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Title

Shark Promiscuity: Investigating Drivers of Shark Polyandry to Advocate for Better Science Based Management

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Shark Promiscuity: Investigating Drivers of Shark Polyandry to Advocate for Better Science Based Management

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Abstract

Stressors since the 1970s like overfishing and habitat degradation, have led to a decline in global shark and ray populations. Direct and indirect fishing pressures on shark populations have reduced the potential suitors for female sharks, while environmental changes may further worsen the ability of most shark species populations to rebound. Limited understanding of shark ecology impedes conservationists' ability to create plans and influence policy. Convenience polyandry was thought to be a rare mating method found with sharks, with the common mechanism involving females accept copulation with any male to avoid excessive harassment. Despite the varied modes of reproduction, multiple paternity behavior in sharks has been recorded in seven elasmobranch orders. Recent studies have increasingly focused on the mechanism behind female choice and physiology in mating interactions generally displayed in post copulatory sperm selection mechanisms focused on "cryptic female choice". In this study we considered a variety of potential drivers of multiple paternity. The models determined that phylogenetic distance is not the only driver of polyandry in sharks. That life history characteristics do hold some influence over the rate of multiple paternity.

Introduction

The abundance of oceanic sharks and rays has declined by about 71% since the 1970s, largely due to fishing pressure.ⁱ The slow growth rate, late sexual maturity, and low fecundity of most chondrichthyans leads to a low rate of recovery in a depleted population.ⁱⁱ Changing environmental conditions is shifting and, in some cases, shrinking the habitat some shark species can inhabit, which could further exacerbate the declining populations of most chondrichthyans.ⁱⁱⁱ Smaller population sizes traditionally risk the chance of extinction due to effects of inbreeding depression caused by the loss of genetic variation or an increase in deleterious alleles.^{iv, v}

In 2016^{vi} the International Union for Conservation of Nature (IUCN) released a report on the endangered status of sharks, rays, and chimeras. Out of 465 species of sharks, 74 are classified as threatened, however, we currently do not have any information on 209 shark species^{vii}. The lack of data and knowledge on shark species inhibits our ability to craft conservation plans and potentially encourage and increase their populations.

Shark populations will have to adapt to changing conditions.^{viii} While marine protected areas (MPAs) are increasingly being established, many still allow fishing which does not help protect biodiversity.^{ix} Only about 2% of MPAs are implemented strongly, with adequate enforcement and monitoring.^x An analysis by the insurance firm Swiss Re, in 2020^{xi} found that more than half of global GDP depends on high functioning biodiversity. Yet about a fifth of countries globally are at risk of their ecosystems collapsing. With changing environmental conditions paired with habitat loss, and fishing pressures sharks, like most species will continue to have significant population declines. Some species of sharks will demonstrate phenotypic plasticity while others will shift their distribution to areas more favorable to their survival.^{xii} However, standing genetic variability will impact how well and fast a species can adapt, especially in those with complex and long-life histories.^{xiii}

Multiple paternity is when a female mates with multiple males. Despite the varied modes of reproduction, multiple paternity behavior in sharks has been recorded in seven elasmobranch orders.^{xiv} Knowledge of the exact mechanism behind this behavior is not known. Many contribute it to "convenience polyandry", where females accept copulation with any male to avoid excessive harassment.^{xv, xvi, xvii} However, as an alternative hypothesis, some studies have suggested that females are able to avoid copulation with undesirable males and choose to

copulate with many suitors.^{xviii} A changing distribution will alter the frequency at which sharks interact conspecifics^{xix} potentially lowering the rate of copulation. A decrease in frequency of interaction may lead to lower rates of insemination, which would reduce the potential genetic variability of some species, lowering their adaptability.

Fishing pressures on shark populations have reduced the potential suitors for female sharks, while environmental changes may further worsen the ability of most shark species populations to rebound. Multiple paternity increases the allelic diversity within a litter when compared to single paternity mating. A better understanding of sharks' geographical and habitat distribution is commonly used to create detailed conservation plans for a species.^{xx} Conservation planning for shark species needs to consider the effects of mate choice patterns and the mating system of the target species to calculate the minimum viable population size.^{xxi}

Genetic variation supports diversity within a species, which can lead to enhanced adaptation and resilience in the face of external stressors. Multiple paternity increases the genetic diversity within each litter or group of offspring and has been found to occur in many species. It may, therefore, be one way to ensure that threatened and at-risk species persist in a changing world. We studied the relationship between the rate of multiple paternity and various life history characteristics of multiple shark species.

Chapter 1: Predictors of multiple paternity

Introduction

Polyandry was once thought to be a rare form of mating^{xxii}, where a female copulates with multiple males, resulting in litters composed of half siblings.^{xxiii} Recent genetic studies have determined that females across the animal kingdom participate in polyandry^{xxiv} which is thought to increase the mother's biological fitness.^{xxv} Despite the varied modes of reproduction, multiple paternity behavior in sharks has been recorded in seven elasmobranch orders.^{xxvi} Available data suggests multiple paternity is abundant in the subclass, indicating the origin of polyandry as a mating method to have come from a common ancestor.^{xxvii}

Knowledge of the exact mechanism behind this behavior is not known, many contribute it to "convenience polyandry", where females accept copulation with any male to avoid excessive harassment.^{xxviii, xxix, xxx} However, some studies have suggested an alternative hypothesis that females are able to avoid copulation with undesirable males and choose to copulate with many suitors.^{xxxi} Current understanding of the drivers of polyandry is lacking, with most studies focusing on the presence and distribution of multiple paternity in a single population.

Recent studies have increasingly focused on the mechanism behind female choice and physiology in mating interactions generally displayed in post copulatory sperm selection mechanisms focused on "cryptic female choice". Some species will have anatomical features that allow for the female to control sperm access to the eggs,^{xxxii} while others secrete a protein that destroys seminal fluid that deteriorates competing seminal fluid from other males^{xxxiii}, reducing post-copulatory competition.

Focus on potential drivers of multiple paternity like the study done by Avise and Liu on viviparous fishes and mammals focused on one covariate, clutch size.^{xxxiv} The study was unable to determine a correlation between the occurrence of multiple paternity and clutch size, but did find that the factors influencing multiple paternity are similar in live bearing species, like fish and mammals or amphibians and reptiles.

In this study we consider a variety of potential drivers of multiple paternity. We investigate the impact evolution has on the prevalence of multiple paternity among the shark species. Species phylogeny will explain a percentage of species richness and variation^{xxxv} as evolution is an intrinsic driver of diversity in a taxa. The life history characteristics of a species can further the explanatory power of statistical models predicting trait prevalence.^{xxxvi} Earlier age of maturity can be a form of adaptive evolution, lending a higher fitness to the individuals that are able to breed faster than their counterparts.^{xxxvii} The adaptive strategy in short lived species may increase the likelihood of an individual becoming pregnant and paired with multiple paternity, the offspring would be more diverse, lending to a higher fitness for the mother.

We studied the relationship between the rate of multiple paternity and various life history characteristics of multiple shark species. We created two Bayesian models to determine the relationship of the above predictors on multiple paternity across all species as well as the difference in predictors and difference of multiple paternity between all pairs of species.

Methods

Data Acquisition

Multiple paternity data were supplied by Lyons, K., Kacev, D., and Mull, C., literary review. The covariates' maximum age and female age of maturity were gathered from the Sharks of the World: A Complete Guide. The potential breeding years were calculated by subtracting the maximum age of the species by the female age of maturation. The endangered status of sharks was collected from the *IUCN Red List of Threatened Species*.

Phylogenetic Analysis

A comprehensive phylogenetic tree for Chondrichthyes with 1192 species was sourced from the phylogenetic analysis in Stein et al.,^{xxxviii} which was sourced from the Chondrichthyan tree of life.^{xxxix} There was a large sampling of phylogenetic trees owing to the combination of taxa for which DNA data was available as well as those for which it was lacking. A single tree which included branch lengths, was sampled into Mesquite^{xl} from their “Chondrichthyan.610sp.1_fossil_Calibration.500treePLtrees” dataset. This tree was trimmed to exclude the chimaeras and rays, leaving 289 species of sharks, encompassed by the Galeomorphii and Squalomorphii. A character matrix was then coded into Mesquite to allow these characters to be mapped onto the phylogenetic tree. The first character was the presence or absence of polyandry for each species as presented in Lamarca et al. (2020). Any species with a rate of polyandry greater than 0.01% was marked as having polyandry present. For many species the status of polyandry was unknown so most terminal nodes were coded as missing. The other character that was coded for each species was the IUCN Red list status.^{xli} This was a binary character with each terminal node being scored as either critically endangered or not. This latter state merged multiple IUCN Red list categories. In this test of an association between polyandry and IUCN we hypothesized that endangered species would have fewer occurrences of polyandry compared to non-endangered species. We believed this to be the case due to the theorized increase to a mother’s fitness, multiple paternity lends. A species that has a higher occurrence of polyandry would not be a severely impacted by stressors that commonly lead to a decline in a population. The two characters were traced using the ‘most parsimonious reconstruction’ option in Mesquite. Then, using the mirror tree function in Mesquite the two characters were juxtaposed to visually assess any association between the two characters traced. Also, tests of association

using the Pairwise comparisons^{xlii} and Pagel's^{xliii} Correlation Method implemented in Mesquite were attempted.

Global Predictive Model

For each shark species with multiple paternity data, we modeled the proportion of litters displaying multiple paternity using a Bayesian generalized logistics model. To account for the rate of multiple paternity given the species, we used a posterior distribution. We have formulated the model to estimate the probability of multiple paternity given varied life history traits of each species. The linear model relating the proportion of litters with multiple paternity (P) to the set of predictors was defined as:

$$\text{Ln} \left(\frac{P}{1-P} \right) = \beta_0 + \beta_1 O + \beta_2 F + \beta_3 G + \beta_4 R + \beta_5 C + \beta_6 P + \beta_7 H$$

$\text{Ln} \left(\frac{P}{1-P} \right)$ = the expected likelihood of multiple paternity

β_0 = the model intercepts

β_{1-7} = refers to the slope of the corresponding predictor variable

O = Order designation of the species of shark

F = Family designation of the species

G = Genus designation of the species

R = Red list endangered status

C = Coarse reproduction mode

P = Reproduction Mode

H = Habitat type

The likelihood was based on a binomial distribution where,

$$m \sim \text{Binomial}(n | P)$$

m = the number of multiple paternity litters in each species

n = the total number of litters surveyed in each species

Posterior distributions were generated for above model using the *runjags* package in R v4.2.1. For the model, 8 independent MCMC chains were run, with 1000 adaptation steps, 100,000 steps for burn-in, and 1,000 sampling steps, thinned every 1,000 steps for a total of 8,000 samples for the posterior. Chain convergence and mixing were assessed with the *coda* package in R.

Statistically significant predictors were identified as those with posteriors that did not have 95% credibility intervals that included zero. Thus, predictors with more than 95% or less than 5% of their distributions greater than zero were considered to have significant influence on the rate of multiple paternity.

Pairwise Predictive Model

For all pairs of shark species with multiple paternity data, we modeled the difference in the proportion of multiple paternity using a Bayesian linear regression model. To account for the rate of multiple paternity given the species, we used a beta distribution. We have formulated the

model to estimate the difference in the probability of multiple paternity between two species given varied life history traits of each species. This formulation also allowed us to model the difference in multiple paternity as a function of phylogenetic distance between the species. The linear model was defined as:

$$Pdiff = \beta_0 + \beta_1 O + \beta_2 F + \beta_3 G + \beta_4 M + \beta_5 A + \beta_6 La + \beta_7 Ua + \beta_8 R + \beta_9 C + \beta_{10} P + \beta_{11} H + \beta_{12} T$$

$Pdiff$ = the estimated difference in multiple paternity

β_0 = the model intercepts

β_{1-12} = refers to the slope of the corresponding predictor variable

O = Order designation of the species of shark

F = Family designation of the species

G = Genus designation of the species

M = Maximum known age for the species

A = Average age of maturity

La = Lower range for age of maturity

Ua = Upper range for age of maturity

R = Red list endangered status

C = Coarse reproduction mode

P = Reproduction Mode

H = Habitat type

T = Phylogenetic distance

The likelihood was defined as:

$$P(MP_{species\ 1}) - P(MP_{species\ 2}) \sim Normal(Pdiff, SD)$$

$P(MP_{species\ 1})$ = probability of multiple paternity for species 1

$P(MP_{species\ 2})$ = probability of multiple paternity for species 2

SD = standard deviation

Beta distributions were fit to describe the binomial uncertainty around multiple paternity for each species. Bayesian models were fit in *runjags* as described above.

Results

The presence or absence of polyandry for each species resulted in 5 species being marked with an absence of polyandry and the other 27 participated in polyandry. Endangered status had a higher number of sharks with data but did have missing species. A visual assessment of the mirror tree function did not result in any obvious pattern or clustering of the characterization of absence or presence of multiple paternity (figure 1). However, there were a few clusters for the characterization of endangered (endangered and critically endangered) and not endangered (near threatened, vulnerable, and least concern) with *Squatina*, *Centrophorus*, and *Sphyrna* showing the most obvious groupings. Endangered classification occurred independently about 10 -15

times, with a few groupings of 2-3 scattered throughout the tree. Of all species marked with the presence or absence of polyandry, five have not been found to participate in this method of mating. For all forms of analysis conducted using Mesquite, there was unfortunately too much missing information in the Polyandry character to get the tests to execute. We were able to also determine that a common ancestor was the most likely origin of polyandry in the clade, a result identical to the one found by Lamarca et al (2020).

The logistic model was run to determine the strength the predictor variables had to influence the prevalence of multiple paternity in sharks. The pairwise linear regression model was run to determine the difference in the rate of multiple paternity between two species based on the difference in predictor values, this model also took into consideration the phylogenetic distance between the species.

For the logistic model, samples drawn from the posterior distributions showed good convergence and the estimated model fits to the data were good. Two covariates showed a significant relationship with the rate of polyandry, female maturity rate ($p=0.000$) and Red List status of endangered ($p=0.010$) (Table 1). The order of a species was nearly significant ($p=0.058$) in describing rate of polyandry.

	Median	HDI.Lower	HDI.Upper	Percent greater than 0
Intercept	3.095	0.232	6.482	0.981
Order lamniformes	-0.614	-9.867	8.631	0.450
Order squaliformes	-1.443	-3.269	0.362	0.058
Family triakidae	-0.448	-2.745	1.829	0.342
Maximum age	0.484	-10.257	11.475	0.531
Average female maturity	0.408	-10.432	11.182	0.528
Lower female maturity	-0.566	-0.844	-0.311	0.000
Upper female maturity	-0.261	-0.885	0.405	0.234
Potential breeding years	-0.506	-11.507	10.206	0.465
Redlist: CE	-1.024	-3.532	1.247	0.213
Redlist: NT	-0.884	-2.567	0.585	0.142
Redlist: V	-1.304	-3.620	1.128	0.138
Redlist: E	-1.470	-2.696	-0.057	0.010
Coarse reproduction mode: Lecithotrophic live bearing	-1.532	-15.320	11.487	0.407
Coarse reproduction mode: Matrotrophic live bearing	-1.725	-11.571	7.995	0.371
Reproduction mode1: Mucoid histotroph	-0.896	-10.025	8.317	0.434
Reproduction mode1: Placental	-0.838	-10.103	8.433	0.428
Reproduction mode 1: Yolk sac live bearing	-1.679	-14.638	12.354	0.426

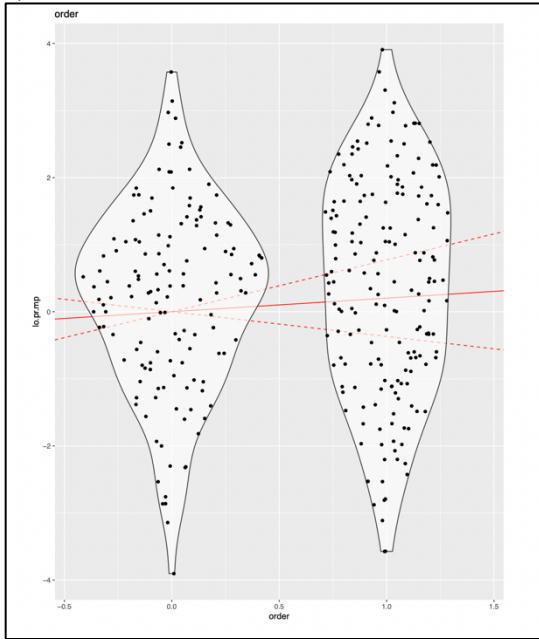
Table 1. Likelihood of covariates influence over rate of multiple paternity.

All but three of the covariates showed a significant influence over multiple paternity. The family classification ($p = 0.002$) indicates a higher likelihood of determining multiple paternity with a slope of -0.762 (figures 2b). The maximum age, lower and upper age of maturity ($p = 0.000$) show the greatest inverse influence over determining multiple paternity when phylogenetic distance is taken into consideration. The slope of maximum age is -0.017 (Figure 2c). The lower and upper ranges of the female age of maturity had similar slopes, -0.364 and -0.324 (figure 2e and f). The average female age of maturity ($p = 1.000$) was the only predictor value with a positive slope, 0.769 (figure 2d). The red list status ($p = 0.020$) indicates a higher likelihood of determining multiple paternity with a slope of -0.096 (Figure 2g). The phylogenetic distance ($p = 0.952$) indicates a higher likelihood of determining multiple paternity with a slope of 0.002 (figures 2j).

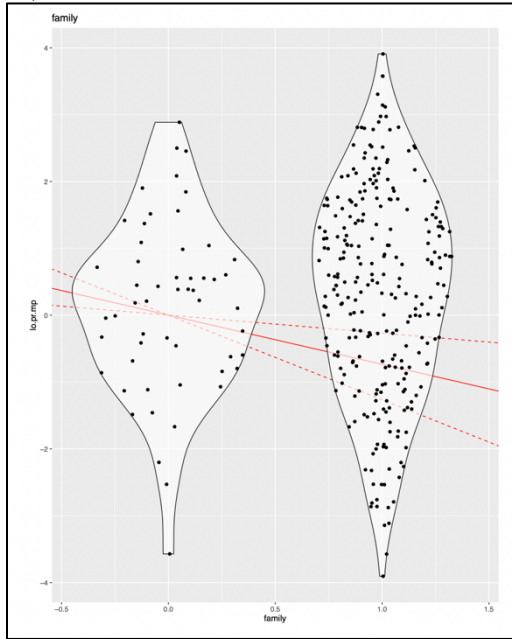
	Median	HDI.Lower	HDI.Upper	Percent greater than 0
Intercept	0.545	0.156	0.896	0.998
Order	0.191	-0.386	0.788	0.751
Family	-0.759	-1.225	-0.300	0.002
Maximum age	-0.017	-0.026	-0.008	0.000
Average female maturity	0.769	0.563	0.963	1.000
Lower female maturity	-0.362	-0.461	-0.263	0.000
Upper female maturity	-0.326	-0.433	-0.207	0.000
Red list	-0.096	-0.184	-0.002	0.018
Coarse reproduction mode	-0.090	-0.468	0.271	0.310
Reproduction mode1	-0.219	-0.640	0.165	0.143
Phylogenetic distance	0.002	0.000	0.004	0.957

Table 2. Likelihood of covariates influence over rate of multiple paternity with phylogenetic distance as a main factor.

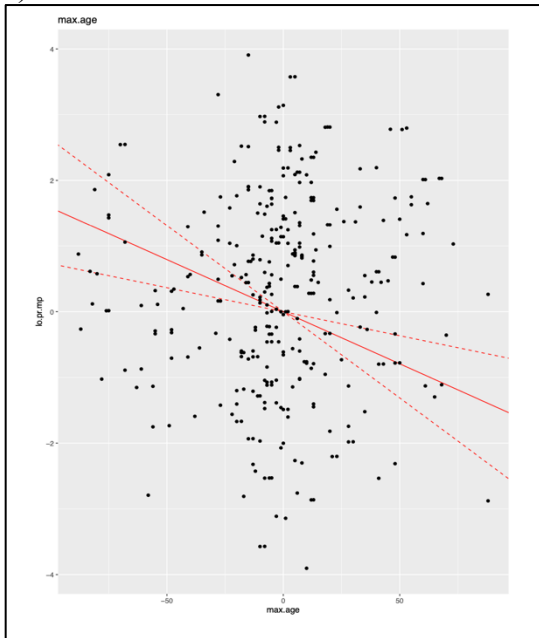
a)



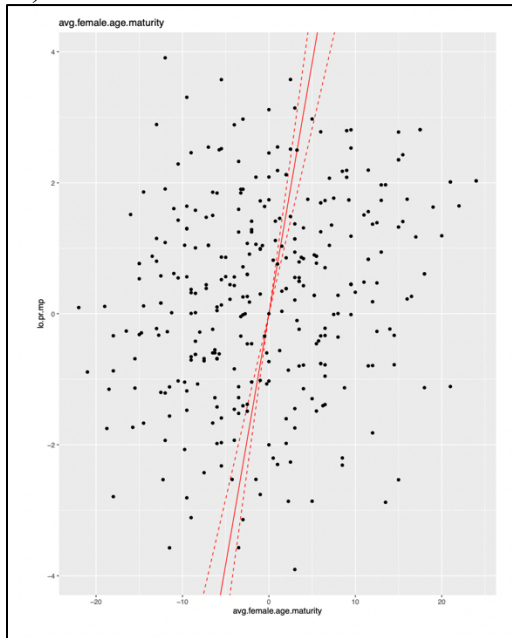
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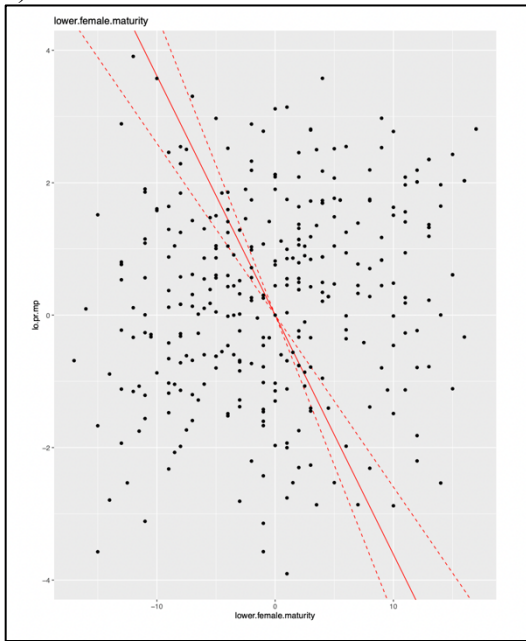
c)



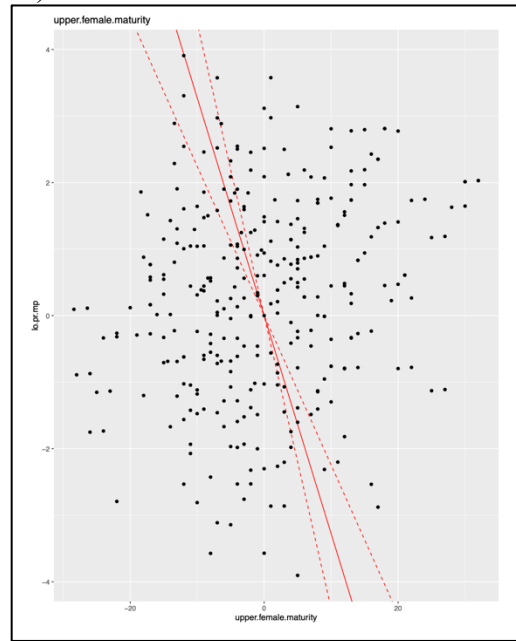
d)



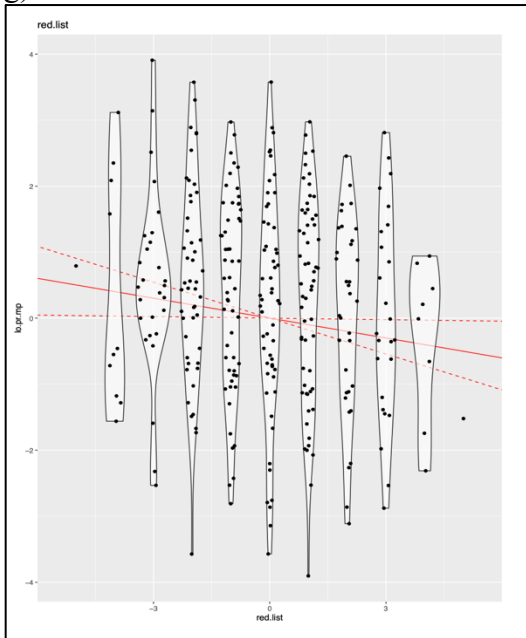
e)



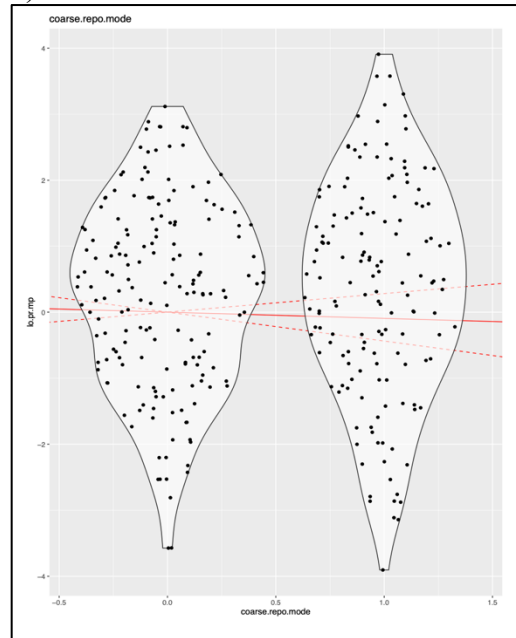
f)

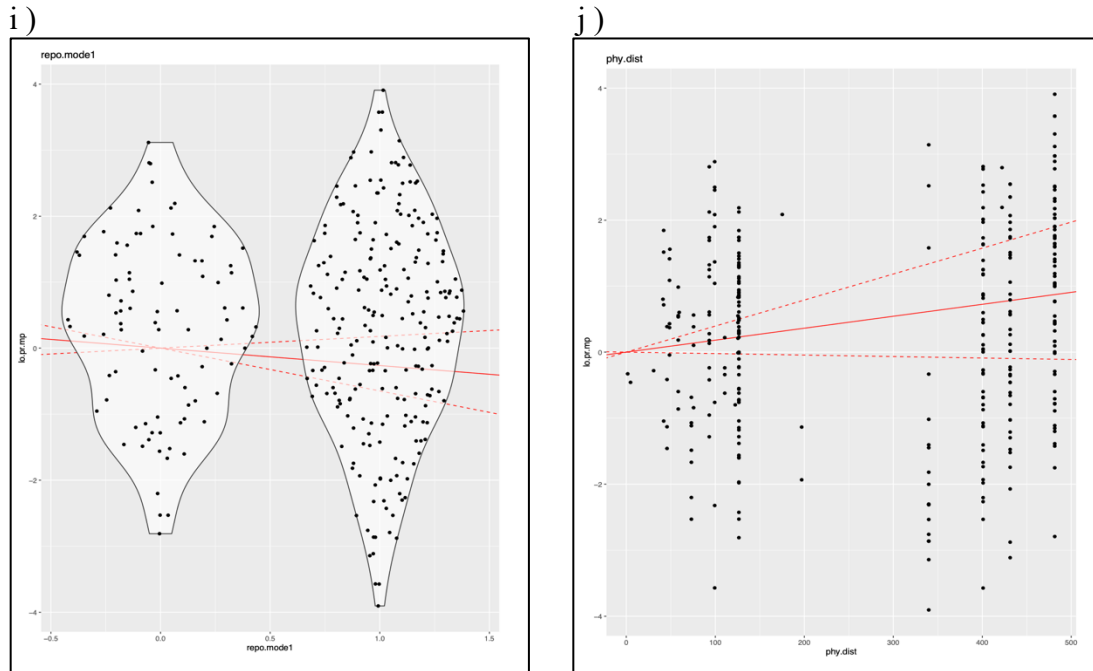


g)



h)





Figures 2 a-j. Models with vases depict the categorical options linked to the predictive value.

Discussion

Drivers of multiple paternity are not well understood, with most hypotheses considering the direct or indirect benefits while others focus on polyandry as a byproduct of competition.^{xliv} Multiple paternity has been viewed in a binary fashion to explain the evolution of polyandry in a clade^{xlv} or as a comparison of the rate of polyandry amongst populations.^{xlvi} We investigated potential predictors that may influence the prevalence of multiple paternity. The results have suggested that phylogenetic distance is not the only driving force for the rate of polyandry in a species (table 2). The female age of maturity seemed to have the strongest relationship with multiple paternity (tables 1 and 2), however the contrast in slopes leads to potential deeper considerations.

Phylogenetic Analysis

Due to the lack of data the tests of association run with Mesquite did not work. Carcharhiniforms have the most species with multiple paternity, however given the lack of data, there may be little significance to this grouping or another explanation. The order Carcharhiniforms is the largest grouping of sharks, leading to a skew in data collection as the chances of catching a member of this order to be higher than others. There is more information on the endangered status compared to data on multiple paternity, however there are still gaps in the data. Data on rates of multiple paternity data has been gathered mainly opportunistically. The challenges involved sampling many shark species makes genetic testing of litters difficult as well as collection of life history characteristics. The only determination made through Mesquite was that polyandry is the ancestral state of all chondrichthyans, this conclusion is also shared by Lamarca, et al. (2020). With the large gaps in data for sharks in general, this conclusion is in line with what the data shows, however may not be representative of the actual cause of polyandry being present in the species.

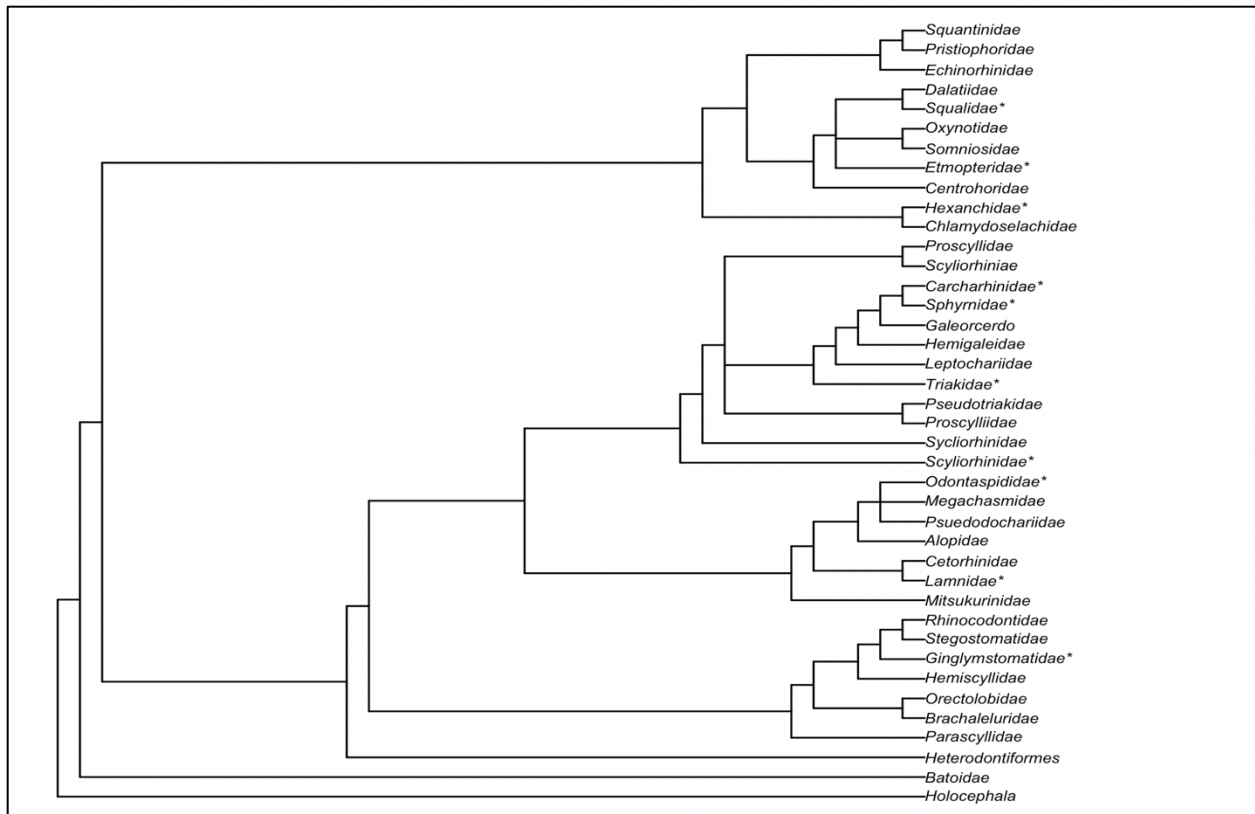


Figure 3. The family classifications of chondrichthyan families applied to a phylogenetic tree. Titles with an asterisk are families with multiple paternity present. Carcharhinidae 9, Etmopteridae 2, Ginglymstomatidae 1, Hexanchidae 1, Lamnidae 2, Odontaspidae 1, Scyliorhinidae 1, Sphyrnidae 2, Squalidae 2, and Triakidae 7.

General logistic model

The order squaliformes held significance above the other four orders present. In the 26 species analyzed only 5 squaliformes displayed polyandry mating. Most squaliformes are deep-water inhabitants^{xlvii}, in the deep many species are known to exhibit extreme mating methods due to the lack of interaction with the opposite sex, the male anglerfish fusing to the body of the female permanently is one such example.^{xlviii} Polyandry could increase the fitness of the females, as their litter of pups would have a diverse array of genetics, leading to a better chance her genetics are passed through the population.

The younger the female of the species becomes sexually mature, the higher the likelihood the species has a high occurrence of polyandry. There is a relationship between a low age of female maturity and reduced potential breeding years (figure 4). Breeding years was calculated by taking the difference in the maximum age and the average female age of maturity, combined with set mating cycles (annual or biannual) some species may only have a few limited chances to mate and reproduce successfully. A female who mates with one male, compared to one who mates with multiple would have less genetic diversity present in her offspring, lowering the chances of her genetics being passed on to future generations. A mother who participates in polyandry has a higher chance of more offspring surviving if they are genetically different, as they are less likely to die from the same stressor, disease, etc. The increase in a mother's fitness by participating in multiple paternity may be an explanation as to why the species with lower age of maturity show higher frequencies of multiple paternity.

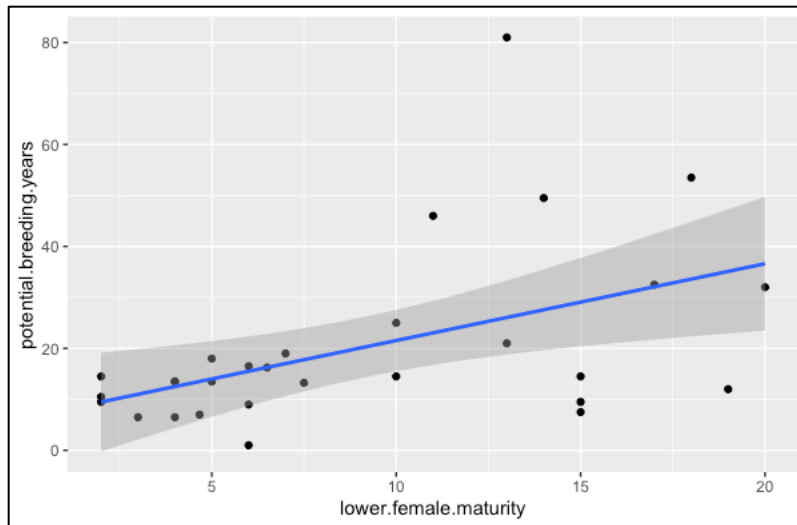


Figure 4. Relationship between the lower age of female maturity and the potential breeding years.

There is a higher likelihood for species with an IUCN Red List status of Endangered to have lower rates of multiple paternity (Table 1). Endangered species are less likely to have high frequencies of multiple paternity. However, with a large gap in data for endangered status and polyandry frequency, the predictive power granted towards the IUCN endangered status may not be of any actual significance.

Pairwise linear model

The family designation of the species has a higher likelihood of determining multiple paternity when phylogenetic distance is taken into consideration. Utilizing the phylogenetic distance from the “Chondrichthyan.610sp.1_fossil_Calibration.500treePLtrees” dataset, the significance identified in the results may be largely due to the type of multiple paternity data available. The top three families represented in the model are Carcharhinidae (10 species), Triakidae (8 species), and Etmopteridae (3 species), the other 9 families have only one or two species. The strength of family designation as a predictor, is therefore heavily biased.

The maximum age of the species has a higher likelihood of determining polyandry when phylogenetic distance is taken into consideration. The higher the age, the lower the frequency of multiple paternity (Figure 2c). This significance is related to the results found in the global model concerning the lower age range of maturity. A species with a longer life history would have longer potential breeding years, allowing them more time to carry genetically diverse litters throughout their lifetime. The fitness gained by species with shorter potential breeding years is not applicable for those with longer breeding years, making the need to participate in multiple paternity less severe. As polyandry originates from a common ancestor, most species are still able to partake in it, however longer-lived species are not under duress to.

Interestingly as the average age of female maturity increased so does the chances of the species having higher rates of multiple paternity however the lower and upper range of female age of maturity have an inverse effect. Future statistical analysis may lend to a better understanding of the inverse relationship the predictors have.

Red list status could be an indirect way to predict the frequency of multiple paternity for a species. However, this predictive power may be severely limited due to the lack of data for sharks in general. There are over 200 species that have not gone through an assessment with the

IUCN and about 30 species that currently have multiple paternity data from the litters. The accuracy of the red list status as a predictor for frequency of multiple in a species may not be as significant as these models show.

Chapter 2: Comic
Main Comic

SHARK PUPS ARE IMPORTANT TO THE ECOSYSTEM?!

GRAPHIC DESIGN BY AZSHA HUDSON
ILLUSTRATED BY ALEJANDRO CANO- LASSO CARRETERO AND AZSHA HUDSON

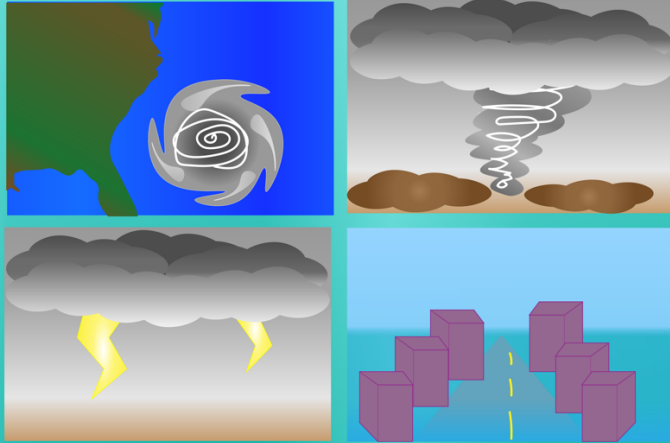
WHO NEEDS KIDS!?!?

TECHNICALLY WE DO...

YEAH, BUT WE DON'T HAVE TO WATCH THEM!

Citations: Ebert, D. A., Dando, M., & Fowler, S. L. (2021). *Sharks of the world a complete guide*. Princeton University Press., Blackburn, Daniel G. "Viviparity and oviparity: evolution and reproductive strategies." (1999), Pacoureau, N., Rigby, C.L., Kyne, P.M. et al. Half a century of global decline in oceanic sharks and rays. *Nature* 589, 567-571 (2021). <https://doi.org/10.1038/s41586-020-03173-9>, Nowicki, R.J, Thomson, J.A, Fourqurean, J.W, Wirsing, A.J, Heithaus, M.R. Loss of predation risk from apex predators can exacerbate marine tropicalization caused by extreme climatic events. *J Anim Ecol.* 2021; 90: 2041- 2052. <https://doi.org/10.1111/1365-2656.13424>
., IPCC Climate Change 2014: Synthesis Report (eds Core Writing Team, Pachauri, R. K. & Meyer L. A.) (IPCC, 2014).

CLIMATE CHANGE IS LEADING TO MORE INTENSE AND EXTREME CLIMATE EVENTS GLOBALLY

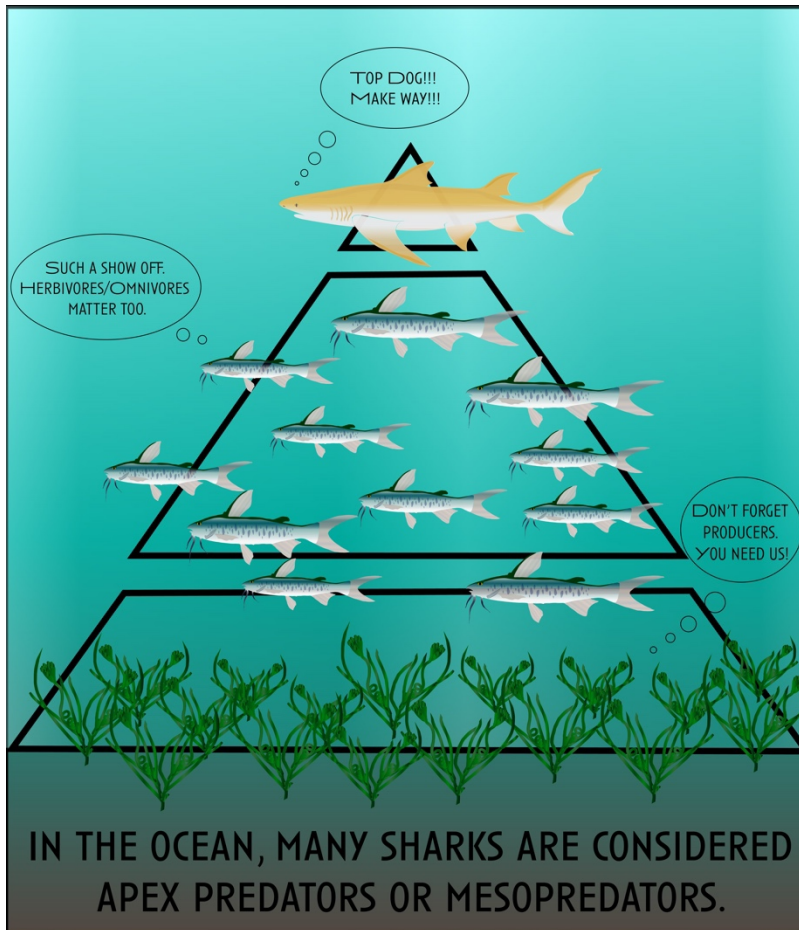


1840S
SMALLER STORMS,
LESS DAMAGE

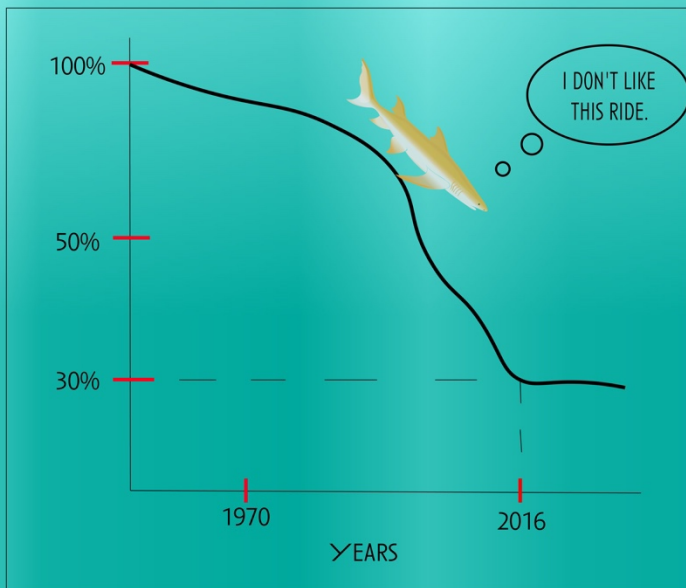
2020S
BIGGER STORMS,
MORE DAMAGE



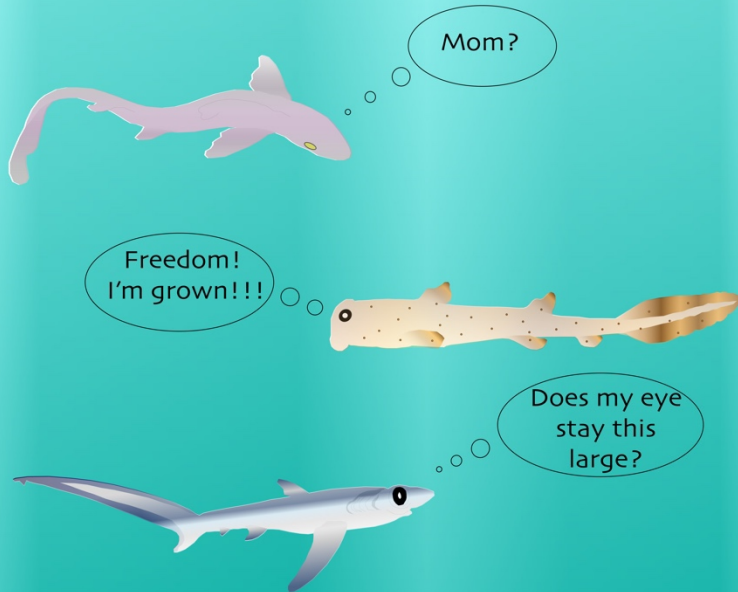
STUDIES SHOW THAT THE LOSS OF PREDATORS IN A MARINE ECOSYSTEMS CAN MAKE THE IMPACT OF EXTREME CLIMATE EVENTS WORSE



SHARK POPULATIONS HAVE DECLINED BY 70% SINCE THE 1970S



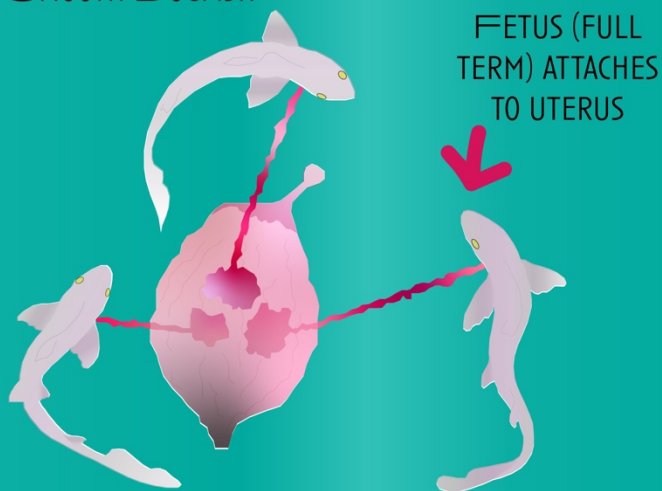
A HEALTHY POPULATION REQUIRES MANY DIVERSE INDIVIDUALS. THE POPULATION IS MAINTAINED BY NEWBORN PUPS.



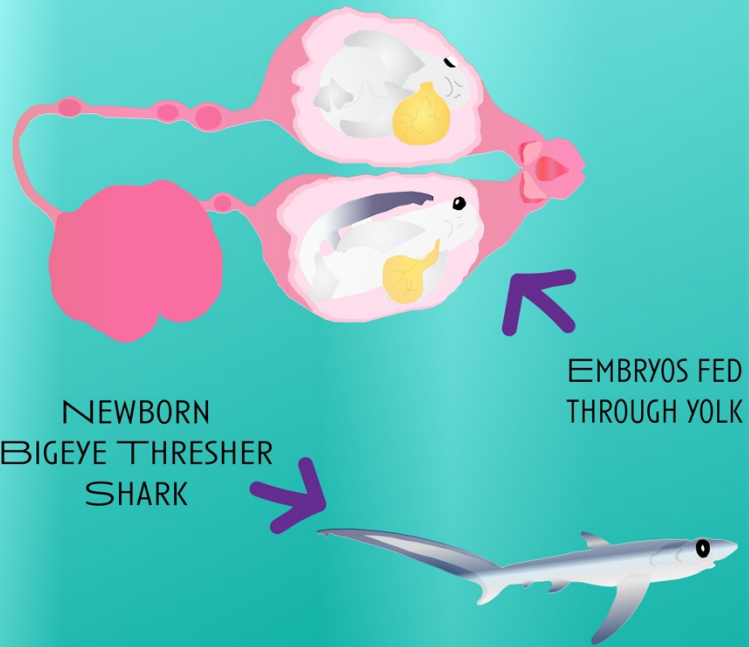
**THERE ARE THREE MODES OF REPRODUCTION FOUND IN SHARKS:
VIVIPARITY, OVIVIPARITY, OVIVIPARITY**

VIVIPARITY: LIVE BIRTH, PLACENTA

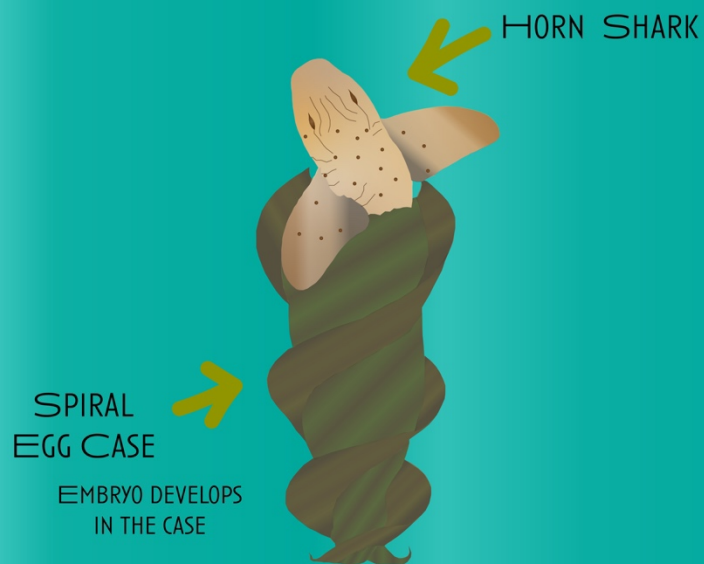
SMOOTH DOGFISH



OVIVIPARITY: LIVE BIRTH, YOLK



OVIPARITY: LAYS EGGS



Multiple Paternity

Multiple Paternity

Rare mating method or common practice in sharks?

Graphic design and illustrations by : Azsha Hudson



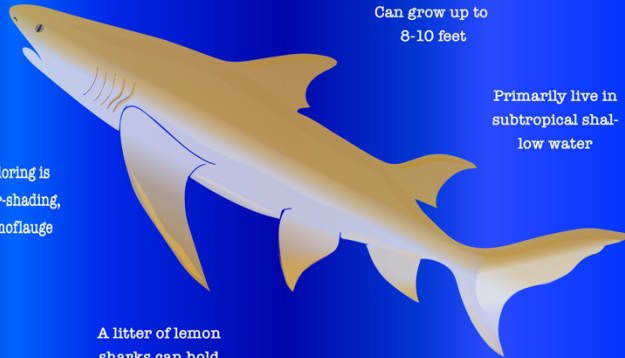
Give live birth, through placental connection

Maximum life expectancy is about 27 years.

Can grow up to 8-10 feet

Primarily live in subtropical shallow water

Two tone coloring is called counter-shading, a form of camouflage

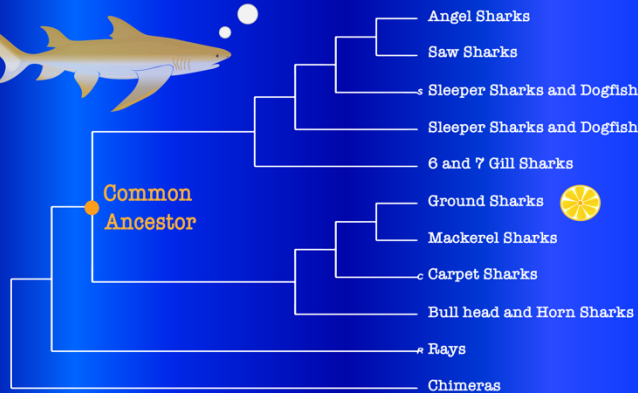


A litter of lemon sharks can hold up to as many as 17 pups.

Lemon sharks have a yellow/brown or olive gray coloring

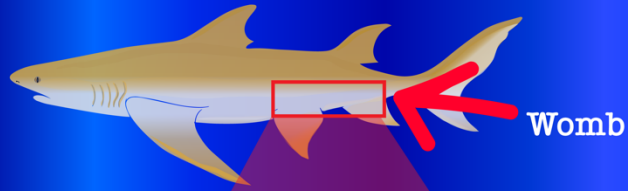
A recent study by Lamarcka, et al., found that multiple paternity most likely evolved in sharks through a common ancestor

Great, Great, great, great, great.....great grandparents!!!!



This is a phylogenetic tree. It helps scientist understand how species are related to each other

Female Lemon Shark is pregnant with pups

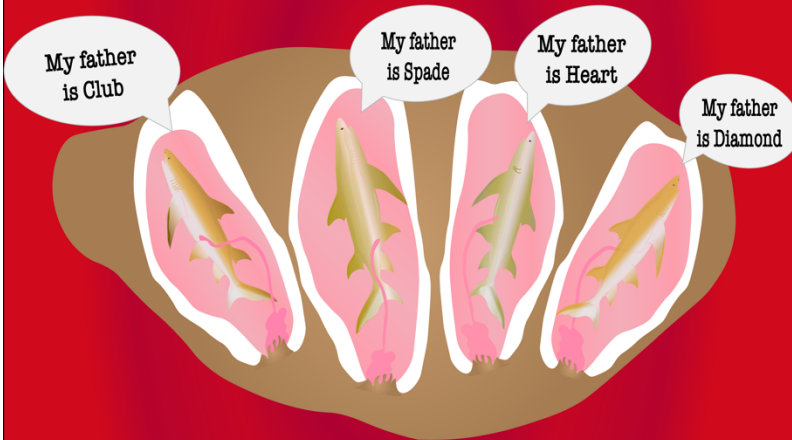


Womb

Inside the
womb



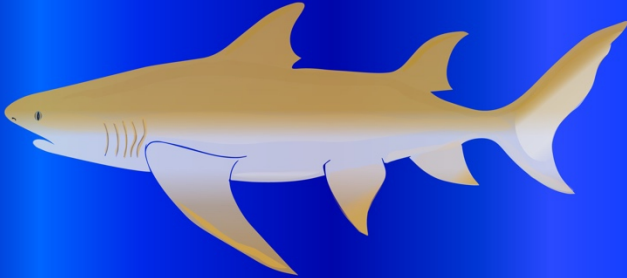
Multiple Paternity is when a female mates with multiple males. Producing offspring that can be half siblings.



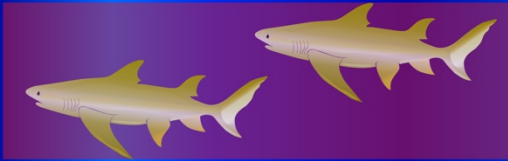
Inside the female shark

When there are many pups,
fathers can sire multiple in a litter

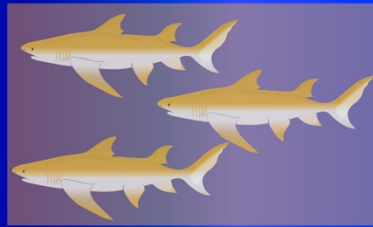
Mother Supreme: aka
mother of litter



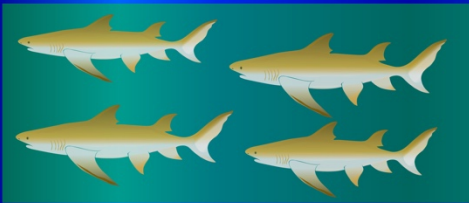
Father North



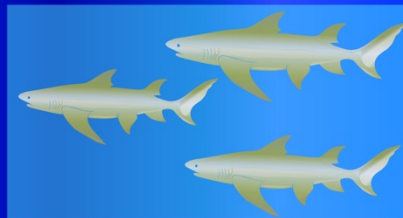
Father
East



Father West



Father
South



Reproduction

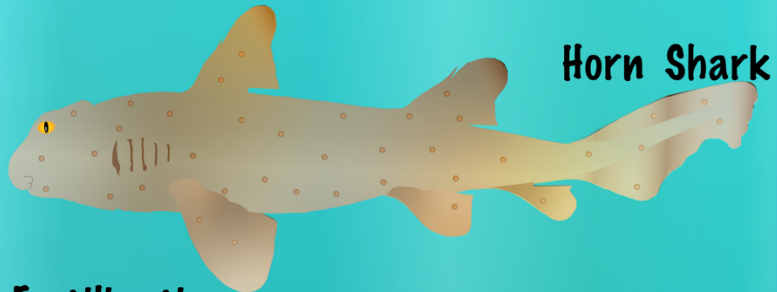
Shark Reproduction

Graphic design by Azsha Hudson
Illustrated by Alejandro Cano- Lasso Carretero

As an offshoot of the main comic, this is to give more explanation as to what each of the 3 modes of reproduction are. Sharks have more than one way of giving birth, some are similar to mammals, some to birds, and others a hybrid of the two. Learning about how certain species reproduce will aid in fcurrrent and future conservation effotrs.

Citations: Ebert, D. A., Dando, M., & Fowler, S. L. (2021). Sharks of the world a complete guide. Princeton University Press.,Blackburn, Daniel G. "Viviparity and oviparity: evolution and reproductive strategies." (1999).

Oviparity: Lays eggs



Fertilization

The fetus with
an attached
yolk sac

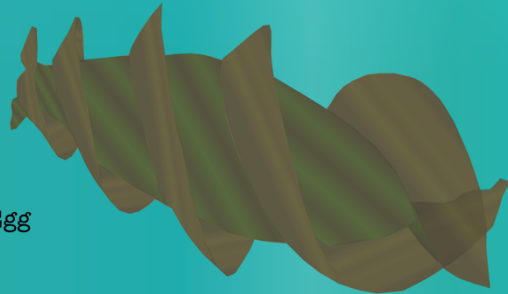


Incubation

Embryo develops
in the case



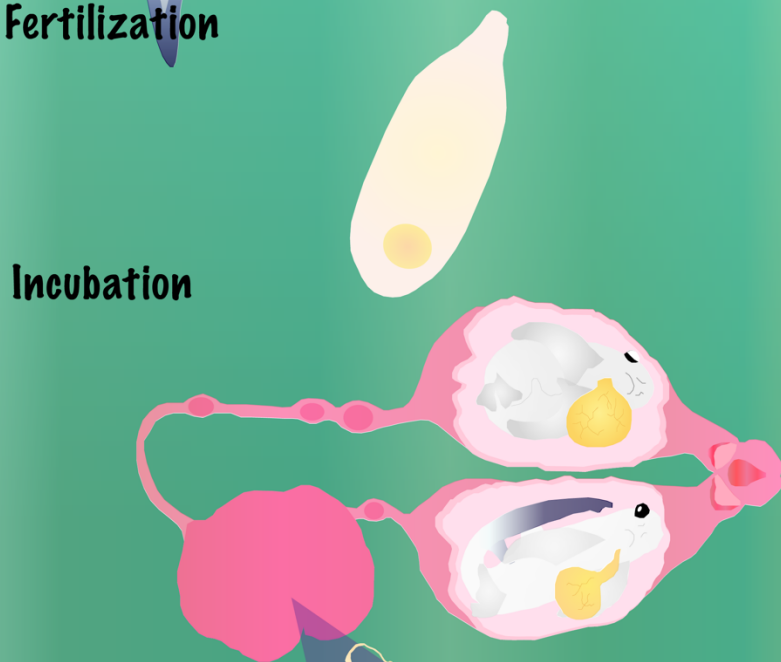
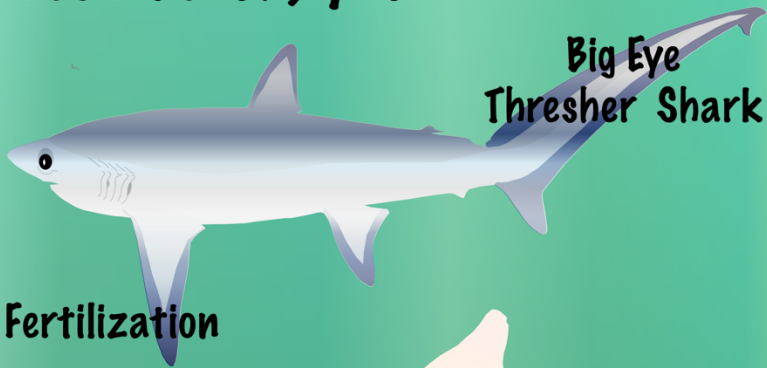
Spiral Egg
Case



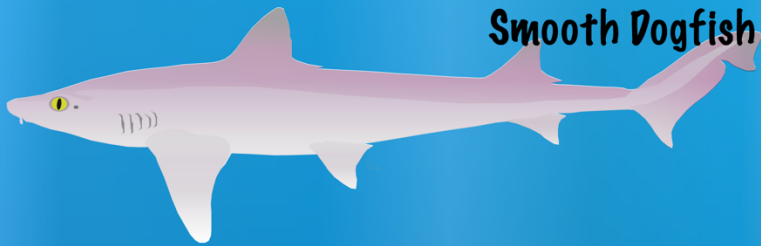
Birth



Oviviparity: Live Birth, yolk



Viviparity: Live birth, placenta

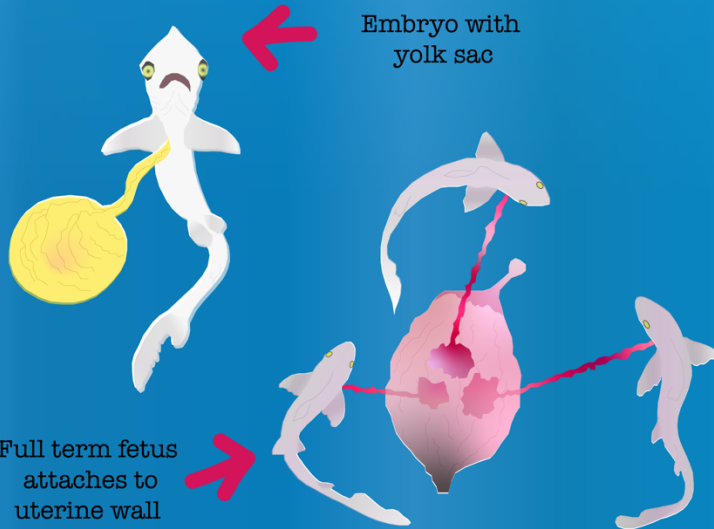


Fertilization

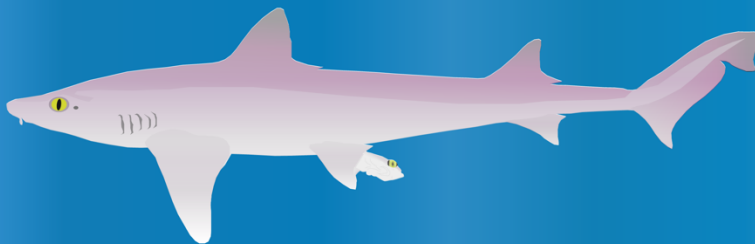
Egg capsule with
developing embryo



Incubation



Birth



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