flow levels: low (LF) and high (HF). Sample size ( n ) for each collection correspond to the total number of individuals analyzed for estimating minimum size at maturity over the number of individuals included in shape analysis after excluding juveniles and curved individuals. Further details about about site and date of collections in Appendix 1.1.

| Species | Collection | Pred. | Flow | n |
| :---: | :---: | :---: | :---: | :---: |
| G. alvarezi | UMMZ 211110 | LP | LF | 30/26 |
| G. atrora | UMMZ 169499, UMMZ 210724 | HP | HF | 43/39 |
| G. atrora | AMNH 40812, AMNH 77929 | HP | HF | 28/26 |
| G. aurata | AMNH 75821, RBL | LP | LF | 28/27 |
| G. baracoana | USNM 204442 | HP | LF | 29/21 |
| G. clarkhubbsi | TCWC 11880-09, TCWC 11882-07, TCWC 11887-08 | LP | HF | 34/33 |
| G. geiseri | TNHC 9132, TNHC 9146 | LP | LF | 58/58 |
| G. hubbsi | UMMZ 202727 | HP | LF | 21/18 |
| G. hurtadoi | UMMZ 196737, UMMZ 211112 | LP | HF | 62/58 |
| G. krumholzi | KU 7341 | HP | LF | 29/24 |
| G. lemaitrei | UIST (uncatalogued material) | HP | LF | 24/24 |
| G. luma | FMNH 87628, FMNH 94163 , UMMZ 197235, UMMZ 197258 | HP | HF | 76/52 |
| G. manni | ANSP 103450, ANSP 103452, RBL | HP | LF | 68/64 |
| G. melapleura | USNM 205559 | LP | HF | 25/23 |
| G. nicaraguensis | UMMZ 199657, UMMZ 199689 | HP | HF | 39/39 |
| G. oligosticta | UMMZ 190129, RBL | HP | LF | 38/36 |
| G. punctata | AMNH 96308 | HP | HF | 20/18 |
| G. punctata | AMNH 96320 | HP | HF | 19/18 |
| G. punctata | USNM 203197, USNM 203198 | HP | HF | 60/54 |
| G. rhizophorae | TCWC 2577-02, TCWC 8671-01, UMMZ 213650, RBL | HP | LF | 36/35 |
| G. sexradiata | UMMZ 210795, UMMZ 196655 | HP | LF | 48/47 |
| G. vittata | AMNH 75838 | HP | HF | 20/14 |
| G. vittata | UMMZ 192503 | HP | HF | 24/23 |
| G. vittata | UMMZ 97513 | HP | HF | 34/31 |
| G. vittata | UMMZ 97517 | HP | HF | 26/25 |
| G. wrayi | USNM 205574, UF 25054 | HP | LF | 48/42 |

Table 1.2. MANCOVAs for the three configuration sets (shapes early in pregnancy, late in pregnancy, and the pregnancy effect). Independent variables were centroid size (CS), predation (P), flow (F), and their interaction $\left(P^{*} F\right)$. F-ratios were estimated from Wilk's $\wedge$. Partial $\eta^{2}$ values indicate effect size. Phylogenetic MANCOVAs used Brownian motion on two phylogenetic trees, one with the original branch lengths proportional to nucleotide differences, and another with constant branch lengths. K indicates phylogenetic signal of the respective divergence vector $(d)$. The correlations of each $d$ with streamlining index (SI) were calculated from non-phylogenetic MANCOVAs. Significant $p$-values ( $p<0.05$ ) in bold.

| Configuration | Indep. variab. | Non-phylogenetic |  |  |  | Original |  | Constant |  | Correlation of $d$ with SI |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | df | F | $p$ | $\begin{gathered} \text { Partial } \\ \mathrm{n}^{2} \end{gathered}$ | p | K | p | K | $\mathrm{R}^{2}$ | Slope $\pm$ SE | p |
| Early in pregnancy | CS | 11,11 | 5.069 | 0.006 | 0.86 | 0.001 | 0.354 | 0.012 | 1.098 | 0.05 | $0.75 \pm 0.67$ | 0.274 |
|  | P | 11,11 | 3.989 | 0.015 | 0.80 | 0.000 | 0.182 | 0.017 | 0.444 | 0.32 | $2.05 \pm 0.61$ | 0.003 |
|  | F | 11,11 | 1.276 | 0.346 | 0.56 | 0.016 | 0.365 | 0.193 | 0.477 | 0.01 | $0.32 \pm 0.57$ | 0.581 |
|  | P*F | 11,11 | 2.128 | 0.113 | 0.68 | 0.003 | 0.275 | 0.069 | 0.363 | 0.04 | $0.64 \pm 0.65$ | 0.334 |
| Late in pregnancy | CS | 11,11 | 1.322 | 0.326 | 0.55 | 0.641 | 0.164 | 0.505 | 0.915 | 0.35 | $2.26 \pm 0.63$ | 0.001 |
|  | P | 11,11 | 3.918 | 0.016 | 0.80 | 0.000 | 0.527 | 0.009 | 0.968 | 0.25 | $1.67 \pm 0.59$ | 0.009 |
|  | F | 11,11 | 0.953 | 0.531 | 0.49 | 0.073 | 0.215 | 0.317 | 0.567 | 0.08 | $0.74 \pm 0.50$ | 0.149 |
|  | P*F | 11,11 | 1.499 | 0.257 | 0.60 | 0.015 | 0.167 | 0.206 | 0.315 | 0.03 | $-0.61 \pm 0.71$ | 0.398 |
| Effect of pregnancy | CS | 13,9 | 1.181 | 0.411 | 0.56 | 0.735 | 0.071 | 0.559 | 0.624 | 0.18 | $2.19 \pm 0.97$ | 0.033 |
|  | P | 13,9 | 1.174 | 0.414 | 0.63 | 0.131 | 0.035 | 0.403 | 0.252 | 0.26 | $3.04 \pm 1.04$ | 0.007 |
|  | F | 13,9 | 1.378 | 0.320 | 0.67 | 0.018 | 0.083 | 0.154 | 0.456 | 0.14 | $2.43 \pm 1.24$ | 0.061 |
|  | P*F | 13,9 | 0.934 | 0.558 | 0.57 | 0.180 | 0.065 | 0.501 | 0.351 | 0.05 | $2.21 \pm 1.89$ | 0.255 |

Table 1.3. Regressions showing best-supported model and average model for each dependent variable. Dependent variables were log of standard length (SL), centroid size (CS), Streamlining index (SI), Fineness Index (FI), surface area (SA) and
caudal peduncle area (CP). Subscripts of dependent variables indicate estimated values early in pregnancy, late in
pregnancy, and the pregnancy effect. Five adaptive models were tested for each dependent variable: $M \sim S, M \sim S+P, M \sim S+F$,
$M \sim S+P+F, M \sim S+P+F+P^{*} F$, where $P=P r e d a t i o n$, and $F=F l o w, ~ a n d ~ S=\log S L$. When size variables (log $S L$ and $C S$ ) were the dependent variables, S was not used as a covariate. The models of character evolution tested were ordinary least squares (OLS, non-phylogenetic multiple regression), Pagel's (RegPagel), and Ornstein-Uhlenbeck (RegOU). Branch-length transformations were either proportional to molecular distances $(M)$ or constant $(C)$ branch lengths. Phylogenetic signal was $\lambda$ for RegPagel, and $d$ for RegOU. Akaike weights ( $w$ ) indicate the percentage of variation explained by each model. Coefficients of the interaction ( $\mathrm{P}^{*} \mathrm{~F}$ ) are not shown because they were invariably zero. Full list and further details of top set
models available in Appendix 1.11.

| Depend. variable | Independent variables | Character Evolution | Tree | w | $\lambda$ or $d$ | Coefficient $\pm$ SE ${ }^{\text {p-value }}$ |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  |  |  | $\log$ SL | Predation | Flow |
| $\log$ SL | P | RegOU | M | 28.6 | 0.047 |  | $0.121 \pm 0.079$ |  |
|  | Average | - | - | - | - |  | $0.077 \pm 0.080$ | $0.014 \pm 0.045$ |
| CS | $P$ | RegOU | M | 35.8 | 0.109 |  | $0.217 \pm 0.114$ |  |
|  | Average | - | - | - | - |  | $0.147 \pm 0.115$ | $0.004 \pm 0.045$ |
| Slearly | S+P | RegPagel | M | 26.3 | 0.715 | $0.124 \pm 0.080^{0.140}$ | $0.091 \pm 0.035$ |  |
|  | Average | - | - | 85.5 | - | $0.036 \pm 0.073$ | $0.025 \pm 0.044$ | $<0.001 \pm 0.004$ |
| Slate | S | RegOU | C | 29.1 | 1.285 | $0.060 \pm 0.066^{0.373}$ |  |  |
|  | Average | - | - | 73.8 | - | $0.028 \pm 0.056$ | $0.004 \pm 0.013$ | $<0.001 \pm 0.004$ |
| SI pregancy | S+P | RegPagel | C | 21.9 | 0.857 | $-0.020 \pm 0.0666^{0.763}$ | $-0.067 \pm 0.025$ |  |
|  | Average | - | - | 87.3 | - | $-0.009 \pm 0.045$ | $-0.016 \pm 0.030$ | $<0.001 \pm 0.004$ |
| Flearly | S | RegOU | M | 30.9 | 0.306 | $-0.026 \pm 0.088^{0.775}$ |  |  |
|  | Average | - | - | 79.9 | - | $-0.017 \pm 0.075$ | $<0.001 \pm 0.013$ | $0.002 \pm 0.013$ |
| Flate | S | OLS | - | 24.1 | - | $-0.070 \pm 0.073^{0.343}$ |  |  |
|  | Average | - | - | 77.7 | - | $-0.034 \pm 0.066$ | $0.001 \pm 0.010$ | $0.003 \pm 0.012$ |
| Fl ${ }_{\text {pregancy }}$ | S | OLS | - | 13.7 | - | $0.086 \pm 0.038{ }^{0.036}$ |  |  |
|  | Average | - | - | 88.3 | - | $0.030 \pm 0.045$ | $-0.003 \pm 0.010$ | $-0.001 \pm 0.005$ |
| SA early | S | RegOU | M | 29.3 | 0.487 | $1.941 \pm 0.082^{<0.001}$ |  |  |
|  | Average | 促 | - | 84.1 | - | $1.220 \pm 0.790$ | $0.005 \pm 0.019$ | $-0.009 \pm 0.023$ |
| SA ${ }_{\text {late }}$ | S | RegOU | M | 23.0 | 0.128 | $1.983 \pm 0.098{ }^{<0.001}$ |  |  |
|  | Average | - | - | 70.9 | - | $1.152 \pm 0.770$ | $-0.001 \pm 0.014$ | $-0.007 \pm 0.021$ |
| SA pregancy | S | OLS | - | 26.9 | - | $-0.068 \pm 0.030^{0.035}$ |  |  |
|  | Average | - | - | 63.8 | - | $-0.031 \pm 0.034$ | $<0.001 \pm 0.003$ | $0.001 \pm 0.004$ |
| CP early | S | RegOU | M | 40.6 | 0.189 | $1.957 \pm 0.071^{<0.001}$ |  |  |
|  | Average | - | - | 70.5 | - | $1.120 \pm 0.749$ | $<0.001 \pm 0.009$ | $-0.004 \pm 0.015$ |
| CP1ate | S | RegOU | M | 23.9 | 0.070 | $2.018 \pm 0.077^{<0.001}$ |  |  |
|  | Average | - | - | 75.8 | - | $1.235 \pm 0.771$ | $-0.001 \pm 0.010$ | $-0.005 \pm 0.016$ |


| Depend. variable | Independent variables | Character Evolution | Tree | w | $\lambda$ ord | Coefficient $\pm$ SE p-value |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  |  |  | log SL | Predation | Flow |
|  | S | OLS | - | 28.2 | - | $0.034 \pm 0.057$ |  |  |
|  | Average | - | - | 69.1 | - | $0.021 \pm 0.046$ | $-0.003 \pm 0.012$ | $0.001 \pm 0.006$ |

Figure 1.1. Map with collection localities and Gambusia phylogeny
superimposed. $\mathrm{LP}=\mathrm{low}$, and HP=high-predation regime. $\mathrm{LF}=$ low, and $\mathrm{HF}=$ highflow regime. Geographic coordinates used WGS84 datum. Branch lengths stretched for the purpose of presentation and not directly proportional to molecular divergence. See Supplementary Material for original phylogeny.


Figure 1.2. (A) Digital fish reconstruction as a composite of 200 elliptical cylinders, used for calculating streamlining index and surface area of each fish. (B) Landmarks (circles) and semilandmarks (squares) digitized for geometricmorphometric analyses. Numbers correspond to the following positions: (1) tip of the snout; (2-3) semilandmarks along dorsal midline between (1) and (4); anterior (4) and posterior (5) terminus of dorsal-fin base; dorsal (6) and ventral (7) terminus of caudal-fin base; posterior (8) and anterior (9) terminus of anal fin; (10) anterior terminus of pelvic-fin base; (11) semilandmark along ventral midline between (10) and (12); bottom of head at junction of border of opercle and body outline; and (13) eye center. Gray polygon indicates caudal peduncle area.


Figure 1.3. Shape variation estimated with MANCOVAs. Configuration sets in columns, independent variables in rows. Scattered and box-whishker plots show the relationship between respective divergence vectors (d) and the corresponding independent variable. Thin-plate splines show the range of shape variation, from low to high values in the independent variable values represented with grey and black outlines, respectively. Length, thickness, and darknes of arrows within shapes indicate the magnitude of change from low to high-values in the independent variable.


Figure 1.3

Figure 1.4. Left panel: Predicted values (mean $\pm$ SE of estimated values) obtained from Ordinary Least Squares models showing the predation effect on streamlining index (SI) of females early and late in pregnancy. Right panel: Lateral outlines of fish with SI values at the extremes of the SI range depicted in the left panel. Horizontal dashed-line indicating optimal SI value of one. Rightside: example outlines of females across the range of SI variation.


Predation Regime
Appendix 1.1. Additional information on collections analyzed. Geographic coordinates use WGS84 datum. Predation levels:
low (LP) and high (HP). Flow levels: low (LF) and high (HF). Sample size ( $n$ ) for each collection correspond to the total
number of individuals analyzed for estimating minimum size at maturity over the number of individuals included in shape
analysis after excluding juveniles and curved individuals.

| Species | Collection | Locality | Long. | Lat. | Date | Pred | Flow | n |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| G. alvarezi | UMMZ 211110 | Ojo de San Gregorio, Chihuahua, Mexico | 27.010 | -105.495 | 22/03/82 | LP | LF | 30/26 |
| G. atrora | UMMZ 169499 | Río Axtla, San Luis Potosí, Mexico. | 21.438 | -98.922 | 31/12/51 | HP | HF | 24/23 |
| G. atrora | UMMZ 210724 | Río Huichihuayán, San Luis Potosí, Mexico. | 21.438 | -98.922 | 22/01/82 | HP | HF | 19/16 |
| G. atrora | AMNH 40812 | Río Huichihuayán, San Luis Potosí, Mexico. | 21.478 | -98.965 | 25/03/72 | HP | HF | 15/15 |
| G. atrora | AMNH 77929 | Río de la Tableta, San Luis Potosí, USA | 21.520 | -98.007 | 10/04/80 | HP | HF | 13/11 |
| G. aurata | AMNH 75821 | Río Mante, Tamaulipas, Mexico | 22.699 | -99.046 | 11/02/86 | LP | LF | 9/9 |
| G. aurata | RBL | Río Guayalejo, Tamaulipas, Mexico. | 22.832 | -99.011 | 22/06/05 | HP | LF | 19/18 |
| G. baracoana | USNM 204442 | Lagunas de Pedro Montiel at Baracoa, Guantánamo, Cuba. | 20.350 | -74.507 | 29/12/43 | HP | LF | 29/21 |
| G. clarkhubbsi | TCWC 11880-0 | San Felipe Creek, Texas, USA. | 29.371 | 100.884 | 03/08/01 | LP | HF | 4/4 |
| G. clarkhubbsi | TCWC 11882-0 | San Felipe Creek, Texas, USA. | 29.371 | 100.884 | 23/03/02 | LP | HF | 16/16 |
| G. clarkhubbsi | TCWC 11887-08 | San Felipe Creek, Texas, USA. | 29.366 | -100.886 | 23/03/02 | LP | HF | 14/13 |
| G. geiseri | TNHC 9132 | San Marcos River, Texas, USA. | 29.872 | -97.931 | 14/12/78 | LP | LF | 25/25 |


| Species | Collection | Locality | Long. | Lat. | Date | Pred. | Flow | n |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| G. geiseri | TNHC 9146 | San Marcos River, Texas, USA. | 29.879 | -97.932 | 04/11/78 | LP | LF | 33/33 |
| G. hubbsi | UMMZ 202727 | Massey Creek, Bimini, Bahamas. | 25.700 | -79.297 | 01/08/51 | HP | LF | 21/18 |
| G. hurtadoi | UMMZ 196737 | Ojo Hacienda Dolores, Chihuahua, Mexico. | 27.030 | -104.915 | 27/03/74 | LP | HF | 28/28 |
| G. hurtadoi | UMMZ 211112 | Ojo Hacienda Dolores, Chihuahua, Mexico. | 27.030 | -104.915 | 28/03/82 | LP | HF | 34/30 |
| G. krumholzi | KU 7341 | Río de Nava, Coahuila, Mexico. | 28 | -100.868 | 14/04/63 | HP | LF | 29/24 |
| G. lemaitrei | UIST <br> (uncataloged) | Ciénaga Totumo, Atlántico, Colombia. | 10.734 | -75.222 | 02/12/06 | HP | LF | 24/24 |
| G. luma | FMNH 87628 | Belize River, Cayo, Belize. | 17.117 | -89.128 | 24/04/76 | HP | HF | 35/24 |
| G. luma | FMNH 94163 | Blue Creek, Toledo, Belize. | 16.202 | -89.036 | 14/07/71 | HP | HF | 24/17 |
| G. luma | UMMZ 197235 | Río Paujila, Izabal, Guatemala. | 15.686 | -88.981 | 12/04/74 | HP | HF | 13/8 |
| G. luma | UMMZ 197258 | Río Dulce, Izabal, Guatemala. | 15.670 | -88.984 | 13/04/74 | HP | HF | 4/3 |
| G. manni | ANSP 103450 | Great Bahama Bank, New Providence Island, Bahamas. | 25.060 | -77.437 | 09/04/55 | HP | LF | 30/27 |
| G. manni | ANSP103452 | Lake Killarney, New Providence Island, Bahamas. | 25.040 | -77.416 | 15/04/55 | HP | LF | 21/20 |
| G. manni | RBL | Lake Killarney, New Providence, Bahamas. | 25.040 | -77.416 | 27/07/05 | HP | LF | 17/17 |
| G. melapleura | USNM 205559 | Shrewsberry River, Westmoreland, Jamaica. | 18.300 | -78.153 | 29/12/49 | LP | HF | 25/23 |
| G. nicaraguensis | UMMZ 199657 | Río Coco, Zelaya, Nicaragua. | 14.745 | -83.976 | 15/05/75 | HP | HF | 21/21 |
| G. nicaraguensis | UMMZ 199689 | Stream at West side of Big Hog Island, Honduras. | 15.971 | -86.479 | 20/05/75 | HP | HF | 18/18 |
| G. oligosticta | RBL | Pool near Port Royal, Kingston, Jamaica. | 17.936 | -76.806 | 30/06/05 | HP | LF | 13/13 |


| Species | Collection | Locality | Long. | Lat. | Date | Pred. | Flow | n |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| G. oligosticta | UMMZ 190129 | Port Henderson, St Catherine, Jamaica. | 17.923 | -76.893 | 12/12/70 | HP | LF | 25/23 |
| G. punctata | AMNH 96308 | Río Taco Taco, Pinar del Río, Cuba. | 22.699 | -83.158 | 17/04/90 | HP | HF | 20/18 |
| G. punctata | AMNH 96320 | Río San Cristóbal, Pinar del Río, Cuba. | 22.721 | -83.042 | 17/04/90 | HP | HF | 19/18 |
| G. punctata | USNM 203197 | Streat 25 mi W of Camagüey, Camaguëy, Cuba. | 21.445 | -78.146 | 20/06/48 | HP | HF | 25/21 |
| G. punctata | USNM 203198 | Rio Gibara, Oriente, Cuba. | 20.788 | -76.103 | 28/07/44 | HP | HF | 35/33 |
| G. rhizophorae | RBL | Tidal creek in Matheson Hammock County Park, Florida, USA. | 25.679 | -80.262 | 13/07/05 | HP | LF | 8/8 |
| G. rhizophorae | TCWC 2577-02 | Key West, Florida, USA. | 24.564 | -81.774 | 09/08/78 | HP | LF | 4/4 |
| G. rhizophorae | TCWC 8671-01 | Salt pond at Key West, Florida, USA. | 24.558 | -81.768 | 18/03/97 | HP | LF | 6/5 |
| G. rhizophorae | UMMZ 213650 | Monroe Lagoon at Hopkins Island, Florida, USA. | 24.629 | -81.380 | 30/12/85 | HP | LF | 18/18 |
| G. sexradiata | UMMZ 196655 | Laguna at Rancho Chapultepec, Tabasco, Mexico. | 17.922 | -93.363 | 10/03/74 | HP | LF | 20/19 |
| G. sexradiata | UMMZ 210795 | Isolated lagoons close to Papalopán, Oaxaca, Mexico. | 18.127 | -96.106 | 26/01/82 | HP | LF | 28/28 |
| G. vittata | AMNH 75838 | Río Tancuilín, San Luis Potosí, Mexico. | 21.338 | -98.867 | 28/02/86 | HP | HF | 20/14 |
| G. vittata | UMMZ 192503 | Río Guayalejo at Llera, Tamaulipas, Mexico. | 23.324 | -99.032 | 09/06/69 | HP | HF | 24/23 |
| G. vittata | UMMZ 97513 | Río Valles, San Luis Potosí, Mexico. | 21.989 | -99.034 | 28/04/30 | HP | HF | 34/31 |


| Species | Collection | Locality | Long. | Lat. | Date | Pred. Flow | n |
| :--- | ---: | :--- | :--- | :--- | :--- | :--- | :--- |
| G. vittata | UMMZ 97517 | Tributary of Río Calabozo, <br> Veracruz, Mexico. | 21.064 | -98.143 | $07 / 05 / 30$ | HP | HF |
| $26 / 25$ |  |  |  |  |  |  |  |
| G. wrayi | UF 25054 | Black River Spa Spring, St <br> Elizabeth, Jamaica. | 18.026 | -77.844 | $18 / 04 / 78$ | HP | LF |
| G. $\mathbf{1 8 / 1 4}$ |  |  |  |  |  |  |  |
| Grayi | USNM 205574 | Black River Spa Spring, St <br> Elizabeth, Jamaica. | 18.023 | -77.847 | $28 / 12 / 49$ | HP | LF |

Appendix 1.2. Fish community of each locality included in analyses. Numbers in Fish Community correspond to the Species Number of Appendix 1.3.

| Species | Collection | Fish Community |
| :---: | :---: | :---: |
| G. alvarezi | UMMZ 211110 | 34, 89 |
| G. atrora | AMNH 40812 | 7, 35, 56, 69, 103, 124, 128 |
| G. atrora | AMNH 77929 | 7, 35, 56, 69, 103, 124, 128 |
| G. atrora | UMMZ 169499 | $\begin{aligned} & 1,6,20,35,54,56,58,65,66,67,70,88 \\ & 90,103,106,107,112,113,114,127,128 \end{aligned}$ |
| G. atrora | UMMZ 210724 | $\begin{aligned} & 1,6,20,35,54,56,58,65,66,67,70,88 \\ & 90,103,106,107,112,113,114,127,128 \end{aligned}$ |
| G. aurata | AMNH 75821 | 75, 102, 103, 112 |
| G. aurata | RBL | $\begin{aligned} & 6,36,49,56,65,66,90,100,103,112 \text {, } \\ & 113 \end{aligned}$ |
| G. baracoana | USNM 204442 | 37, 84 |
| G. clarkhubbsi | TCWC 11880-09 | 21, 25, 32, 38, 55 |
| G. clarkhubbsi | TCWC 11882-07 | 21, 25, 32, 38, 55 |
| G. clarkhubbsi | TCWC 11887-08 | 21, 25, 32, 38, 55 |
| G. geiseri | TNHC 9132 | 31, 39, 78 |
| G. geiseri | TNHC 9146 | 31, 39, 78 |
| G. hurtadoi | UMMZ 196737 | 23, 41 |
| G. hurtadoi | UMMZ 211112 | 23, 41 |
| G. krumholzi | KU 7341 | 2, 33, 42, 65, 79 |
| G. lemaitrei | UIST (uncatalogued material) | 43, 71, 98, 99, 110 |
| G. Iuma | FMNH 87628 | $4,6,9,11,16,18,44,68,96,118,122$ |
| G. Iuma | FMNH 94163 | $\begin{aligned} & 6,10,12,44,44,63,68,68,108,117 \\ & 125,125 \end{aligned}$ |


| Species | Collection | Fish Community |
| :---: | :---: | :---: |
| G. Iuma | UMMZ 197235 | $4,5,6,9,11,13,14,15,16,18,19,26$, $29,44,63,64,73,80,93,95,103,108$, 109, 116, 119, 125 |
| G. Iuma | UMMZ 197258 | $\begin{aligned} & 4,5,6,9,13,16,18,44,63,83,91,95 \\ & 119 \end{aligned}$ |
| G. manni | ANSP 103450 | 22, 40, 45, 85 |
| G. manni | ANSP 103452 | 22, 40, 45, 85 |
| G. manni | RBL | 22, 40, 45, 85 |
| G. hubbsi | UMMZ 202727 | 45, 86 |
| G. melapleura | USNM 205559 | 46 |
| G. nicaraguensis | UMMZ 199657 | $3,6,9,11,47,74,92,95,97,101,111$ |
| G. nicaraguensis | UMMZ 199689 | 47, 84, 104 |
| G. oligosticta | RBL | 48, 86 |
| G. oligosticta | UMMZ 190129 | 24, 48, 84 |
| G. punctata | AMNH 96308 | 50, 61, 84 |
| G. punctata | AMNH 96320 | 50, 51, 59, 60, 62, 82, 84, 87 |
| G. punctata | USNM 203197 | 50, 84 |
| G. punctata | USNM 203198 | 50, 61, 84 |
| G. rhizophorae | RBL | 52, 86 |
| G. rhizophorae | TCWC 2577-02 | 52, 86 |
| G. rhizophorae | TCWC 8671-01 | 52,86 |
| G. rhizophorae | UMMZ 213650 | 52, 86 |
| G. sexradiata | UMMZ 196655 | $\begin{aligned} & 4,6,8,16,17,28,53,72,96,103,105 \\ & 121,122,123,126 \end{aligned}$ |


| Species | Collection | Fish Community |
| :---: | :---: | :---: |
| G. sexradiata | UMMZ 210795 | $\begin{aligned} & 6,11,16,27,53,72,94,103,106,108 \text {, } \\ & 109,120,126 \end{aligned}$ |
| G. vittata | AMNH 75838 | $\begin{aligned} & 6,35,49,56,65,66,69,76,103,106, \\ & 113,115,124,127,128,129 \end{aligned}$ |
| G. vittata | UMMZ 192503 | $\begin{aligned} & 6,20,28,56,65,66,77,100,102,103 \\ & 112,113,129 \end{aligned}$ |
| G. vittata | UMMZ 97513 | $6,20,49,56,65,66,76,77,112,113,129$ |
| G. vittata | UMMZ 97517 | 6, 49, 56, 65, 66, 127 |
| G. wrayi | UF 25054 | 30, 57, 81, 84 |
| G. wrayi | USNM 205574 | 30, 57, 81, 84 |

Appendix 1.3. Diet of fish inhabiting localities of this study. Species numbers match numbers in Appendix 1.2.
Synonym was the name in field notes if it is different from the current valid name. Predation indicates whether the

## species never eats other fish (low-predation, LP), rarely eats fish (middle-predation, MP), or it is feeds mainly on <br> fish (high-predation, HP). Food items per species listed in descending order of importance. Abbreviations with <br> references correspond to method used to estimate feeding habits. FE, field experiment; ISO, isotope analysis; LE, laboratory experiment; LR, literature review; ND, no data; NS, not specified; OBS, direct observation; PO, All

Poeciliids except for Belonesox belizanus were assumed not to predate strongly on Gambusia (Bussing, 1998;
Meffe and Snelson, 1989); SCA, stomach content analysis; XR, X-ray observations.

| Species <br> Number | Species | Synonym | Pred. |
| :---: | :---: | :---: | :---: |
|  | NA |  | Food items and comments |
| Agonostomu |  |  |  |
| s monticola |  |  |  |$\quad$ NA | Invertebrates, algae, detritus(Aiken, 1998: SCA). Mostly insects, |
| :--- |
| also algae and occasionaly fish (Cruz, 1987:SCA). Mostly insects |
| and insect larvae, also plant material, and probably algae |
| (Hildebrand, 1935: SCA). Plant material, invertebrates, rarely fish |
| (Phillip, 1993: SCA). Invertebrates, algae, rarely plant material or |
| fish (Torres-Navarro and Lyons, 1999: SCA). |


| Species Number | Species | Synonym | Pred. | Food items and comments |
| :---: | :---: | :---: | :---: | :---: |
| 2 | Ameiurus natalis | NA | HP | Detritus, fishes, plant material and invertebrates (Walters et al., 2003: LR). Trophic level 2.9-3.6 in a scale where 2 is herbivore, 3 carnivore, and 4-4.3 is piscivore (Fry et al., 1999: ISO). Ate fish when used as bait (Schneider, 1998: FE). Larvae of other fish (Carpenter and Mueller, 2008: OBS). Population in the Everglades of Florida, USA, is mainly predatory (Murie et al., 2009: LR). |
| 3 | Amphilophu <br> $s$ margaritifer | Cichlasoma margaritiferu m | NA | ND |
| 4 | Amphilophu s robertsoni | Cichlasoma robertsoni | LP | Mostly insects, zooplankton, and molluscs (Valtierra-Vega and Schmitter-Soto, 2000: SCA). Algae and invertebrates by sifting mud (Conkel, 1993: OBS). |
| 5 | Anchoa parva | NA | LP | Plankton (Miller, 2005: LR) |
| 6 | Astyanax fasciatus | NA | MP | Algae, invertebrates, and fish material (Esteves, 1996: SCA). ostly invertebrates and plant material (Vilella, et al., 2002: SCA). |
| 7 | Astyanax mexicanus | NA | HP | Plant material, invertebrates, detritus, fish eggs, larvae and juveniles (Miller, 2005: LR). Omnivorous but important predator of swordtails (Xiphophorus, Poeciliidae) (Rosenthal, et al., 2001: LE). |


| Species Number | Species | Synonym | Pred. | Food items and comments |
| :---: | :---: | :---: | :---: | :---: |
| 8 | Atherinella alvarezi | NA | NA | ND |
| 9 | Atherinella $s p$. | NA | NA | ND. Some species of Atherinella eat insects and fruits (Miller, 2005: LR). |
| 10 | Awaous tajasica | NA | LP | Aquatic insects, foraminífera, and plant material (Miller, 2005: LR). |
| 11 | Belonesox belizanus | NA | HP | Fish and insects (Miller, 2005: LR). Fish (Bussing, 1998: LR). Fish (Meffe and Snelson, 1989: OBS). |
| 12 | Brycon guatemalens is | NA | MP | Insects when young, switching to plant material herbivorous as adults. A population in Lago Arenal (Costa Rica) also feeds heavily on fishes (silversides, Atherinidae) (Bussing, 1998: LR). |
| 13 | Carlhubbsia stuarti | NA | LP | PO |
| 14 | Centropomu s ensiferus | NA | MP | Crustaceans, rarely in fish (Alvarez-Lajonchère and Tsuzuki. 2008: LR). |
| 15 | Centropomu $s$ undecimalis | NA | HP | Mainly fish (including Gambusia), also shrimp, polychaetes, amphipods, and calenoid copepods (Luczkovich et al., 1995: SCA, OBS). |


| Species Number | Species | Synonym | Pred. | Food items and comments |
| :---: | :---: | :---: | :---: | :---: |
| 16 | Cichlasoma salvini | NA | MP | Opportunistic omnivore with tendency to herbivory, although some populations are zooplanctivorous (Miller, 2005: LR). <br> Macroinvertabrates and some small fish (Conkel, 1993: OBS). Mostly aquatic invertebrates and vegetative detritus (Cochran, 2008: SCA). |
| 17 | Cichlasoma urophthalmu m | Cichlasoma urophthalmus | MP | Mainly fish, also detritus, ostracods, algae, snails, and terrestrial insects (Bergmann and Motta, 2002: SCA). Plant material and invertebrates (Chávez-López et al., 2004: SCA). Invertebrates, vegetal material, and in less extent fish (Martínez-Palacios and Ross, 1988: OBS, SCA,). |
| 18 | Cryptoheros spilurus | Cichlasoma spilurum | LP | Mostly algae and invertebrates (Valtierra-Vega and SchmitterSoto, 2000: SCA). |
| 19 | Cryptoheros spilurus | Cichlasoma spinosissimu m | LP | Mostly algae and invertebrates (Valtierra-Vega and SchmitterSoto, 2000: SCA). |
| 20 | Cyprinella lutrensis | Notropis lutrensis | LP | Detritus, invertebrates, and algae, rarely on fish scales (Gido et al 1999: SCA). |
| 21 | Cyprinella proserpina | NA | LP | Invertebrates (Thomas et al., 2007: LR). Invertebrates (Bonner et al., 2008: LR). |
| 22 | Cyprinodon laciniatus | NA | LP | Plant matter and detritus (Barton, 1999: OBS). |


| Species Number | Species | Synonym | Pred. | Food items and comments |
| :---: | :---: | :---: | :---: | :---: |
| 30 | Eleotris pisonis | NA | HP | Plant material, fish, and invertebrates (Nordlie, 1981: SCA). Molluscs, crustaceans, and fish (Teixeira, 1994: SCA). Crustaceans, fish, and molluscs Winemiller and Ponwith 1998: SCA). Insects and fish (Brian Langerhans, pers. obs.: SCA). |
| 31 | Etheostoma fonticola | NA | LP | Inmature insects and microcrustacea (Thomas et al., 2007: LR). |
| 32 | Etheostoma grahami | NA | LP | ND. Etheostoma grahami was assumed to be non-predatory of Gambusia geiseri (a sympatric species) because it is a small fish that does not exceed 60 mm in total length (Thomas et al., 2007), and its congeners consume invertebrates and microcrustacea (e.g. Paine et al., 1982). |
| 33 | Gambusia affinis | NA | LP | PO |
| 34 | Gambusia alvarezi | NA | LP | PO |
| 35 | Gambusia atrora | NA | LP | PO |


| Species Number | Species | Synonym | Pred. | Food items and comments |
| :---: | :---: | :---: | :---: | :---: |
| 54 | $\begin{gathered} \text { Gambusia } \\ \text { sp. } \end{gathered}$ | NA | LP | PO |
| 55 | Gambusia speciosa | NA | LP | PO |
| 56 | Gambusia vittata | NA | LP | PO |
| 57 | Gambusia wrayi | NA | LP | PO |
| 58 | Girardinichth ys viviparus | $\begin{aligned} & \text { Girardinichth } \\ & \text { ys } \\ & \text { innominatus } \end{aligned}$ | LP | Omnivorous with a tendency to carnivory (Armando Vega-López, per. com.). Microcrustacea (Vega-López et al., 2007: LE). The maximum size of this species ( 65 mm SL, Miller, 1965) indicates that it is unlikely to be a dangerous predator for Gambusia. |
| 59 | Girardinus falcatus | NA | LP | PO |


| Species <br> Number | Species | Synonym | Pred. | Food items and comments |
| :---: | :---: | :---: | :---: | :---: |
| 60 | Girardinus metallicus | NA | LP | PO |
| 61 | Girardinus sp. | NA | LP | PO |
| 62 | Girardinus uninotatus | NA | LP | PO |
| 63 | Gobiomorus dormitor | Gobiomorus dormitator | HP | Shrimp larvae and fish (Nordlie, 1981: SCA). Fish (Miller, 2005: LR). Fish (B. Langerhans, unpub.). |
| 64 | Gobiosoma $s p$. | NA | NA | ND. Some species of Gobiosoma eat insects and fish (Miller, 2005: LR). |
| 65 | Herichthys cyanoguttatu $s$ | Cichlasoma cyanoguttatu m | HP | Fish (Brosnan at al., 2003: LE). |
| 66 | Herichthys labridens | Cichlasoma labridens | MP | Mostly snails, rarely fish (Rosenthal et al., 2001: SCA). |


| Species <br> Number | Species | Synonym | Pred. | Food items and comments |
| :--- | :--- | :--- | :--- | :--- | :--- |
| 67 | Herichthys <br> steindachner <br> $i$ | Cichlasoma <br> steindachneri | HP | Fish (Miller, 2005: LR). |
| 68 | Heterandria <br> bimaculata | NA | LP | PO |
| 69 | Heterandria <br> jonesi | NA | LP | PO |
| 70 | Heterandria <br> sp. | NA | LP | PO |
| 71 | Hoplias <br> malabaricus | NA | HP | Fish (Dahl, 1971: LR, OBS). |
| 72 | Hyphessobr <br> ycon <br> compressus | NA | MP | Omnivore, with an intermediate trophic level (Winemiller et al., <br> 2011: ISO). |


| Species Number | Species | Synonym | Pred. | Food items and comments |
| :---: | :---: | :---: | :---: | :---: |
| 73 | Hyphessobr ycon milleri | NA | NA | ND |
| 74 | Hyphessobr ycon tortuguerae | NA | NA | ND |
| 75 | Ictiobus bubalus | NA | LP | Detritus, insects and microinvertebrates (Gido, 2001: SCA). Ostracods, insect larvae, snails, algae, and detritus (Miller, 2005: LR). |
| 76 | Ictiobus labiosus | NA | NA | ND |
| 77 | Lepisosteus osseus | NA | HP | Fish, rarely on invertebrates (Lagler and Hubbs, 1940: SCA). |
| 78 | Lepomis macrochirus | NA | LP | Zooplankton and invertebrates (Olson et al., 2003: SCA). |


| Species Number | Species | Synonym | Pred. | Food items and comments |
| :---: | :---: | :---: | :---: | :---: |
| 79 | Lepomis megalotis | NA | MP | Insects, other small invertebrates, and occasionally fish (Miller, 2005: LR). |
| 80 | Leptophilypn us fluviatilis | NA | MP | Invertebrates (Winemiller and Leslie, 1992: LR, OBS). |
| 81 | Limia melanogaste $r$ | NA | LP | PO |
| 82 | Limia vittata | NA | LP | PO |
| 83 | Lophogobius cyprinoides | NA | LP | Algae, secondarily on amphipods, isopods, copepods, tanaids, ostracods, insects, polychaetes,mollusks, and barnacles (Darcy, 1981: SCA). |
| 84 | LowlandMarine | NA | HP | Marine predators can ascend freshwater streams. Most of lowland streams in the Neotropics have a number of piscivore fishes (D. Reznick, pers. obs). |
| 85 | Lutjanus griseus | NA | HP | Shrimp, fish, and crabs (Harrigan et al., 1989: SCA, ISO). |


| Species Number | Species | Synonym | Pred. | Food items and comments |
| :---: | :---: | :---: | :---: | :---: |
| 86 | Marine | NA | HP | Predators such as needlefish and barracudas are ubiquitous in marine habitats inhabited by Gambusia. |
| 87 | Nandopsis tetracanthus | Cichlasoma tetracanthus | MP | Worms, small fish, shrimps, and water insects (Froese et al., 2011: LR). Poecilia reticulata (as lure) (Hulsey et al., 2010: LE). |
| 88 | Neoheteran dria tridentiger | NA | LP | PO |
| 89 | Notropis chihuahua | Notropis sp. | LP | Invertebrates (Burr and Mayden, 1981: SCA). Invertebrates (De La Maza-Benignos, 2009: NS). |
| 90 | Notropis tropicus | NA | NA | ND |
| 91 | Oligoplites palometa | NA | MP | Fish scales, benthic and planktonic crustaceans, rarely smaller fishes and polychaetes (Froese et al., 2011: LR). |


| Species Number | Species | Synonym | Pred. | Food items and comments |
| :---: | :---: | :---: | :---: | :---: |
| 92 | Parachromis managuensi s | Cichlasoma managuense | HP | Fish (Bussing, 1998: LR). |
| 93 | Parachromis motaguensis | Cichlasoma motaguense | MP | Invertebrates and fish (Froese et al., 2011: LR). |
| 94 | Paraneetropl us fenestratus | Cichlasoma fenestratum | LP | Mainly vegetable material and invertebrates (Froese et al., 2011: LR). |
| 95 | Paraneetropl us maculicauda | Cichlasoma maculicauda | LP | Detritus and vegetable matter (Froese et al., 2011: LR). |
| 96 | Petenia splendida | NA | HP | Fish (Miller, 2005: LR). |
| 97 | Phallichthys amates | NA | LP | PO |
| 98 | Poecilia caucana | NA | LP | PO |
| 99 | Poecilia cuneata | NA | LP | PO |


| Species <br> Number | Species | Synonym | Pred. | Food items and comments |  |
| :--- | :--- | :--- | :--- | :--- | :--- |
| 100 | Poecilia <br> formosa | NA | LP | PO |  |
| 101 | Poecilia gilli | NA | LP | PO |  |
| 102 | Poecilia <br> latipunctata | NA | LP | PO |  |
| 103Poecilia <br> mexicana | NA | LP | PO |  |  |
| 104 | Poecilia orri | NA | LP | PO |  |
| 105 | Poecilia <br> petenensis | NA | LP | PO |  |
| 106 | Poecilia <br> Sphenops | NA | LP | PO |  |


| Species Number | Species | Synonym | Pred. | Food items and comments |
| :---: | :---: | :---: | :---: | :---: |
| 107 | Poeciliidae sp. | NA | NA | ND |
| 108 | Rhamdia guatemalens is | NA | MP | Aquatic insects, crustaceans, and small fishes (Bussing, 1998: LR). Considered a predator of the Poeciliidae Brachirhaphis rhabdophora (Langerhans and DeWitt, 2004: LR). |
| 109 | Rocio octofasciata | Cichlasoma octofasciatu m | MP | Invertebrates and algae (Valtierra-Vega and Schmitter-Soto, 2000: SCA). Worms, crustaceans, insects and fish (Froese et al., 2011: LR). |
| 110 | Roeboides dayi | NA | LP | Invertebrates and fish scales (Peterson and Winemiller, 1997: SCA). |
| 111 | Roeboides guatemalens is | NA | NA | ND |
| 112 | Tampichthys erimyzonops | Dionda erimyzonops | LP | Filamentous algae and detritus (Miller, 2005: LR). |


| Species Number | Species | Synonym | Pred. | Food items and comments |
| :---: | :---: | :---: | :---: | :---: |
| 113 | Tampichthys ipni | Dionda ipni | LP | Insects, water mites, algae, and detritus (Miller, 2005: LR). |
| 114 | Tampichthys rasconis | Dionda rasconis | NA | ND |
| 115 | Tampichthys $s p$. | Dionda sp. | LP | ND. However, the only species of Tampichthys in this region of Rio Panuco are T. ipni and T. erimyzonops, both non-piscivorous species (Miller, 2005). |
| 116 | Theraps bocourti | Cichlasoma bocourti | NA | ND |
| 117 | Theraps godmani | Cichlasoma godmani | LP | Fresh vegetation (Froese et al., 2011: LR). |
| 118 | Theraps intermedius | Cichlasoma intermedium | NA | ND |
| 119 | Thorichthys aureus | Cichlasoma aureum | NA | ND |


| Species Number | Species | Synonym | Pred. | Food items and comments |
| :---: | :---: | :---: | :---: | :---: |
| 120 | Thorichthys ellioti | Cichlasoma ellioti | NA | ND |
| 121 | Thorichthys helleri | Cichlasoma helleri | NA | ND |
| 122 | Thorichthys meeki | Cichlasoma meeki | MP | Invertebrates, algae, and rarely fish (Valtierra-Vega and SchmitterSoto, 2000: SCA). |
| 123 | Thorichthys pasionis | Cichlasoma pasionis | NA | ND. This species shows molariform teeth on their pharyngeal jaws, a character associated with a molluscivore diet (Chakravarty, 2007). |
| 124 | Xiphophorus cortezi | NA | LP | PO |
| 125 | Xiphophorus hellerii | NA | LP | Invertebrates, algae, rarely fish scales (Arthington, 1989: SCA). |


| Species <br> Number | Species | Synonym | Pred. | Food items and comments |
| :--- | :--- | :--- | :--- | :--- |
| 126Xiphophorus <br> maculatus | NA | LP | Invertebrates and algae (Arthington, 1989: SCA). |  |
| 127Xiphophorus <br> montezuma <br> $e$ | NA | LP | PO |  |
| 128Xiphophorus <br> pygmaeus | NA | LP | PO |  |
|  | Xiphophorus <br> variatus | NA | LP | PO |

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## Appendix 1.4. Calculation of streamlining

Streamlining Index (SI) is based on a comparison of the distributions of the masses of a fish and a streamlined foil (McHenry and Lauder 2006). To calculate distributions of mass, the volumes of the fish and the foil were approximated as composites of multiple slices (elliptical cylinders, Figure 2A). For the fish, the dimensions of the elliptical cylinders were obtained by measuring the height and width from lateral and ventral pictures, respectively, at equidistant positions along the longitudinal axis. Fins were digitally removed from pictures before analyses using Photoshop CS5 (Adobe Systems Inc.). In our study we made 200 sections because exactitude does not increase with more sections (McHenry and Lauder 2006). For the ideal shape the widths and heights of the sections are estimated using the equation for NACA foils with no chamber (Jacobs et al. 1933):

$$
h_{N A C A}(x)=0.4 h_{\max }\left(0.2969 \sqrt{\frac{x}{S L}}-0.1260 \frac{x}{S L}-0.3516\left(\frac{x}{S L}\right)^{2}+0.2843\left(\frac{x}{S L}\right)^{3}-0.1015\left(\frac{x}{S L}\right)^{4}\right)
$$

where $h_{\text {NACA }}$ is the estimated width (or height) at a particular position in the $x$-axis (i.e. the anterior-posterior axis), $h_{\max }$ is the maximum width (or height) in the profile, $x$ is the distance between the tip of the fish and the current position along the $x$-axis, and $S L$ is the standard length. The distributions of mass of either the actual fish volume or the ideal volume are estimated as the moments of inertia of their respective cylinders. The total moment of inertia for each body is the sum of
the moments of inertia of its cylinders, according to the parallel axis theorem (Meriam and Kraige 2006). The moment of inertia is calculated as if the body were rotating along a vertical axis located at its anterior tip, with the equation

$$
I=\frac{\rho \pi}{4}\left(\sum_{i=1}^{n}\left(\frac{w^{3} h}{16}+w h x^{2}\right)_{i}\right) \Delta x
$$

where $l$ is the moment of inertia, $\rho$ is density (assumed as 1 in this study), $w$ and $h$ are respectively the width and height of the fish at the position $x$ of the ith section, $n$ the number of sections, and $\Delta x$ is the distance between sections (SL/ 200 in this study). SI is the ratio between the moments of inertia of the fish and its respective estimated NACA foil, $\mathrm{SI}=I_{\text {fish }} / I_{\text {NACA }}$.

Fineness Index (FI), is calculated as:

$$
F I=1-\left|1-\frac{S L}{4.5 D_{\max }}\right|
$$

where $S L$ is the standard length and $D_{\max }$ is the maximum body depth. The value 4.5 comes from the experimental observation that at this ratio the drag coefficient is minimum (Blake 1983). The Matlab code used to calculate streamlining (streamline_analysis_20120312_for_distribution.m) is available upon request.

## References Appendix 1.4

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## Appendix 1.5. Phylogeny of Gambusia

Majority (50\%) consensus tree of Gambusia using three genes (ND2, Cyt b, S7) in Newick format (R. B. Langerhans, unpub.). Tip labels correspond to species and collection names linked by underscores, and node labels to bootstrapping support.
(((()._clarkhubbsi_-

TCWC_11880-09_TCWC_11882-07_TCWC_11887-08:0.004177,G._krumholzi_-KU_7341:0.007942)1.00:0.035231,G._geiseri_-

TNHC_9132_TNHC_9146:0.12442)0.99:0.130828,(((G._alvarezi_-UMMZ_211110:0.042105,G._hurtadoi_-

UMMZ_196737_UMMZ_211112:0.023829)1.00:0.164551,(G._atrora_-AMNH_40812_AMNH_77929:0.00461,G._atrora_-UMMZ_169499_UMMZ_210724:0.00461):0.146954)0.75:0.029413,(G._aurata_-AMNH_75821_RBL:0.164195,(G._vittata_-UMMZ_192503:0.00461,G._vittata_-UMMZ_97513:0.00461,G._vittata_-UMMZ_97517:0.00461,G._vittata_AMNH_75838:0.00461):0.120073)0.96:0.028746)1.00:0.029974, ((()._oligosticta_-UMMZ_190129_RBL:0.015952,G._baracoana_-USNM_204442:0.002092)1.00:0.133733,(G._hubbsi_-UMMZ_202727:0.023658,G._manni_-ANSP_103450_ANSP_103452_RBL: 0.02423)0.66:0.112589)1.00:0.04566,G._nicaraguensis_-

UMMZ_199657_UMMZ_199689:0.139127)1.00:0.039811,(G._lemaitrei_-UIST_uncatalogued:0.256976,(G._melapleura_-

USNM_205559:0.060682,G._wrayi_-USNM_205574_UF_25054:0.058121) 1.00:0.105819)1.00:0.04822)0.67:0.041355,((G._punctata_-

AMNH_96308:0.00461,G._punctata_-AMNH_96320:0.00461,G._punctata_-USNM_203197_USNM_203198:0.00461):0.045904,G._rhizophorae_-

TCWC_2577-02_TCWC_8671-01_UMMZ_213650_RBL:0.062711) 0.99:0.092292)1.00:0.058663,G._sexradiata_-

UMMZ_210795_UMMZ_196655:0.258672)0.59:0.07495,G._luma_FMNH_87628_FMNH_94163_UMMZ_197235_UMMZ_197258:0.451326)1.00;

## Appendix 1.6. Phylogenetic tree of Gambusia with branch lengths proportional

 to the units of inferred nucleotide substitution.

## Appendix 1.7. Phylogenetic tree of Gambusia with constant branch lengths.



Appendix 1.8. Shape variation of females early in pregnancy, as described by Principal Components (PC). Overlapping figures represent the extreme configurations in each PC, from lowest (grey outline) to highest values (black outline). Within parentheses: Percentage of shape variation explained for each PC, and factor of magnification of differences.

PC 1 (47\%; 1x)


PC 2 (23\%; 2x)


PC 6 (3\%; 4x)


PC 7 (2\%; 4x)


PC 8 (2\%; 4x)


PC 5 (4\%; 2x)


PC 3 (10\%; 2x)


PC 4 (6\%; 2x)


PC 10 (1\%; 5x)


PC $9(1 \% ; 5 x)$


PC 11 (<0.5\%; 5x)


Appendix 1.9. Shape variation of females late in maturity. Further details in caption of Appendix 1.8.


PC 9 (1\%; 5x)


PC 6 (3\%; 2x)
PC 10 (1\%; 5x)


PC 11 (1\%; 5x)


Appendix 1.10. Difference in shape between females early and late in pregnancy, with shape variation arranged in Principal Components. Overlapping figures are the deformations related to pregnancy on the average-shape female. Further details in caption of Appendix 1.8.

Appendix 1.11. Canditate set $\left(\Delta A I C_{C}=4\right)$ of regressions for size variables and each morphological trait. Subscripts
pregnancy effect. Five adaptive models were tested for each dependent variable: $M \sim S, M \sim S+P, M \sim S+F, M \sim S+P+F$,
$M \sim S+P+F+P^{*} F$, where $S=\log S L, P=P r e d a t i o n$, and $F=F l o w$. The same models without $S$ as the covariate were
tested with body size variables (log SL, Centroid Size) as dependent variables. Branch-length transformations were
either proportional to molecular distances (M) or constant (C) branch lengths. Phylogenetic signal was $\lambda$ for
RegPagel, and $d$ for RegOU. $\mathrm{k}=$ number of parameters, $\operatorname{InML}=\log$ Maximal Likelihood, $\mathrm{AIC}_{\mathrm{C}}=$ small sample corrected
Akaike Information Criterium, and w=Akaike weights. Evidence Ratio (ER) indicates the number of times the most-
supported model of the set is better supported than each row's model. Coefficients of the interaction (P*F) are not
shown because they were invariably zero.

|  | Model | Character Evolution | Tree k InML |  | $\mathrm{AlC}_{c}$ | w | $\lambda$ ord ER |  | Coefficients $\pm$ SE |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  |  | log SL |  |  |  | Predation |  | Flow |
| Body size |  |  |  |  |  |  |  |  |  |  |  |  |
| $\log$ SL | P | RegOU | M | 412.2 |  | -14.6 | 28.6 | 0.047 | 1.00 |  | $0.121 \pm 0.079$ | 0.143 |  |
|  | P | RegOU | C | 411.5 | -13.1 | 13.9 | 0.698 | 0.49 |  | $0.116 \pm 0.075$ | 0.142 |  |
|  | F | RegOU | M | 411.2 | -12.6 | 10.5 | 0.014 | 0.37 |  |  |  | $0.029 \pm 0.074{ }^{0.701}$ |
|  | P | RegPagel | C | 411.2 | -12.5 | 10.1 | 0.983 | 0.35 |  | $0.125 \pm 0.074$ | 0.107 |  |
|  | P+F | RegOU | M | 512.4 | -11.8 | 7.1 | 0.036 | 0.25 |  | $0.126 \pm 0.081$ | 0.142 | $0.037 \pm 0.075^{0.631}$ |
|  | F | RegOU |  | 410.7 | -11.6 | 6.4 | 0.565 | 0.22 |  |  |  | $0.047 \pm 0.065{ }^{0.484}$ |



[^0]|  | Model | Character Evolution | Tree k InML |  | AICc | w | $\lambda$ or $d$ | ER | Coefficients $\pm$ SE |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  |  | log SL |  |  |  |  | Predation |  | Flow |
|  | S | RegPagel | C | 438.0 |  | -66.2 | 5.0 | 0.658 | 4.35 | $-0.049 \pm 0.069$ | 0.489 |  |  |  |
|  | S+P | RegOU | M | 539.5 | -66.1 | 4.8 | 0.006 | 4.55 | $-0.029 \pm 0.072$ | 0.692 | $-0.045 \pm 0.029$ | 0.135 |  |
|  | S+P | RegPagel | M | 539.5 | -66.0 | 4.5 | 0.669 | 4.76 | $-0.029 \pm 0.066$ | 0.668 | $-0.068 \pm 0.029$ | 0.034 |  |
|  | $\mathrm{S}+\mathrm{P}+\mathrm{F}$ | RegPagel | C | 641.1 | -65.8 | 4.3 | 0.865 | 5.00 | $-0.026 \pm 0.069$ | 0.709 | $-0.066 \pm 0.026$ | ${ }^{0.023}$ | $0.008 \pm 0.020{ }^{0.703}$ |
|  | $\mathrm{S}+\mathrm{P}+\mathrm{F}$ | RegOU | C | 640.8 | -65.1 | 3.0 | 0.807 | 7.14 | $-0.042 \pm 0.070$ | 0.554 | $-0.066 \pm 0.027$ | 0.027 | $0.007 \pm 0.021{ }^{0.727}$ |
| Fineness Index |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Flearly | S | RegOU | M | 430.5 | -51.1 | 30.9 | 0.306 | 1.00 | $-0.026 \pm 0.088$ | 0.775 |  |  |  |
|  | S | RegPagel | M | 430.2 | -50.6 | 24.4 | 0.878 | 1.27 | $-0.015 \pm 0.083$ | 0.854 |  |  |  |
|  | S+F | RegOU | M | 530.6 | -48.2 | 7.5 | 0.329 | 4.17 | $-0.014 \pm 0.090$ | 0.876 |  |  | $0.019 \pm 0.037{ }^{0.614}$ |
|  | S+F | RegPagel | M | 530.6 | -48.1 | 7.1 | 0.878 | 4.35 | $-0.014 \pm 0.084$ | 0.870 |  |  | $0.023 \pm 0.030{ }^{0.460}$ |
|  | S+P | RegOU | M | 530.5 | -48.0 | 6.6 | 0.327 | 4.76 | $-0.016 \pm 0.097$ | 0.872 | $-0.007 \pm 0.043$ | 0.870 |  |
|  | S+P | RegPagel | M | 530.3 | -47.5 | 5.2 | 0.874 | 5.88 | $-0.021 \pm 0.094$ | 0.828 | $0.004 \pm 0.042$ | 0.922 |  |
|  | S | OLS | - | 327.3 | -47.4 | 5.0 | - | 6.25 | $-0.156 \pm 0.095$ | 0.115 |  |  |  |
| Flate | S | OLS | - | 334.2 | -61.4 | 24.1 | - | 1.00 | $-0.070 \pm 0.073$ | 0.343 |  |  |  |
|  | S | RegOU | M | 435.3 | -60.6 | 16.3 | 0.052 | 1.47 | $-0.039 \pm 0.080$ | ${ }^{0.631}$ |  |  |  |
|  | S | RegPagel | M | 435.0 | -60.2 | 12.8 | 0.768 | 1.89 | $-0.021 \pm 0.072$ | 0.774 |  |  |  |
|  | S+F | OLS | - | 434.6 | -59.4 | 8.8 | - | 2.70 | $-0.086 \pm 0.075$ | 0.268 |  |  | $0.023 \pm 0.028{ }^{0.407}$ |
|  | S+P | OLS | - | 434.4 | -59.0 | 7.1 | - | 3.45 | $-0.080 \pm 0.075$ | 0.302 | $0.019 \pm 0.033^{0.563}$ |  |  |
|  | S | RegOU | C | 434.4 | -59.0 | 7.1 | 0.190 | 3.45 | $-0.068 \pm 0.079$ |  |  |  |  |
|  | S+F | RegPagel | M | 535.4 | -57.8 | 4.0 | 0.770 | 5.88 | $-0.026 \pm 0.072$ | 0.725 |  |  | $0.022 \pm 0.026^{0.411}$ |
|  | S+F | RegOU | M | 535.4 | -57.8 | 3.9 | 0.063 | 6.25 | $-0.037 \pm 0.081$ | 0.653 |  |  | $0.015 \pm 0.031^{0.630}$ |
|  | S+P | RegOU | M | 535.3 | -57.5 | 3.5 | 0.059 | 6.67 | $-0.038 \pm 0.086$ | 0.660 | $0.001 \pm 0.035{ }^{0.984}$ |  |  |
|  | S | OLS | - | 350.8 | -94.5 | 13.7 | - | 1.00 | $0.086 \pm 0.038$ | 0.036 |  |  |  |
|  | S | RegPagel | C | 452.1 | -94.3 | 12.5 | 0.923 | 1.10 | $0.022 \pm 0.040$ |  |  |  |  |
|  | S | RegOU | M | 451.9 | -93.9 | 9.8 | 0.002 | 1.39 | $0.059 \pm 0.042$ | 0.182 |  |  |  |
|  | S | RegOU | C | 451.9 | -93.8 | 9.8 | 1.013 | 1.39 | $0.014 \pm 0.040$ | 0.725 |  |  |  |
|  | $S+P$ | OLS | - | 451.7 | -93.6 | 8.5 | - | 1.61 | $0.096 \pm 0.039$ | 0.021 | $-0.022 \pm 0.017$ | 0.207 |  |
|  | S+P | RegPagel | C | 552.9 | -92.9 | 6.0 | 0.929 | 2.27 | $0.038 \pm 0.042$ | 0.382 | $-0.019 \pm 0.016$ | ${ }^{0.241}$ |  |


|  | Model | Character Evolution | Tree k InML AICc |  |  | W | $\lambda$ ord ER |  | Coefficients $\pm$ SE |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  |  |  | $\log$ SL |  |  | Predation |  | Flow |
| $F l_{\text {preg }}$. | S+F | OLS | - | 451.3 | -92.7 |  | 5.5 | - | 2.50 | $0.094 \pm 0.0400^{0.027}$ |  |  | $-0.014 \pm 0.014^{0.360}$ |
|  | S | RegPagel | M | 451.3 | -92.7 | 5.4 | 0.646 | 2.56 | $0.036 \pm 0.039{ }^{0.362}$ |  |  |  |
|  | S+P | RegOU | C | 552.7 | -92.4 | 4.7 | 1.040 | 2.94 | $0.031 \pm 0.042^{0.465}$ | $-0.020 \pm 0.016$ | 0.239 |  |
|  | $S+P$ | RegOU | M | 552.4 | -91.8 | 3.5 | 0.001 | 3.85 | $0.070 \pm 0.043^{0.123}$ | $-0.016 \pm 0.017$ | 0.355 |  |
|  | $S+F$ | RegPagel | C | 552.3 | -91.7 | 3.3 | 0.882 | 4.17 | $0.029 \pm 0.041^{0.487}$ |  |  | $-0.008 \pm 0.013^{0.561}$ |
|  | $S+P+F$ | OLS | - | 552.3 | -91.5 | 3.1 | - | 4.35 | $0.105 \pm 0.040^{0.016}$ | $-0.022 \pm 0.017$ |  | $-0.014 \pm 0.014^{0.348}$ |
|  | $S+P$ | RegPagel | M | 552.1 | -91.1 | 2.5 | 0.628 | 5.56 | $0.053 \pm 0.041^{0.207}$ | $-0.021 \pm 0.018$ | 0.260 |  |
|  | $S+F$ | RegOU | C | 551.9 | -90.9 | 2.2 | 0.985 | 6.25 | $0.016 \pm 0.041^{0.700}$ |  |  | $-0.004 \pm 0.013^{0.736}$ |
|  | $S+F$ | RegOU | M | 551.9 | -90.9 | 2.2 | 0.001 | 6.25 | $0.061 \pm 0.043^{0.181}$ |  |  | $-0.004 \pm 0.016^{0.794}$ |
| Surface Area |  |  |  |  |  |  |  |  |  |  |  |  |
| SA ${ }_{\text {early }}$ | S | RegOU | M | 430.2 | -50.5 | 29.3 | 0.487 | 1.00 | $1.941 \pm 0.082^{<0.001}$ |  |  |  |
|  | S | RegPagel | M | 429.8 | -49.7 | 19.6 | 0.927 | 1.49 | $1.946 \pm 0.081<0.001$ |  |  |  |
|  | S+F | RegOU | M | 531.2 | -49.3 | 16.4 | 0.613 | 1.79 | $1.893 \pm 0.078^{<0.001}$ |  |  | $-0.051 \pm 0.033^{0.144}$ |
|  | $S+F$ | RegPagel | M | 530.8 | -48.5 | 11.2 | 0.945 | 2.63 | $1.920 \pm 0.0788^{<0.001}$ |  |  | $-0.042 \pm 0.030^{0.179}$ |
|  | $S+P$ | RegOU | M | 530.7 | -48.3 | 9.9 | 0.644 | 2.94 | $1.873 \pm 0.085^{<0.001}$ | $0.052 \pm 0.041$ | 0.219 |  |
|  | $S+P$ | RegPagel | M | 529.9 | -46.9 | 4.9 | 0.949 | 5.88 | $1.906 \pm 0.089<0.001$ | $0.029 \pm 0.041$ | 0.489 |  |


| SAlate | S | RegOU | M | 429.5 | -49.1 | 23.0 | 0.128 | 1.00 | $1.983 \pm 0.098^{<0.001}$ |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | S | RegPagel | M | 429.0 | -48.1 | 13.8 | 0.813 | 1.67 | $1.968 \pm 0.090^{<0.001}$ |  |  |  |
|  | S | OLS | - | 327.2 | -47.4 | 9.7 | - | 2.38 | $2.040 \pm 0.095^{<0.001}$ |  |  |  |
|  | $S+F$ | RegOU | M | 530.1 | -47.3 | 9.2 | 0.218 | 2.50 | $1.959 \pm 0.095^{<0.001}$ |  |  | $-0.044 \pm 0.038{ }^{0.255}$ |
|  | S+F | RegPagel | M | 529.9 | -46.8 | 7.3 | 0.833 | 3.13 | $1.969 \pm 0.088<0.001$ |  |  | $-0.042 \pm 0.032^{0.204}$ |
|  | $S+F$ | OLS | - | 428.3 | -46.6 | 6.5 | - | 3.57 | $2.071 \pm 0.096{ }^{<0.001}$ |  |  | $-0.048 \pm 0.035^{0.187}$ |
|  | $S+P$ | RegOU | M | 529.5 | -46.0 | 4.9 | 0.188 | 4.76 | $1.962 \pm 0.105^{<0.001}$ | $0.016 \pm 0.045$ | 0.732 |  |
|  | $S+P$ | OLS | - | 427.9 | -45.9 | 4.7 | - | 5.00 | $2.062 \pm 0.097^{<0.001}$ | $0.046 \pm 0.042$ | 80 |  |
|  | S | RegOU | C | 427.9 | -45.9 | 4.6 | 0.325 | 5.00 | $2.024 \pm 0.104^{<0.001}$ |  |  |  |
|  | S | OLS | - | 357.0 | -106.9 | 26.9 | - | 1.00 | $-0.068 \pm 0.030{ }^{0.035}$ |  |  |  |
|  | S | RegOU | C | 457.5 | -105.2 | 11.5 | 0.338 | 2.33 | $-0.035 \pm 0.033^{0.308}$ |  |  |  |
| c^ | S+F | OLS | - | 457.5 | -105.2 | 11.3 | - | 2.38 | $-0.075 \pm 0.031^{0.025}$ |  |  | $0.011 \pm 0.011^{0.333}$ |



## Chapter 2

Interspecific life history variation in livebearing female fishes of the genus Gambusia (Poeciliidae)

Abstract: Evolutionary processes may form a continuum from micro- to macroevolutionary scales, such that microevolutionary processes can explain macroevolutionary patterns. Here we analyze macroevolutionary pattern of life history variation in female Gambusia. Life history theory, largely developed and tested at the microevolutionary level, predicts that an increase in mortality later in life reduces age at maturity and increases reproductive allocation before and during the age when mortality increases. Life history theory also predicts that higher mortality at later ages selects for more and smaller embryos. Predation and flow are key factors for freshwater fish, in part because of the high mortalities that they can exert. We used life history theory to propose how life history in Gambusia could respond to variation in predation and flow regimes. We collected life history data from preserved specimens of 20 Gambusia species and found remarkable life history variation across the genus. At the intraspecific level, life history traits were related to female body size and stage of embryo development. However, these allometric and pregnancy correlations varied among species. At the interspecific level, the best predictor of life history variation was female body size. Moreover, body size also explained the allometric variation in life-history traits among collections. The effect of predation on life histories coincided with
most of the predictions from life-history theory: species from high-predation sites tended to have larger gonads and more and smaller embryos. However, the differences of species between high-and low-predation species were relatively small. Latitude, flow, predation intensity, and female body size showed statistically significant phylogenetic signal, but life history traits did not.

## Introduction

A general concept in evolutionary biology is that adaptation at the microevolutionary level (within species) can explain macroevolutionary patterns of variation (among higher taxa; Darwin 1872: 49; Watson et al. 1936: 58; Charlesworth et al. 1982; Arnold et al. 2001). Under this view, the same selective factors can drive populations and higher taxa in similar directions towards optimal areas of the adaptive space, forming a continuum between micro- and macroevolution (Charlesworth et al. 1982). However, it has been suggested that the direction of adaptive divergence can be modified by other evolutionary processes (e.g. random genetic drift), which can blur microevolutionary patterns at the long term (Stanley 1979: 189). Moreover, some evolutionary scenarios may not fit the concept of a micro-macroevolutionary continuum. For example, the direction of selection across the adaptive landscape may not correspond between micro-and macroevolutionary scales if the adaptive landscape peaks vary in position among higher taxa (Arnold et al. 2001) or if different taxa find alternative morphological solutions to the same functional problem (Losos 2011). These points favor an alternative view that microevolutionary divergence cannot always be extrapolated to explain divergence at the macroevolutionary scale (Goldschmidt 1940; Van Valen 1974; Eldredge and Cracraft 1980). A useful approach to test the connection between micro- and macroevolutionary scales is to produce models of divergence from microevolutionary patterns to predict
patterns at the macroevolutionary level (Arnold et al. 2001; Losos and Ricklefs 2009). We used this strategy to explain the interspecific patterns of life history in female Gambusia, testing predictions derived from models of life history evolution that were developed to assess microevolutionary processes.

Explaining the remarkable diversity of life histories in nature has been addressed with a large body of theory based on models at the population level (Roff 1992; Stearns 1992; Roff 2002). Theoretically, natural selection should act upon life-history variation to maximize Darwinian fitness (Cole 1954). Organisms are expected to invest optimal proportions of their limited resources into different body compartments (growth, reproduction, maintenance; Williams 1966). Thus, an increase in mortality at a given age is predicted to reduce age at maturity (Gadgil and Bossert 1970), and increase reproductive allocation before and during the age when mortality increases (Gadgil and Bossert 1970; Schaffer 1974; Law 1979; Michod 1979). Life history theory also predicts that higher mortality at later ages selects for smaller embryos (Sibly and Calow 1986). Given a necessary trade-off between number and size of offspring (Roff 2002; p. 257), higher mortality late in life is expected to simultaneously increase the number of embryos as embryo size decreases.

These predictions are largely supported by intraspecific field studies of various species found across gradients of predation in fishes (Poecilia reticulata: Reznick et al. 1996 and references herein; Gambusia hubbsi: Downhower et al. 2000; Brachyrhaphis rhabdophora: Johnson and Belk 2001; Brachyrhaphis
episcopi: Jennions and Telford 2002; Rivulus hartii: Walsh and Reznick 2009), an amphipod (Hyalella azteca: Wellborn 1994), a copepod (Daphnia ambigua: Walsh and Post 2011), and a lizard (Sceloporus undulatus: Tinkle and Ballinger 1972). These predictions are also supported by laboratory (Drosophila melanogaster: Gasser et al. 2000) and field (P. reticulata: Reznick et al. 1990) experimental evolution studies that have manipulated mortality rate and measured evolved changes in life history phenotype. Moreover, data from fisheries are consistent with these models. Maturation at younger age is observed as a by-product of heavy fishing pressure - where larger fish are often the most intensively harvested (Sharpe and Hendry 2009). Here we extend life history predictions to the interspecific level, asking if life histories of species living in contrasting environmental regimes vary as predicted by theory. At the same time, we incorporate other, potentially interacting, factors that might affect life history evolution.

Predation, latitude, and disturbance regimes are potentially important environmental factors in shaping life histories. Predation is a key factor in nature (Lima 1998; Langerhans 2006; Hawlena and Schmitz 2010), structuring communities (Paine 1966; Sih et al. 1985), acting as a selective factor that induces phenotypic divergence (Endler 1995; Vamosi 2005), and influencing life history patterns in fishes (see above). Latitude is also associated with life history patterns in fishes (Vila-Gispert et al. 2002; Heibo et al. 2005), squamates (James and Shine 1988; Angilletta et al. 2004), and birds (Griebeler et al. 2010). This
relationship may be a by-product of higher predation levels at lower latitudes (Sih et al. 1985; Pennings and Silliman 2005), or a consequence of resource seasonality or length of breeding seasons (Griebeler et al. 2010). Flow regime is one of the most important disturbance factors in freshwaters (Poff et al. 1997). The correlation between flow regime and life history variation has been proposed (Johnson and Bagley 2011), but has yet to be tested. Floods in mountain rivers cause high mortailities, specially in fish of smaller size (Chapman and Kramer 1991; Grether et al. 2001). Theoretically, these high differential mortalities could have an effect on life history evolution.

The genus Gambusia is an excellent system for a macroevolutionary lifehistory study. Gambusia species are naturally distributed along a large latitudinal gradient from North America to Northern Colombia (Rosen and Bailey 1963; Lucinda 2003). Moreover, many species are restricted to distinct predation and flow regimes (Langerhans et al. 2007). For example, G. alvarezi lives only in ponds with other non-piscivorous fish, whereas G. luma lives in streams with multiple predatory fish in the community. These gradients have promoted phenotypic divergence in Gambusia, where predation (Langerhans et al. 2007; Chapter 1), and flow regime (Langerhans and Reznick 2010; Chapter 1) are related to body shape. Here we study the effects of predation and flow regime on life history variation of Gambusia, using the same specimens previously used in analyses of body shape variation (Chapter 1).

Previous studies on several Gambusia species demonstrated a large range of life history variation in the genus (e.g., Hubbs and Mosier 1985; Reznick and Miles 1989; Downhower et al. 2000; Riesch et al. 2010a; Riesch et al. 2010b; Johnson and Bagley 2011; Pires et al. 2011a). However, few of these data were useful to test our adaptive hypothesis for three reasons. First, our main objective was to study interspecific variation across the genus, while most previous reports focused on intraspecific variation. Second, previous studies have methodological differences that make comparison difficult (e.g., studies differ in the way they account for the effect of female body size). Third, one of our aims was to use a multivariate approach to account for covariation among life history traits, while accounting for size and pregnancy. Previous studies vary in the traits analyzed and they dealt with the effect of size and pregnancy in different ways.

Our main objective was to analyze interspecific life history variation in female Gambusia using 20-species from varying predation and flow regimes. Our survey includes those Gambusia species that show little intraspecific habitat variation. We analyzed size at maturity, embryo size, fecundity, reproductive allotment, and mode of maternal provisioning (matrotrophy). Additionally, the variation in intraspecific allometric coefficients of embryo size, fecundity, and ovary weight were examined. We analyzed life history traits individually and, to account for their correlation, as composite variables. We used phylogenetically
informed statistical methods to test whether interspecific life history variation is explained by female body size, predation, flow, and latitude.

## Methods

## Source of specimens and habitat characterization

We analyzed preserved specimens from museum and personal collections (Table 2.1). The same collections were used for a study of body shape (Chapter 1), where further details about sampling, localities, and habitat characterization can be obtained (Table 1.1 and Appendix 1.1). Briefly, predation and flow regimes of each locality were determined by analyzing original field notes. The predation regime of each site was estimated from the inventory of the fish community at that site. Low-predation (LP) localities had only non-piscivorous fish and highpredation (HP) sites had piscivorous fish. Flow regime was characterized into two levels, low flow (LF, lakes and ponds) and high flow (HF, streams). Geographic coordinates were obtained from plots of data in Google Earth (Google Inc., 2011). Latitude of merged collections (see below) was the average of the original collections' latitudes. After merging collections from the same species that had nearby sites (Table 2.1) there were a total of 1012 specimens representing 20 species from 26 locations. The number of females was reduced to 695 after calculating the minimum size at maturity and excluding females that had partial broods (details below) or were not pregnant.

## Life history data

Following Pires et al. (2011b), we measured female standard length (SL $\pm 0.1$ $\mathrm{mm})$, female wet weight in alcohol ( $\mathrm{W}_{\mathrm{fem}} \pm 0.001 \mathrm{~g}$ ), fecundity ( $\mathrm{N}_{\mathrm{emb}}$, number of embryos), number of broods, ovarian tissue dry weight ( $W_{\text {ovary }} \pm 0.01 \mathrm{mg}$ ), mean embryo weight (Wemb, dry weight of batch of embryos/fecundity, to the nearest 0.01 mg ), and stage of development of embryos. Embryo development was measured using the scale of Haynes (1995) as modified by Pires et al. (2011b). This scale goes from egg (fertilized or not, Stage 0) to embryo ready for birth (Stage 50). When females had an advanced batch of embryos and a group of unfertilized vitellogenic eggs, the weight of the unfertilized eggs were added to the ovarian tissue weight and only the advanced group of embryos was counted as a brood (Turner 1940).

## Statistical analysis: estimation of variables

Minimum size at maturity (SLmin) was estimated for each collection as the SL of the smallest pregnant female with developing embryos (Stage $\geq 2$ ). After calculating SLmin, non-pregnant females were excluded from all analyses. Females with eggs only (Stage 0) were considered non-pregnant because we could not unambiguously discriminate between fertilized and unfertilized eggs. Four females with partially recruited broods and nine with partially spawned broods were excluded because their actual fecundities are unknown. They were
recognized, respectively, by their broods at early- (Stage $\leq 10$ ) or late-stage (Stage 45-50) and by their low fecundities (relative to other females of the same size).

The effects of intraspecific allometry and pregnancy condition on individual-based life history traits ( $\mathrm{N}_{\text {emb }}, \mathrm{W}_{\text {emb }}$, and $\mathrm{W}_{\text {ovary }}$ ) were accounted for by estimating trait values for the hypothetical average-size female late in pregnancy (Stage 50) for each collection. The estimated values were obtained from linear models (Monteiro 1999; Berner 2011), as follows:

$$
\begin{gathered}
\log \text { trait }=\mathrm{I}+\varepsilon \\
\log \text { trait }=\mathrm{I}+\beta_{\text {size }}(\log \mathrm{SL})+\varepsilon \\
\log \text { trait }=\mathrm{I}+\beta_{\text {stage }}(\text { stage })+\varepsilon \\
\log \text { trait }=\mathrm{I}+\beta_{\text {size }}(\log \mathrm{SL})+\beta_{\text {stage }}(\text { stage })+\varepsilon
\end{gathered}
$$

where $I$ is the intercept, trait is each life history trait, $\beta$ is the respective coefficient, stage is the stage of embryo development, and $\varepsilon$ is the error term. Fitting of models to data was quantified with small sample corrected Akaike information criterion (AICC; Anderson and Burnham 2002). The amount of evidence explained by each model was estimated with Akaike weights (Anderson 2008), Bayesian posterior probabilities (i.e. model probabilities) that range from zero (model not explaining variation) to one (model fully explaining variation). Average coefficients and their respective standard errors were calculated as the respective values obtained from each model, weighted with their respective Akaike weight. Model averaging was performed with unconditional estimation (using all models instead of only those including each parameter; Anderson

2008; Grueber et al. 2011). The estimated life history values (Table 2.1) and their respective allometric coefficients ( $\beta_{\text {size }}$ ) were used in further analyses. The allometric coefficients $\left(\beta_{\text {size }}\right)$ of $N_{\text {emb }}$ and $W_{\text {ovary }}$ were considered isometric when if they were equal to three because fecundity and ovary size are a function of body volume, which scales to the third power of SL (Calder 1984). Hence, allometry was positive when $\beta_{\text {size }}>3$ and negative when $\beta_{\text {size }}<3$.

Viviparous organisms, such as Gambusia, can allocate nutrients to embryos throughout the course of pregnancy (Wourms et al. 1988). Modes of allocation vary from lecithotrophy, where mothers allocate nutrients to embryos prior to fertilization via fully yolked eggs, to matrotrophy, where mothers continually provide nutrients to embryos during gestation (Wourms 1981). Matrotrophy ranges from unspecialized, when embryos maintain their weight during gestation using maternal provisioning that compensates metabolic mass loss, to extreme, where embryos increase in weight several times during development (Wourms 1981). Extreme matrotrophy has evolved more than 30 times in vertebrates (Dulvy and Reynolds 1997), including in Poeciliidae (Reznick et al. 2002; Pollux et al. 2009; Pires et al. 2010; Pires et al. 2011b). Some Gambusia species appear to show unspecialized matrotrophy (Marsh-Matthews et al. 2005), although a more thorough survey of matrotrophy of the genus has not been accomplished. In this study we quantify the degree of maternal provisioning in many species of Gambusia allowing for a fuller understanding of their reproductive mode.

We quantified maternal provisioning using the Matrotrophy Index (MI), a measurement of the change in dry embryo weight between fertilization and parturition (Scrimshaw 1945; Wourms et al. 1988; Blackburn 1994; Reznick et al. 2002). It is calculated as $\mathrm{W}_{\text {emb }}$ estimated at birth (Stage 50) divided by $\mathrm{W}_{\text {emb }}$ estimated at fertilization (Stage 0). These estimated values were obtained from a linear regression between $W_{\text {emb }}$ and stage of embryo development. We evaluate whether MI of each collection was higher than 0.7 following Reznick et al. (2002). This threshold of 0.7 is derived from the observation that eggs of oviparous fish species lose on average $30 \%$ of their dry weight during gestation due to metabolism (Wourms 1981). This threshold value is not critical- a value of 0.6 is not much different from 0.8 . However, it is a reasonable benchmark for comparative purposes.

To determine whether life histories match a fast-slow continuum pattern, life history variation was condensed using a Principal Component Analysis (PCA) based on the estimated life-history values for each collection. If life histories form a fast-slow continuum a single principal component (PC) will account for most of the life history variation (Bielby et al. 2007), once interspecific allometry has been accounted for. The variables included in the PCA were SL, SLmin, $\mathrm{N}_{\text {emb }}, \mathrm{W}_{\text {emb }}$, Wovary, all log-transformed. Principal components with eigenvalues larger than one were retained (Tabachnick and Fidell 2001). Scores of retained PCs were used in further analyses. PCA results were represented with Burnaby Back

Projection (Berner 2011), which allows to project variation of each PC in an orthogonal plane from previous PCs.

## Phylogenetic analysis

For each morphological trait $\left(\log S L, \log W_{f e m}, \log S L_{m i n}, \log N_{\text {emb }}, \log W_{\text {emb }}, \log \right.$ $\mathrm{W}_{\text {ovary, }}$ MI, $\beta_{\text {size }}-\mathrm{N}_{\text {emb }}, \beta_{\text {size }}-\mathrm{W}_{\text {emb, }}, \beta_{\text {size }}-\mathrm{W}_{\text {ovary, }}$ MI, and PC scores), we evaluated five adaptive models (models that include independent variables putatively indicating variation in the selective regime):

$$
\begin{gathered}
\text { trait }=\mathrm{I}+\log \mathrm{SL}+\varepsilon \\
\text { trait }=\mathrm{I}+\log \mathrm{SL}+\text { predation }+\varepsilon \\
\text { trait }=\mathrm{I}+\log \mathrm{SL}+\text { flow }+\varepsilon \\
\text { trait }=\mathrm{I}+\log \mathrm{SL}+\text { latitude }+\varepsilon \\
\text { trait }=\mathrm{I}+\log \mathrm{SL}+\text { predation }+ \text { flow +predation*flow }+\varepsilon .
\end{gathered}
$$

The covariate log SL was dropped from the models to avoid autocorrelation when the trait was $\log \mathrm{SL}$, log female wet weight, or PC scores.

We tested three regression models of character evolution (i.e. error structure). The first model was Ordinary Least Squares (OLS), equivalent to a non-phylogenetic approach (i.e., assuming a star phylogeny with no hierarchical structure and contemporaneous tips). The second model (RegPagel; Pagel 1999; Garland et al. 2005; Lavin et al. 2008) begins with a specified hierarchical phylogenetic tree and simultaneously estimates parameter coefficients and $\lambda$, a factor that multiplies the off-diagonal elements of the variance-covariance matrix
of relatedness (Freckleton et al. 2002). The value $\lambda$ indicates strength of phylogenetic signal, from zero (no signal) to one (phylogeny fully explains error structure). The third model was the Ornstein-Uhlenbeck process (RegOU; Lavin et al. 2008), which assumes that divergence tends to be restrained back towards an optimum determined by selection (Garland et al. 1993; Hansen 1997; Butler and King 2004). In this model the regression coefficients and a measure of phylogenetic signal (d) are again estimated simultaneously (Lavin et al. 2008). The value of $d$ ranges from zero (no signal) to one (phylogeny fully explains error structure), to more than one (the optimal error structure comes from a tree that is more hierarchical than the original).

We also used a univariate measure of phylogenetic signal, the parameter K of Blomberg et al. (2003). Vales of K range from zero (variation independent of phylogeny), to less than one (variation departing from Brownian motion), to one (resemblance among relatives fits the expectation of Brownian motion evolution, averaged across the phylogeny), to more than one (resemblance among relatives is higher than expected under Brownian motion). For each variable analyzed, we calculated K and its probability of being larger than zero. This was performed with a randomization procedure that calculates the probability of $\mathrm{K}>0$ as the frequency that the observed phylogenetically correct mean (MSE) was larger than $n$ randomized MSE (Blomberg et al. 2003). In this study, $n=9,999$ replicates. These analyes were performed using phylosignal in the R package picante (Kembel et al. 2010).

The Gambusia phylogeny was the same as that of Chapter 1 (B. Langerhans, unpub., Appendices 1.5-1.7). This molecular phylogeny is a majority (50\%) consensus based upon mitochondrial (ND2, Cyt b) and nuclear (S7) genes. All phylogenetic tests were performed twice, the first time with the original branch lengths (proportional to the units of inferred nucleotide substitution) and the second time with branch lengths set to a constant value of one. The latter alternative reduces the magnification of phenotypic differences that occur when contrasting closely related taxa and assumes that variation occured when clades branch (punctuated evolution). The Gambusia phylogeny had three soft polytomies (multifurcations resulting from lack of resolution at a given node), which may increase the Type I error when calculating the significance of F-values for each coefficient of GLS models. We corrected for polytomies by reducing the degrees of freedom with the equation $N-k-1-z$, where $N$ are the number of tips in the phylogeny, $k$ the number of parameters estimated for the respective model, and $z$ (five in this study) are the number of branches that were set to zero length (i.e., polytomies; Garland and Díaz-Uriarte 1999).

The most supported regression models were chosen using model selection, preferring the models within $\Delta \mathrm{AIC} \mathrm{C}_{\mathrm{C}}=4$. This set of best-supported models was averaged with unconditional estimation (including all models from top set) by weighting coefficients with the respective Akaike weight (Anderson 2008). To facilitate the comparison between models, Evidence Ratios (ER; Anderson 2008) were calculated as $W_{\text {best model }} / w_{i}$, indicating how many times
better a model is against the $i$-th model. OLS, RegPagel, and RegOU analyses were performed using the Matlab program RegressionV2.m (A. R. Ives and T. Garland Jr.; Lavin et al. 2008). Other analyses used R (R Development Core Team 2011), implementing the package ape (Paradis et al. 2004), and code from Berner (2011).

## Results

## Life history variation

Female Gambusia showed a large range of interspecific life history variation. The ranges of individual variation were 17.84-53.30 mm for SL (a 2.99-fold), $0.033-3.127 \mathrm{~g}$ for $\mathrm{W}_{\text {fem }}\left(\mathrm{a} 94.758\right.$-fold), 1-47 for $\mathrm{N}_{\mathrm{emb}}, 0.46-8.12 \mathrm{mg}$ for $\mathrm{W}_{\text {emb }}$ (a 17.66 -fold), and $1.90-195.53 \mathrm{mg}$ for $\mathrm{W}_{\text {ovary }}$ (a 102.91 -fold). Table 2.1 shows the interspecific ranges of variation after accounting for intraspecific allometry and pregnancy condition. Maternal provisioning was lecitotrophic for most species, but incipient matrotrophy was observed in G. atrora, G. luma, G. rhizophorae, and G. vittata (Table 2.1). Only one female exhibited more than one brood (G. nicaraguensis, UMMZ 199689, with 16 embryos at stage 20 and eight at stage 45). This female was excluded from further analyses.

At the intraspecific level, body size and pregnancy condition accounted for a considerable proportion of variation in $N_{\text {emb }}, W_{\text {emb }}$, and $W_{\text {ovary }}$ (Appendix 2.1). In most species, larger females had more embryos and heavier ovaries (positive
$\beta_{\text {size }} N_{\text {emb }}$ and $\beta_{\text {size }} W_{\text {ovary }}$ values, respectively). However, the proportionality between female size and fecundity and gonadal weight showed considerable variation. The allometric coefficient of $\mathrm{N}_{\text {emb }}\left(\beta_{\text {size }} \mathrm{Nemb}\right.$ ) varied from negative allometry ( $\beta_{\text {size }} N_{\text {emb }}<3$ in three collections of three species) to isometry ( $\beta_{\text {size }}$ $N_{\text {emb }}=3$ ) in remaining collections. $\beta_{\text {size }} W_{\text {ovary }}$ varied from negative allometry ( $\beta_{\text {size }}$ $W_{\text {ovary }}<3$ in $G$. aurata), to isometry ( $\beta_{\text {size }} W_{\text {ovary }}=3$ ), to positive allometry ( $\beta_{\text {size }}$ $W_{\text {ovary }}>3$ in nine collections). Wemb increased with female body size ( $\beta_{\text {size }} W_{\text {emb }}>$ 0 ) in eight collections of six species. The number of embryos remained constant through pregnancy ( $\beta_{\text {stage }} \mathrm{N}_{\text {emb }}=0$ ) except for three collections with embryo loss ( $\beta_{\text {stage }} N_{\text {emb }}<0$ ). In the majority of collections, embryo and gonadal weight decreased throughout pregnancy ( $\beta_{\text {stage }} \mathrm{W}_{\text {emb }}$ and $\beta_{\text {stage }} \mathrm{W}_{\text {ovary }}<0$ ), but in others these weights remained constant.

Interspecific analyses showed patterns of correlation among traits and a phylogenetic effect on environmental factors and body size but not on life-history traits. PCA produced two PCs that condensed $94 \%$ of variation (Table 2.2). PC 1 was strongly related to body size; species with larger mean female size matured at larger sizes and had heavier embryos and ovaries. PC 2 showed a negative correlation between fecundity and embryo weight (Figure 2.1). Phylogenetic signal (K) was high for latitude, low for predation and size variables (SL, $\mathrm{W}_{\text {fem }}$, PC 1), and negligible for life history traits (Table 2.3). Regression results showed that the best-supported models for $\log \mathrm{SL}, \log \mathrm{W}_{\text {fem }}, \log \mathrm{SL}_{\text {min }}$, and PC 1 were RegOU models with low levels of phylogenetic signal ( $\mathrm{d}=0.007-0.159$ ). The best-
supported models for the remaining life-history traits were non-phylogenetic (Table 2.4). For the RegOU and RegPagel models, the phylogenetic tree that best-fit the data was the molecular phylogeny with branch lengths proportional to nucleotide substitution rate.

At the interspecific level, body size and predation were correlated with life history traits. Larger species had heavier embryos and heavier ovaries (Table 2.4). Larger species also had higher $\beta_{\text {size }} N_{\text {emb }}$ and $\beta_{\text {size }} N_{\text {emb }}$ (Table 2.4), indicating that when they grow their fecundities and reproductive allocations increase at a higher rate. As predicted by theory, high predation species tended to have higher fecundities (log $\mathrm{N}_{\mathrm{emb}}$ ) and heavier gonads ( $\mathrm{W}_{\mathrm{emb}}$ ). However, these patterns were not significant. Predation was correlated with $\beta_{\text {size }} W_{\text {ovary }}$ (Table 2.4, Figure 2.3), suggesting that HP species allocate proportionally more to ovaries with growth. Flow or latitude were not strong predictors of any life history trait.

## Discussion

We found remarkable life history variation across Gambusia, in agreement with previous reviews of poeciliid life history (Johnson and Bagley 2011; Pires et al. 2011a). At the intraspecific level, female body size and stage of embryo development proved to be significant factors for life histories of many species, although in variable ways. At the interspecific level, phylogeny had a small effect on female body size but its effect on life history traits was null. The best predictor
of interspecific life history variation was female body size and predation. Body size also explained the allometric variation in life-history traits among collections ( $\beta_{\text {size }}$ coefficients). The effect of predation on life histories coincided with some of the predictions (high predation species tended to have more embryos and heavier gonads), but that pattern was tenuous. Interestingly, we observed a rare life-history pattern, high-predation species allocated proportionally more to ovaries when growing (i.e., high-predation was correlated with high $\beta_{\text {size }} W_{\text {ovary }}$ ).

The response of interspecific life history of female Gambusia to predation regime showed a pattern that partially matched the predictions derived from life history theory. We predicted that HP females would have lower size at maturity, higher fecundity, smaller embryos, and higher reproductive allocation. Instead, we observed a tenuous pattern of HP females having larger size at maturity, higher fecundity, and higher reproductive allocation (Table 2.4). This pattern is blurry in comparison with the sharp contrasts in life histories that have been documented at the intraspecific level for several species living along predation gradients (e.g., Reznick and Endler 1982). A mischaracterized predation regime may be responsible of this blurry pattern. However, we observed in Chapter 1 a clear effect of predation on female body shape of these same females analyzed here. Moreover, predation was strongly correlated with one life history trait ( $\beta_{\text {size }}$ Wovary, further discussion below). This mitigated predictive power of life history theory at the macroevolutionary level may result from the nature of life history traits. These traits experience strong levels of selection in different directions
from multiple ecological factors (Arnold et al. 2001). This strong selection erodes additive genetic variation, what may explain the common observation of low heritabilities in life history traits (Roff 1992: 12). In agreement with this idea of selection quickly moving life history phenotypes in multiple directions, life history traits typically show low levels of phylogenetic signal (Blomberg et al. 2003; this study). This implies that close phylogenetic relatedness accounts for a small proportion of the larger observed variation in these traits. If life history traits are influenced by multiple selective factors, the adaptive landscape of life history traits is relatively flat, as it has been suggested (Arnold et al. 2001). In this case, the direction of evolutionary divergence may differ between micro- and macroevolutionary scales, what would explain the mismatch between this study and the previous ones about the effect of predation on life histories. Only the negative correlation between fecundity and embryo size showed a continuum between evolutionary scales (Table 2.2, Figure 2.1). This negative association between fecundity and embryo size has been previously observed in populations of some poeciliid species (e.g., Riesch et al. 2010b; Ponce de León et al. 2011), and there is accumulating evidence on the trade-off between number and size of offspring in multiple organisms at different taxonomic scales (Smith and Fretwell 1974; Roff 2002; p. 257).

Flow was not related to Gambusia life history. Two issues could obscure a possible correlation between flow and life history. First, there is a negative correlation between predation and flow regimes in the samples that we studied
here ( $r=-0.75$, Chapter 1 ). Such high correlation indicate multicollinearity (Slinker and Glantz 1985). Therefore, linear models that had both factors as independent variables could have results with one factor obscuring the effect of the other (Tabachnick and Fidell 2001). However, flow was not a good predictor of life histories, even when it was the only dependent variable in the model (Table 2.2). The second issue was the flow regime was classified coarsely, contrasting lotic (streams) vs. lentic (lacustrine) habitats. This typically used contrast is problematic because lotic and lentic systems differ in multiple aspects beside flow velocity (Wetzel and Likens 2000). Moreover, each habitat may vary spatially (microhabitat heterogeneity; Church 2002; Wohl and Merritt 2008) or temporarily (flow seasonality; Sabo and Post 2008). Further studies on the effect of flow on the phenotype of Gambusia could refine this characterization of flow with more hydrologically-informed methods (e.g., Sabo and Post 2008).

Latitudinal values were related with Gambusia's phylogeny but not with its life history. Latitudinal distribution is commonly related with phylogenetic relatedness (Blomberg et al. 2003; Rezende et al. 2004; Oufiero et al. 2011), indicating that closely related species are distributed in proximity to their closer relatives. Latitude is also commonly related to life history patterns in vertebrates (James and Shine 1988; Vila-Gispert et al. 2002; Angilletta et al. 2004; Heibo et al. 2005; Traynor and Mayhew 2005; Griebeler et al. 2010), although the relation sometimes is absent (Hubble 2003). The underlying explanation for this pattern is not clear. One alternative is that predation is higher at lower latitudes (Pennings
and Silliman 2005). Here, regardless of the wide latitudinal range covered by our sampling (> $18^{\circ}$ of latitude), we found no correlation of life histories with latitude.

Body size was a strong predictor of some aspects of Gambusia life histories (Appendix 2.1, Table 2.4). Larger female size was correlated with higher fecundities among females within each collection and among species (the latter marginally). Similarly, female body size was related with ovary weight at intraand interspecific levels. The correlations between body size and fecundity, and body size and reproductive investment are very common patterns in nature (Roff 1992; Sokolovska et al. 2000; Roff 2002). These correlations may indicate that larger females can invest more in reproduction because they have more abdominal space, or are better able to acquire resources (Roff 1992). Regarding embryo size, species with larger females had larger embryos. The correlation between female body size and propagule size is common in nature, although its functional explanation is not fully understood (Roff 1992: 347; 2002 :171; Davis et al. 2012). Larger offspring may have higher fitness, e.g., due to higher survivorship (Roff 2002: p. 258), and larger females may have more space or resources to allocate to each embryo (Forsman and Shine 1995). We did not find support for the idea that female body size limits embryo size in Gambusia. If abdominal size was the limitation for embryo size, then species with larger females would have shown the least increase in embryo size with increases with body size ( $\beta_{\text {size }} W_{\text {emb }}$ smaller in larger species), but we found a marginally significant opposite trend (Table 2.4).

Allometric coefficients of life history traits exhibited a relation with body size and, in the case of ovarian weight, with predation. The adaptive significance of allometric coefficients have been frequently studied in the context of sexual selection. Typically, larger individuals exhibit larger sexually-selected traits (Baker and Wilkinson 2001). In contrast, in ecomorphological analysis, variation in allometric coefficients is commonly seen as an inconvenience in the data rather than data itself (e.g., heterogeneity of slopes is a violation of an ANCOVA assumption). Here we took a different approach, accounting for allometric heterogeneity and testing the effect of body size and environmental factors on the allometric coefficients. We found that females of larger species increase in fecundity, embryo size, and ovary size at greater rates as they grow (Table 2.4). The latter also occurs in Gambusia affinis, where females invest more in reproduction at larger body sizes (Billman 2011). Few studies have tested the effect of an ecological factor on allometry (Kelly et al. 2000; Jennions and Kelly 2002; Egset et al. 2011), and this is the first to do so with life history traits or at the interspecific level. Previous studies have analyzed the allometry of morphological characters, across populations, and in relation with predation regime. They found no differences among populations (Egset et al. 2011), or small differences not related with predation (Kelly et al. 2000; Jennions and Kelly 2002). Here we found considerable allometric differences among species (Appendix 2.2), and an effect of predation on the allometric coefficient of ovary
weight (Table 2.4, Figure 3). To the best of our knowledge, this is the first report of an allometric coefficient responding to an environmental selective regime.

The pattern of covariation among life history traits in Gambusia did not fit a "fast-slow continuum". Macroevolutionary patterns of life history variation have been traditionally fitted along a "pace of life" axis, from "slow" to "fast" life histories. Few studies have assessed the prevalence of this continuum, and fewer still do so while accounting for phylogeny (Clobert et al. 1998; Sæther and Bakke 2000; Bielby et al. 2007). Two life history traits in Gambusia aligned along a fast-slow continuum: species with higher fecundities had smaller embryos (a fast pace of life). However, fast-pace-of-life female Gambusia wither did not mature at smaller sizes or have larger reproductive allocation, two characteristics expected in a fast pace of life mode. The absence of these traits in the life history axis was not likely because of a lack of variation (Table 2.1). As an alternative, this could be another example of the variability in the patterns of life history trait covariation (Jeschke and Kokko 2009), which, in addition to reports of life history alignment along more than one axis of variation (Bielby et al. 2007), limit the utility of the slow-fast continuum to represent life histories.

Maternal provisioning showed little variation in Gambusia (MI range from 0.45 to 1.24 ). These values indicate that maternal provisioning within the genus ranges from lecithotrophy to incipient matrotrophy, as previously concluded for some species of Gambusia in studies with radiolabeled transfer methods (MarshMatthews et al. 2010). Another reproductive strategy found in some poeciliid
fishes is superfetation - a pregnant female simultaneously carrying two or more litters of embryos at different developmental stages. Superfetation has been observed in several families of viviparous fish including Poeciliidae and it has been reported for few species of Gambusia (Turner 1940; Scrimshaw 1945; but see Meffe 1985). In our survey we only found one superfetatious female (of $G$. nicaraguensis). Our results indicate that, in the species of Gambusia analyzed, superfetation is a rare irregularity expressed in few specimens rather than a regular mode of breeding. Such rare cases of isolated individuals expressing superfetation have previously been reported for some members of Poeciliidae (Hubbs 1971; Meffe 1985; Pires et al. 2011a; DNR, pers. obs.).

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Table 2.1. Environmental characteristics and average life histories of Gambusia samples. Predation (P) and Flow
(F) levels were either low (L) or high (H). Sample size (n) for each collection corresponds to the total number of
individuals analyzed for estimating $S L_{\text {min }}$ over the number of individuals used in further analyses. Embryo number,
and embryo and ovary dry weights are estimated values at birth for the average SL female.

| ID Species | Collection ${ }^{\text {a }}$ | P | F | Latitude | n | $\begin{gathered} \mathrm{SL} \\ (\mathrm{~mm}) \end{gathered}$ | Fem. wet w. (g) | $\begin{aligned} & \mathrm{SL}_{\text {min }} \\ & (\mathrm{mm}) \end{aligned}$ | $\begin{gathered} \# \\ \text { emb. } \end{gathered}$ | Emb. weight (mg) | Ovary weight (mg) | MI |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1 G. alvarezi | UMMZ 211110 | L | L | 27.010 | 30/16 | 28.79 | 0.507 | 25.13 | 9.0 | 2.51 | 24.93 | 0.69 |
| 2 G. atrora | AMNH 40812, AMNH 77929 | H | H | 21.499 | 35/28 | 27.74 | 0.289 | 22.49 | 4.8 | 2.68 | 13.59 | 0.93 * |
| 3 G. atrora | UMMZ 169499, UMMZ210724 | H | H | 21.438 | 59/41 | 25.29 | 0.200 | 19.86 | 3.5 | 2.59 | 10.07 | 0.72 |
| 4 G. aurata | AMNH75821, RBL | L | L | 22.765 | 18/13 | 24.05 | 0.232 | 18.20 | 4.9 | 1.08 | 4.62 | 0.81 |
| 5 G. baracoana | USNM 204442 | H | L | 20.350 | 30/12 | 28.25 | 0.317 | 24.13 | 9.7 | 1.12 | 11.58 | 0.75 |
| 6 G. clarkhubbsi | TCWC 11880-09, TCWC 11882-07, TCWC 11887-08 | L | H | 29.369 | 34/24 | 27.58 | 0.312 | 20.40 | 3.9 | 2.03 | 9.43 | 0.45 |
| 7 G. geiseri | TNHC 9132, TNHC 9146 | L | L | 29.876 | 70/55 | 25.21 | 0.212 | 17.86 | 6.8 | 0.71 | 4.87 | 0.54 |
| 8 G. hurtadoi | UMMZ 196737, UMMZ 211112 | H | H | 27.030 | 59/28 | 24.74 | 0.286 | $19.91{ }^{\text {b }}$ | 7.3 | 1.75 | 14.00 | 0.74 |
| 9 G. krumholzi | KU 7341 | H | L | 28.412 | 30/23 | 37.97 | 0.835 | 29.21 | 17.0 | 3.19 | 60.99 | 0.55 |
| 10 G. lemaitrei | UIST (uncatalogued) | H | L | 10.734 | 21/13 | 22.79 | 0.223 | 18.47 | 8.0 | 1.21 | 9.73 | 0.89 |
| 11 G. luma | FMNH 87628, FMNH 94163 , UMMZ 197235, UMMZ 197258 | H | H | 16.169 | 69/29 | 30.06 | 0.466 | 23.93 | 5.5 | 1.65 | 9.26 | $0.89{ }^{(*)}$ |
| 12 G. manni | ANSP 103450, ANSP 103452, RBL | H | L | 25.047 | 75/48 | 27.12 | 0.322 | 20.49 | 3.8 | 2.55 | 11.16 | 0.75 |
| 13 G. hubbsi | UMMZ 202727 | H | L | 25.700 | 21/16 | 27.02 | 0.362 | 19.98b | 8.1 | 0.88 | 8.02 | 0.56 |
| 14 G. melapleura | USNM 205559 | L | H | 18.300 | 26/21 | 33.02 | 0.712 | 24.01 | 6.3 | 2.11 | 14.64 | 0.81 |
| 15 G. nicaraguensis | UMMZ 199657, UMMZ 199689 | H | H | 15.358 | 40/30 | 28.75 | 0.418 | $20.41^{\text {b }}$ | 15.4 | 0.99 | 19.38 | 0.87 |
| 16 G. oligosticta | UMMZ 190129, RBL | H | L | 17.929 | 38/31 | 22.48 | 0.189 | 17.84 | 7.7 | 0.92 | 7.78 | 0.48 |
| 17 G. punctata | AMNH 96308 | H | H | 22.699 | 20/14 | 40.24 | 1.222 | 33.61 | 7.6 | 3.32 | 29.14 | 0.84 |
| 18 G. punctata | AMNH 96320 | H | H | 22.721 | 20/14 | 46.30 | 1.685 | 33.49 | 7.7 | 4.43 | 39.61 | 0.63 |


| ID Species | Collection ${ }^{\text {a }}$ | P | F | Latitude | n | $\begin{gathered} \mathrm{SL} \\ (\mathrm{~mm}) \end{gathered}$ | Fem. wet w. (g) | SLmin (mm) | $\begin{gathered} \# \\ \text { emb. } \end{gathered}$ | Emb. weight (mg) | Ovary weight (mg) | MI |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 19 G. punctata | USNM 203197, USNM 203198 | H | H | 21.117 | 60/50 | 41.79 | 1.290 | 32.04 | 11.7 | 3.24 | 38.27 | 0.78 |
| 20 G. rhizophorae | TCWC 2577-02, TCWC 8671-01, UMMZ 213650, RBL | H | L | 24.857 | 39/15 | 29.13 | 0.516 | 18.32 | 3.7 | 2.10 | 6.71 | 1.24 |
| 21 G. sexradiata | UMMZ 210795, UMMZ 196655 | H | L | 18.024 | 58/39 | 29.17 | 0.590 | 24.63 | 10.7 | 1.16 | 13.81 | 0.73 |
| 22 G. vittata | AMNH 75838 | H | H | 21.338 | 20/15 | 31.63 | 0.405 | 28.50 | 5.4 | 3.26 | 19.26 | 0.96** |
| 23 G. vittata | UMMZ 192503 | H | H | 23.324 | 27/24 | 26.44 | 0.255 | 20.36 | 4.6 | 1.71 | 7.79 | 0.64 |
| 24 G. vittata | UMMZ 97513 | H | H | 21.989 | 30/29 | 23.24 | 0.191 | $19.48{ }^{\text {b }}$ | 9.9 | 0.92 | 10.60 | 0.65 |
| 25 G. vittata | UMMZ 97517 | H | H | 21.064 | 30/25 | 27.98 | 0.285 | 22.95 | 12.4 | 1.13 | 18.04 | 0.81 |
| 26 G. wrayi | USNM 205574, UF 25054 | H | L | 18.024 | 55/42 | 37.50 | 0.888 | 27.80 | 13.6 | 1.65 | 23.74 | 0.70 |
|  | Minimum |  |  | 10.734 | - | 22.48 | 0.189 | 17.84 | 3.5 | 0.71 | 4.62 | 0.45 |
|  | Maximum |  |  | 29.876 |  | 46.30 | 1.685 | 33.61 | 17.0 | 4.43 | 60.99 | 0.89 |
|  | Times-Fold |  |  | 2.783 | - | 2.06 | 8.909 | 1.88 | 4.9 | 6.22 | 13.20 | 1.98 |

$\mathrm{SL}=$ standard length. SLmin=minimum size at maturity. $\mathrm{Ml}=$ matrotrophy index. ${ }^{\text {a }}$ Institutional abbreviations follow Sabaj-Perez (2010), except for RBL, a personal collection of one of the authors. Collections with multiple catalog numbers correspond to data from nearby collections (same species and environmental regimes) that were merged to increase sample size. Further details in Table 1.1 and Appendix 1.1.
${ }^{\mathrm{b}}$ These are the only collections without juvenile females smaller than the minimum size at maturity. These $\mathrm{SL}_{\text {min }}$ values were rather low compared with other Gambusia species, suggesting an overestimation of size at maturity was unlikely. P-values of MI: $0.1>$ (*) $^{*}>0.05>*$.

Table 2. 2. Principal Component Analysis of log-transformed life history traits.

|  | PC 1 | PC 2 | PC 3 | PC 4 | PC 5 |
| :--- | :---: | :---: | :---: | :---: | :---: |
| \% Variance | 69.4 | 24.7 | 4.3 | 1.4 | 0.1 |
| Cumul. \% Variance | 69.2 | 94.2 | 98.5 | 99.9 | 100.0 |
| Eigenvalue | 3.5 | 1.2 | 0.2 | 0.1 | 0.0 |
| Loadings |  |  |  |  |  |
| Standard Length | -0.505 | 0.070 | 0.629 | 0.584 | 0.065 |
| Size at Maturity | -0.519 | 0.018 | 0.320 | -0.792 | -0.028 |
| Number embryos | -0.245 | -0.796 | -0.148 | 0.101 | -0.523 |
| Embryo dry weight | -0.394 | 0.581 | -0.433 | 0.116 | -0.554 |
| Ovary dry weight | -0.510 | -0.154 | -0.542 | 0.089 | 0.644 |

Table 2.3. Phylogenetic signal (K) of dependent and independent variables. Dependent variables are the estimated values for the hypothetical mean-size female. $\beta_{\text {size }}=$ allometric coefficient. K was calculated with the original tree ( $\mathrm{K}_{\mathrm{m}}$ ) with branch lengths proportional to rate of nucleotide substitution, and with a tree with arbitrary constant branch lengths (all $=1, \mathrm{~K}_{\mathrm{c}}$ ). $P$-values indicate the probability that phylogenetic signal is present based on a randomization test of the mean squared error (Blomberg et al., 2003).

| Variable |  | $\mathrm{K}_{\mathrm{M}}$ | $P$ |  | $\mathrm{~K}_{\mathrm{C}}$ | $P$ |
| :--- | :--- | :--- | :--- | :--- | :---: | :---: |
|  |  | 0.138 | 0.077 |  | 0.361 | 0.334 |
| Predation |  | 0.195 | $\mathbf{0 . 0 0 6}$ |  | 0.406 | 0.118 |
| Flow |  | 0.824 | $\mathbf{0 . 0 0 0}$ |  | 1.307 | $\mathbf{0 . 0 0 0}$ |
| Latitude |  | 0.126 | 0.058 |  | 0.515 | $\mathbf{0 . 0 0 7}$ |
| Standard Length |  | 0.183 | $\mathbf{0 . 0 1 1}$ |  | 0.649 | $\mathbf{0 . 0 0 1}$ |
| Female wet weight |  | 0.091 | 0.138 |  | 0.398 | 0.100 |
| Minimum size at maturity |  | 0.09 |  |  |  |  |
| $\beta_{\text {size }}$ number of embryos |  | 0.059 | 0.138 |  | 0.604 | 0.691 |
| Number of embryos |  | 0.048 | 0.707 |  | 0.282 | 0.808 |
| $\beta_{\text {size }}$ mean emb. dry w. |  | 0.103 | 0.087 |  | 0.449 | 0.063 |
| Mean embryo dry weight |  | 0.092 | 0.110 |  | 0.437 | 0.062 |
| $\beta_{\text {size }}$ ovary dry w. |  | 0.103 | 0.134 |  | 0.764 | 0.060 |
| Ovary dry weight |  | 0.077 | 0.262 |  | 0.379 | 0.350 |
| Matrotrophy Index |  | 0.087 | 0.276 |  | 0.451 | 0.210 |
| Principal Component 1 |  | 0.091 | 0.137 |  | 0.395 | 0.092 |
| Principal Component 2 |  | 0.053 | 0.579 |  | 0.303 | 0.551 |

Table 2.4. Regressions, showing best-supported model and average model for each trait. $\mathrm{S}=\log \mathrm{SL} . \mathrm{P}=$ Predation.
$F=F l o w . L=L a t i t u d e$. Five adaptive models were tested for each dependent variable: $M \sim S, M \sim S+P, M \sim S+F, M \sim S+L$,
$M \sim S+P+F+L$, where $S=\log S L, P=P r e d a t i o n, F=F l o w$, and $L=L$ atitude. When log $S L$ or $P C$ scores were the
dependent variables, S was not used as a covariate. The three models of character evolution tested were ordinary
least-squares (OLS, non-phylogenetic), Pagel's (RegPagel), and Ornstein-Uhlenbeck (RegOU). Branch-length
transformations were either proportional to molecular distances $(M)$ or constant $(C)$ branch lengths. The value $w$ is
the Akaike weight for the best model or the cummulative weight (within $\Delta A I C_{C}=4$ ) for the average model of each
trait. The value $d$ is the phylogenetic signal for RegOU models. $\mathrm{SL}=$ standard length, $\mathrm{W}_{\text {fem }}=$ female wet weight.
$S_{\text {min }}=$ minimum size at maturity. $\beta_{\text {size }}=$ allometric coefficient. Nemb $=$ number of embryos. $W_{\text {emb }}=m e a n$ embryo weigh.
$W_{\text {ovary }}=$ ovary dry weight. $\mathrm{MI}=$ matrotrophy index. $\mathrm{PC}=$ principal component. Full list and further details of top-set
models in Supplementary Materials.

| Trait | Model | Character Evolution | Tree | w | d | Coefficient $\pm$ SE ${ }^{\text {p-value }}$ |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  |  |  | $\log$ SL | Predation |  | Flow | Latitude |  |
| $\log$ SL | P | RegOU | M | 23.5 | 0.039 |  | $0.107 \pm 0.086$ | 0.234 |  |  |  |
|  | Average | - | - | 84.7 | - |  | $0.039 \pm 0.070$ |  | $0.011 \pm 0.042$ | $<0.001 \pm 0.004$ |  |
| $\log \mathrm{W}_{\text {fem }}$ | P | RegOU | M | 29.4 | 0.159 |  | $0.404 \pm 0.260$ |  |  |  |  |
|  | Average | - | - | 82.3 | - |  | $0.153 \pm 0.242$ |  | $-0.013 \pm 0.114$ | $<0.001 \pm 0.014$ |  |
| $\log \mathrm{L}_{\text {min }}$ | $P$ | RegOU | M | 22.3 | 0.007 |  | $0.114 \pm 0.093$ | 0.240 |  |  |  |
|  | Average | - | - | 90.8 | - |  | $0.044 \pm 0.080$ |  | $0.029 \pm 0.061$ | $<0.001 \pm 0.004$ |  |
| $\beta_{\text {size }} \mathrm{N}_{\text {emb }}$ | S | OLS | - | 25.2 | - | $2.044 \pm 0.761^{0.013}$ |  |  |  |  |  |
|  | Average | - | - | 76.1 | - | $1.691 \pm 0.758$ | $0.162 \pm 0.309$ |  | $-0.004 \pm 0.077$ | $-0.004 \pm 0.015$ |  |
| $\log \mathrm{N}_{\text {emb }}$ | S | OLS | - | 20.1 | - | $0.832 \pm 0.462{ }^{0.086}$ |  |  |  |  |  |
|  | Average | - | - | 66.9 | - | $0.634 \pm 0.444$ | $0.017 \pm 0.086$ |  | $-0.029 \pm 0.098$ | $-0.007 \pm 0.015$ |  |
| $\beta_{\text {size }} \mathrm{W}_{\text {emb }}$ | S | OLS | - | 23.3 | - | $0.902 \pm 0.520{ }^{0.097}$ |  |  |  |  |  |
|  | Average | - | - | 70.3 | - | $0.622 \pm 0.528$ | $0.009 \pm 0.074$ |  | $0.056 \pm 0.142$ | $<0.001 \pm 0.005$ |  |
| $\log$ Wemb | S | OLS | - | 16.4 | - | $1.828 \pm 0.394<0.001$ |  |  |  |  |  |
|  | Average | - | - | 78.3 | - | $1.637 \pm 0.432$ | $0.001 \pm 0.039$ |  | $0.057 \pm 0.121$ | $0.003 \pm 0.010$ |  |
| $\beta_{\text {size }} \mathrm{W}_{\text {ovary }}$ | S+P | OLS | - | 45.5 | - | $2.955 \pm 0.612<0.001$ | $0.824 \pm 0.292$ | 0.010 |  |  |  |
|  | Average | - | - | 80.5 | - | $2.397 \pm 0.756$ | $0.659 \pm 0.299$ |  | $<0.001 \pm<0.001$ | $<0.001 \pm<0.001$ |  |
| $\log \mathrm{W}_{\text {ovary }}$ | S | OLS | - | 25.4 | - | $2.739 \pm 0.402<0.001$ |  |  |  |  |  |
|  | Average | - | - | 76.3 | - | $2.402 \pm 0.494$ | $0.087 \pm 0.165$ |  | $0.003 \pm 0.043$ | $-0.001 \pm 0.006$ |  |
| MI | S+L | OLS | - | 29.5 | - | $0.085 \pm 0.169{ }^{0.622}$ |  |  |  | $-0.014 \pm 0.007$ | 0.069 |
|  | Average | - | - | 78.3 | - | $0.068 \pm 0.167$ | $0.009 \pm 0.038$ |  | $0.002 \pm 0.018$ | $-0.006 \pm 0.008$ |  |
| PC 1 | $P$ | RegOU | M | 30.6 | 0.015 |  | $1.428 \pm 0.87$ | 0.118 |  |  |  |
|  | Average | - | - | 76.1 | - |  | $0.615 \pm 0.85$ |  | $0.169 \pm 0.479$ | $-0.002 \pm 0.026$ |  |
| PC 2 | F | OLS | - | 20.6 | - |  |  |  |  | $-0.073 \pm 0.048$ | 0.140 |
|  | Average | - | - | 84.9 | - |  | $0.038 \pm 0.229$ |  | $-0.291 \pm 0.420$ | $-0.029 \pm 0.046$ |  |

Figure 2.1. Representation of the Principal Component 2, showing the relationship between the two variables with loadings $>0.32$ in that axis (following the criterium of Tabachnick and Fidell, 2001). Values were estimated using Burnaby back projection, which projects them in a plane orthogonal Principal Components 1 (Berner, 2011). It is similar to estimating the residuals of PC1, except for producing scores of values in their original scale.


Figure 2.2. Association between mean values of log Standard Length and mean values of life history traits. Original values on left side, phylogenetic independent contrasts (PIC) on right side. Best-fit lines in black. Bottom-left panel with gray line that indicates the threshold value for Matrotrophy Index ( $\mathrm{MI}=0.7$ ). Axes in logarithmic scale. Histograms beside boxes have bar widths proportional to intervals in linear scale. PIC were calculated with original branch lenght tree.


Figure 2.3. Relationship between predation and the allometric coefficient of ovary dry weight for each collection. Filled dots = Low Predation, empty dots = High Predation.

for each rait and each collection. Values were obtained by model averaging the general model (log trait $=I+\beta_{\text {size }}\left(\mathrm{log}\right.$ SL) $+\beta_{\text {stage }}$
stage) $+\varepsilon$ ) and its nested models. ID numbers match Table 2.1. Values of $\beta_{\text {stage }} \pm$ SE are multiplied by 102. Bold indicate (stage) $+\varepsilon$ ) and its nested models. ID numbers match Table 2.1. Values of $\beta_{\text {stage }} \pm S E$ are multiplied by 10 e 2 . Bold indicates

 $-6.40 \pm 2.372 .63 \pm 0.70-0.45 \pm 0.38 \quad 2.22 \pm 1.68-0.27 \pm 0.50-\mathbf{0 . 8 0} \pm \mathbf{0 . 3 2}-10.95 \pm 1.612 .33 \pm 0.48-\mathbf{1 . 1 2} \pm \mathbf{0 . 2 5}$ $\begin{array}{lll}-15.88 \pm 0.69 & 3.65 \pm 0.21 & -1.11 \pm 0.23 \\ -12.92 \pm 0.81 & 2.66 \pm 0.25 & -0.56 \pm 0.31\end{array}$ $-10.39 \pm 1.33 \quad 1.93 \pm 0.41 \quad-2.28 \pm 0.64$ $-17.91 \pm 3.31 \quad 4.13 \pm 1.02-0.67 \pm 0.65$ $-14.11 \pm 0.99 \quad 3.07 \pm 0.30-1.45 \pm 0.30$ $-14.27 \pm 0.92 \quad 3.02 \pm 0.30-1.58 \pm 0.39$ $-17.58 \pm 1.28 \quad 4.19 \pm 0.39-0.29 \pm 0.30$ $-19.23 \pm 1.57 \quad 4.54 \pm 0.43-0.19 \pm 0.39$ $-14.69 \pm 1.97 \quad 3.38 \pm 0.62-1.00 \pm 0.64$ $-19.19 \pm 1.70 \quad 4.47 \pm 0.50-1.38 \pm 0.44$ $\begin{array}{lll}-12.74 \pm 0.92 & 2.48 \pm 0.28 & 0.09 \pm 0.31\end{array}$ $\begin{array}{lll}-15.76 \pm 1.52 & 3.87 \pm 0.51 & -3.66 \pm 0.90 \\ -14.40 \pm 1.35 & 3.06 \pm 0.39 & -1.03 \pm 0.50\end{array}$
 $-12.89 \pm 1.09 \quad 2.61 \pm 0.33-0.21 \pm 0.56$ $-21.46 \pm 1.99 \quad 5.04 \pm 0.55-1.39 \pm 0.40$ $-22.08 \pm 2.63 \quad 4.97 \pm 0.68-0.39 \pm 0.37$ $-21.53 \pm 1.11 \quad 4.95 \pm 0.29-0.42 \pm 0.28$
 $-19.55 \pm 1.89 \quad 4.66 \pm 0.56-0.90 \pm 0.38$ $-19.12 \pm 1.94 \quad 4.59 \pm 0.55-1.39 \pm 0.39$
 $-14.52 \pm 1.63 \quad 3.20 \pm 0.50-0.19 \pm 0.45$

 $0.99 \pm 0.53 \quad 0.09 \pm 0.16-0.68 \pm 0.21$ $2.23 \pm 1.82-0.65 \pm 0.57-0.18 \pm 0.62$
 $3.41 \pm 071 \quad 1.31 \pm 0.23-1.70 \pm 0.30$ $-0.51 \pm 1.06 \quad 0.41 \pm 0.32-0.48 \pm 0.24$ $-0.48 \pm 1.29 \quad 0.60 \pm 0.35-1.05 \pm 0.35$ $3.27 \pm 1.59 \quad 1.12 \pm 0.51-0.05 \pm 0.32$ $-0.69 \pm 1.10 \quad 0.37 \pm 0.32-0.17 \pm 0.24$ $1.23 \pm 0.47-0.01 \pm 0.14-0.53 \pm 0.33$ $0.97 \pm 1.03 \quad 0.54 \pm 0.35-1.84 \pm 0.58$ $0.47 \pm 0.88 \quad 0.41 \pm 0.25-\mathbf{- 0 . 4 6} \pm 0.30$
 $-1.03 \pm 1.04 \quad 0.47 \pm 0.30-1.04 \pm 0.63$ $-2.69 \pm 2.17 \quad 1.13 \pm 0.60-0.60 \pm 0.43$ $-3.12 \pm 2.90 \quad 1.31 \pm 0.74-\mathbf{0 . 8 0} \pm 0.39$ $2.22 \pm 1.82 \quad 0.93 \pm 0.48-0.19 \pm 0.33$ $-2.39 \pm 0.98 \quad 0.95 \pm 0.30-0.11 \pm 0.35$ $0.21 \pm 1.00 \quad 0.20 \pm 0.30-0.66 \pm 0.20$ $2.83 \pm 1.11 \quad 1.15 \pm 0.32 \quad 0.11 \pm 0.19$


 $8.94 \pm 0.953 .29 \pm 0.29-0.83 \pm 0.34$ $-6.34 \pm 0.962 .36 \pm 0.30-0.06 \pm 0.25$ $-5.34 \pm 2.372 .34 \pm 0.73-1.05 \pm 1.1$ $-9.66 \pm 3.47 \quad 3.58 \pm 1.05-0.07 \pm 0.5$ $-4.88 \pm 1.66 \quad 1.88 \pm 0.50-0.02 \pm 0.36$ $-4.02 \pm 0.98 \quad 1.77 \pm 0.32-0.47 \pm 0.44$ $-11.40 \pm 2.03 \quad 3.86 \pm 0.55 \quad 0.38 \pm 0.56$ $-4.30 \pm 2.532 .15 \pm 0.80-0.70 \pm 0.73$ $-10.48 \pm 1.783 .71 \pm 0.53-0.89 \pm 0.50$ $-7.98 \pm 1.04 \quad 2.73 \pm 0.31 \quad 0.61 \pm 0.51$
 $-4.74 \pm 1.272 .40 \pm 0.37-1.18 \pm 0.79$ $-4.48 \pm 1.33 \quad 2.04 \pm 0.39 \quad 0.36 \pm 0.71$ $\pm \pm 2.983 .86 \pm 0.82-1.06 \pm 0.64$ $-12.42 \pm 1.924 .00 \pm 0.51-0.11 \pm 0.34$ $-2.84 \pm 3.051 .26 \pm 0.93-0.23 \pm 0.99$ $-12.03 \pm 2.204 .30 \pm 0.65-0.19 \pm 0.35$ $-9.30 \pm 2.313 .43 \pm 0.66-1.73 \pm 0.47$ $\begin{array}{lll}-3.59 \pm 1.62 & 1.49 \pm 0.51 & 0.48 \pm 0.51 \\ -7.83 \pm 1.76 & 3.16 \pm 0.54 & 0.37 \pm 0.54\end{array}$

 25 G. vittata
Appendix 2．2．Canditate set $(\triangle A I C C=4)$ of regressions for size variables and each life history trait．Five adaptive models were tested for each dependent variable：$M \sim S, M \sim S+P, M \sim S+F, M \sim S+L, M \sim S+P+F+L$ ，where $S=\log S L, P=P r e d a t i o n, F=F l o w, ~ a n d$ $L=L a t i t u d e$ ．The same models without $S$ as the covariate were tested when Standard Length，female weight，size at maturity， and Principal Components as dependent variables．The three models of character evolution tested were ordinary least－ squares（OLS，non－phylogenetic），Pagel＇s（RegPagel），and Ornstein－Uhlenbeck（RegOU）．Branch－length transformations were either proportional to molecular distances（M）or constant（C）branch lengths．$k=$ number of parameters， $\mathrm{InML}=\log$ Maximal Likelihood， AIC $_{c}=$ small sample corrected Akaike Information Criterium，and w＝Akaike weights．Evidence Ratio（ER） indicates the number of times the most－supported model of the set is better supported than each row＇s model．Phylogenetic signal was $\lambda$ for RegPagel，and $d$ for RegOU．


|  | $0.028 \pm 0.0770 .716$ |  |
| :--- | :---: | :---: |
| $0.080 \pm 0.078$ | 0.325 |  |
|  | $0.045 \pm 0.0680 .515$ |  |
| $0.089 \pm 0.078$ | 0.268 |  |
|  | $0.068 \pm 0.0650 .313$ |  |
|  |  | $0.004 \pm 0.0090 .681$ |
|  |  | $0.004 \pm 0.0090 .687$ |

## $0.004 \pm 0.0090 .687$

$-0.008 \pm 0.027 \quad 0.770$
$0.200 \pm 0.2340 .404 \quad-0.008 \pm 0.0270 .770$
$0.008 \pm 0.0290 .778$
$0.030 \pm 0.2030 .8850 .012 \pm 0.0310 .699$
$-0.021 \pm 0.1960 .914$
$\begin{array}{ll}0.030 \pm 0.2030 .885 & 0.008 \pm 0.0290 .778 \\ -0.021 \pm 0.1960 .914 & 0.012 \pm 0.0310 .699\end{array}$
$0.030 \pm 0.2030 .8850 .012 \pm 0.0310 .699$
$-0.021 \pm 0.1960 .914$
1.0
G．
0.2
6.1
0.1
3.1
0
$\infty$
$\begin{array}{ccc}29.4 & 0.159 & 1.0 \\ 11.3 & 0.118 & 2.6 \\ 11.1 & 0.087 & 2.7 \\ 9.4 & 0.787 & 3.1\end{array}$

$\underset{\forall}{\forall} \stackrel{n}{+}$

log Female weight
12.6







$\downarrow$
$\Sigma$
$\Sigma \Sigma \Sigma \cup \cup \cup \cup \cup \cup$


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| Model | Character Evolution | Tree k |  | lnML | AICc | w | $\lambda \text { or } d E$ | Coefficients $\pm$ SE ( $P$-value) |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  |  |  |  |  | $\log$ SL |  | Predation | Flow | Latitude |
| P | RegOU | M | 4 |  | 8.7 | -7.5 | 22.3 | 0.007 | 1.0 |  |  | $0.114 \pm 0.0930 .240$ |  |  |
| F | RegOU | M | 4 | 8.2 | -6.6 | 14.0 | 0.001 | 1.6 |  |  |  | $0.058 \pm 0.0810 .480$ |  |
| F | OLS | - | 3 | 6.7 | -6.4 | 12.8 | - | 1.7 |  |  |  | $0.106 \pm 0.0760 .179$ |  |
| L | RegOU | M | 4 | 8.0 | -6.1 | 11.2 | 0.005 | 2.0 |  |  |  |  | $-0.003 \pm 0.0090 .765$ |
| P | OLS | - | 3 | 6.3 | -5.6 | 8.5 | - | 2.6 |  |  | $0.105 \pm 0.0980 .297$ |  |  |
| P | RegOU | C | 4 | 7.2 | -4.6 | 5.1 | 0.328 | 4.4 |  |  | $0.104 \pm 0.0920 .276$ |  |  |
| F | RegOU | C | 4 | 7.2 | -4.4 | 4.8 | 0.224 | 4.7 |  |  |  | $0.076 \pm 0.0770 .339$ |  |
| L | OLS | - | 3 | 5.7 | -4.4 | 4.7 | - | 4.7 |  |  |  |  | $-0.001 \pm 0.0090 .917$ |
| F | RegPagel | C | 4 | 6.9 | -3.9 | 3.7 | 0.260 | 6.0 |  |  |  | $0.097 \pm 0.0730 .205$ |  |
| P | RegPagel | C | 4 | 6.9 | -3.9 | 3.7 | 0.358 | 6.0 |  |  | $0.131 \pm 0.0930 .178$ |  |  |
| Allometric coefficient of number of embryos |  |  |  |  |  |  |  |  |  |  |  |  |  |
| S | OLS | - |  | -27.6 | 62.3 | 25.2 | - | 1.0 | $2.044 \pm 0.761$ | 0.013 |  |  |  |
| S+P | OLS | - |  | -26.4 | 62.7 | 21.1 | - | 1.2 | $1.870 \pm 0.750$ | 0.021 | $0.540 \pm 0.3570 .146$ |  |  |
| S+L | OLS | - |  | -27.0 | 63.9 | 11.2 | - | 2.3 | $2.087 \pm 0.761$ | 0.012 |  |  | $-0.033 \pm 0.0320 .309$ |
| S+F | OLS | - |  | -27.6 | 65.1 | 6.3 | - | 4.0 | $2.081 \pm 0.798$ | 0.016 |  | $-0.061 \pm 0.3000 .841$ |  |
| S | RegOU | C |  | -27.6 | 65.1 | 6.2 | <0.001 | 4.1 | $2.044 \pm 0.761$ | 0.016 |  |  |  |
| S | RegOU | M |  | -27.6 | 65.2 | 6.1 | <0.001 | 4.1 | $2.044 \pm 0.762$ | 0.016 |  |  |  |
| S+P | RegOU | C |  | -26.4 | 65.8 | 4.5 | <0.001 | 5.6 | $1.870 \pm 0.750$ | 0.024 | $0.540 \pm 0.3570 .150$ |  |  |
| S+P | RegOU | M |  | -26.4 | 65.8 | 4.4 | <0.001 | 5.7 | $1.870 \pm 0.752$ | 0.024 | $0.540 \pm 0.3580 .150$ |  |  |
|  |  |  |  |  |  |  |  |  | log Number | of emb | ryos |  |  |
| S | OLS | - |  | -14.7 | 36.4 | 20.1 | - | 1.0 | $0.832 \pm 0.462$ | 0.086 |  |  |  |
| S+L | OLS | - |  | -13.5 | 36.8 | 16.2 | - | 1.2 | $0.868 \pm 0.452$ | 0.068 |  |  | $-0.028 \pm 0.0190 .153$ |
| S+F | OLS | - |  | -13.7 | 37.3 | 12.6 | - | 1.6 | $0.972 \pm 0.468$ | 0.050 |  | $-0.231 \pm 0.1760 .204$ |  |
| S+P | OLS | - |  | -14.1 | 38.2 | 8.2 | - | 2.5 | $0.763 \pm 0.469$ | 0.118 | $0.213 \pm 0.2230 .351$ |  |  |
| S | RegOU | C |  | -14.7 | 39.2 | 4.9 | <0.001 | 4.1 | $0.832 \pm 0.462$ | 0.090 |  |  |  |
| S | RegOU | M |  | -14.7 | 39.2 | 4.9 | <0.001 | 4.1 | $0.832 \pm 0.463$ | 0.090 |  |  |  |
| S+L | RegOU | C |  | -13.5 | 39.9 | 3.4 | <0.001 | 5.9 | $0.868 \pm 0.452$ | 0.073 |  |  | $-0.028 \pm 0.0190 .158$ |
| S+L | RegOU | M |  | -13.5 | 39.9 | 3.4 | <0.001 | 5.9 | $0.869 \pm 0.454$ | 0.073 |  |  | $-0.028 \pm 0.0190 .157$ |


| Mode | Character Evolution | Tree | $k$ InML AICc |  | w | $\lambda$ ord ER |  | Coefficients $\pm$ SE ( $P$-value) |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  |  | $\log$ SL |  |  | Predation | Flow | Latitude |
| S | OLS | - | 3-17.7 | 42.5 |  | 23.3 | - | 1.0 | $0.902 \pm 0.5200 .097$ |  |  |  |
| S+F | OLS | - | 4-16.9 | 43.8 | 12.0 | - | 1.9 | $0.761 \pm 0.5300 .166$ |  | $0.233 \pm 0.2000 .256$ |  |
| S | RegPagel | M | 4-17.3 | 44.5 | 8.6 | 0.492 | 2.7 | $0.726 \pm 0.5340 .191$ |  |  |  |
| S | RegOU | M | 4-17.4 | 44.7 | 7.7 | 0.001 | 3.0 | $0.790 \pm 0.5840 .193$ |  |  |  |
| S+P | OLS | - | 4-17.5 | 45.0 | 6.7 | - | 3.5 | $0.859 \pm 0.5340 .123$ | $0.135 \pm 0.2540 .602$ |  |  |
| S | RegOU | C | 4-17.6 | 45.2 | 6.2 | 0.279 | 3.8 | $0.561 \pm 0.5750 .343$ |  |  |  |
| S+L | OLS |  | 4-17.7 | 45.3 | 5.8 | - | 4.0 | $0.897 \pm 0.5310 .106$ |  |  | $0.004 \pm 0.0220 .858$ |
| S+F | RegPagel | M | 5-16.3 | 45.7 | 4.7 | 0.625 | 5.0 | $0.510 \pm 0.5260 .346$ |  | $0.343 \pm 0.1940 .097$ |  |
| S | RegPagel | C | 4-18.1 | 46.1 | 3.8 | 0.396 | 6.1 | $0.524 \pm 0.5790 .379$ |  |  |  |
| S+F | RegOU | C | 5-16.6 | 46.3 | 3.5 | 0.442 | 6.7 | $0.249 \pm 0.5790 .673$ |  | $0.324 \pm 0.1970 .119$ |  |
| log Embryo dry weight |  |  |  |  |  |  |  |  |  |  |  |
| S | OLS | - | 3-10.5 | 28.1 | 16.4 | - | 1.0 | $1.828 \pm 0.394$ |  |  |  |
| S+F | OLS | - | $4-9.3$ | 28.5 | 13.5 | - | 1.2 | $1.693 \pm 0.395$ |  | $0.223 \pm 0.1490 .149$ |  |
| S+L | OLS | - | $4-9.8$ | 29.6 | 8.1 | - | 2.0 | $1.804 \pm 0.393$ |  |  | $0.019 \pm 0.0170 .273$ |
| S | RegPagel | C | $4-9.9$ | 29.8 | 7.2 | 0.434 | 2.3 | $1.939 \pm 0.417$ |  |  |  |
| S | RegOU | M | 4-10.0 | 29.8 | 7.1 | 0.006 | 2.3 | $1.894 \pm 0.4420 .001$ |  |  |  |
| S | RegPagel | M | 4-10.2 | 30.2 | 5.7 | 0.324 | 2.9 | $1.888 \pm 0.396$ |  |  |  |
| S | RegOU | C | 4-10.4 | 30.6 | 4.7 | 0.315 | 3.5 | $1.853 \pm 0.436$ |  |  |  |
| S+F | RegPagel | C | $5-8.9$ | 30.9 | 4.2 | 0.333 | 3.9 | $1.804 \pm 0.4210 .001$ |  | $0.173 \pm 0.1420 .240$ |  |
| S+P | OLS | - | 4-10.5 | 30.9 | 4.0 | - | 4.1 | $1.822 \pm 0.4080 .000$ | $0.016 \pm 0.1940 .934$ |  |  |
| S+F | RegPagel | M | $5-9.0$ | 31.0 | 3.9 | 0.162 | 4.2 | $1.758 \pm 0.389$ |  | $0.193 \pm 0.1510 .217$ |  |
| S+F | RegOU | M | $5-9.1$ | 31.3 | 3.5 | 0.002 | 4.7 | $1.817 \pm 0.439$ |  | $0.198 \pm 0.1630 .244$ |  |
| S+L | RegPagel | C | $5-9.3$ | 31.5 | 3.0 | 0.368 | 5.5 | $1.920 \pm 0.419$ |  |  | $0.011 \pm 0.0160 .519$ |
| S+L | RegPagel | M | $5-9.3$ | 31.6 | 2.9 | 0.284 | 5.7 | $1.872 \pm 0.392$ |  |  | $0.020 \pm 0.0180 .290$ |
| S+F | RegOU | C | $5-9.3$ | 31.6 | 2.9 | 0.177 | 5.7 | $1.735 \pm 0.4270 .001$ |  | $0.193 \pm 0.1520 .224$ |  |
| S+L | RegOU | M | $5-9.4$ | 31.7 | 2.7 | 0.005 | 6.1 | $1.886 \pm 0.4420 .001$ |  |  | $0.018 \pm 0.0180 .321$ |
| Allometric coefficient of ovary dry weight |  |  |  |  |  |  |  |  |  |  |  |
| S+P | OLS | - | 4-21.1 | 52.1 | 45.5 | - | 1.0 | $2.955 \pm 0.612<0.001$ | $0.824 \pm 0.2920 .010$ |  |  |
| S+P | RegPagel | M | 5-20.6 | 54.2 | 15.6 | 0.097 | 2.9 | $3.066 \pm 0.594<0.001$ | $0.796 \pm 0.2940 .015$ |  |  |
| $S+P$ | RegOU | C | 5-21.1 | 55.2 | 9.7 | <0.001 | 4.7 | $2.955 \pm 0.612<0.001$ | $0.824 \pm 0.2920 .012$ |  |  |
| $S+P$ | RegOU | M | $5-21.1$ | 55.2 | 9.7 | <0.001 | 4.7 | $2.952 \pm 0.615<0.001$ | $0.824 \pm 0.2920 .012$ |  |  |


| Model | Character Evolution | Tree | k InML AICc |  | w | $\lambda$ ord ER |  | Coefficients $\pm$ SE ( $P$-value) |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  |  | $\log$ SL |  |  | Predation | Flow | Latitude |
| log Ovary dry weight |  |  |  |  |  |  |  |  |  |  |  |
| S | OLS | - | 3-11.0 | 29.2 |  | 25.4 | - | 1.0 | $2.739 \pm 0.402$ |  |  |  |
| S | OLS |  | $4-9.9$ | 29.8 | 19.0 | - | 1.3 | $2.652 \pm 0.398<0.001$ | $0.273 \pm 0.1900 .165$ |  |  |
| S+L | OLS |  | 4-10.8 | 31.5 | 7.8 | - | 3.3 | $2.753 \pm 0.408$ |  |  | -0.011 0.0170 .527 |
| S+F | OLS |  | 4-11.0 | 31.9 | 6.6 | - | 3.9 | $2.708 \pm 0.421$ |  | $0.051 \quad 0.1590 .751$ |  |
| S | RegOU |  | 4-11.0 | 32.0 | 6.2 | 0.008 | 4.1 | $2.748 \pm 0.405$ |  |  |  |
| S | RegOU |  | 4-11.0 | 32.0 | 6.2 | <0.001 | 4.1 | $2.765 \pm 0.415$ |  |  |  |
| S | RegPagel | M | 4-11.2 | 32.4 | 5.1 | <0.001 | 5.0 | $2.769 \pm 0.387$ |  |  |  |
| S | RegOU |  | 5 -9.9 | 32.9 | 4.0 | 0.081 | 6.4 | $2.724 \pm 0.419<0.001$ | $0.283 \pm 0.1900 .157$ |  |  |
| S | RegOU | M | $5-9.9$ | 32.9 | 4.0 | <0.001 | 6.4 | $2.715 \pm 0.436<0.001$ | $0.287 \pm 0.1950 .160$ |  |  |
| S | RegPagel | M | 5-10.1 | 33.1 | 3.5 | 0.375 | 7.3 | $2.945 \pm 0.421<0.001$ | $0.330 \pm 0.1970 .113$ |  |  |
| Matrotrophy Index |  |  |  |  |  |  |  |  |  |  |  |
| S+L | OLS | - | 412.1 | -14.3 | 29.5 | - | 1.0 | $0.085 \pm 0.1690 .622$ |  |  | $-0.014 \pm 0.0070 .069$ |
| S | OLS | - | 310.2 | -13.2 | 17.5 | - | 1.7 | $0.067 \pm 0.1780 .710$ |  |  |  |
| S | OLS | - | 410.9 | -11.9 | 9.1 | - | 3.2 | $0.035 \pm 0.1790 .846$ | $0.100 \pm 0.0850 .255$ |  |  |
| S+L | RegOU | C | 512.1 | -11.2 | 6.3 | 0.144 | 4.7 | $0.081 \pm 0.1820 .662$ |  |  | $-0.014 \pm 0.0080 .091$ |
| S+L | RegOU | M | 512.1 | -11.2 | 6.2 | 0.001 | 4.8 | $0.160 \pm 0.1930 .418$ |  |  | $-0.013 \pm 0.0080 .098$ |
| S+F | OLS | - | 410.4 | -10.8 | 5.2 | - | 5.7 | $0.042 \pm 0.1850 .823$ |  | $0.041 \pm 0.0700 .560$ |  |
| S | RegOU | C | 410.2 | -10.5 | 4.5 | 0.199 | 6.6 | $0.058 \pm 0.1940 .767$ |  |  |  |
| S | RegOU | M | 410.2 | -10.5 | 4.5 | 0.003 | 6.6 | $0.177 \pm 0.2030 .396$ |  |  |  |


| Principal Component 1 |  |  |  |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| P | RegOU | M | 4-49.1 | 108.2 | 30.6 | 0.015 | 1.0 | 1.4 |  |  |
| F | RegOU | M | $4-50.2$ | 110.3 | 10.9 | 0.001 | 2.8 |  | $0.460 \pm 0.7640 .555$ |  |
| F | OLS | - | $3-51.7$ | 110.5 | 9.9 | - | 3.1 |  | $0.936 \pm 0.7230 .209$ |  |
| L | RegOU | M | 4-50.3 | 110.6 | 9.2 | 0.005 | 3.3 |  |  | $-0.020 \pm 0.0830 .813$ |
| P | OLS | - | $3-51.8$ | 110.7 | 8.6 | - | 3.6 | 1.0 |  |  |
| P | RegOU | C | $4-50.6$ | 111.2 | 6.9 | 0.363 | 4.4 | 1.2 |  |  |
| F | RegOU | C | 4-51.1 | 112.2 | 4.2 | 0.245 | 7.3 |  | $0.633 \pm 0.7270 .397$ |  |
| Principal Component 2 |  |  |  |  |  |  |  |  |  |  |
| L | OLS | - | 3-37.9 | 83.0 | 20.6 | - | 1.0 |  |  | $-0.073 \pm 0.0480 .140$ |
| F | OLS | - | 3-38.0 | 83.0 | 20.2 | - | 1.0 |  | $-0.648 \pm 0.4270 .143$ |  |


| Model | Character Evolution | Tree k InML |  | $\mathrm{AlC}_{\mathrm{c}}$ | w | $\lambda$ ord |  | Coefficients $\pm$ SE ( $P$-value) |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  |  |  |  | $\log$ SL | Predation | Flow | Latitude |
| P | OLS | 3 | 3-38.9 |  | 84.9 | 7.7 | - | 2.7 |  | $0.368 \pm 0.5600 .518$ |  |  |
| F | RegPagel | C 4 | $4-37.5$ | 85.0 | 7.5 | <0.001 | 2.8 |  |  | $-0.757 \pm 0.3980 .074$ |  |
| P+F+L | OLS | 5 | 5-36.3 | 85.6 | 5.4 | - | 3.8 |  | $0.175 \pm 0.5760 .764$ | $-0.721 \pm 0.4220 .104$ | $-0.074 \pm 0.0510 .161$ |
| L | RegOU | $C$ | 4-37.9 | 85.8 | 5.0 | <0.001 | 4.1 |  |  |  | $-0.073 \pm 0.0480 .144$ |
| L | RegOU | M | 4-37.9 | 85.8 | 5.0 | <0.001 | 4.1 |  |  |  | $-0.073 \pm 0.0480 .144$ |
| F | Regou | C 4 | $4-38.0$ | 85.8 | 5.0 | <0.001 | 4.1 |  |  | $-0.648 \pm 0.4270 .147$ |  |
| F | RegOU | M 4 | $4-38.0$ | 85.8 | 4.9 | <0.001 | 4.2 |  |  | $-0.650 \pm 0.4280 .147$ |  |
| L | RegPagel | M | 4-38.3 | 86.5 | 3.6 | <0.001 | 5.7 |  |  |  | $-0.081 \pm 0.0510 .128$ |

Appendix 2.3. List of software files used in analyses.

All files within the folder Gambusia/ANALYSES/LH/20120311

## Input Data:

Life history data: Gambusia_LH_20110827.csv
Feeding habits of fish communities:
Gambusia_list_fish_community_20110811.csv
Site description: GAMBUSIA_MD_20120204.csv
Fish community in each site:
Gambusia_Predator_List_Per_Collection_20120516.csv
Folder with SI and related data txt files, used to corroborate SL:
Gambusia_SI_data

## Code to process data:

Data input and preparation, matching databases; Table 1:
Gambusia_LH_Data_Preparation_20120516.R
Preparation of tree: Gambusia_LH_Tree_Preparation_20120313.R
Estimation of matrotrophy index, ranges; exporting data later used in
RegressionV2: Gambusia_LH_MIN_MAX_20120516.R
Folder with RegressionV2, files used to run the program, and folder with RegressionV2 results: Phylogenetics_w_REGRESSIONv2

Processing of output from RegressionV2: Gambusia_LH_Comparative_After_ REGRESSIONv2_for_results_of_20120315c.R

Preparation of Figure 1: Gambusia_LH_Figure1_size_vs_traits_20120518.R
Preparation of Figure 2: Gambusia_LH_Figure 2_PCA_plot_20120517.R
Preparation of Figure 3: Gambusia_LH_Figure_SLvsGONADDRY_20120517.R

## Chapter 3

## Variation in body shape of Trinidadian guppies along a geomorphological gradient

Abstract: Disturbances are ubiquitous disruptive phenomena in nature, but organisms may respond adaptively to the selective forces that they exert. Here we study the body shape of guppies (Poecilia reticulata, Poeciliidae) in response to flow regime in mountain streams of Trinidad. In these habitats, floods are short-lived, severe, and may cause high mortalities of fish. We analyzed the body shape of females and males of 22 guppy populations from the Northern Range of Trinidad. We measured body shape with geometric morphometrics and with Streamlining Index. We tested the correlation between guppy shape and three geomorphological variables, watershed area, relief, and shape, which are indicative of flow regime. We also measured site characteristics that may influence fish shape, including pool volume, canopy cover, flow velocity, and the abundance of prawns and Rivulus hartii (previously known to ecologically interact with guppies). We observed a correlation between body shape and geomorphological features of the watersheds. However, the results varied between sexes. We predicted that guppies have larger caudal areas in more circular watersheds or in steeper watersheds, but we only observed the former in females and the latter in males. Despite our efforts to reduce environmental variation other than flow regime, we found gradients of prawn and Rivulus
abundances that explained some of the body shape variation. Surprisingly, watershed area was not a strong predictor of guppy shape. Additionally, we found that pregnancy dissipated the correlations between environmental variables and shape. We observed that body shape was partially explained by geographical proximity of the sites, specially the watershed of origin; however, the statistical significance of the results were almost the same when the hierarchical structure of the sampling was taken into account.

## Introduction

Disturbances are ubiquitous phenomena (e.g. fires, hurricanes, droughts, floods) that disrupt and may even drive populations to extinction (Pickett and White 1985). However, organisms may have the potential to may adapt to the strong selective forces that disturbances exert (Lytle 2001). Moreover, organisms adapted to certain patterns of disturbance may be negatively impacted by their alteration (for example by fire prevention, levees, dams, etc.; Lytle and Poff 2004). Whereas the ecological effects of disturbance have received considerable attention (Pickett and White 1985), their evolutionary consequences have been rarely addressed (Lytle 2001). Here we study the body shape of guppies in response to flow regime in mountain streams of Trinidad.

Floods in mountain streams are excellent phenomena to understand the ecological and evolutionary implications of disturbances. In such habitats, floods are short-lived but severe because adjacent steep banks confine waters to the stream channel (Swanson et al. 1998). Flash-floods are a recurrent disturbance that cause economic and social catastrophes (Wohl 2000), and are a major cause of mortality for aquatic fauna (Meffe 1984; Dawson 1988; Chapman and Kramer 1991; Peterson 1996; Lytle 2000; Fausch et al. 2001; Grether et al. 2001). For example, 13 populations of a molly in mountain streams of Costa Rica suffered an average of $75 \%$ reduction in size after a flash-flood (Chapman and Kramer 1991). Similarly, guppy populations living in six Trinidadian mountain
streams suffered 22-92\% biomass reduction after a flooding event (Grether et al. 2001). Here we perform a comparative field study of guppy body shape across a gradient of flow regimes in rivers of the Northern Range of Trinidad.

Flow regime is more complex than just water flow velocity (Poff et al. 1997). Sites with the same base flow velocity can have very different patterns of flooding. These floods (and in general any disturbance) can be characterized by their frequency, magnitude, seasonality, and timing (Lytle and Poff 2004; Sabo and Post 2008). However, measuring these characteristics is very datademanding (e.g., the daily flow time series should be at least 20 years long; Sabo and Post 2008), and such flow data are extremely rare for mountain streams (Wohl 2006). To overcome this issue, we relied on geomorphological variables known to be well correlated with flow regime: watershed area, relief, and shape (Gordon et al. 2004). Watershed area is a major factor in freshwaters, influencing stream flow, sediment transportation, streambed grain size, nutrient flux, and channel morphology (Strahler 1964; Church 2002). Larger watersheds collect more rainfall and consequently their floods discharge more water (i.e., flood disturbance have a higher frequency and magnitude). Watersheds with a steeper relief have stronger and shorter-lived floods because rainfall water runs down in a shorter time (i.e., a higher discharge peak; Gordon et al. 2004). Watershed shape also influences discharge peak. Whereas more rounded watersheds act as a funnel (i.e. rainfall water runs down in a short time period causing strong and short-lived flood), elongated watersheds work as a pipe (i.e., rainfall water is
evacuated with weaker and more prolonged flows; Strahler 1964). We predict that fish living in watersheds with larger areas, steeper relief, and more rounded shapes will have body shapes better suited for dealing with stronger floods. This morphology may be predicted by applying biomechanical theory to fish.

Biomechanical theory predicts that fish maximize swimming performance by having body shapes more efficient for the type of swimming they use. Streamlined shapes (outlines similar to foils that minimize flow drag) can cruise at constant velocity (steady swimming) for longer periods (Langerhans and Reznick 2010). Conversely, bodies with deeper caudal areas displace more water when undulating, generating more acceleration (unsteady swimming; Lighthill 1971; Webb 1982; Walker 1997). These two shapes thus exhibit a tradeoff; maximizing unsteady swimming alters the outline in a way that increases drag (Langerhans 2009). We predict that fish from sites with stronger floods (i.e., with larger, steeper, and more rounded watersheds) will have deeper caudal areas. This morphology would allow them to reduce costly swimming in turbulent flows (Enders et al. 2003; Liao 2007), like those created by floods (Webb 2004), by optimizing unsteady (non-constant velocity) swimming (Langerhans and Reznick 2010). Since fish seem to show a morphological trade-off between the optimal streamlined shape for steady swimming and a larger caudal region optimal for unsteady swimming, we predict that fish from sites with stronger floods will depart more from the optimal streamlined shape.

We analyzed natural populations of Trinidadian guppies to test our hypotheses. The Trinidadian guppy system is well known for showing a gradient of predation pressure (Reznick and Endler 1982; Reznick et al. 1996b). Guppies from high-predation sites are exposed to piscivore fishes that readily prey on them, increasing their mortality rates (Reznick et al. 1996a). Multiple aspects of guppy phenotype are related with this predation gradient, including body shape (Hendry et al. 2006), coloration (Endler 1995), life history (Reznick and Endler 1982), and diet (Zandonà et al. 2011), among many others (Magurran 2005). Here we study the less-known geomorphological gradient of this system. Previous studies have hinted at the existence of this gradient. Reznick et al. (1996b; unpub. data) observed considerable variation in life histories of guppies even within low-predation sites in Trinidad. Similarly, Grether et al. (2001) observed large variation in the guppy biomass reduction after a flooding event that affected multiple low-predation Trinidadian sites. Here we focuse on the effects this geomorphological gradient has on guppy morphology by minimizing variation due to predation regime (by selectin only low-predation sites). We also minimized the effect of flow velocity, a factor strongly correlated with body shape in fishes (Langerhans 2008), by exclusively sampling pools (i.e., sites with low flow velocity).

## Methods

## Source of specimens

Trinidadian guppies were collected from 22 wild populations (Table 3.1, Figure 3.1). Guppies are found in most Trinidadian streams in populations isolated from each other by waterfalls, land, and ocean. We focused on the Northern Range of Trinidad, a region with relatively homogeneous weather, soil, and vegetation cover (mostly primary and secondary forest; Cooper and Bacon 1981; Gopeesingh 1989; pers. obs.). Specifically, we sampled four watersheds, two on the North slope of the range mountains (Madamas and Paria), and two on the Southern slope of the range (Guanapo and Quare). We selected sites with contrasting geomorphological variation in watershed area, Relief Ratio, and Elongation Ratio (see Habitat Characterization below). We also applied previous knowledge of the fish communities of these watersheds, and selected only those reaches that were categorized as low predation (LP) sites. These LP sites lack piscivorous fish (e.g., Hoplias malabaricus and Crenicichla alta in the South slope, Eleotris pisonis, Gobiomorus dormitor, and Dorrnitator maculatus in the North slope; Reznick et al., 1996). However, LP sites have other aquatic organisms that can exert relatively mild predation pressure on guppies. All LP sites have the ubiquitous Rivulus hartii, an omnivore that rarely preys on guppies (Magurran 2005). LP sites in the Guanapo and Madamas have Rhamdia quelen, an omnivore that feeds mainly on invertebrates and plant material, and rarely fish
(Maldonado-Ocampo et al. 2006). In the Quare, Paria, and Madamas, there are prawns (Macrobrachium spp.), which may feed on guppies (Magurran 2005; pers. obs.). North-slope sites (Paria and Madamas) have Agonostomus monticola and Sicydium puctatum. The former species mainly feeds on invertebrates, plant material and algae (Phillip 1993), and the latter on algae (Coat et al. 2009).

In each site we looked for a population of guppies living in a pool delimited up- and downstream by waterfalls. Fish were captured with hand nets, an attempt was made to include the full range of body sizes for each sex. Soon after capture, fish were euthanized in MS-222 and preserved in 5\% formalin. For sites that were sampled more than once, we pooled together individuals after confirming that the distribution of their shape variables was not statistically different. After excluding juveniles and bent specimens, we analyzed 568 females and 386 males (Table 3.1).

## Habitat characterization

Three characteristics of the watershed were measured from cartographic maps (1:25000 scale), using Adobe Photoshop CS5 (Adobe Systems, Seattle, WA, USA). Watershed area (AREA) was the projected drainage area upstream of each site. The steepness of the watershed was measured with the Relief Ratio (REL), the elevation difference between site and maximum watershed height, divided by maximum watershed length (Schumm 1956). Steeper watersheds
have larger REL values. The shape of the watershed was quantified with the Elongation Ratio (ELO), the ratio between the diameter of a circle with the same area of the watershed, and the maximum watershed length (Morisawa 1958). ELO values range from less than one, indicating elongated watersheds, to values close to one for more circular watersheds.

We aimed to minimize environmental variation not related with the flow regime by sampling only pools from LP localities with pristine basins.

Nevertheless, we measured five local variables known to influence guppy phenotypes to test whether shape variation was better explained by factors different from the three geomorphological watershed variables. Pool volume (VOL) was calculated as one half of an ellipsoid (4mabc/3, where a=maximum
 measured with a laser distance measurer (Leica Disto D5), and depths with a measuring rod coupled with a rod level. The percentage of canopy cover (CAN) was measured with a concave spherical densiometer (Forest Densiometers, Bartlesville, OK), averaging measurements made in all four cardinal directions (from the same point). Water flow velocity (VEL) was measured with an electromagnetic flow meter (Marsh-McBirney Flo-Mate Model 2000) at the deepest point of the pool, positioning the probe at a depth equal to maximum depth (Gordon et al. 2004). The abundance of prawn (PRW) and R. hartii (RIV) was estimated using a catch per unit effort (CPUE) measure. Two collapsible minnow traps (Models TR-501 and TR-503, Promar Company, Gardena, CA)
were baited with five dog food pellets and left undisturbed for 15 minutes. The traps were placed in portions of the pool were guppies were observed and water depth was deep enough to cover the entrances of the traps. The relative abundance of prawns and $R$. hartii was the number of individuals of each taxa collected in both traps.

Geographic coordinates were measured in each site using Global Positioning System equipment, which was set to the Universal Traverse Mercator projection and the Naparima 1955 datum.

## Photographs and Dissections

Lateral and ventral views of preserved fish were photographed following the recommendations of Zelditch et al. (2004). Standard length (SL) of specimens was measured with calipers (to the nearest 0.1 mm ). Females were dissected to estimate stage of embryo development using the scale of Haynes (1995), as modified by Pires et al. (2007). Stages in this scale range from egg (stage 0) to fully-formed pre-birth embryo (stage 50). We only included mature individuals to eliminate the morphological variation associated with immaturity. For females, we excluded individuals smaller than the minimum size at maturity for each collection (i.e., the SL of the smallest female with stage of development of embryos $\geq 2$ ). For males, individuals without a fully formed gonopodial tip were excluded.

## Measurements of shape

Shape was measured with two complimentary methods. The first method was two-dimensional geometric morphometrics (Zeldtich et al. 2004). Eleven lardmarks (homologous coordinates) and five sliding landmarks (nonhomologous coordinates along the outline) were digitized on lateral photographs using TpsDig2 2.12 (Rohlf 2008), as explained in Appendix 3.1. Semilandmarks were slid to minimize the bending energy criterion (Zeldtich et al. 2004), with code adapted from Morpho (Stefan Schlager, unpub). Landmarks and slid semilandmarks were Procrustes superimposed (to extract variation independent of location, scale, and rotation of the specimens in the images) using R-code adapted from Claude (2008).

Three mean-shape configurations were estimated for guppies from each site: mean-size female early in pregnancy (when embryos were at developmental stage 0), mean-size female late in pregnancy (embryos at stage 50), and meansize male. Body size was measured as the centroid size (CS; Zeldtich et al. 2004). For females, the two morphologies were estimated using a multiple regression model (Monteiro 1999; Berner 2011), with projected landmark positions as dependent variables, and centroid size and stage of development of embryos as independent variables. Dimensionality was reduced with a Principal Component Analysis on the superimposed coordinates for each of the three configuration sets, retaining 95\% of the variation. Principal Component scores
were used in further analyses. Modified thin-plate splines were used to visualize shape differences, as explained in Chapter 1.

The second method used to estimate shape was the tridimensional estimation of body mass distribution of the Streamlining Index (McHenry and Lauder 2006). SI is a ratio of the mass distributions of a fish over an optimally streamlined foil of the same length, width, and depth as the fish (McHenry and Lauder 2006). SI ranges from less than one (proportionally larger anterior body regions), to one (optimal body mass distribution along the longitudinal fish axis), to more than one (proportionally larger caudal regions). SI was calculated using Matlab 7.5 with Image Processing Toolbox 6.0 (MathWorks, Natick, MA), as explained in Chapter 1. As in the geometric morphometric analyses, three SI values were estimated for the hypothetical averaged-size individual of each sex in each population: one value for females early in pregnancy, another for late-inpregnancy females, and the last for males.

## Statistical analyses

Thirteen adaptive hypotheses were tested for each dependent variable (DV):

$$
\begin{gathered}
\text { DV } \sim \mathrm{CS}+\text { Watershed }+\varepsilon \\
\mathrm{DV} \sim \mathrm{CS}+\mathrm{AREA}+\text { Watershed }+\varepsilon \\
\mathrm{DV} \sim \mathrm{CS}+\mathrm{REL}+\text { Watershed }+\varepsilon \\
\mathrm{DV} \sim \mathrm{CS}+\mathrm{ELO}+\text { Watershed }+\varepsilon \\
\mathrm{DV} \sim \mathrm{CS}+\mathrm{CAN}+\text { Watershed }+\varepsilon
\end{gathered}
$$

$$
\begin{gathered}
\mathrm{DV} \sim \mathrm{CS}+\mathrm{VOL}+\text { Watershed }+\varepsilon \\
\mathrm{DV} \sim \mathrm{CS}+\mathrm{VEL}+\text { Watershed }+\varepsilon \\
\mathrm{DV} \sim \mathrm{CS}+\mathrm{PRAWN}+\text { Watershed }+\varepsilon \\
\mathrm{DV} \sim \mathrm{CS}+\mathrm{RIV}+\text { Watershed }+\varepsilon \\
\mathrm{DV} \sim \mathrm{CS}+\mathrm{AREA}+\mathrm{REL}+\mathrm{ELO}+\mathrm{Watershed}+\varepsilon \\
\mathrm{DV} \sim \mathrm{CS}+\mathrm{CAN}+\mathrm{VOL}+\mathrm{VEL}+\text { Watershed }+\varepsilon \\
\mathrm{DV} \sim \mathrm{CS}+\mathrm{PRW}+\mathrm{RIV}+\text { Watershed }+\varepsilon \\
\mathrm{DV} \sim \mathrm{CS}+\mathrm{AREA}+\mathrm{REL}+\mathrm{ELO}+\mathrm{CAN}+\mathrm{VOL}+\mathrm{VEL}+\mathrm{PRW}+\mathrm{RIV}+\text { Watershed } \\
+\varepsilon,
\end{gathered}
$$

where AREA, CAN, VOL, VEL, PRW, and RIV were log-transformed values, $\varepsilon$ was the error term, and DV were the geometric morphometric shape variables, CS, or SI (more details below). These models were evaluated with Ordinary Least Squares (OLS) and with a phylogenetic framework to account for the potentially hierarchical structure of the data, which could be produced by the hierarchical nature of river networks. The phylogeny used originally had branch lengths proportional to geographical distances between sites along the streambed (Appendix 3.2). To prevent the negative effect of some disproportionally long branches on the comparative analyses, branch lengths were transformed using Grafen's (1989) power transformation (Appendix 3.3). One soft politomy at the base of the river watershed tree was resolved prior to analyses by making the tree dichotomous (function multi2di in the package ape; Paradis et al. 2004) and setting the branch length of the new branches to zero
length. Type I error produced by this polytomy was corrected by reducing the degrees of freedom when estimating P-values (Garland and Díaz-Uriarte 1999).

Two different methods were used to test the adaptive hypotheses, depending on whether the dependent variables were geometric morphometric shape variables or not (CS or SI). For the former, we used phylogenetic MANCOVAs (Garland et al. 1993; Revell et al. 2007; Chapter 1), with PC scores as dependent variables, watershed as a factor, and other predictors (CS, AREA, REL, ELO, VOL, CAN, VEL, PRAWN, and RIV) as covariates. We tested two models of character evolution, OLS (non-phylogenetic) and Brownian Motion (BM, random divergence). For the phylogenetic MANCOVA, the P-values of the F-statistics obtained from OLS were estimated using an empirical null distribution calculated from Monte Carlo simulations of tip data (999 simulations), using the original topology as the phylogenetic structure, and observed root values as starting values. To visualize the shape variation explained by predictors of MANCOVA, we used a canonical analysis (Langerhans 2009; Chapter 1). We calculated the phylogenetic signal (K; Blomberg et al. 2003) and the probabililty of $\mathrm{K}=0$ for each canonical vector, using phylosignal in the R package picante (Kembel et al. 2010).

When the dependent variables were CS or SI, we used regression models to analyze the adaptive hypotheses. Specifically, we used phylogenetic Generalized Least Squares (GLS; Grafen 1989), which has the option of hierarchically structuring the error term by multiplying it by a phylogenetic
variance-covariance matrix (Martins and Hansen 1997; Garland and Ives 2000; Rezende and Diniz-Filho 2012). We tested three models of character evolution, OLS (non-phylogenetic, the error term multiplied by the identity matrix), Pagel's (RegPagel, a regression model that assumes Brownian motion and simultaneously estimates the parameter coefficients and a measurement of phylogenetic signal; Pagel 1999; Garland et al. 2005), and the OrnsteinUhlenbeck process (RegOU, which assumes Brownian motion that tends to drift towards an optimum determined by selection and simultaneously estimates regression coefficients and a measure of phylogenetic signal; Hansen 1997; Butler and King 2004). When CS was the dependent variable, it was not used as a covariate in the models.

For both MANCOVA and GLS analyses, we selected the best supported model for each dependent-variable set using model selection (Burnham and Anderson 2002). Because of our relatively small sample size, we used small sample corrected Akaike information criterion (AICc; Anderson and Burnham 2002; Hansen et al. 2008). Akaike weights ( $w$, the amount of evidence explained by each model) and Evidence Ratios (ER, the number of times each model is worse than the best supported model) were also estimated. GLS regressions were calculated using the Matlab program RegressionV2.m (A. R. Ives and T. Garland Jr.; Lavin et al. 2008). Other analyses were executed using code written in $R(R$ Development Core Team 2011).

## Results

Some of the habitat characteristics (Table 3.1) were strongly correlated (Table 3.2). Specifically, larger watershed area was associated with larger pool volume and larger water flow velocity; steeper relief was associated with more elongated watersheds and a reduction in canopy cover.

## MANCOVAS of geometric morphometric shape variables

In females, the best supported MANCOVAs (for both sets of configurations, early and late in pregnancy) were the adaptive models with all terms ( $\Delta \mathrm{AIC} \mathrm{C}_{\mathrm{c}}>8$ ). For females early in pregnancy, AREA was the only geomorphological variable significantly related with geometric morphometric shape variables, other significantly related predictors were biotic (CS, PRW, and RIV; Table 3.3, Figure 3.2). The divergence (d) vectors of these signficant results showed phylogenetic signal (Table 3.3). The Phylogenetic MANCOVA showed that only AREA, PRW, and RIV were significant after accounting for phylogenetic relatedness (Table 3.3). The d vectors for AREA and PRW (but not RIV), were significantly related with SI (Table 3.3), indicating that early-in-pregnancy females have proportionally larger anterior areas in sites with larger watershed areas and more prawns (Figure 3.2). Female shape late in pregnancy showed the same tendencies as early in pregnancy, but none of the p-values were significant (results not shown).

In males, the best supported MANCOVA was the full model ( $\triangle \mathrm{AIC} C^{C}$ between best and second best supported models was 20.488). For males, only REL and PRW were significantly predictors of shape, in both OLS and phylogenetic MANCOVAs (Table 3.4). The divergence vectors of these two relationships showed significant levels of phylogenetic signal (Table 3.4). Both vectors were positively related with SI , indicating that species living in steeper watersheds and in sites with more prawns have larger caudal areas (Table 3.4, Figure 3.2).

## Regressions of CS and SI

Centroid size of females and males were best explained by watershed; specimens from the Guanapo river were larger (Figure 3.3 A-B). For females, CS was also related with VOL; larger females were found in larger pools (Figure 3.3 A). The best supported model for SI of early in pregnancy females was SI~CS+ELO+watershed and explained $36.7 \%$ of the variation (w value, Appendix 3.4). In this model, SI early in pregnancy was independent of $C S(p=0.420)$, but was correlated with ELO (estimated coef. $\pm$ SE=0.346 $\pm 0.133, \mathrm{p}=0.021$ ) and watershed ( $p=0.021$ ). The best supported model for SI of females late in pregnancy was SI~CS+REL+watershed, but none of the predictors in this or in the other models was statistically significant. For males, SI was best explained by the model SI~CS+VEL+watershed (w=60.7, Appendix 3.4). In this model, CS
was not correlated with $\mathrm{SI}(\mathrm{p}=0.949)$, but VEL $(0.200 \pm 0.073, p=0.016)$ and watershed $(p=0.002)$ were.

## Discussion

Here we tested the correlation between guppy shape and three geomorphological variables indicative of flow regime. We observed a correlation between body shape and geomorphological features of the watersheds. However, the results varied between sexes. We predicted that guppies have larger caudal areas in more circular (funnel-shape) watersheds or in steeper watersheds, but we only observed the former in females (Figure 3.3) and the latter in males (Figure 3.2). Despite our efforts to reduce environmental variation other than flow regime, we found gradients of prawn and Rivulus abundances that explained some of the body shape variation (Tables 3.3-3.4, Figure 3.2). Surprisingly, watershed area was not a strong predictor of guppy shape (Figures 3.2-3.3). Additionally, we found that pregnancy dissipated the correlations between environmental variables and shape. We observed that body shape was partially explained by geographical proximity of the sites, specially the watershed of origin; however, the statistical significance of the results were almost the same when the hierarchical structure of the sampling was taken into account.

Some relationships between flow regime (estimated by geomorphological features) and body shape matched our predictions. There are several examples
of flow regime effects on freshwater fish. The structure of fish communities is so well correlated with aspects of flow regime that it can be used as their indirect index (Chang et al. 2011; Huang et al. 2011). Flow regime not only affects the structure of the fish community, but also the life history traits of the species in the community (Mims et al. 2010). Flow regime variation also affects fish at the intraspecific level. In Cyprinella robusta, a small cyprinid, populations experiencing human-made alteration of the flow regime (river impoundment) showed a small but consistent change in body shape, specially in the size and orientation of the head (Haas et al. 2010). However, to the best of our knowledge, the present study is the first one to analyze the correlation between a natural geomorphological gradient and fish body shape.

The association between geomorphology and body shape morphology was not consistent between sexes. Guppy body shape is sexually dimorphic, females have larger abdomens and males have more anterior anal fins (Hendry et al. 2006; Figure 3.2). According to our results, female and male guppies may be responding differently to selection pressures that flow regime may be causing. These differences between sexes are likely independent of pregnancy. We accounted for pregnancy in this study, observing that pregnancy reduced the phenotypic divergence across environments, what coincides with previous studies that reported pregnancy as a burden that reduces adaptive divergence (Ghalambor et al. 2004; Wesner et al. 2011; Chapter 1). Instead of a pregnancy effect, the intersexual differences observed here may lay on intersexual
differences in mortality regimes. This idea was previously suggested in a study that found intersexual differences in guppy body shape across gradients of predation, water flow velocity, and canopy cover (Hendry et al. 2006). This hypothesis is supported by the observation that males suffer higher mortality rates in high-predation sites than females (Reznick et al. 1996a). In the case of the mortality exerted by flow regime, there is evidence that males are recaptured less frequently than females after mountain flooding episodes (Chapman and Kramer 1991). The intersexual differences in shape and size in this species may be associated with differences in swimming performace, which in turn may confer fitness advantages when facing selective events occurring at peak flows.

We also found inconsistencies in the results obtained with different variables used to measure shape (geometric morphometrics and Streamlining Index). In females, geometric morphometric shape variables were best explained by AREA, PRW, and RIV (Table 3.3), whereas SI was more strongly correlated with ELO. Similarly, in males the shape variation depicted by geometric morphometrics was correlated with REL and PRW, whereas male SI was correlated with VEL. The discrepancy between the results using different methods is not surprising, geometric morphometrics is a very good method to condense shape variation (Zeldtich et al. 2004), but the variable extracted may not necessarily be related with biomechanical function (Chapter 1). The results using these two commonly used methods should be seen as complementary rather than fully overlapping (Chapter 1 ).

Watershed relief, shape, and (indirectly) area, were related with fish shape in a pattern that matched our predictions. Larger caudal areas were observed in males from steeper relief watersheds and in females from more rounded watersheds. Regarding watershed area, females early in pregnancy had slightly deeper bodies in sites with larger basins (Figure 3.2). Since watershed area and flow velocity were strongly correlated (Table 3.2), the result of males having larger caudal areas in sites with stronger water flow velocity could be also interpreted as a watershed area effect. Despite all these significant results, given the large influence of watershed area in multiple stream ecology factors (Church 2002), we were expecting a larger watersheda area effect. Our use of watershed area as a proxy to estimate flow regime characteristics has been done before (Lytle et al. 2008). Our sampling sites did not lack variation in watershed area, they ranged from 0.06 to $20.50 \mathrm{~km}^{2}$. Instead, it may be that watershed area is a complex factor that correlates with multiple habitat characteristics, which ultimately may balance-out each other effects on the flow regime. For example, low stream order streams have smaller areas, what reduces flow peak height, but typically have steep slope and a reduced floodplain, what increases flow peak height (Church 2002). Recent analysis of the very few available hydrological datasets with high geographical density for mountain streams (e.g., Pike and Scatena 2010) are a promising strategy to understand the fine scale relationships between geomorphology of mountain streams and flow regime.

We found a relationship between body shape (as measured with geometric morphometrics) and the abundance of prawns in both sexes. We originally measured this variable to confirm that it had no effect on guppy body shape in our homogeneous site sample (as occurred for canopy cover). We found that both sexes coincided in having proportionally larger areas in sites with more prawns (Tables 3.3-3.4 and Figure 3.2). It could be hypothesized that this is a watershed effect, prawn populations went extinct in the Guanapo river few decades ago (D. Reznick, pers. obs.), they are rare in the Quare river, and are common in Northern range streams. Our analysis, however, accounted for watershed effects in the models, and yet prawn abundance showed a significant relationship with guppy shape. The observed relationship was actually counterintuitive, fish from sites with more prawns had larger abdominal areas, but if prawns are predators of fish and escaping from prawns utilizes unsteady swimming, guppies with higher prawn density should have had larger caudal areas. An alternative explanation could be that instead of predators, prawns act as competitors of guppies. Prawns have an omnivorous diet mainly based in detritus, algae, and invertebrates, and only in minor proportions containing fish (Lewis et al. 1966; Collins and Paggi 1997; Albertoni et al. 2003). This diet largely overlaps with guppy feeding habits (Zandonà et al. 2011). If prawns and guppies compete for food, guppies in sites with more prawns would have to search more for food, what would require a more frequent use of steady swimming, and
therefore more streamlined bodies (Langerhans and Reznick 2010) with less prominent caudal areas.

We also found that females early in pregnancy have shallower bodies in sites where Rivulus are more abundant (Table 3.3, Figure 3.2). This variation was not significantly related with SI (Table 3.3), therefore it is not indicative of differences in swimming performance. The interaction between guppies and Rivulus is complex, each species seems to prey on each other juveniles (Magurran 2005), and adults compete for food resources (de Villemereuil and López-Sepulcre 2011). The functional explanation of the shape response to Rivulus abundance observed here is not clear.

There are some future directios that could complement the results of this study. One limitation of this study was the use of wild populations, which may be affected by unmeasured environmental aspects. This caveat of any comparative study (Garland and Adolph 1991; Garland et al. 2005) could be overcomed by a "common garden" experiment that keep populations in a controlled environment for one or more generations. Using a common garden approach it would be possible to estimate the proportion of phenotypic divergence that corresponds to phenotypic plasticity and to genetic variation. Nevertheless, despite we ignore whether the shape variation observed here has a plastic of genetic origin, our observations are indicative of morphological adaptive divergence.

Another important aspect not explored here is the behavioral response of fish to flow regime. Fish escape from flushing flows by orienting their body with
the direction of flow as soon as water velocity increases (Meffe 1984), by hiding behind barriers (Meffe 1984; Liao 2007), or by swimming close to the shore where stream flow velocity is reduced (pers. obs.). A more complete ecomorphological picture (Garland and Losos 1994) of the effect of flow regime on fish should include morphology, behavior, and fitness measures.

Human impact is dramatically changing flow regimes all around the world, specially in the delicate mountain rivers (Wohl 2006). Mountain rivers are important ecosystems for biodiversity and human development, but are suffering from an increasing anthopogenic pressure (e.g. by damming, water extraction for irrigation, channelization, and deforestation). Moreover, ongoing climate change is expected to increase the frequency and magnitude of flash-floods (Walters and Post 2008), making urgent a better understanding of the biological implications of such disturbances. Our study goes in that direction, we showed here that guppy body shape responds adaptively to flow regime.

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Table 3.1. Environmental data from collections sites. The first three letters of each site code indicate the watershed (Gua=Guanapo, Mad=Madamas, Par=Paria, and Qua=Quare). Sample size ( $n$ ) for each collection correspond to the number | of females over number of males, after excluding juveniles and curved individuals. |  |  |  |  |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Site | n | Latitude | Longit. | $\begin{array}{c}\text { Area } \\ \left(\mathrm{km}^{2}\right)\end{array}$ |  |  |  |  |  |  |  |
| Relief | Ratio | Ratio | $\begin{array}{c}\text { Canopy } \\ \text { cover }(\%)\end{array}$ | Pool Vol. $\left(\mathrm{m}^{3}\right)$ |  | $(\mathrm{m} / \mathrm{s})$ | CPUE | CPUE |  |  |  |
| Gua07 | $20 / 9$ | 1183420 | 689820 | 0.61 | 0.33 | 0.41 | 80.33 | 27.04 | 0.02 | 0.00 | 5.00 |
| Gua08 | $20 / 4$ | 1183810 | 689850 | 2.85 | 0.29 | 0.71 | 89.79 | 610.74 | 0.04 | 0.00 | 2.00 |
| Gua12 | $31 / 17$ | 1184888 | 689101 | 1.38 | 0.25 | 0.52 | 84.45 | 313.25 | 0.03 | 0.00 | 2.00 |
| Mad04 | $32 / 10$ | 1188012 | 693194 | 1.76 | 0.36 | 0.71 | 71.84 | 125.22 | 0.12 | 16.25 | 1.25 |
| Mad07 | $12 / 14$ | 1188185 | 693766 | 0.62 | 0.34 | 0.50 | 72.5 | 17.49 | 0.01 | 18.00 | 0.00 |
| Mad18 | $37 / 24$ | 1188030 | 695400 | 0.29 | 0.21 | 0.65 | 90.3 | 21.93 | 0.06 | 9.00 | 3.00 |
| Mad22 | $22 / 16$ | 1188200 | 696900 | 0.64 | 0.13 | 0.59 | 84.32 | 34.55 | 0.03 | 10.00 | 0.00 |
| Mad24 | $21 / 28$ | 1188300 | 695500 | 5.57 | 0.23 | 0.92 | 76.43 | 237.86 | 0.08 | 11.00 | 0.00 |
| Mad28 | $18 / 13$ | 1188591 | 694295 | 6.12 | 0.24 | 0.84 | 91.78 | 1172.30 | 0.01 | 1.00 | 0.00 |
| Par03 | $37 / 31$ | 1191900 | 691630 | 3.12 | 0.18 | 0.91 | 86.95 | 130.24 | 0.03 | 12.67 | 2.67 |
| Par04 | $38 / 30$ | 1192052 | 691050 | 20.50 | 0.15 | 0.89 | 83.94 | 885.17 | 0.06 | 3.80 | 0.20 |
| Par06 | $43 / 31$ | 1191873 | 690546 | 2.00 | 0.1 | 0.84 | 84.8 | 113.43 | 0.14 | 4.50 | 0.50 |
| Par10 | $34 / 19$ | 1189434 | 690573 | 6.64 | 0.22 | 0.93 | 83.45 | 1398.28 | 0.11 | 13.00 | 5.00 |
| Par11 | $35 / 18$ | 1190775 | 689621 | 0.80 | 0.21 | 0.92 | 80.66 | 11.20 | 0.03 | 5.50 | 9.50 |
| Par18 | $38 / 26$ | 1191530 | 689200 | 1.00 | 0.12 | 1.08 | 86.01 | 179.15 | 0.04 | 5.50 | 9.50 |
| Par21 | $15 / 16$ | 1188765 | 691351 | 1.44 | 0.33 | 0.59 | 77.04 | 63.14 | 0.03 | 11.00 | 0.00 |
| Par28 | $17 / 13$ | 1189475 | 689818 | 1.10 | 0.1 | 0.79 | 78.45 | 16.49 | 0.08 | 7.00 | 0.00 |
| Par29 | $16 / 18$ | 1189150 | 691400 | 0.07 | 0.38 | 0.68 | 80.62 | 29.32 | 0.00 | 8.00 | 1.00 |
| Qua08 | $24 / 9$ | 1181310 | 697050 | 1.76 | 0.17 | 0.56 | 82.35 | 315.25 | 0.03 | 1.00 | 6.00 |
| Qua09 | $19 / 22$ | 1181000 | 697060 | 0.11 | 0.29 | 0.69 | 78.34 | 3.24 | 0.00 | 0.00 | 9.00 |
| Qua10 | $24 / 8$ | 1180670 | 696970 | 0.42 | 0.45 | 0.65 | 72.03 | 31.66 | 0.06 | 0.00 | 3.00 |
| Qua20 | $15 / 10$ | 1181000 | 696830 | 0.06 | 0.3 | 0.74 | 83.44 | 30.16 | 0.00 | 0.00 | 17.00 |

Table 3.2. Bivariate correlations between predictor variables. Correlation coefficients below diagonal, P -values above diagonal. $\mathrm{P}<0.05$ and respective correlation coefficients in bold. AREA=watershed area, REL=Relief Ratio, ELO=Elongation Ratio, VOL=Pool volume ( $\mathrm{m}^{3}$ ), VEL=water flow velocity ( $\mathrm{m} / \mathrm{s}$ ), CAN=canopy cover (\%), PRW = Macrobrachium spp. abundance (CPUE), RIV=Rivulus hartii abundance (CPUE).

|  | log <br> AREA | REL | ELO | log <br> VOL | log <br> CAN | log <br> VEL | $\log$ <br> PRW | log <br> RIV |
| :--- | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| log AREA | - | $\mathbf{0 . 0 3 6}$ | $\mathbf{0 . 0 1 7}$ | $\mathbf{0 . 0 0 0}$ | 0.549 | $\mathbf{0 . 0 0 0}$ | 0.166 | $\mathbf{0 . 0 1 2}$ |
| REL | $\mathbf{- 0 . 3 7 1}$ | - | $\mathbf{0 . 0 0 2}$ | 0.221 | $\mathbf{0 . 0 0 1}$ | 0.076 | 0.301 | 0.858 |
| ELO | $\mathbf{0 . 4 1 9}$ | $\mathbf{- 0 . 5 2 9}$ | - | 0.068 | 0.223 | 0.074 | $\mathbf{0 . 0 3 3}$ | 0.369 |
| log VOL | $\mathbf{0 . 8 0 4}$ | -0.222 | 0.326 | - | 0.089 | $\mathbf{0 . 0 1 3}$ | 0.893 | 0.189 |
| log CAN | 0.110 | $\mathbf{- 0 . 5 7 2}$ | 0.222 | 0.305 | - | 0.647 | 0.282 | 0.302 |
| log VEL | $\mathbf{0 . 6 1 9}$ | -0.318 | 0.320 | $\mathbf{0 . 4 3 4}$ | -0.084 | - | $\mathbf{0 . 0 1 4}$ | 0.070 |
| log PRW | 0.251 | -0.189 | $\mathbf{0 . 3 7 8}$ | 0.025 | -0.196 | $\mathbf{0 . 4 3 0}$ | - | 0.069 |
| log RIV | $\mathbf{- 0 . 4 3 8}$ | 0.033 | 0.164 | -0.238 | 0.188 | -0.325 | -0.326 | - |

Table 3.3. MANCOVAs for the configurations of females early in pregnancy. F-ratios were estimated from Wilk's $\Lambda$. Partial $\eta^{2}$ values indicate effect size. Phylogenetic MANCOVA used Brownian motion on a phylogenetic tree with the original branch lengths proportional to geographic distances along the river channel. These branch lengths were transformed with Grafen (1989)'s method to proportionally reduce long branches. K indicates phylogenetic signal of the respective divergence vector (d). The correlations of each $d$ with streamlining index (SI) were calculated from non-phylogenetic MANCOVAs. Significant $p$-values ( $p<0.05$ ) in bold.

| Independent variable | Non-phylogenetic |  |  |  | Phylogenetic |  |  | Correlation of $d$ with SI |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | df | F | $p$ | Partial $\eta^{2}$ | p | K | p (K) | $\mathrm{R}^{2}$ | Slope $\pm$ SE | p |
| CS | 1,7 | 9.277 | 0.047 | 0.96 | 0.305 | 1.238 | <0.001 | 0.30 | $-4.50 \pm 1.43$ | 0.005 |
| $\log$ AREA | 1,7 | 32.538 | 0.008 | 0.99 | 0.042 | 1.751 | <0.001 | 0.17 | $-3.15 \pm 1.35$ | 0.031 |
| REL | 1,7 | 1.954 | 0.313 | - | 0.341 | 0.701 | 0.020 | <0.01 | $-0.01 \pm 2.44$ | 0.995 |
| ELO | 1,7 | 5.027 | 0.106 | - | 0.212 | 1.190 | <0.001 | 0.18 | $-3.86 \pm 1.62$ | 0.027 |
| $\log$ CAN | 1,7 | 5.554 | 0.093 | - | 0.152 | 0.507 | 0.260 | 0.10 | $-4.56 \pm 2.48$ | 0.081 |
| $\log \mathrm{VOL}$ | 1,7 | 1.969 | 0.311 | - | 0.389 | 0.610 | 0.058 | 0.17 | $-5.00 \pm 2.17$ | 0.032 |
| $\log$ VEL | 1,7 | 2.007 | 0.305 | - | 0.327 | 0.431 | 0.539 | <0.01 | $-0.49 \pm 2.37$ | 0.839 |
| $\log$ PRW | 1,7 | 51.500 | 0.004 | 0.99 | 0.014 | 1.911 | <0.001 | 0.20 | $-3.39 \pm 1.34$ | 0.020 |
| log RIV | 1,7 | 16.879 | 0.020 | 0.98 | 0.022 | 1.690 | <0.001 | 0.08 | $2.75 \pm 1.60$ | 0.102 |
| Watershed | 3,21 | 1.677 | 0.212 | - | 0.511 | - | - | - | - | - |

Table 3.4. MANCOVA for the configurations of males. Explanation of variables as in Table 3.2.

| Independent variable | Non-phylogenetic |  |  |  | Phylogenetic |  |  | Correlation of $d$ with SI |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | df | F | p | Partial | p | K | $\mathrm{p}(\mathrm{K})$ | $\mathrm{R}^{2}$ | Slope $\pm$ SE | p |
| CS | 1,7 | 2.940 | 0.203 | - | 0.587 | 1.641 | <0.001 | 0.53 | $6.29 \pm 1.26$ | <0.001 |
| $\log$ AREA | 1,7 | 5.177 | 0.102 | - | 0.293 | 1.296 | <0.001 | 0.35 | $4.17 \pm 1.19$ | 0.002 |
| REL | 1,7 | 14.756 | 0.025 | 0.97 | 0.023 | 1.195 | <0.001 | 0.16 | $5.15 \pm 2.31$ | 0.038 |
| ELO | 1,7 | 7.781 | 0.060 | - | 0.175 | 1.175 | <0.001 | 0.33 | $-5.07 \pm 1.52$ | 0.003 |
| $\log$ CAN | 1,7 | 2.602 | 0.232 | - | 0.306 | 0.370 | 0.868 | 0.01 | $-3.34 \pm 2.98$ | 0.277 |
| $\log \mathrm{VOL}$ | 1,7 | 5.178 | 0.102 | - | 0.099 | 0.646 | 0.043 | <0.01 | $3.75 \pm 4.12$ | 0.374 |
| $\log$ VEL | 1,7 | 0.236 | 0.947 | - | 0.975 | 0.364 | 0.885 | 0.25 | $-5.84 \pm 2.04$ | 0.010 |
| log PRW | 1,7 | 18.663 | 0.018 | 0.98 | 0.050 | 1.628 | <0.001 | 0.36 | $4.86 \pm 1.36$ | 0.002 |
| $\log$ RIV | 1,7 | 2.003 | 0.305 | - | 0.280 | 0.555 | 0.172 | <0.01 | $1.97 \pm 2.36$ | 0.414 |
| Watershed | 3,21 | 2.451 | 0.081 | - | 0.327 | - | - | - |  | - |

Figure 3.1. Sampling localities. Upper panel shows the Northern range of
Trinidad island. Lower panel zooms the rectangle in the upper panel, showing sites and watersheds. Par=Paria, Mad=Madamas, Gua=Guanapo, Qua=Quare.


Figure 3.2. Shape variation estimated with MANCOVAs. A. Females early in pregnancy. B. Males. C. Females late in pregnancy. Only significant effects shown. Shapes are represented with thin-plate splines, grey and black outlines are the extreme low- and high-values, respectively. Arrows inside outlines are proportional to the magnitude and direction of shape differences. Scatterplots beside splines show the relationship between each factor and the canonical vector of divergence. Shape differences have a four-fold magnification.


Figure 3.3. Body size and shape variation estimated with regressions. $A$ and $B$ are regressions with body size of females and males, respectively. C and D are regressions with Streamlining Index of females and males, respectively, Symbols in all panels indicate watershed origin, following arrangement of panel B.


Appendix 3.1. Position of landmarks (circles) and semilandmarks (squares) in lateral view of guppies. Numbers correspond to the following positions: (1) tip of the snout; (2-3) semilandmarks along dorsal midline between (1) and (4); anterior (4) and posterior (5) terminus of dorsal-fin base; (6) semilandmark along dorsal midline between (5) and (7); dorsal (7) and ventral (8) terminus of caudal-fin base; (9) semilandmark along ventral midline between (8) and (10); posterior (10) and anterior (11) terminus of anal fin (gonopodium in males); (12) anterior terminus of pelvic-fin base; (13) semilandmark along ventral midline between (12) and (14); (14) bottom of head at junction of border of opercle and body; (15) anterior terminus of pectoral fin; and (16) eye center.


Appendix 3.2. Phylogeny derived from river network hierarchy. Branch lengths proportional to geographical distances between sites along the streambed. First three letters of site name correspond to watershed names (Par=Paria, Mad=Madamas, Qua=Quare, and Gua=Guanapo).


Appendix 3.3. Phylogeny depicted in Appendix 3.2. after transformation of branch lengths using Grafen's (1989) power transformation method. This transformation was performed to reduce the negative influence of long branches in calculations.


Appendix 3.4. Canditate set of regression models for Centroid Size (CS) and Streamlining Index (SI) of females (F, early and late in pregnancy) and males (M). Only best supported models $\left(\triangle A I C_{C}=4\right)$ shown. Models indicated with a regression equation, where AREA= watershed AREA (km², log), REL= REL Ratio, ELO= ELO Ratio, CAN= percentage of CAN cover (log), VOL=Pool VOL ( $\mathrm{m}^{3}$, log), VEL=water flow VEL ( $\mathrm{m} / \mathrm{s}$, $\log$ ), Macrobrachium=CPUE abundance of Macrobrachium spp. (log), and RIV=CPUE abundance of $R I V$ hartii (log). When CS was the dependent variable, it was not included as a covariate. For each model the following features are listed: number of parameters (k), logarithm of its Maximal Likelihood (InL), small-sample Akaike Information Criterium (AICc), correlation coefficient ( $\mathrm{R}^{2}$ ), Akaike weights ( $w$, the percentage of variation explained by each model), and Evidence Ratio (ER, the number of times that each model is worse than the best supported model of each set).

| Stage <br> Pregnancy |  |  |  |  |  |  |  | Model |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| F | - | CS~VOL+Watershed | 6 | 28.0 | -38.41 | 0.75 | 38.9 | 1.0 |
| F | - | CS~AREA+Watershed | 6 | 26.7 | -35.76 | 0.72 | 10.4 | 3.8 |
| F | - | CS~VEL+Watershed | 6 | 26.6 | -35.55 | 0.72 | 9.3 | 4.2 |
| F | - | CS $\sim$ Watershed | 5 | 24.6 | -35.42 | 0.66 | 8.7 | 4.5 |
| F | Early | SI~CS+ELO+Watershed | 7 | 28.7 | -35.42 | 0.61 | 36.7 | 1.0 |
| F | Early | SI~CS+REL+Watershed | 7 | 28.3 | -34.66 | 0.60 | 25.1 | 1.5 |
| F | Early | SI~CS+Watershed | 6 | 24.8 | -32.05 | 0.45 | 6.8 | 5.4 |
| F | Early | SI~CS+VEL+Watershed | 7 | 26.8 | -31.59 | 0.54 | 5.4 | 6.8 |
| F | Late | SI~CS+REL+Watershed | 7 | 23.5 | -25.02 | 0.47 | 33.4 | 1.0 |
| F | Late | SI~CS+Watershed | 6 | 20.8 | -23.97 | 0.33 | 19.7 | 1.7 |
| F | Late | SI~CS+CAN+Watershed | 7 | 21.9 | -21.82 | 0.39 | 6.7 | 5.0 |
| F | Late | SI~CS+PRW+Watershed | 7 | 21.8 | -21.70 | 0.39 | 6.3 | 5.3 |
| F | Late | SI~CS+VEL+Watershed | 7 | 21.6 | -21.29 | 0.38 | 5.2 | 6.5 |
| M | - | CS~Watershed | 5 | 30.5 | -47.18 | 0.43 | 29.5 | 1.0 |
| M | - | CS~VOL+Watershed | 6 | 31.6 | -45.50 | 0.48 | 12.8 | 2.3 |
| M | - | CS~VEL+Watershed | 6 | 30.8 | -44.07 | 0.45 | 6.3 | 4.7 |
| M | - | CS~ELO+Watershed | 6 | 30.8 | -44.00 | 0.45 | 6.0 | 4.9 |
| M | - | CS~AREA+Watershed | 6 | 30.8 | -43.90 | 0.44 | 5.7 | 5.2 |
| M | - | CS~PRW+Watershed | 6 | 30.7 | -43.84 | 0.44 | 5.6 | 5.3 |
| M | - | CS~REL+Watershed | 6 | 30.6 | -43.56 | 0.43 | 4.8 | 6.1 |
| M | - | CS~CAN+Watershed | 6 | 30.5 | -43.35 | 0.43 | 4.4 | 6.8 |
| M | - | CS~Watersheda | 6 | 30.5 | -43.33 | 0.43 | 4.3 | 6.9 |
| M | - | CS~Watershed | 6 | 30.5 | -43.33 | 0.43 | 4.3 | 6.9 |
| M | - | CS~RIV+Watershed | 6 | 30.5 | -43.33 | 0.43 | 4.3 | 6.9 |
| M | - | SI~CS+VEL+Watershed | 7 | 28.6 | -35.28 | 0.72 | 60.7 | 1.0 |

Notes: Twelve adaptive models were tested for each dependent variable (DV): DV~CS +Watershed, DV~CS+AREA+Watershed, DV~CS+REL+Watershed, DV~CS+ELO +Watershed, DV~CS+CAN+Watershed, DV~CS+VOL+Watershed, DV~CS+VEL +Watershed, DV~CS+Macrobrachium+Watershed, DV~CS+RIV+Watershed, DV~CS +AREA+REL+ELO+Watershed, DV~CS+CAN+VOL+VEL+Watershed, DV~CS +Macrobrachium+RIV+Watershed, DV~CS+AREA+REL+ELO+CAN+VOL+VEL +Macrobrachium+RIV+Watershed. The models of character evolution tested were ordinary least squares (OLS, non-phylogenetic multiple regression), Pagel's (RegPagel), and Ornstein-Uhlenbeck (RegOU). Most of the resulting best supported models were OLS. The exceptions are marked with superscripts: a) RegPagel, with phylogenetic signal $=1.30 \mathrm{E}-17$; and b) RegOU, with phylogenetic signal $=1.30 \mathrm{E}-17$.

## Concluding Remarks

In this dissertation I studied complex adaptive processes that involved multiple environmental and phenotypic interacting variables. In the first two chapters I used the Gambusia female system to test whether processes commonly observed at the intraspecific level were also present at the interspecific level. The first chapter was an interspecific analysis in body shape of females of 20 species of Gambusia. The main question here was whether predation and flow regimes explain body shape in these females. The main result was that, as predicted by biomechanical theory and in agreement with microevolutionary studies, female Gambusia showed relatively larger caudal regions in high-predation sites. This indicates that there is a continuum from micro- to macroevolutionary scales in the effect of predation on body shape of these females. At least in this system, microevolutionary patterns of phenotypic divergence were useful to predict macroevolutionary patterns of body shape variation. Unexpectedly, flow explained very little of the wide range of variation observed. As later explored in Chapter 3, flow may be a complex variable not always related to shape. One of the novel aspects of this analysis was that it accounted for pregnancy condition and for phylogenetic relatedness. The results show the importance of taking pregnancy into account because the way shape changed through pregnancy was related with predation regime, that is, pregnancy reduced the magnitude of phenotypic divergence between females from contrasting predation regimes.

Further studies may try to assess whether the different ways to be pregnant may explain the differences in locomotive performance of livebearing species (Ghalambor et al. 2004). The phylogenetic analysis had the challenge to deal with multivariate shape data (in the case of geometric morphometrics). Here I developed new software that allows such analysis. Our observation here agrees with the generality that phylogenetic signal is typically strong in shape variation (Blomberg et al. 2003), indicating that accounting for phylogeny in shape analysis of hierarchically structured samples should be the default analytical strategy. Also regarding methods, we observed that different currently widespreas methods to measure body shape were not interchangeable, but rather complementary. Further functional shape analysis should complement the currently ubiquitous application of geometric morphometrics with other estimations of shape that are more directly connected with functional aspects of shape.

The second chapter I also explored the continuation of adaptive divergence from micro- to macroevolutionary scales, this time with the life history of Gambusia females as the focal traits. In contrast to the analysis of shape, and despite theoretical predictions and previous observations at the microevolutionary level, predation or flow did not predict the wide range of life history observed in this genus. This negative results may be a consequence of the large sensitivity of life history traits to environmental conditions, perhaps in these case some conditions that we did not measure such as food availability or conspecific density. Nevertheless, this analysis showed interesting novel aspects,
such as the observation of incipient matrotrophy in few species and the first data on the life history of several species (some of them with a delicate conservation status). Moreover, we observed a rare life history phenomenon with unexplored theoretical implications: allometric coefficients vary with predation regime. Specifically, species from High-Predation sites increased in gonadal size at a higher rate with growth. This phenomenon deserves further theoretical and empirical investigation.

One interesting avenue for future studies on the Gambusia system would be to simulaneously analyze both sexes at intra- and interspecific scales. The data collected here, in addition to data from previously published studies (Langerhans et al. 2007; Langerhans and Reznick 2010) are a readily available source for such analysis.

In the third chapter I focused more specifically in flow regime to explain body shape of male and female guppies. The broad theme of this question was the study of adaptation to a disturbance. We observed a correlation between body shape and geomorphological features of the watersheds, but the results varied between sexes. A stronger predictor of shape was, interestingly, the abundance of prawns and Rivulus. That is, two biotic factors (the abundance of two competing or mildy predatory species) were more important for explaining body shape variation than abiotic factors associated with flow regime. This result pays homage to Darwin, who always favored biotic over abiotic factors when explaining evolutionary patterns in nature.

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[^0]:    S RegOU C $438.4-66.9 \quad 29.1 \quad 1.285 \quad 1.00$ $\begin{array}{llll}15.1 & 1.045 & 1.92 & 0.052 \pm 0.069\end{array}$ $\begin{array}{llll}2.5 & 1.287 & 2.33 & 0.032 \pm 0.070\end{array}$ $\begin{array}{lllll}9.4 & 0.696 & 3.13 & 0.105 \pm 0.066 & 0.129\end{array}$ $\begin{array}{llll}6.6 & 1.282 & 4.35 & 0.058 \pm 0.067\end{array} \quad 0.400$
    $6.5 \quad 0.989 \quad 4.55 \quad 0.028 \pm 0.073^{0.711} \quad 0.031 \pm 0.028^{0.276}$ $-0.067 \pm 0.025^{0.018}$ $-0.067 \pm 0.026^{0.021}$
    $-0.043 \pm 0.028^{0.137}$ $\begin{array}{lllll}6.5 & 0.002 & 3.33 & -0.046 \pm 0.071 & 0.526 \\ 5.0 & 0.549 & 4.35 & -0.072 \pm 0.071 & 0.324\end{array}$
    
    

