Biometric and allometric relationships for large pelagic species collected in Reunion Island: contribution to an IOTC database?

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Abstract

Biometric relationships are critical to convert measurement performed at landings (fish with head, tail cut or gutted and gilled) to standardized measurements which can be used in stock assessment and scientific purposes. In the Indian Ocean, while tuna species are relatively well described, there is a critical lack of information for billfish and the interannual and seasonal variations of these relationships are rarely investigated. To cope with this issue, the relationships used at IOTC are coming from other oceans or close species which is not scientifically satisfactory. In this document, we present the biometric relationships for 6 large pelagic species over 267 individuals in 2017 and 2018 from catches of Reunionese longliners. The classical length and weights are established for this species. While the relationships are very neat, further collections are needed to provide robust relationship. This document question our ability to share and build a global biological database at IOTC which can be regularly updated and provided the best scientific knowledge for these relationship. These data could be also used for other scientific needs and could be easily freely accessible as they are not sensitive.

Introduction

An effort is needed to improve basic biological and ecological knowledge about exploited species as stock assessment models are very sensitive to these key parameters. While a substantial amount of information is available on tuna species, there is a critical lack of knowledge for billfish. Moreover, data are collected at specific time and locations and subsequent analysis for allometric and biometric relationship are established on this subset of data.

Data collection in Reunion Island

Sampling of large pelagic landings by Reunionese longline fisheries is carried out twice a month in order to meet the reporting obligations for the Indian Ocean Tuna Commission (IOTC; DCF/DCMAP funding). Most of the individuals landed are prepared on board. Depending on the species and size, they are eviscerated, headed or without tail. The measurements at landing are thus converted into fork length from size-size relationships that come from different sources (IOTC, scientific articles, Fishbase, IFREMER samples, etc.). Length-weight relationships are then used to obtain the entire weight of individuals. These relationships are also defined by the IOTC, scientific articles, FishBase or IFREMER samples.

Some problems on these biometric relationships used have been noted:

1- For some species, the geographical location of the individuals on which these relationships are established is not adapted to the Indian Ocean context (most length-length relationships and half of length-weight relationships)

2- The number of samples that allowed these relationships to be established is very low (e.g., the length-length relationship of wahoo)

3- The conversion from a measured length to a length that can be used for a length-weight relationship is not direct and requires conversions to another length first. This leads to error propagation.

Table 1: Length-weight relationships available for the species landed in Reunion Island

English name	FAO code	L	a	b	Area	Reference
Albacore	ALB	FL	3e-05	2.955	Indian	1
Bigeye	BET	FL	2.7e-05	2.951	Indian	2
Yellowfin	YFT	FL	1.585e-05	3.046	Indian	2
Blue marlin	BUM	LJFL	1.2e-06	3.366	Atlantic	3
Black marlin	BLM	LJFL	6.61e-05	2.611	Pacific	4
Stripped marlin	MLS	EFL	1.33e-06	3.413	Pacific	4
Wahoo	WAH	FL	0.0016	3.275	Atlantic	3
Swordfish	SWO	LJFL	0.000206	2.273	Reunion	6
Sailfish	SAI	EFL	6.9e-05	2.524	Pacific	4

(1) IFREMER Germon project, (2) IOTC-2006-WPTT-09, (3) ICCAT, (4) South Pacific Commission, (6) Poisson & Taquet (2001)

Material and methods

Fish sampling

Over 2017 and 2018, 313 whole individuals of albacore (*Thunnus alalunga*), bigeye (*Thunnus obesus*), yellowfin (*Thunnus albacares*), blue marlin (*Makaira nigricans*), sailfish (*Istiophorus platypterus*), dolphinfish (*Coryphaena hippurus*), and swordfish (*Xiphias gladius*) have been landed for this project. For each individuals, measurement of whole weight, gutted and gilled weight, gutted and headed, standard length, pectoral-fork length and equivalent curved length as well as kneel-cleithrum length for swordfish. The half circumference, the jaw (dentary) length, and the tip of dentary to pre-operculum and operculum lengths has been taken too. Length were measured to the nearest lower centimeter and weight to the nearest decigram. The information about sex and maturity stage were also noted.

Model fitting

We used the "lm" function to estimate the different length-length and weight-weight relationships. For the length-weight relationships, we first log-transformed the data prior to estimate the parameter of the linear model.

Table 2: Sampling features for each species

FAO Code	Sample size	Min. Weight	Max. weight	Mean weight
ALB	50	17.4	31.1	23.8
				42.7
				78.5
				11.4
				38.7
				35.7

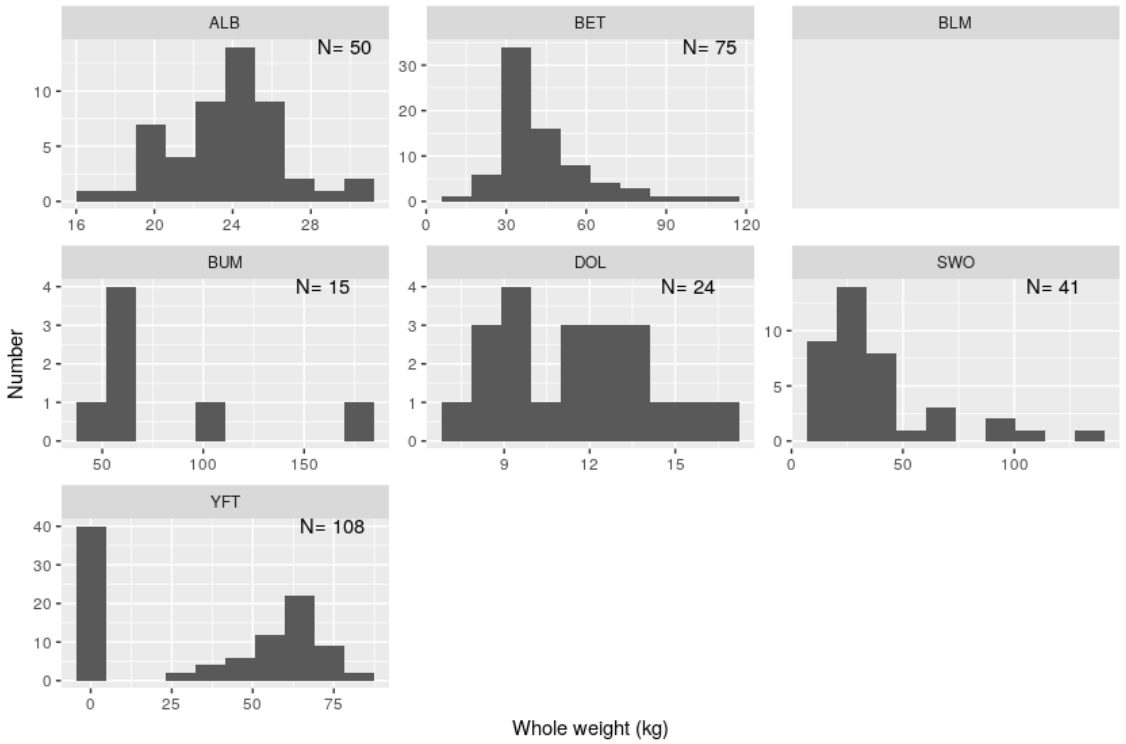

Figure 1: Weight distribution of the sampled fish

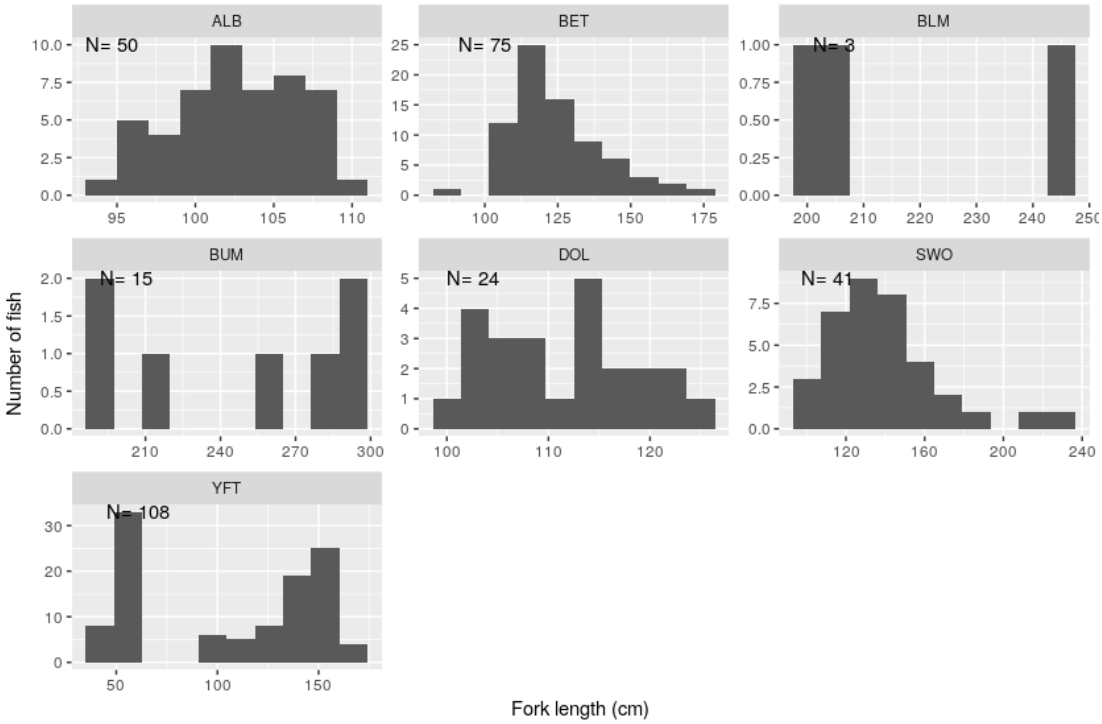

Figure 2: Fork length distribution of sampled fish

Results

The different length-length, weight-weight, and length-weight relationships are given in the following tables and figures. The fit to data is remarkably good with very few outliers.

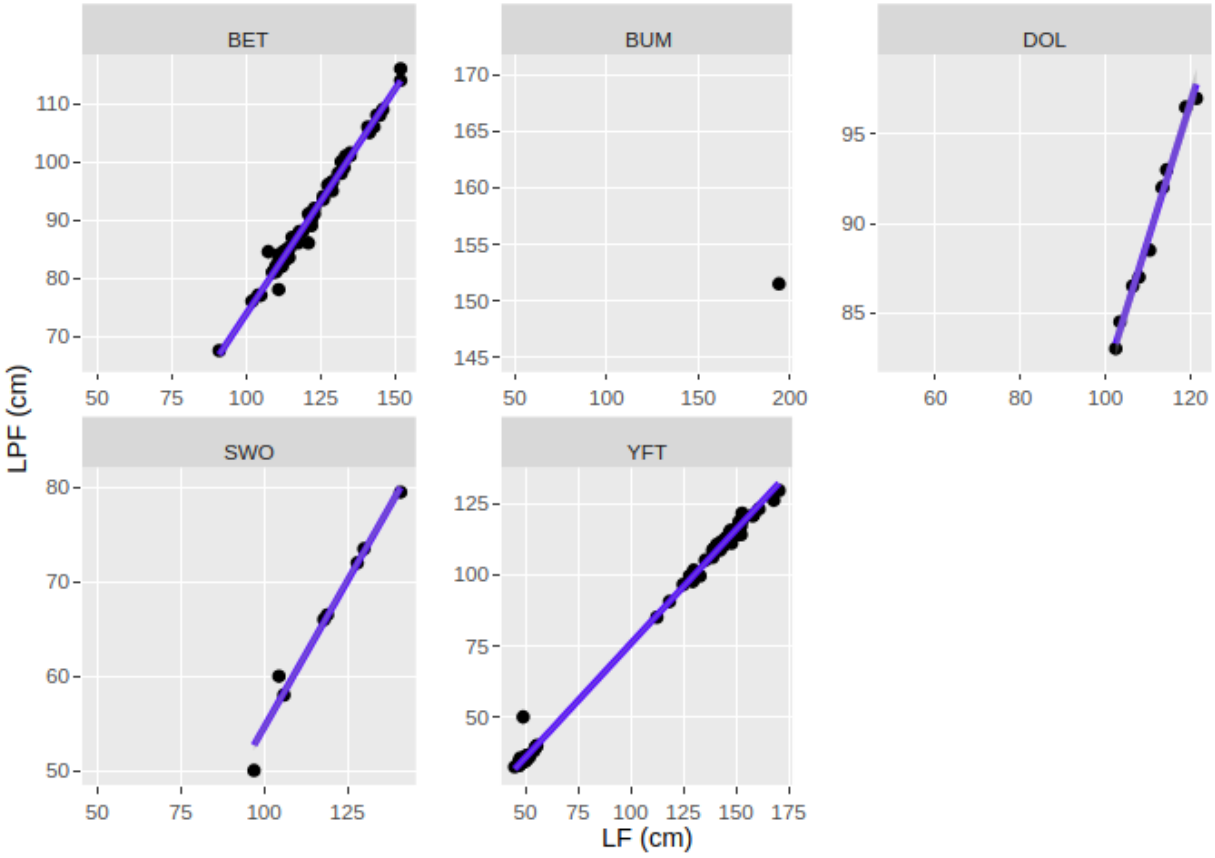

Figure 3: Pectoral-fork length relationships for the different species

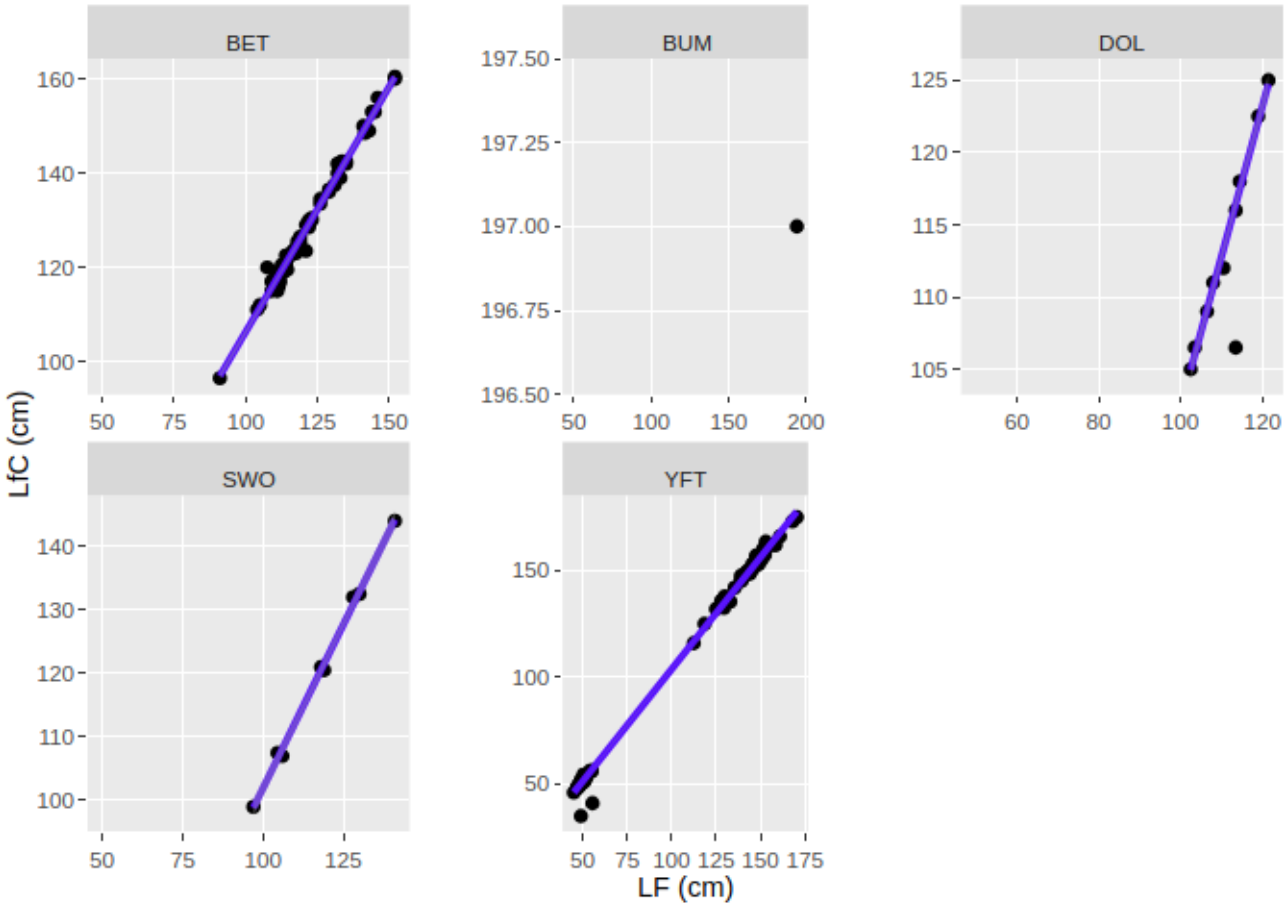

Figure 4: Fork – curved fork length relationship

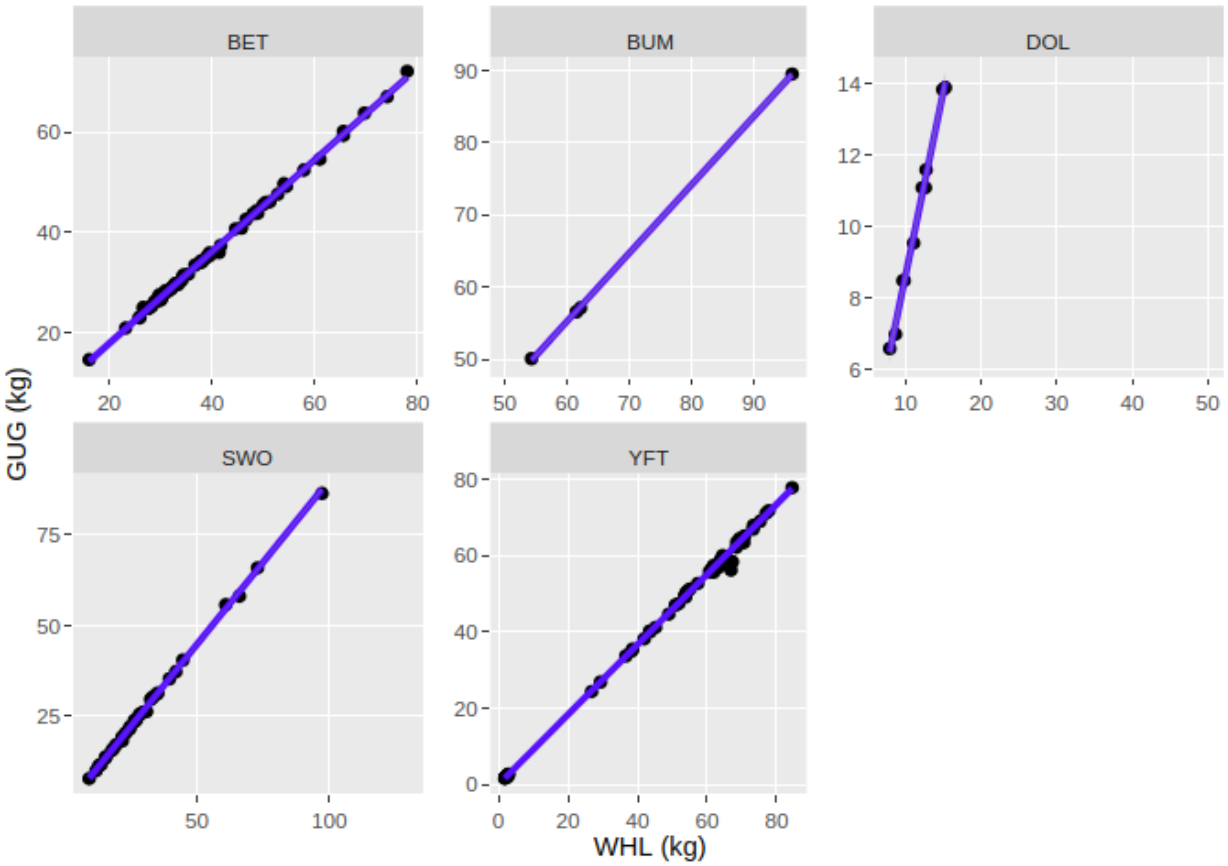

Figure 5: Example of a weight-weight relationship (gutted and gilled weight *vs* whole weight)

Table 3: Coefficients for the weight-weight relationships

	Relation	Code.FAO	a	N	R2
1	WHL - GUG	ALB	1.08	50	1
2	WHL - GUG	BET	1.1	75	1
3	WHL - GUG	BUM	1.21	15	0.99
4	WHL - GUG	DOL	1.12	24	1
5	WHL - GUG	SWO	1.11	41	1
6	WHL - GUG	YFT	1.09	108	1
7	WHL - GHT	ALB	1.19	50	1
8	WHL - GHT	BET	1.23	75	1
9	WHL - GHT	BUM	1.09	15	0.96
10	WHL - GHT	SWO	1.24	41	1
11	WHL - GHT	YFT	1.18	108	1

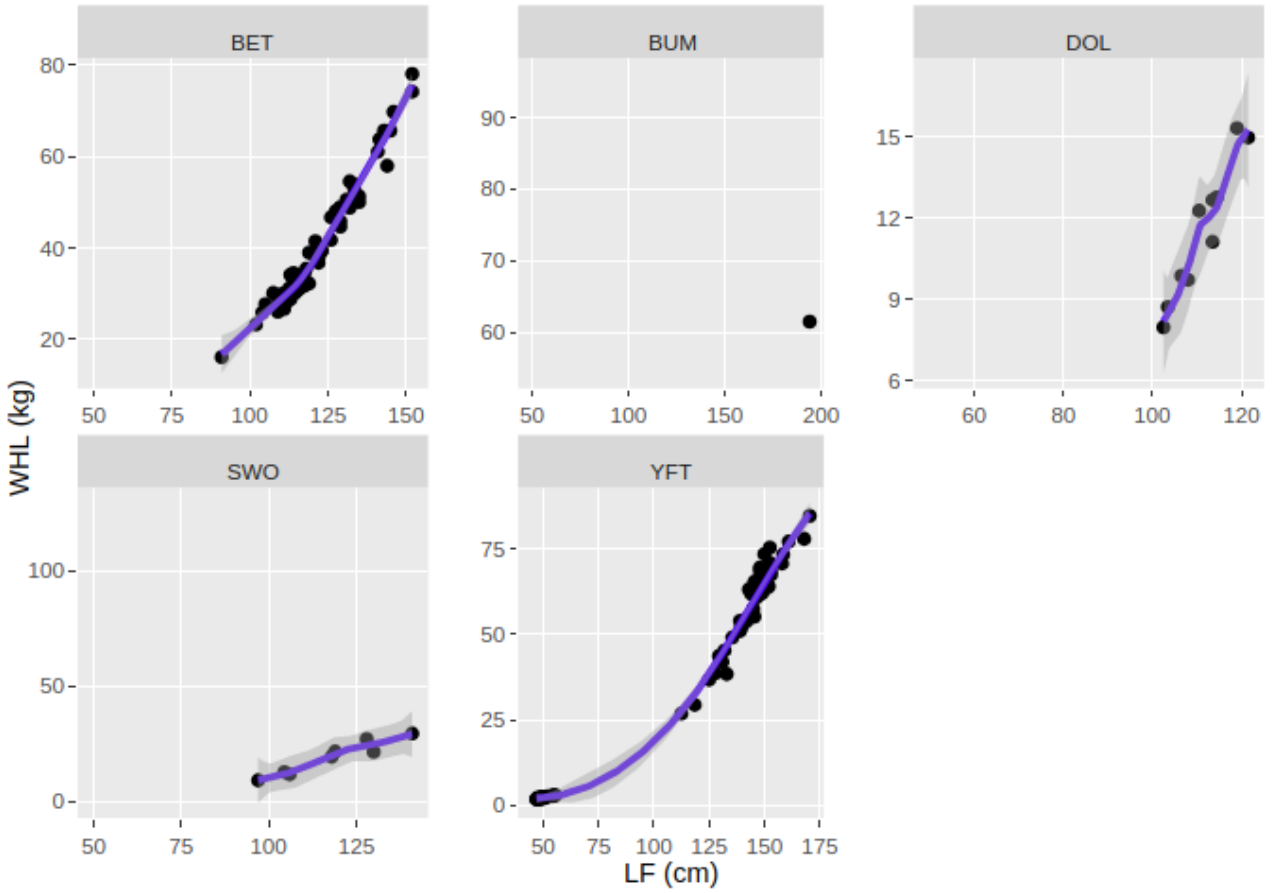

Figure 6: Example of a weight-length relationship (whole weight *vs* fork length)

Table 4: Coefficients for the weight-length relationships W=aL^b

	Relation	Code.FAO	a	b	N	R2
1	W - L	ALB	0.0001537	2.578	50	0.84
2	W - L	BET	0.0000235	2.981	75	0.98
3	W - L	BUM	0.0000101	2.948	15	1
4	W - L	DOL	1e-7	3.858	24	0.96
5	W - L	SWO	0.0000082	3.07	41	0.99
6	W - L	YFT	0.000016	3.036	108	0.99

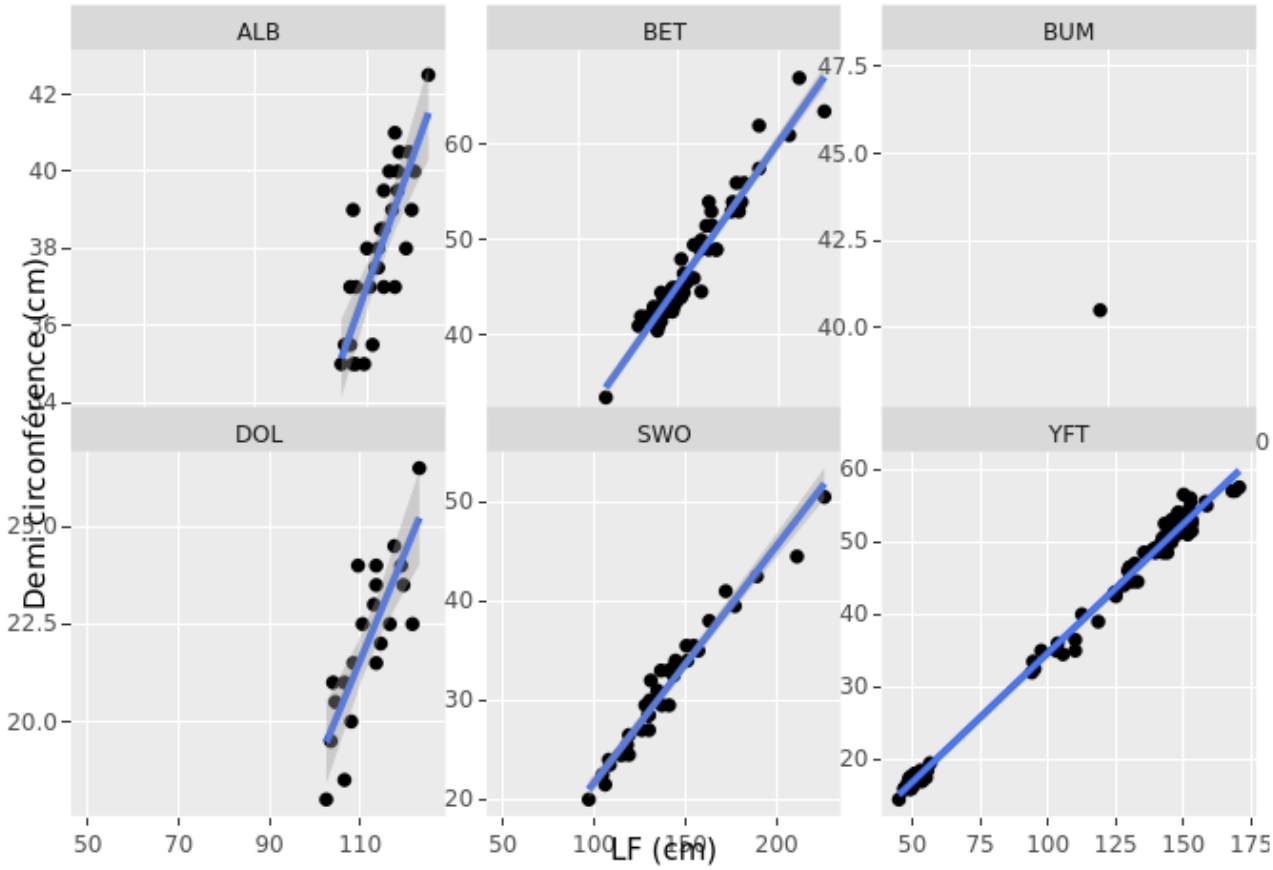

Figure 7: Example of half circumference (HC) – standard length (SL) relationships (SL = a.HC+b)

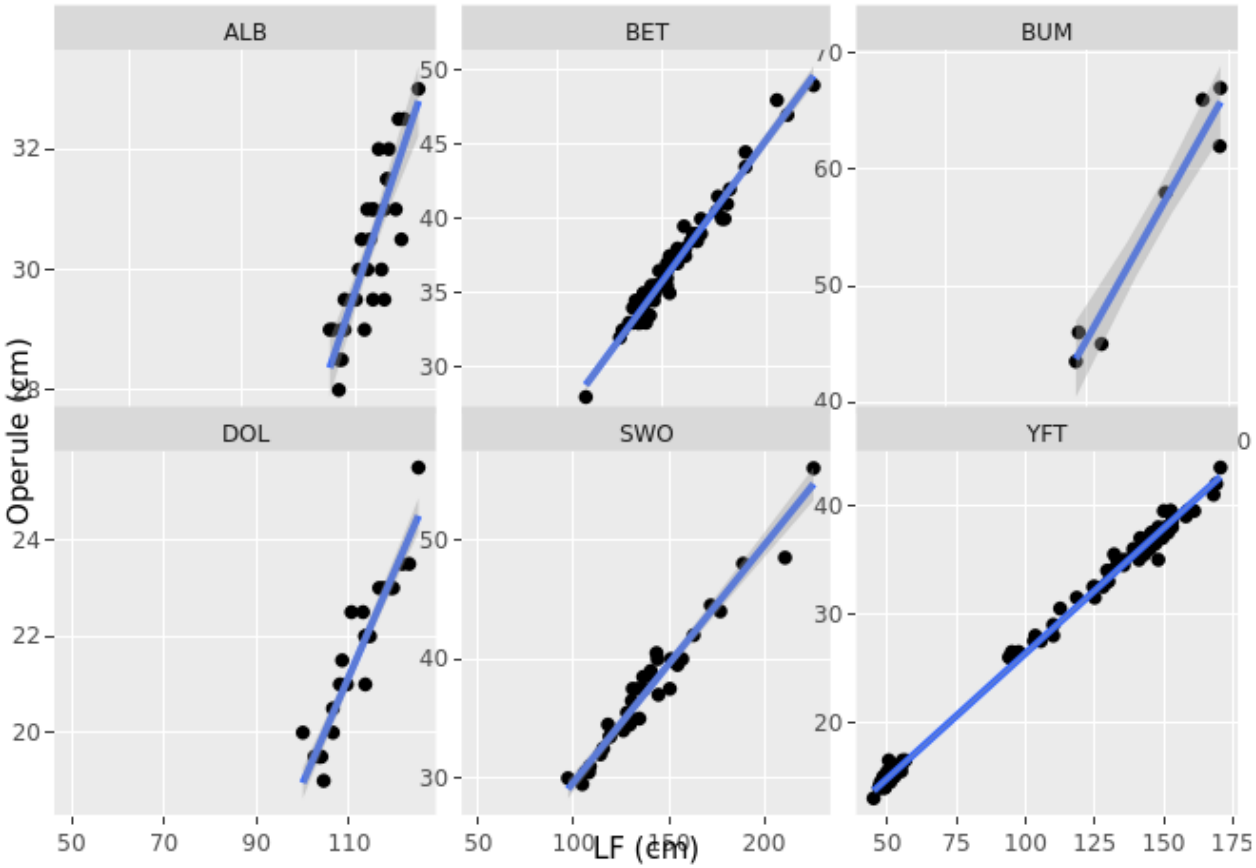

Figure 8: Example of jaw (dentary) relationships

Table 5: Coefficients for the different jaw – standard length relationships

	Relation	Code.FAO	a	b	N	R2
1	LF - OP	ALB	-6.79	103.79	50	0.48
2	LF - OP	BET	-37.33	128.33	75	0.93
3	LF - OP	BUM	18	192	15	1
4	LF - OP	DOL	-1.13	104.5	24	0.96
5	LF - OP	SWO	-7.5	104.5	41	0.99
6	LF - OP	YFT	2.98	45	108	1

Discussion – Conclusion

The different relationships that were derived from the sampling in Reunion Island are a first step to provide more accurate information about allometric relationships for large pelagics in the Indian Ocean. These relationships are critical for stock assessments and more generally for the quality of the data collected at sea, landings or in factories.

With continued effort to collect these data over time, the different relationships could also be investigated over seasonal, yearly, and spatially subsets. As these data are not sensitive, a global effort should be done so a common database of biological measurements and even sampling should be hosted at IOTC to be able to derive robust relationships which can be updated “on the fly” for the different stock assessments.

References