

**Final report to the Caribbean Fishery Management Council on project “Priority 1 to improve understanding of Queen Conch conversion factors by reanalyzing existing data”**

by

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**EXECUTIVE SUMMARY**

The advantages and limitations of the use of conversion factors (CFs) used to expand weight categories of processed queen conch (QC) meat to total live weight equivalent (i.e. the weight of the meat plus shell) were discussed at different meetings of the WECAFC technical and advisory working groups on queen conch. It was concluded that FAO statistics should be expressed in live weight, while dirty or total flesh weight was a better expression of biomass collected from an ecosystem in which shells could well be considered part of the habitat.

A study by Horsford et al., (2011), although not statistically tested, suggested the possibility of potential allometric differences in queen conch shell growth in relation to their meat weight, sex, and location. Such a condition can impact the estimated average CF over a range of processed meat categories; therefore, the condition of disaggregated shell growth in relation to meat growth is worrisome and needs to be studied.

The WECAFC QC conservation and management plan (Prada et al., 2017) mentions that estimation of global yield and number of individuals in QC landings should be reported or collected by clean meat categories and that the CF should be statistically comparable between fishing areas and between countries to generate more accurate and precise information on the overall yield of queen conch populations. Therefore, the Plan does not refer to live weight, but to the weight of meat and the number of individuals landed. This last statistic is essential to relate exploitation to the possible Allee effects mentioned in Stoner and Ray-Culp (2000). This is especially critical information when stock densities are to serve as exploitation benchmarks that frame annual clean meat quotas reported to CITES as well as QC conservation programs adopted by countries.

Therefore, there is a clear need to accurately account for landings of QC in different processing units of measurement in order to: 1. Report the country's production by live weight to FAO, 2. The country's annual non-detrimental landings by processed meat categories reported to CITES, and 3. Numbers of QC landed to assess the effect of selective removals from the stocks needed to assess the impact of exploitation on population densities.

This study consists of a re-assessment of the CFs addressing the estimation of QC dirty meat weight from weight of processed meat categories by using the existing data already used to estimate the CFs necessary to obtain whole live weight from processed meat categories. In addition, it addresses the recommendation that an average CF be available for the entire region

in order to estimate live weight (i.e. the weights of flesh plus shell) from landings expressed in dirty weight in those countries that do not have such CF. This average CF will be used for the purposes of FAO landing reports on live weight of the species. Therefore, this report has the following objectives:

1. To carry out a statistical review and validation of the existing data used in previous CF estimates for live weight and assess the suitability of the data for estimating new CFs for estimating "dirty" meat weights originated from different percent meat processing categories.
2. To carry out statistical analyses of the effects of "dirty weight" on the % of clean meat weights in order to elucidate the statistical validity of using such data under potential morphometric effects of the QC. Such analyses should also portray the effects of differences in QC processing observed among fisheries in the Caribbean region.
3. Contribute new CFs referred to the "dirty weight" classification from various weights of % of meat processing categories reported by countries, and
4. Estimate a regional average CF in order to reconstruct FAO fishery landing statistics from average "dirty" weight to live weight statistics (i.e. dirty or tissue weight + shell weight).

The statistical significance of differences between slopes, intercepts, and residual variances on linear regressions used to analyze QC morphometrics were assessed following a standard Analysis of Covariance (ANCOVA) procedure designed to test differences between linear regressions (e.g., Draper and Smith 1966). ANCOVA first tests the hypothesis of equal slopes and, if this test fails, no further testing of the intercepts is necessary, as differences in slopes imply differences in the morphometric nature of the individual growth of the QC in the datasets.

In the specific situations where comparisons were made between countries and/or fisheries (i.e., Objective 1), and significant differences in slopes were observed between "dirty" meat weight and the weight of the shell, independent Pearson's Chi-square ( $\chi^2$ ) tests were applied to the classifications of dirty meat weight.

The data to be re-assessed from previous CF estimations were from samples previously collected and submitted by The Bahamas, Nicaragua, Honduras, Mexico, Martinique, Belize and Barbados. Data on shell weight was estimated as the difference between live weight and dirty weight data available for the analyses. Such data were used to identify and evaluate the effects of phenotypic conditions on the data used for the estimation of CFs.

There was a highly significant difference between the databases of Mexico and Belize despite the fact that the QC inhabits the same Mesoamerican Reef coastal ecosystem. The disparity in clean meat weights for the two countries is for the same statistical range of dirty meat weights. Such disparities were not resolved, and it is recommended that Mexico and Belize develop a verifiable statistical sampling design to generate new data for the estimation of CF.

The results of ANCOVA to test the phenotypic characteristics of the QC showed that the landings from populations in Nicaragua, Honduras, the Bahamas, Barbados, and Martinique have slopes that are statistically equal, implying that linear regressions adjusted for dirty weight on shell weight are parallel lines. Such a condition is indicative that the changes in dirty weight due to changes in shell weight observed in the comparative databases are approximately similar across countries. However, the differences in intercepts are significantly different between the countries compared, except in the case of Honduras-Bahamas where the lines are statistically identical. All comparisons using the Mexico database resulted in significantly different linear relationships, adding uncertainty to the origin of the significantly heavier flesh weight of the individuals per unit shell weight observed in the Mexican database. The implication of this result is that the QC in Mexico is phenotypically different from those in the other countries, which was an unexpected result. The differences between Martinique-Barbados, Nicaragua-Honduras, Nicaragua-The Bahamas and Honduras-Barbados were not significant for slopes, but were significant for intercepts. Such differences may be due to geographic identity conditions in the growth characteristics of the QC shell.

The large dispersion of dirty weight about regression on shell weight generated a low degree of association between the two variables, indicating that QC shell weight is not a good predictor of meat weight. The results obtained are in agreement with the existing information on the morphometric characteristics of the growth and development of the QC shell.

The geographic identity of QC shell growth, as well as the significant changes in shell structure and shape expected with the onset of sexual maturity, may be significant processes responsible for the low correlations observed between shell weight and dirty weight in available regional data sources. Such potential differences in growth processes that appear in the analyzed data lead to the conclusion that the CF of QC relative to live weight would be more imprecise if attempts to estimate QC live weight from % clean meat weight categories are attempted with these data.

The results of the analyses show that while the QCs are phenotypically very similar between Honduras, Nicaragua and the Bahamas, the difference in intercepts under equal slopes between Honduras and Barbados may explain that the data from the two countries, which are distributed far apart within the habitat range of the species, are significantly different in size. These differences reflect considerable differences in the estimated body weight for QCs in those two regions. Such differences may suggest that the regional harmonization of conversion factors at the live weight level may not be entirely correct with regard to the reconstruction of the total catch for the purposes of FAO landing statistics. Therefore, it is recommended that countries that do not yet have adequate CFs urgently establish work to calculate them in order to avoid the use of regionally harmonized CF estimates.

The results of the statistical analyses showed a fairly low statistical significance of shell weight as a predictor of dirty weight. Analyses and results show that dirty weight data best correlates with different levels of % clean meat processing. These results are important when considering the estimation of live weight conversion factors (shell weight + tissue weight), which will introduce a

large and significant variance due to the greater variance of shell weight relative to meat weight variance.

The averages of the total dirty weights reconstructed from the % clean meat levels using the corresponding re-assessed mean CFs for the categories estimated in this study always resulted in total weight values greater than 99% of the original dirty weight observed in the samples. This finding supports the validity of the CFs estimated in this study.

The mean regional conversion factor for live weight (i.e. shell weight + tissue weight) from dirty weight was 5.36, which is similar to that estimated in FAO (2014).

### **ABSTRACT**

The queen conch databases (number and weight of individuals per % meat processing category) from 7 Caribbean countries were re-analyzed in order to validate the statistical databases used to estimate conversion factors. Regression and covariance analyses were used to classify the information used in the % clean meat weight conversion factor estimates.

The results of the statistical analyses showed that the shell weight of the queen conch is not a good predictor of dirty meat weight a conclusion supported by a low statistical significance of shell weight as a predictor of dirty weight. Analyses and results show that dirty weight data best correlates with different levels of % clean meat processing. These results are important for the estimation of live weight conversion factors (shell weights + tissue weights), which will introduce a large and significant variance due to the greater variance of shell weight relative to meat weight variance.

The averages of the total dirty weights expanded from corresponding % clean meat levels using the corresponding mean CFs for the categories estimated in this study always resulted in total weight values greater than 99% of the original dirty weight observed in the samples.

A mean regional conversion factor for live weight (i.e. shell weight + tissue weight) from dirty weight was 5.36, which is similar to that estimated in FAO (2014). A new regression method was developed to estimate conversion factors based on queen conch morphometry, which allows the application of conversion factors by individual size frequencies in the different categories of % clean meat of juvenile and adult queen conch.

### **PROBLEM IDENTIFICATION**

At the 3rd Meeting of the CFMC/ OSPESCA/ WECAFC/ CRFM/ CITES Working Group on Queen Conch in Panama City, Panama, on 30 October-1 November 2018 and then at the Scientific, Statistical and Technical Advisory Working Group (SSTAG) meeting held in Miami, Florida, on 24-26 April 2019 discussions were held regarding the statistical merits and constraints of using Conversion Factors (CF) to expand processed queen conch (QC) meat weight categories to whole

live weight (i.e. weight of flesh plus shell). The SSTAG concluded that FAO statistics need to be expressed in live weight, while dirty or flesh weight was a better expression of the biomass cropped from an ecosystem where shells may well be considered as part of the habitat. The reasoning for these considerations was based on the fact that QC has limited seasonal movements resulting in reduced home range (<8 ha; Glazer et al. 2003). As such, reduced mobility necessarily imprints geographic identity regarding the character of shell growth. In addition, it was noted that unless shell weight is directly proportional (isometric) relative to tissue weight, any CF that considers expansions of % processed weight categories to live weight (i.e. flesh + shell weights) should introduce a large, yet unknown and difficult to measure uncertainty (e.g. see data in figures 1 and 2). In this regard, reference was made to Horsford's et al. (2011) who found that most variability of QC CFs for % processed categories to live weight in Antigua and Barbuda were due to location and individual maturity effects (i.e. growth of shell lip at the onset of sexual maturity). Such finding, although not statistically tested, suggests the possibility of potential allometric differences in the growth of QC shells relative to their flesh weight. Such condition may impact CF estimated as average over a range of processed meat categories; therefore, the condition of disaggregated shell growth relative to flesh growth is of concern and deemed necessary to research such condition.

The Group also addressed the need of exporting countries to declare their annual non detrimental queen QC quotas to CITES in corresponding % meat processed weights that originate from landings mostly expressed in pre-processed meat weights (e.g. see figure 3). This is an important operational condition given the fact that in QC industrial fisheries shells are usually not landed. Furthermore, it was argued that annual non-detrimental QC catch quotas should be assessed considering the effects of exploitation on wild population densities for levels that are necessary to secure successful seasonal mating (i.e. the Allee effect expressed in Stoner and Ray-Culp 2000). As such, numbers of conch landed are very important to elucidate densities left in the wild stocks and the per unit of weight at the individual level of meat processing is mandatory.

The Group noted that the proposed QC conservation and management plan (Prada et al. 2017) mentions estimation of overall yield and numbers of individuals from QC landings should be reported or collected by clean meat categories and that CF should be statistically comparable among fishing grounds and among countries to generate more accurate and precise information on overall QC yield. Therefore, the Plan does not refer to live weight but flesh weight and number of individuals landed. The latter statistic is fundamental to link exploitation to the potential Allee effects mentioned in Stoner and Ray-Culp (2000). The above is particularly critical information when population densities should serve as exploitation reference points framing annual flesh quotas reported to CITES and adopted country QC conservation programs.

Therefore, the group identified that there is a distinct need to accurately account for QC landings in different processing measurement units in order to: 1. Report country production in live weight to the FAO, 2. Country annual non-detrimental landings by processed meat categories to the CITES, and 3. Numbers landed to assess selective retrievals from stocks needed to assess impact of exploitation on population densities.

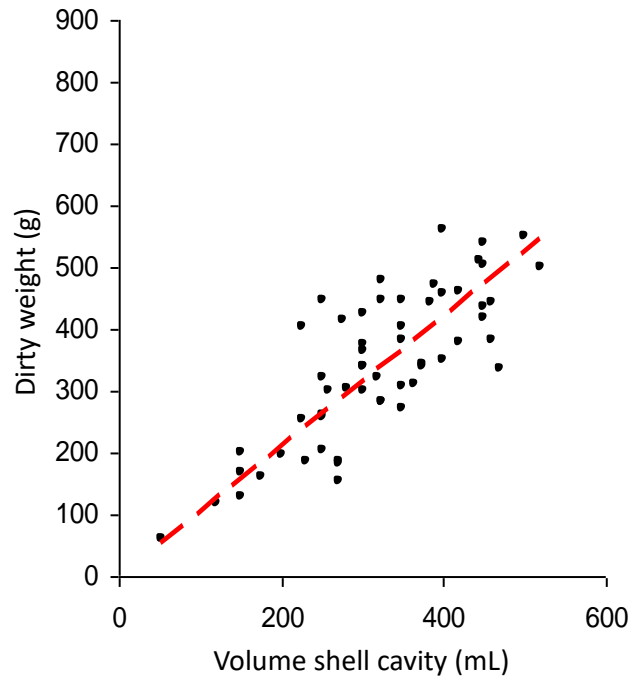


Figure 1. Dirty weight (g) is statistically proportional to shell cavity volume (From Ehrhardt and Romero, 2010).

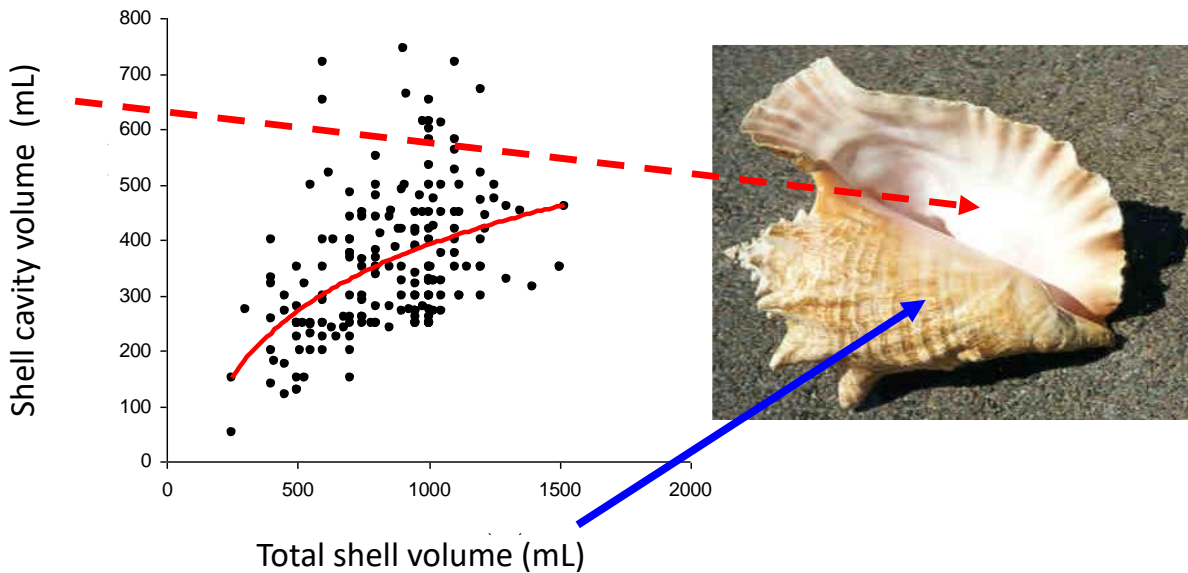


Figure 2. Queen Conch shell volumetric relationship (mL) (From Ehrhardt and Romero 2010).



Figure 3. Pre-processed queen conch in industrial fisheries (From Ehrhardt and Romero 2010).

### **OBJECTIVES OF THIS WORK**

The works included in this report consist of a re-assessment of CF addressing dirty weight equivalent of processed QC meat weight categories by using existing data already used to estimate CF pertaining estimation of whole live weight from processed meat weight categories. In addition, this consulting work addresses the recommendation of the SSTAG that an average CF should be made available for the entire region to raise country landings expressed in dirty weight to whole live weight (i.e. flesh plus shell weights). Such average CF will serve the purpose of FAO catch reporting for the species. Therefore, this report includes the following objectives:

1. To statistically review and validate existing data used in previous CF estimations for live weight and assess adequacy of the data for estimating new CF to estimate “dirty” meat weight from different percentages of meat processing categories.
2. To carry out statistical analysis of the effects of “dirty weight” on % clean meat weights to elucidate the statistical validity of using such data under potential QC morphometric effects. Such analyses should also portray the effects of differences in QC processing observed among fisheries in the Caribbean region.
3. To provide new CF to “dirty weight” from various % processing weights reported by the countries.
4. To estimate a regional average CF for the purpose of reconstructing FAO fishery statistics from average “dirty” weight statistics to live weight (i.e. dirty weight + shell weight).

## METHODS AND MATERIALS

The statistical data evaluations pertaining objectives 1 and 2 were carried out following a statistical analysis frame that considered QC phenotype characteristics. This is possible because phenotypes are observable expressions of the results of genes (i.e., the genotypes), combined with spatial environmental and ecological influences on QC appearance and behavior. Such influences are determinants on the reported QC geographic identity reflected by phenotypic characterizations in QC shell and flesh growth. Since phenotypes can be determined by direct observations (i.e., measurements) of animals before any meat processing, then shell weight and corresponding dirty weight (i.e., weight of all flesh) statistics found in the morphometric databases used to determine previous CF should allow statistical evaluations of data quality. Likewise, phenotype characterizations should be reflected in the resulting meat processing under standard QC cleaning practices.

Linear regression and analysis of covariance techniques were used regarding:

- 1) QC meat morphometric growth characterizations defined by slopes found in linear functional relationships (i.e., regressions) between shell weight and dirty weight as well as between different meat processing levels (i.e., % clean meat as required for the product market demands) on dirty weight (i.e., the individual weight of total flesh as extracted from the shell). All weights categories were expressed in grams,
2. The degree of weight reduction due to processing from dirty weight is portrayed by the difference in intercepts of the morphometric linear regression functions, and
- 3) The “disparity” of phenotype as well as meat cleaning process is expressed by the variance of the residuals of the observations about regressions (i.e., the standard error of the estimates).

The statistical significance of differences among slopes, intercepts, and variances of the residuals about regressions were evaluated following a standard procedure of Analysis of Covariance (ANCOVA) for testing the differences among linear regressions (e.g., Draper and Smith 1966). ANCOVA first tests the hypothesis of equal slopes and if such test fails, no further tests on the intercepts are necessary based on the fact that differences in slopes imply differences in the morphometric nature of individual QC growth in the data sets.

In the specific situation when comparisons among countries and/or fisheries were performed (i.e., Objective 1), and showed significant differences in slopes between dirty meat weight on shell weight, independent Pearson’s Chi-square ( $\chi^2$ ) tests were applied to the dirty meat weight classifications. Pearson’s test is a statistical test applied to sets of categorical data to evaluate how likely it is that any observed difference between the two sets of dirty meat weight arose by chance alone. Pearson Chi-square tests were performed following a rxc contingency table design, where c represented two countries and/or fisheries being compared in the test, and n is the number of meat weight categories included in the samples from countries or fisheries. All



methods were implemented in Microsoft Excel to facilitate potential explanations to users and equally important to visualize data structure, deviations and outliers.

The computational formulations required for the various analyses are given below.

1. Analysis of Covariance is summarized in the generic ANCOVA Table as follows:

ANCOVA table

Line	Group	d.f	$\sum y^2$	$\sum xy$	$\sum x^2$	d.f.	SS	MS
1	A	$n_A-1$	Equation 1	Equation 2	Equation 3	$n_A-2$	$SS_A$	$MS_1=SS_A/(n_A-2)$
2	B	$n_B-1$	Equation 1	Equation 2	Equation 3	$n_B-2$	$SS_B$	$MS_2=SS_B/(n_B-2)$
3	Total					N-4	$SS_A+SS_B$	$MS_3=(SS_A+SS_B)/(N-4)$
4	Lines 5-3		Difference for testing slopes			1	$SS_A+SS_B-SS_{AB}$	$MS_4=(SS_A+SS_B-SS_{AB})$
5	Lines 1+2	N-2	$\sum \sum y^2$	$\sum \sum xy$	$\sum \sum x^2$	N-3	$SS_{AB}$	$MS_5=SS_{AB}/(N-3)$
6	Lines 7-5		Difference for testing intercepts			1	$SS_{Pooled}-SS_{AB}$	$MS_6=(SS_{Pooled}-SS_{AB})$
7	Pooled data	N-1	Equation 1	Equation 2	Equation 3	N-2	$SS_{Pooled}$	

Where Groups A and B can be two different % clean meat category levels within a given country or fishery, or the same % clean meat category levels for two different countries or fisheries. Headers in the table are d.f. for degrees of freedom, SS for Sum of Squared Deviations, MS for Mean Squares or variance. Total sample size, N, is equal to the sum of the group sample sizes  $n_A$  and  $n_B$ .

SS in Lines 1, 2, 5, and 7 are given by the following equations for each data group

$$\sum y^2 - \frac{(\sum xy)^2}{\sum x^2}$$

where Equation 1  $\sum y^2 = \sum (Y - \bar{Y})^2$   
Equation 2  $\sum xy = \sum (X - \bar{X})(Y - \bar{Y})$   
Equation 3  $\sum x^2 = \sum (X - \bar{X})^2$

The test of hypothesis for equal slopes follows a F-statistic equals to  $MS_4/MS_3$  with 1 and N-4 degrees of freedom. If the test of equal slopes is accepted, then the test for equal intercepts is given by an F-statistic equals to  $MS_6/MS_5$  with 1 and N-2 degrees of freedom.

## 2. Pearson's Chi-square ( $\chi^2$ ) test

In this case, an "observation" consists of the values of two outcomes and the null hypothesis is that the occurrence of these outcomes is statistically independent. Each observation is allocated to one cell of a multi-dimensional array of cells (i.e., a contingency table) according to the values

of the multiple outcomes. If there are  $r$  rows and  $c$  columns in the table, the "theoretical frequency" for a cell, given the hypothesis of independence, is

$$E_{i,j} = Np_i.p_j$$

where  $N$  is total sample size and the fraction of observations across columns is  $p_i$ , and the fraction across rows is  $p_j$ ; therefore,

$$p_i = \frac{O_i}{N} = \sum_{j=1}^c \frac{O_{i,j}}{N} \quad \text{and} \quad p_j = \frac{O_j}{N} = \sum_{i=1}^r \frac{O_{i,j}}{N}$$

Where  $O$  stands for numbers observed in a given category. The value of the Chi-square statistic is given as

$$\chi^2 = \sum_{i=1}^r \sum_{j=1}^c \frac{(O_{i,j} - E_{i,j})^2}{E_{i,j}}$$

where the degrees of freedom are given by  $(r-1)(c-1)$

The test of independence, or test of homogeneity, with a chi-squared probability of less than or equal to 0.05 was interpreted as justification for rejecting the null hypothesis that the row variable, or clean meat class frequency, is independent of the column variable, or the country or fishery.

### 3. Conversion Factors

The Conversion Factors (CF) are estimated taking into consideration a linear regression of the individual QC dirty meat weights  $D$  (i.e., values on the Y-axis) on the resulting % clean meat weight classifications after processing  $C\%$  (i.e., values on the X-axis). The regression assumes a statistically valid regressional range between the two variables (i.e., ample X range values correlated with a wide Y range values); therefore, a CF to obtain the average estimated dirty meat weight from the average weight of individuals from a sample drawn from a given % clean meat category is expressed as

$$CF = \frac{\widehat{D}}{C\%}$$

In the formulation,  $\widehat{D}$  corresponds to the predicted average of Dirty weight ( $D$ ) estimated from the regression of  $D$  on  $C\%$  at the point of average  $\bar{C}\%$ . This method is new and the main purpose for its development is that will allow estimation of QC CFs for any size (i.e., weight) of individuals in landings with a % meat clean weight category.

The data subjected to CF re-analysis corresponded to samples collected and previously submitted by The Bahamas, Nicaragua, Honduras, Mexico, Martinique, Belize and Barbados. The variables measured, their size ranges and corresponding sample sizes are presented in Table 1.

Table 1. Queen conch minimum and maximum shell and dirty weights in grams and sample size by % clean meat for countries available to assess databases and to re-estimate conversion factors.

Country	Minimum-Maximum (g)		% Clean Meat Processing (Sample size in #)		
	Shell weight	Dirty weight	50%	85%	100%
The Bahamas	663-3159	175-638	261		262
Nicaragua	646-2967	215-804	712		711
Honduras	425-2800	101-674		404	402
Mexico	435-2850	125-950	372		372
Martinique	1355-3454	303-743	210		210
Belize	602-2311	128-510	400	287	687
Barbados	410-3390	190-862			26

## RESULTS

### Objective 1. Statistical assessment of databases

The existing morphometric paired data on individual shell weight and dirty weight as well as the raw data on individual weight reductions due to cleaning to different QC market processing categories were available for 7 countries (see Table 1). Such databases were evaluated concerning identification of outliers originated from different sources, missing measurements among some of the variables measured per individuals, sample size selectivity issues that create differences in regression ranges in the data used to estimate average CF, as well as identification of duplicated observations reported in different samples.

Data on shell weight were estimated as the difference between live weight and dirty weight, and used to identify and assess the effects of phenotype conditions on the data used for CF estimation. Such data were measured without altering the animal's natural weight conditions while allowing relative ease on measuring weights. Thus, the data were expected to reflect accuracy and precision in samples drawn from the statistical populations of weights. It is thought that such data are also comparable across regions and fisheries if in fact there is enough QC stock mixing.

#### Data from Mexico

Four individual QC entries in the database from Mexico were identified with dirty weights classified as highly significant outliers that fell well outside possible data ranges but well positioned along the projected linear regression function fitted to the data of dirty weight on shell weight. Such outliers dominated the significance of the regression fits. It was not known if

the outliers were due to data entry errors or true outliers. For example, the average QC dirty weight in the 4 outliers was 1,463 grams, 1,341 grams when 50% clean, and 241 grams when 100% clean. Such results contrasts very significantly when compared with the data for the remaining 368 individuals in the sample from Mexico, which had an average dirty weight of 412 grams, 309 grams when 50% clean and 187 grams when 100%, respectively. Also, the average live weight measured for the 4 individual entries was 3,281 grams, which is well above the average the 1,894 g live weight for the 368 individuals in the sample. Pearson's Chi-square ( $\chi^2$ ) test result for the comparison of the 50% clean meat weight category data from Mexico and the integer (i.e., decimals equal zero) clean meat data available for neighboring Belize (see explanation for Belize data given below) generated a highly significant difference between the two databases (Table 2). This finding was not expected given that samples from Mexico and Belize are for QC populations inhabiting the same Mesoamerican Reef coastal ecosystem and for the same statistical size range of dirty weights. Such significant disparity in the data from Mexico could not be resolved in consultations with the originators of the Mexican data, therefore, outliers were considered an error that needs to be addressed in the future.

In addition, results of the analyses carried out to compare potential morphometric differences in the QC regional databases (see Table 3), show that the database from Mexico is the only regional sample that consistently rejects the null hypothesis of equal slopes (Table 3) relative to all the other country samples. This finding is indicative of significant growth differences between QC populations in Mexico relative to the other 5 countries for which valid statistical data were available. The unexpected results led to the conclusion that data from Mexico should be re-assessed with new observations that must be collected under a known and verified sampling statistical design such that biological morphometric characteristics of QC from Mexico could be defined as compatible with those of other countries in the region.

Table 2. Pearson's Chi-square ( $\chi^2$ ) test for the comparisons of 50% clean meat weight data from Mexico and Belize.

	Estimated	Tabulated
Chi Square	174.62	12.59
Degrees of freedom:	6	6
P-value for Chi Square:	4.7043E-35	0.05

#### Data from Belize

It was found that entire columns for some of the clean meat weight categories (e.g. 100% clean meat weight) in the Belizean database contained weights in grams expressed with a very large number of decimal values. This may be possible only if such variables would have been estimated through an arithmetic operation instead of measured directly on the individuals. This was a significant recurrent issue that could not be resolved with the originator of the data. Given that the level of precision to measure in decimal grams was not available in the balances used to measure such weights (i.e., a situation declared by the originator), then it had to be assumed that such data was estimated and not directly measured. The originator claimed a formatting error in Excel, which could not be verified as it affected only a fraction of the observations (i.e., the 100% clean meat weight data) in the database. This decimal point effect was not present in any of the

other variables (i.e., live weight, 50% clean meat weight, etc.) measured in the same QC specimens. Following discussions on this data issue, the Belize Department of Fisheries recommended that we do not use data exhibiting extended decimal points in any of the analyses and as such a large fraction of the database was discarded. Further analyses of the remaining database for Belize resulted in the identification of a large number of individual QC data sets that were identical in a file of data collected in two different areas at two different times (i.e., August of 2014 and October of 2014). Such observations contradicted the information on the origin and time of the two databases. This critical issue was not resolved with the originator despite the documented findings. Therefore, based on the analyses carried out by this consultancy, the two Belizean CF databases were classified as non-validated and statistically uncertain for inclusion in the analyses in this work.

#### Data for Nicaragua, Honduras, The Bahamas, Barbados and Martinique

The ANCOVA results for testing differences in phenotypic characteristics of the QC samples reported by Nicaragua, Honduras, The Bahamas, Barbados and Martinique have slopes that are statistically equal (Table 3 and figures 4 to 11). These results imply that linear regressions fitted to dirty weight on shell weight are parallel lines indicating that changes in dirty weight per unit change in shell weight are approximately similar among the compared country databases. Differences in intercepts, however, are statistically significant among the countries, excepting the case of Honduras-Bahamas where the lines are statistically identical. Such differences in intercepts may be interpreted in the databases as a geographic identity effect on similar phenotypic growth characterizations observed among the different QC stocks.

Contrary to the previous results, all slope and intercept comparisons using the QC database from Mexico resulted in significantly different linear relationships (Table 3) adding uncertainty to the origin of the significantly larger individuals per unit of shell weight and lower slopes observed in the Mexican database. The implication of this result is that QC in Mexico is phenotypically different from the QC in all the other countries, which is an unexpected result.

Table 3. Values of the F-statistic and the resulting probability for accepting (in red) null hypotheses regarding equality of slopes and intercepts in the ANCOVA comparison of linear regressions.

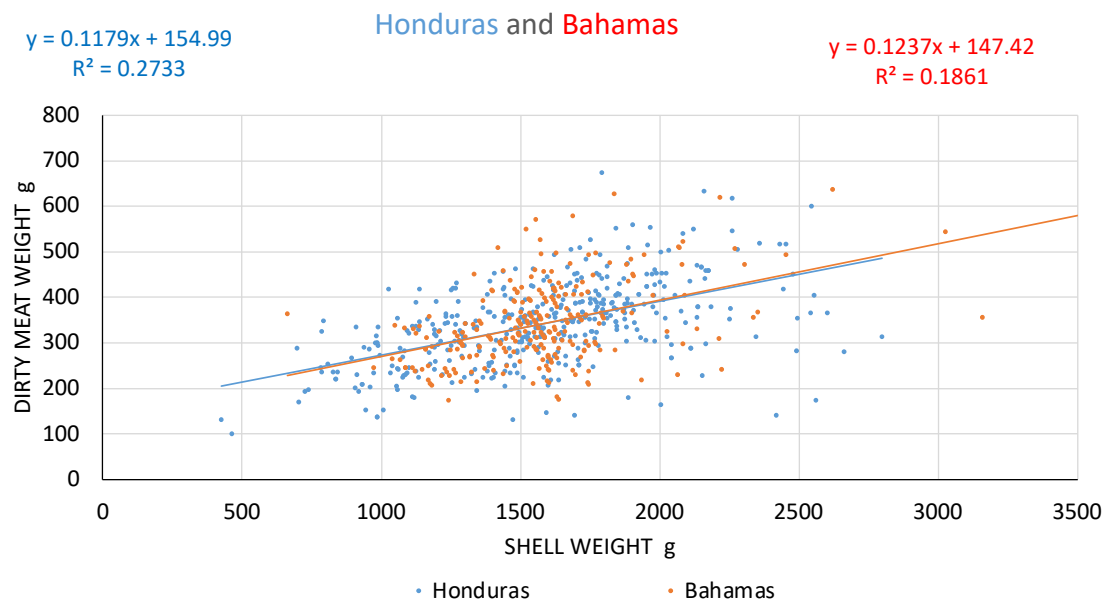
<b>Pair comparisons</b>	<b>Slopes (F;Probability)</b>	<b>Intercepts (F;Probability)</b>
Mexico - Nicaragua	12.04; 5.4E-04	68.04; 4.6E-16
Mexico - Honduras	21.43; 4.3E-06	135.58; 5.8E-29
Mexico - Bahamas	8.7; 3.1E-09	43.58; 8.7E-11
Mexico - Martinique	27.61; 2.1E-07	9.89; 1.7E-03
Mexico - Barbados	15.47; 9.3E-05	8.76; 3.2E-08
Martinique - Barbados	<b>2.01; 0.16</b>	18.96; 1.7E-05
Martinique - Bahamas	<b>5.56; 1.9E-02</b>	77.23; 2.9E-17

Martinique - Honduras	6.73; 0.01	103.11; 0.000
Honduras - Bahamas	0.09; 0.77	0.60; 0.44
Honduras - Barbados	0.0; 0.949	256.48; 1.05E-48
Nicaragua - Bahamas	1.87; 0.17	51.51; 1.4E-12
Nicaragua - Honduras	5.99; 1.4E-02	96.62; 6.2E-22
Nicaragua - Barbados	4.46; 0.035	156.86; 2.20E-33
Barbados - Bahamas	0.24; 0.624	231.31; 1.09E-42

Several important aspects can be observed in the data shown in figures 4 to 11, such as the large dispersion (i.e., large residuals) about regression resulting in low degree of association between the variables (i.e., low  $R^2$  given in the figures). These are indicative that QC shell weight is not a good predictor of flesh weight; and in fact shell cavity volume while being a good predictor of dirty weight (Figure 1), total shell volume (i.e., another indicator of shell size) is a very poor indicator of cavity volume that defines individual weight (Figure 2). Consequently, the analyzed databases provide sufficient statistical evidence to support the concept of geographic identity of QC and that CF pertaining to live weight would be more imprecise if % clean meat weight to live weight CF are attempted with this data.

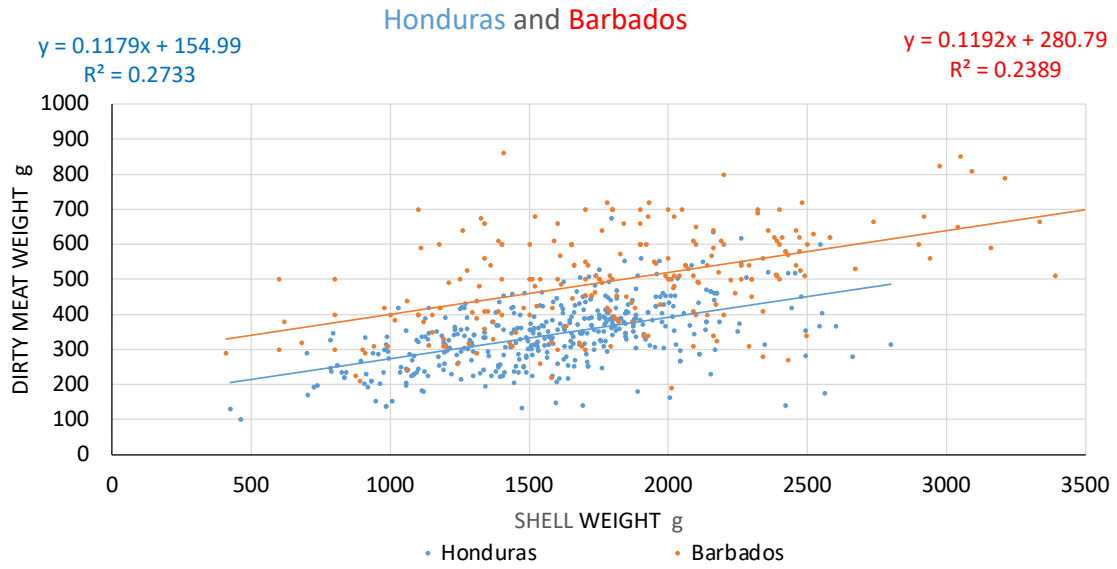
Figures 4 to 11 show that while QC are phenotypically very similar between Honduras, Nicaragua and The Bahamas, the difference in intercept but equality of slopes between Honduras and Barbados may explain that the data for the latter two countries, which are distributed far apart within the habitat range of the species, are significantly different in dirty weight (Figure 5). These differences should reflect considerable differences in the live weight CF estimated for each of these two regions. Such differences may suggest that regionally harmonizing CF at the live weight level may not be entirely correct regarding reconstruction of total catch for FAO landing statistical purposes.

Results of the analyses presented here validate the use of the CF databases presented by The Bahamas, Nicaragua, Honduras, Martinique, and Barbados.



Line	Group	d.f.	Sum y2	Sum xy	Sum x2	d.f.	SS	MS
1	Hon(Residuals)	404	3342688	7746308	65685781	403	2429168	6027.71
2	Bah(Residuals)	257	1929814	2902678	23456705	256	1570618	6135.23
3								
4					Total	659	3999786	6069.48
5	Line 6-Line 4	Difference for testing slopes				1	585	584.75
6	Lines 1+2	661	5272502	10648986	89142486	660	4000371	6061.17
7	Line 8-Line 6	Difference for testing levels				1	405	405.31
8	Pooled values	662	5272619	10648142	89148560	661	4000776	
							Tabulated probability of F	
	F slopes	0.10	d.f.	1	659		0.7564	
	F levels	0.07	d.f.	1	660		0.7960	

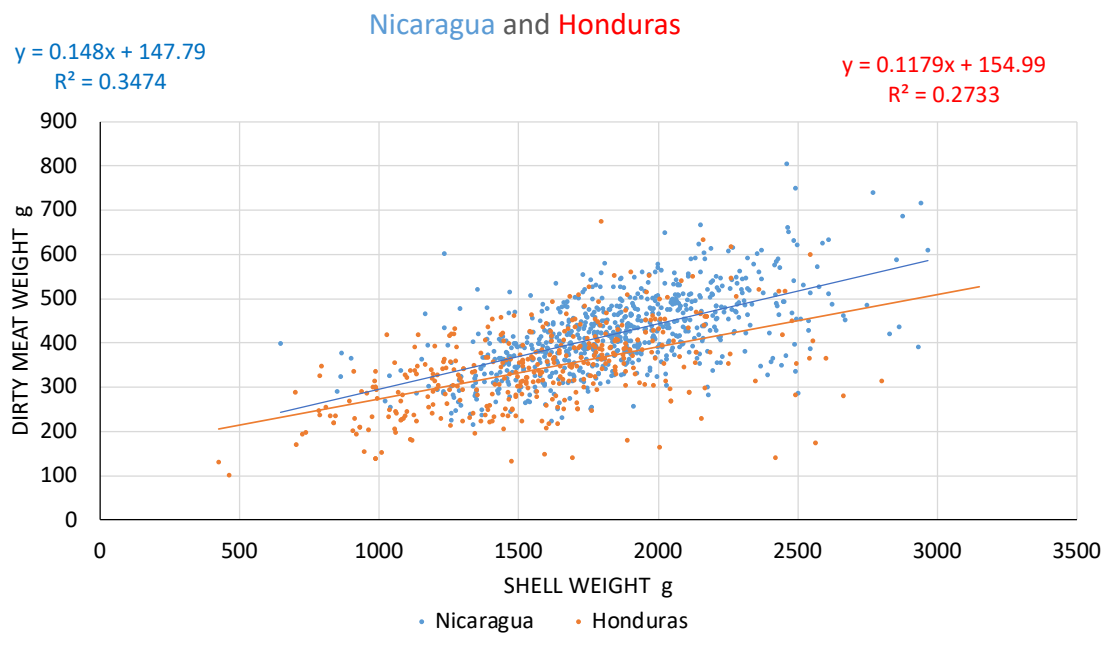
Figure 4. Plot of dirty meat weight on shell weight for the comparison of databases in Honduras and The Bahamas. Lower panel is the ANCOVA table developed according to the methods to estimate F-tests for the significance of the differences between two regressions.



Line	Group	d.f.	Sum y2	Sum xy	Sum x2	d.f.	SS	MS
1	Hon(Residuals)	403	3338381	7759525	65645220	402	2421174	6022.82
2	Barb(Residuals)	230	4197647	8410111	70529035	229	3194798	13951.08
3								
4					Total	631	5615973	8900.11
5	Line 6-Line 4	Difference for testing slopes				1	37	36.72
6	Lines 1+2	633	7536028	16169636	136174255	632	5616009	8886.09
7	Line 8-Line 6	Difference for testing levels				1	2279136	2279135.81
8	Pooled values	634	11127773	21606162	144410778	633	7895145	
							Tabulated probability of F	
	F slopes	0.00	d.f.	1	631		0.9488	
	F levels	256.48	d.f.	1	632		1.05421E-48	

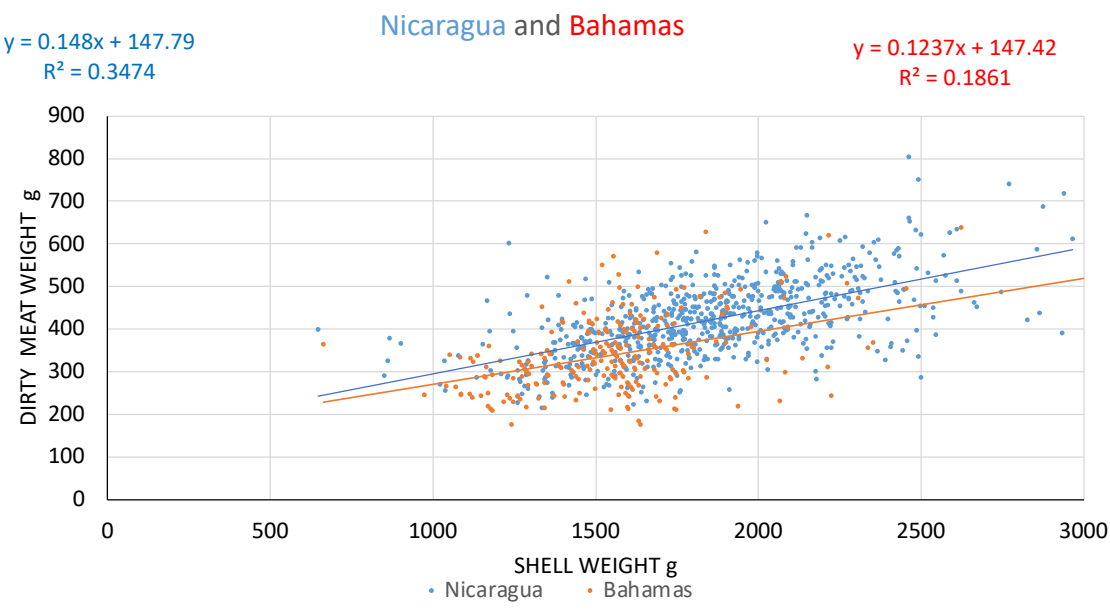
Figure 5. Plot of dirty meat weight on shell weight for the comparison of databases in Honduras and Barbados. Lower panel is the ANCOVA table developed according to the methods to estimate F-tests for the significance of the differences between two regressions.





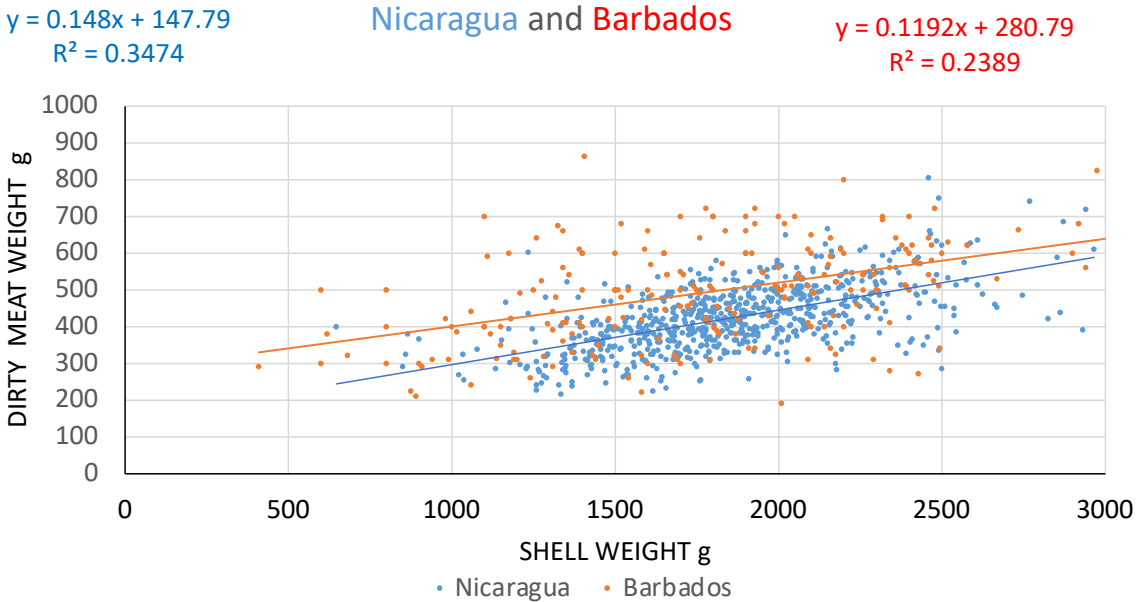
Line	Group	d.f.	Sum y <sup>2</sup>	Sum xy	Sum x <sup>2</sup>	d.f.	SS	MS
1	Nic(Residuals)	710	5356722	12574993	84980570	709	3495939	4930.80
2	Hon(Residuals)	404	3297078	7693302	64845422	403	2384339	5916.47
3								
4								
4						Total	1112	5880278
5	Line 6-Line 4	Difference for testing slopes				1	31649	31649.21
6	Lines 1+2	1114	8653800	20268295	149825992	1113	5911927	5311.70
7	Line 8-Line 6	Difference for testing levels				1	513208	513208.10
8	Pooled values	1115	10375578	25899384	169798218	1114	6425135	
							Tabulated probability of F	
	F slopes	5.99	d.f.	1	1112		0.0146	
	F levels	96.62	d.f.	1	1113		6.36439E-22	

Figure 6. Plot of dirty meat weight on shell weight for the comparison of databases in Honduras and Nicaragua. Lower panel is the ANCOVA table developed according to the methods to estimate F-tests for the significance of the differences between two regressions.



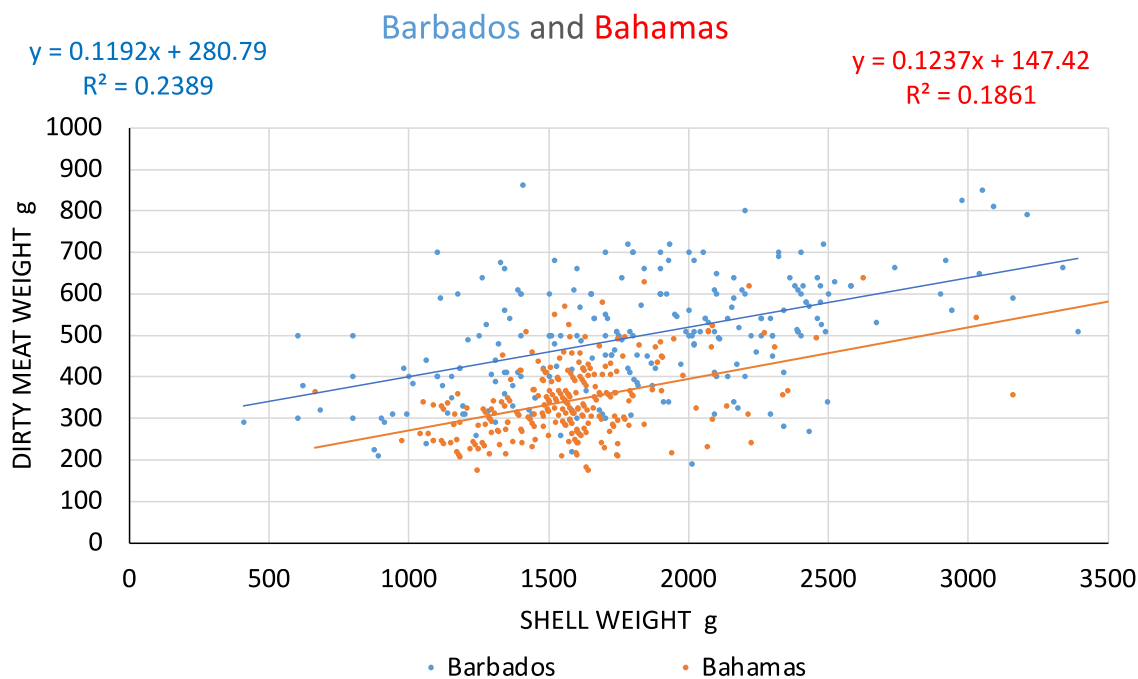
Line	Group	d.f.	Sum y <sup>2</sup>	Sum xy	Sum x <sup>2</sup>	d.f.	SS	MS
1	Nic(Residuals)	710	5356722	12574993	84980570	709	3495939	4930.80
2	Bah(Residuals)	257	1929785	2902678	23264324	256	1567620	6123.51
3								
4					Total	965	5063558	5247.21
5	Line 6-Line 4	Difference for testing slopes				1	9835	9835.16
6	Lines 1+2	967	7286507	15477671	108244893	966	5073393	5251.96
7	Line 8-Line 6	Difference for testing levels				1	270509	270508.81
8	Pooled values	968	8490135	19681666	123121215	967	5343902	
							Tabulated probability of F	
	F slopes	1.87	d.f.	1	965		0.1713	
	F levels	51.51	d.f.	1	966		1.42126E-12	

Figure 7. Plot of dirty meat weight on shell weight for the comparison of databases in Nicaragua and The Bahamas. Lower panel is the ANCOVA table developed according to the methods to estimate F-tests for the significance of the differences between two regressions.



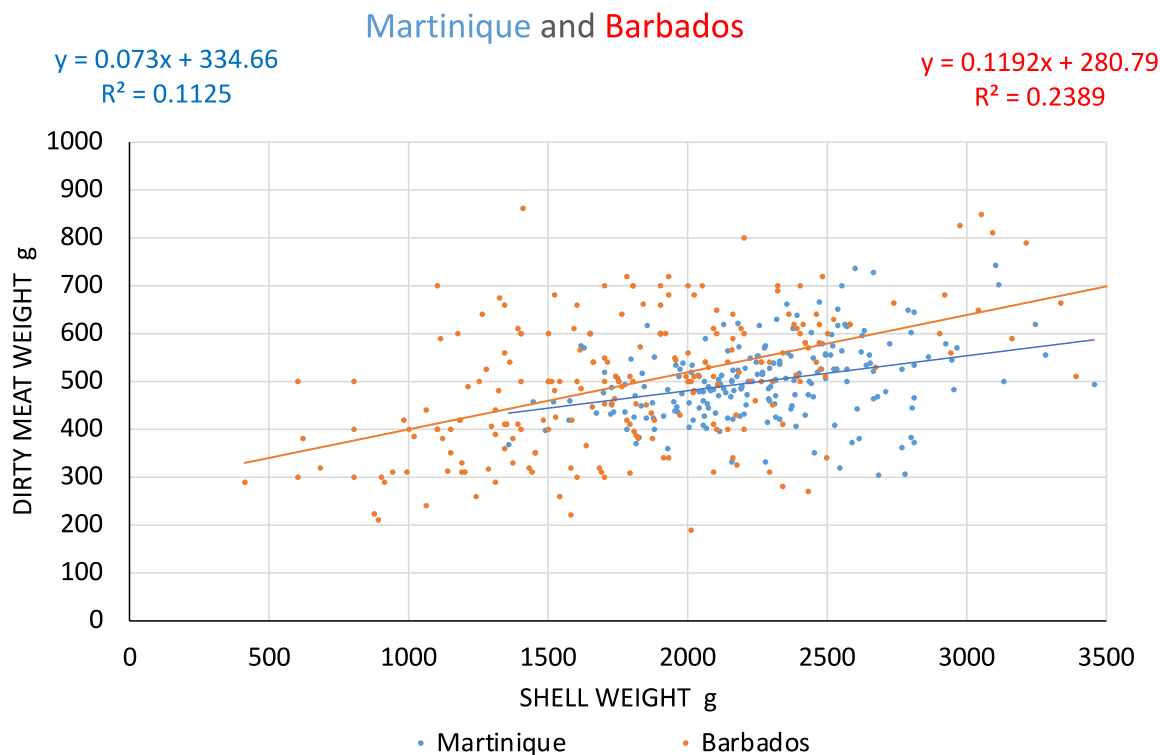
Line	Group	d.f.	Sum y2	Sum xy	Sum x2	d.f.	SS	MS
1	Nic(Residuals)	710	5356722	12574993	84980570	709	3495939	4930.80
2	Bar(Residuals)	230	4197647	8410111	70529035	229	3194798	13951.08
3								
4					Total	938	6690737	7132.98
5	Line 6-Line 4	Difference for testing slopes				1	31816	31816.49
6	Lines 1+2	940	9554369	20985104	155509605	939	6722553	7159.27
7	Line 8-Line 6	Difference for testing levels				1	1122738	1122737.53
8	Pooled values	941	10550050	20523059	155724016	940	7845291	
							Tabulated probability of F	
	F slopes	4.46	d.f.	1	938		0.0350	
	F levels	156.82	d.f.	1	939		2.20455E-33	

Figure 8. Plot of dirty meat weight on shell weight for the comparison of databases in Nicaragua and Barbados. Lower panel is the ANCOVA table developed according to the methods to estimate F-tests for the significance of the differences between two regressions.



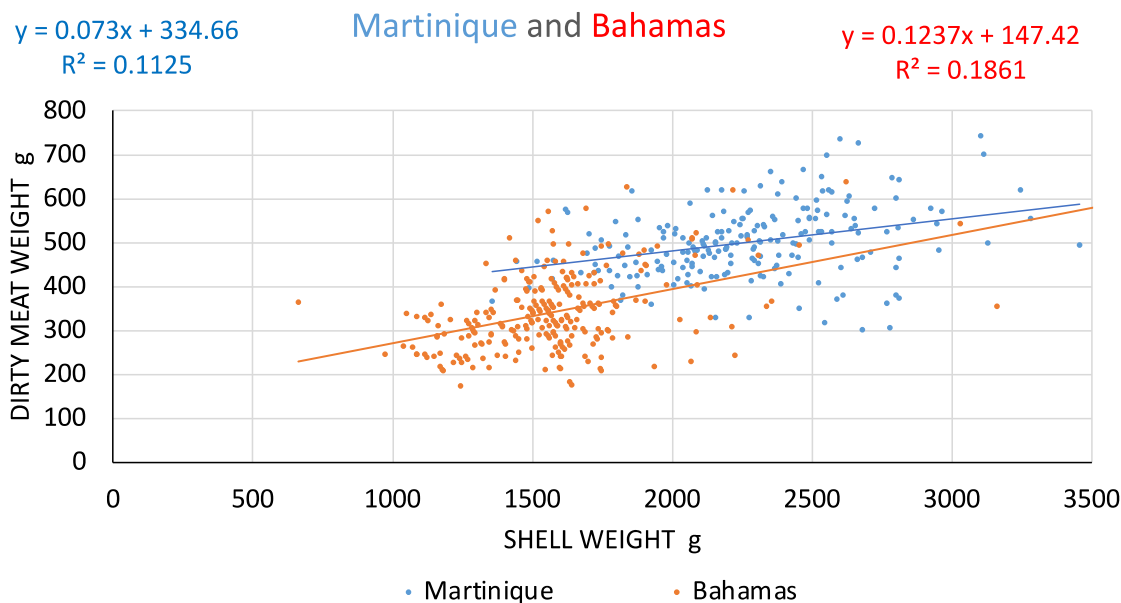
Line	Group	d.f.	Sum y2	Sum xy	Sum x2	d.f.	SS	MS
1	Barb(Residuals)	209	3793420	7097838	63384534	208	2998600	14416.35
2	Bah(Residuals)	257	1929814	2902678	23456705	256	1570618	6135.23
3								
4					Total	464	4569218	9847.45
5	Line 6-Line 4	Difference for testing slopes				1	2370	2370.02
6	Lines 1+2	466	5723233	10000516	86841238	465	4571588	9831.37
7	Line 8-Line 6	Difference for testing levels				1	2274064	2274064.12
8	Pooled values	467	8239376	11360963	92609040	466	6845652	
							Tabulated probability of F	
	F slopes	0.24	d.f.	1	464		0.623951864	
	F levels	231.31	d.f.	1	465		1.08915E-42	

Figure 9. Plot of dirty meat weight on shell weight for the comparison of databases in Barbados and The Bahamas. Lower panel is the ANCOVA table developed according to the methods to estimate F-tests for the significance of the differences between two regressions.



Line	Group	d.f.	Sum y2	Sum xy	Sum x2	d.f.	SS	MS
1	MTQ(Residuals)		209	1331118	2051846	208	1181379	5679.71
2	Bar(Residuals)		230	4197647	8410111	229	3194798	13951.08
3								
4					Total	437	4376177	10014.13
5	Line 6-Line 4	Difference for testing slopes				1	43029	43028.75
6	Lines 1+2		439	5528765	10461957	438	4419206	10089.51
7	Line 8-Line 6	Difference for testing levels				1	183034	183034.22
8	Pooled values		440	5529555	10595022	439	4602240	
							Tabulated probability of F	
	F slopes		4.30	d.f.	1	437	0.038769725	
	F levels		18.14	d.f.	1	438	2.51229E-05	

Figure 10. Plot of dirty meat weight on shell weight for the comparison of databases in Martinique and Barbados. Lower panel is the ANCOVA table developed according to the methods to estimate F-tests for the significance of the differences between two regressions.



Line	Group	d.f.	Sum y2	Sum xy	Sum x2	d.f.	SS	MS
1	MTQ(Residuals)	209	1331118	2051846	28116012	208	1181379	5679.71
2	Bah(Residuals)	257	1929814	2902678	23456705	256	1570618	6135.23
3								
4					Total	464	2751997	5931.03
5	Line 6-Line 4	Difference for testing slopes				1	32960	32959.95
6	Lines 1+2	466	3260932	4954524	51572717	465	2784957	5989.15
7	Line 8-Line 6	Difference for testing levels				1	462529	462528.78
8	Pooled values	467	6150484	17662065	107457348	466	3247486	
							Tabulated probability of F	
	F slopes	5.56	d.f.	1	464		0.018819092	
	F levels	77.23	d.f.	1	465		2.96017E-17	

Figure 11. Plot of dirty meat weight on shell weight for the comparison of databases in Martinique and The Bahamas. Lower panel is the ANCOVA table developed according to the methods to estimate F-tests for the significance of the differences between two regressions.

## Objective 2

Results of the statistical analysis in objective 1 showed a rather low statistical significance of shell weight as a predictor of dirty weight (e.g., Figures 4 to 11 with  $R^2$  values ranging from 0.11 to 0.35). Such findings are supported by previous comments regarding QC flesh morphometric features and shell phenotypic developments (i.e., Figures 1 and 2). Analyses and results pertaining to objective 2, which are independent of shell weight, demonstrate that dirty weight data are better correlated to the different % levels of meat processing (Figure 12) with  $R^2$  values ranging from 0.58 to 0.91 for 50% and 100% clean meat weight levels (e.g., Figures 13 to 16). These results are important if considering the estimation of conversion factors to live weight (shell + flesh weights) from % clean meat weight categories. In such case large and significant variance will be introduced in the CF estimates due to the higher variance of shell weight relative to the variance of flesh weight.

#### Case of 100% clean meat category

Results of the ANCOVA for the comparison of functional morphometric data expressed as % clean meat weight on dirty weight among countries, show that 100% clean meat weight on dirty weight exhibits significant correspondence among two country groups: Nicaragua-Honduras-Bahamas (Figure 13) and Bahamas-Martinique (Figure 14). Such groupings are statistically supported by the resulting ANCOVA F-test values for the equality of slopes hypotheses given by  $F = 3.78$  with 2 and 1,369 degrees of freedom with a probability of 0.023, and  $F = 0.44$  with 1 and 468 degrees of freedom with probability 0.558 as shown in the lower panel in figures 13 and 14, respectively. This finding is indicative that statistics of dirty weight and 100% clean meat weight may in some cases be regionally comparable due to common morphometric features expressed by the equality of slopes found in QC within some regions. These results are plausible due to the well-defined final product characterization representing 100% QC clean muscle weight where remnants of other tissue parts are not included.

#### Case of 50% clean meat category

Furthermore, the analysis of data portrayed in figures 15 and 16 show that 50% clean meat has slightly higher variance about regression on dirty weight relative to the 100% clean meat condition (see Table 4 for comparison of relative standard error of the estimates). In this instance, analyses of the 50% clean meat level on dirty meat reject the null hypotheses of equal slopes for the two cases for which valid statistical data were available ( $F = 137.06$  for 1 and 969 degrees of freedom and  $F = 23.65$  with 1 and 467 degrees of freedom in the lower panels of Figures 15 and 16, respectively). Thus, the existing databases carry the expected statistical signals of higher natural variability of the less precise and sometime more subjective definitions for partial (i.e., 50% and 85%) meat cleaning process level definitions. Rejection of the null hypotheses of equal slopes results in the rejection of any natural grouping of the samples at 50% according to countries or regions.

The significant and well-defined linear trends observed in data expressing different levels of meat processing relative to dirty weight, support the statistical validity of using the existing country specific data for the purpose of re-constructing (i.e., expanding) diverse national QC % clean meat weights to dirty weight.

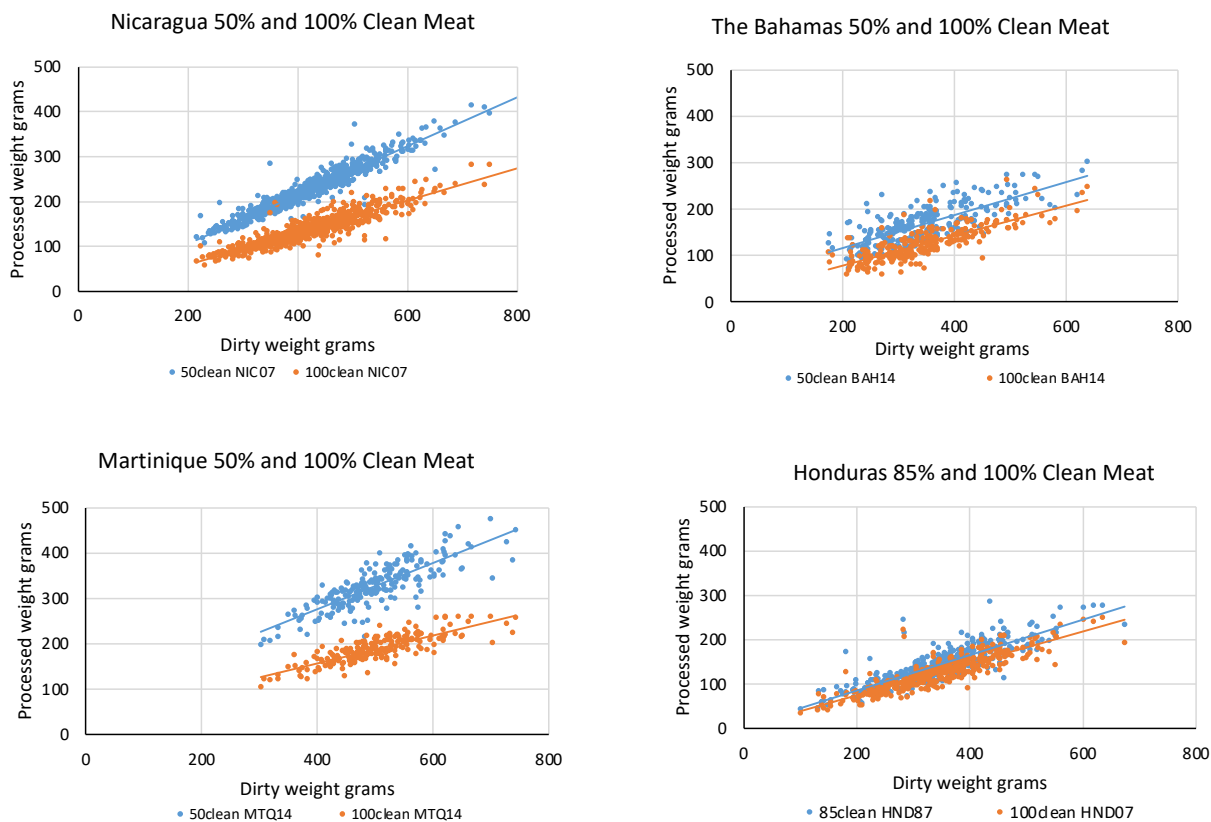
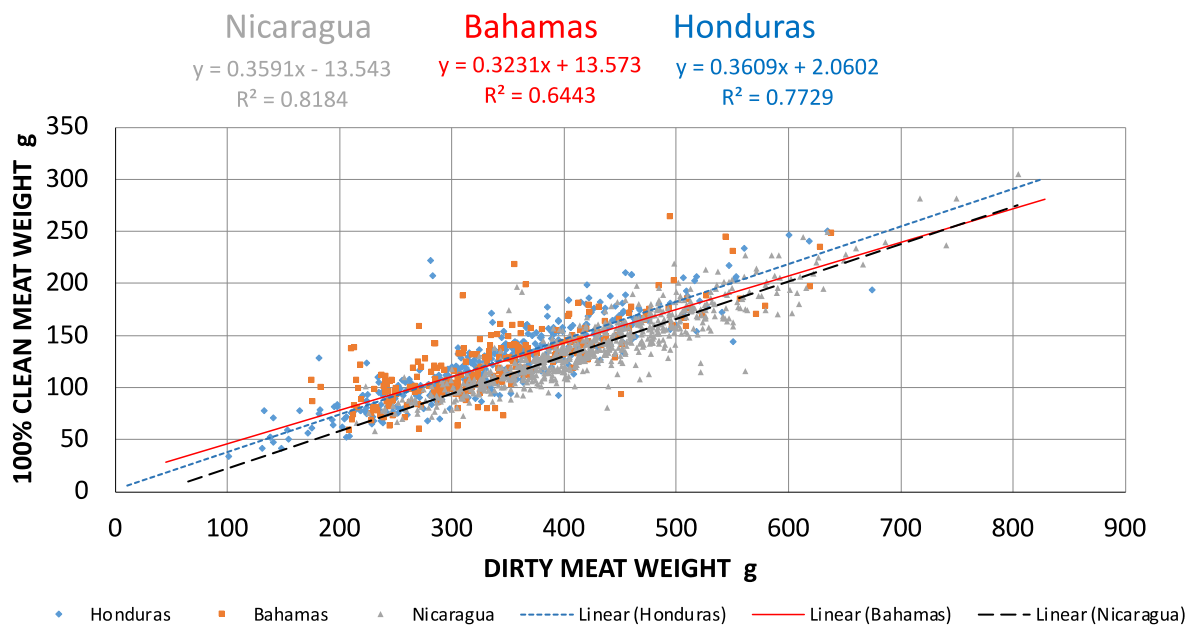


Figure 12. Data distributions between levels of % clean meat processing and dirty meat weight for different countries.

Table 4. Standard errors of estimated % meat processed level regressions on dirty meat weight.

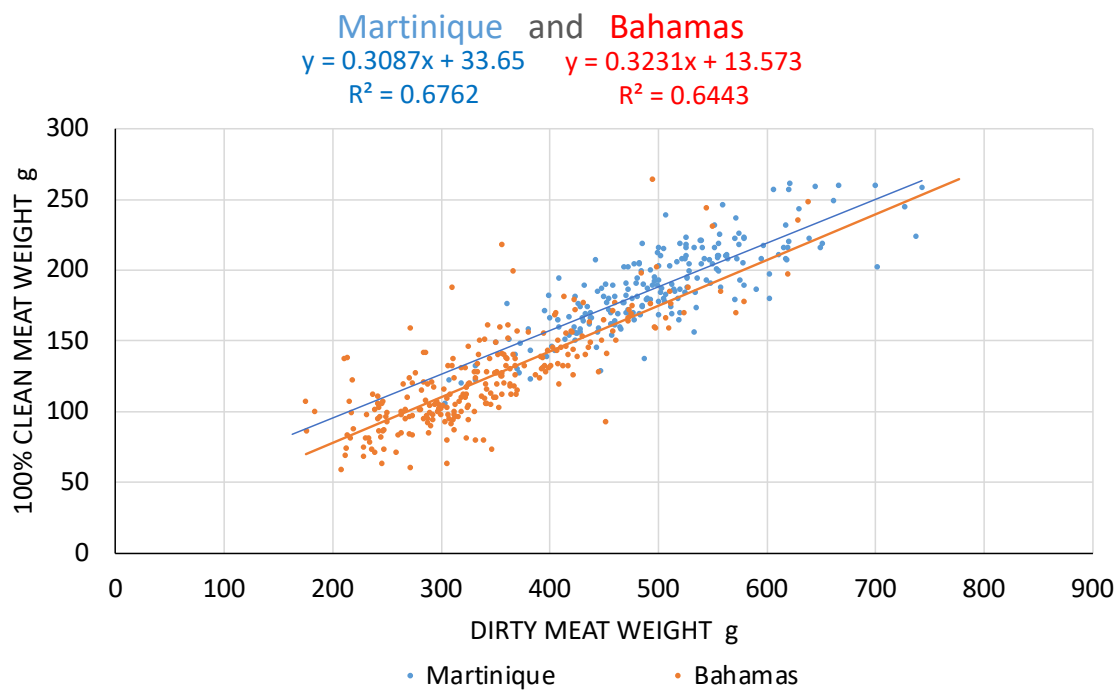
Country	100% Clean	85% Clean	50% Clean
Honduras	17.85	21.66	
Bahamas	20.97		26.43
Nicaragua	14.70		14.63
Martinique	17.09		28.15
Barbados		22.65	





Line	Group	d.f.	Sum y2	Sum xy	Sum x2	d.f.	SS	MS
1	Hond(Residuals)	401	560995	1201242	3328163	400	127427	318.57
2	Bahm(Residuals)	261	321422	640864	1983355	260	114345	439.79
3	Nic(Residuals)	710	844144	1923725	5356722	709	153289	216.20
4					Total	1369	395061	288.58
5	Line 6-Line 4	Difference for testing slopes				2.00	2181	1090.45
6	Lines 1+2+3	1372	1726560	3765832	10668240	1371	397242	289.75
7	Line 8-Line 6	Difference for testing levels				2	65773	32886.54
8	Pooled values	1374	1784351	4120050	12846707	1373	463015	
							Tabulated probability of F	
	F slopes	3.78	d.f.	2	1369		0.023	
	F levels	113.50	d.f.	2	1371		2.43685E-46	

Figure 13. Plot of 100% clean meat weight on dirty meat weight for the comparison of databases in Nicaragua, The Bahamas, and Honduras. Lower panel is the ANCOVA table developed according to the methods to estimate F-tests for the significance of the differences between the three countries.



Line	Group	d.f.	Sum y2	Sum xy	Sum x2	d.f.	SS	MS
1	MTQ(Residuals)	209	187612	410947	1331118	208	60743	292.03
2	Bah(Residuals)	261	321422	640864	1983355	260	114345	439.79
3								
4					Total	468	175088	374.12
5	Line 6-Line 4	Difference for testing slopes				1	165	165.12
6	Lines 1+2	470	509034	1051812	3314473	469	175253	373.67
7	Line 8-Line 6	Difference for testing levels				1	11874	11873.98
8	Pooled values	471	979485	2212719	6179182	470	187127	
							Tabulated probability of F	
	F slopes	0.44	d.f.	1	468		0.5068	
	F levels	31.78	d.f.	1	469		2.99062E-08	

Figure 14. Plot of 100% clean meat weight on dirty meat weight for the comparison of databases in Martinique and The Bahamas. Lower panel is the ANCOVA table developed according to the methods to estimate F-tests for the significance of the differences between the two countries.

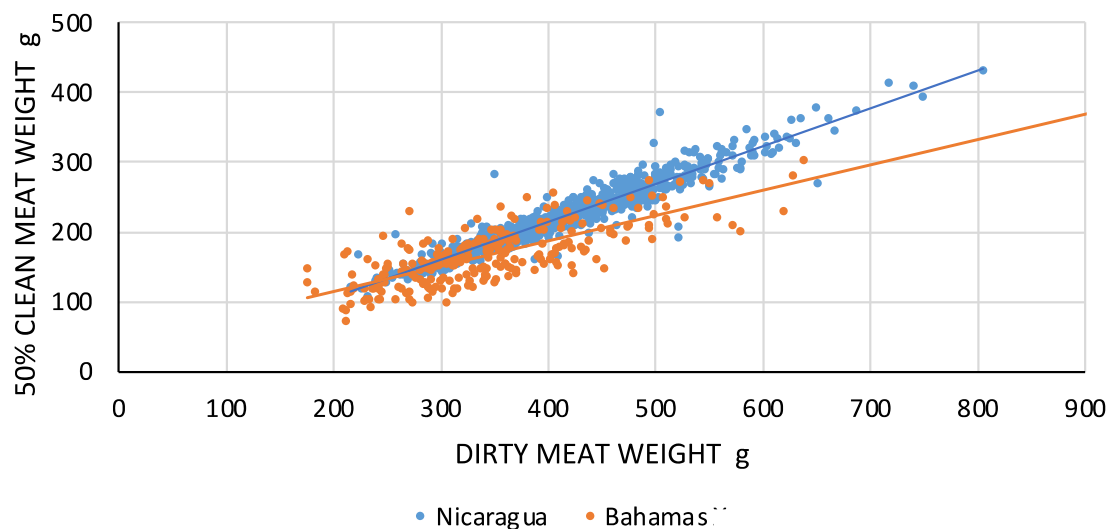
$$y = 0.5426x - 2.5425$$

$$R^2 = 0.9121$$

## Nicaragua and Bahamas

$$y = 0.3616x + 43.026$$

$$R^2 = 0.587$$



Line	Group	d.f.	Sum y <sup>2</sup>	Sum xy	Sum x <sup>2</sup>	d.f.	SS	MS
1	Nic(Residuals)	711	1729144	2906898	5357685	710	151960	214.03
2	Bah(Residuals)	260	438212	711271	1966789	259	180987	698.79
3								
4					Total	969	332947	343.60
5	Line 6-Line 4	Difference for testing slopes				1	47093	47093.01
6	Lines 1+2	971	2167356	3618169	7324474	970	380040	391.79
7	Line 8-Line 6	Difference for testing levels				1	67915	67914.54
8	Pooled values	972	2839869	4513097	8515374	971	447955	
							Tabulated probability of F	
	F slopes	137.06	d.f.	1	969		1.05306E-29	
	F levels	173.34	d.f.	1	970		1.52895E-36	

Figure 15. Plot of 50% clean meat weight on dirty meat weight for the comparison of databases in Nicaragua and The Bahamas. Lower panel is the ANCOVA table developed according to the methods to estimate F-tests for the significance of the differences between the two countries.

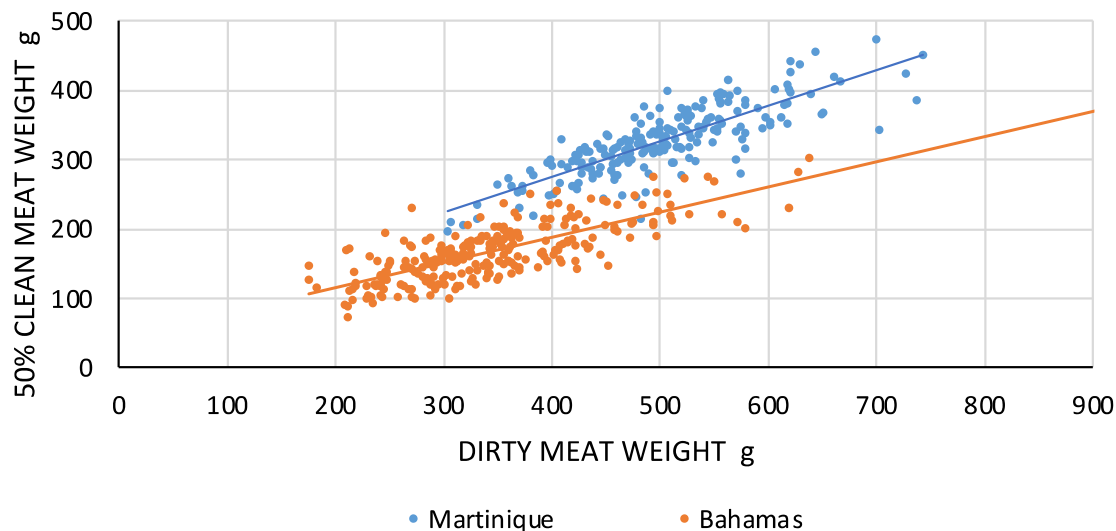
$$y = 0.5102x + 71.429$$

$$R^2 = 0.6776$$

## Martinique and Bahamas

$$y = 0.3616x + 43.026$$

$$R^2 = 0.587$$



Line	Group	d.f.	Sum y2	Sum xy	Sum x2	d.f.	SS	MS
1	MTQ(Residuals)	209	511257	679082	1331118	208	164817	792.39
2	Bah(Residuals)	260	438212	711271	1966789	259	180987	698.79
3								
4					Total	467	345804	740.48
5	Line 6-Line 4	Difference for testing slopes				1	17510	17510.43
6	Lines 1+2	469	949469	1390353	3297907	468	363315	776.31
7	Line 8-Line 6	Difference for testing levels				1	540710	540710.06
8	Pooled values	470	3912818	4310625	6175726	469	904025	
							Tabulated probability of F	
	F slopes	23.65	d.f.	1	467		1.58371E-06	
	F levels	696.51	d.f.	1	468		1.09043E-94	

Figure 16. Plot of 50% clean meat weight on dirty meat weight for the comparison of databases in Martinique and The Bahamas. Lower panel is the ANCOVA table developed according to the methods to estimate F-tests for the significance of the differences between the two countries.

### Objective 3

Considering the results of the statistical analyses carried out with the validated data for five of the seven countries that provided information and included in objectives 1 and 2, analyses in this objective 3 addressed the re-estimation of the CF necessary to expand categories of meat with a % clean weight to dirty weight. According to the regression analysis methodology that is proposed for the analyses, the conversion factors were estimated using an estimate of the average dirty weight (on the Y-axis) obtained from a linear regression function evaluated at the average weight of processed meat corresponding to a given % clean meat category (on the X-axis). Intercepts and slopes as parameters for the simple linear regression models were obtained by least squares procedures in Excel and are shown in Table 5. For example, using data from Honduras on individual dirty meat weight and the corresponding weight of 100% clean meat in a

sample collected at random for the determination of CF were plotted in Figure 17. The average weight of the clean meat in the sample was 125.38 grams; therefore, from Table 5 the intercept and slope of the regression line fitted to the data observed in Figure 17 are 73.198 and 2.1413, respectively. In this way the average weight of dirty meat estimated for the average weight of clean meat is given by:

$$\text{Average weight of dirty meat in Honduras} = 73.198 + 2.1413 \times 125.38 = 341.67 \text{ grams}$$

Therefore, the conversion factor from 100% clean meat to dirty meat weight will be:

$$FC = \frac{341.67}{125.38} = 2.72$$

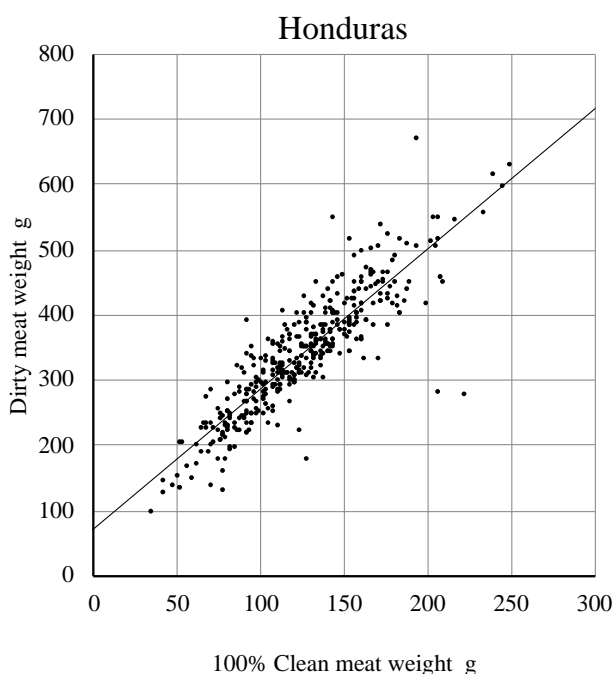


Figure 17. Graph of dirty meat weight as a function of 100% clean meat weight in Honduras used for the estimation of conversion factors according to sizes by weight of processed individuals. Parameters of the linear equation for Honduras are shown in Table 5.

Table 5. Estimated parameters for intercepts (a), slopes (b), coefficient of determination ( $R^2$ ) and regressional range of the data in dirty weight regressions fitted as a function of 100%, 85% and 50% clean meat categories.

Dirty meat weight as function of 100% clean meat in grams				
	Intercept	Slope	$R^2$	Range
Honduras	73.198	2.1413	0.773	50-250

Nicaragua	107.5	2.2789	0.818	50-250
Bahamas	95.149	1.9938	0.644	50-200
Martinique	88.273	2.1900	0.676	120-260

Dirty meat weight as function of 85% clean meat in grams

	Intercept	Slope	R <sup>2</sup>	Range
Honduras	79.86	1.848	0.739	50-270
Barbados	64.30	1.605	0.891	140-370

Dirty meat weight as function of 50% clean meat in grams

	Intercept	Slope	R <sup>2</sup>	Range
Nicaragua	41.361	1.681	0.912	120-350
Bahamas	71.844	1.623	0.587	100-250
Martinique	66.408	1.328	0.677	200-400

The confidence intervals for the CF require conceptual explanations to understand the origin of the 95% confidence interval values shown ahead in Table 8. From a biological standpoint the proportionality among morphometric flesh weight characteristics that exist between definitions of dirty meat and the resulting weights of usable % clean meat of the organisms are not directly proportional to each other. For this reason, the fitted linear functions between two flesh weight variables do not pass through the coordinates at the origin (0,0) as shown in Figures 12 to 17. This implies that the ratios between estimated dirty meat values and those of the corresponding % clean meat values used in the calculations of CF are not constant values but change as a function of the size of the individuals in the processed meat weights. In fact, it is observed that CF estimated for small specimens in the 100% clean meat category have higher CF values than CF estimated for larger individuals in the same meat processed category. For the example, using dirty and 100% clean weight data found in the sample from Honduras resulted in regressional parameters with intercept 73.178 and slope 2.1413 (Table 5). Using arbitrarily chosen individual 100% clean meat weight values of 50 grams, 200 grams and the average 125.38 grams, the CF according to % clean weight size turn out to be:

Meat weight 100 % clean (grams)	CF
50	3.60
125.38	2.72
200	2.51

This implies that larger individuals have a higher fraction of usable meat per unit of dirty weight than smaller individuals; therefore, larger (i.e., heavier) individuals have a lower CF, and vice versa. Consequently, the CF commonly used in the regional fisheries usually correspond to an average of % clean meat weight category and they may not be representative of the different individual group sizes of QC that may be landed in different regions or from different QC stocks (e.g., landings from shallower areas characterized by juveniles versus landings from deeper fishing grounds characterized by having older individuals). Therefore, it is important to have the

regression estimation procedure presented here as a tool for estimating CF corresponding to each of the individual average % clean meat weight observed in the landings or in groups of QC products already processed. Such regressional functions will greatly facilitate estimation of the CF by simply estimating an average weight of the individuals in processed products with which estimate an average dirty weight. The CF is simply the ratio between the two weights.

The confidence intervals for the CF given in Table 8 correspond to the 95% confidence levels of the parameters of the linear functions fitted to the data that are used in the estimation of the dirty weights. Those linear regression parameters (i.e., intercepts and slopes) and their confidence levels are the result of the least squares procedure applied to dirty meat weights as a function of the percentage levels of clean meat obtained from samples obtained for this purpose. They are found in the output tables when using the regression function in Data Analysis in Excel. An example of such an output table is presented in Table 6 for data on dirty meat weights and 100% clean meat weights in the samples from Honduras. A list of regression parameters and their confidence intervals for all countries that provided information are found in Table 7.

Table 6. Summary output of a linear regression fit using such a function in Excel. The data correspond to individual dirty weights and the 100% clean meat weights resulting from the queen conch cleaning process in Honduras. Data plotted figure 17.

SUMMARY OUTPUT Honduras dirty weight as a function of meat weight 100% clean

<i>Regression Statistics</i>	
Multiple R	0.8791215
R Square	0.7728547
Adjusted R Square	0.7722868
Standard Error	43.473458
Observations	402

#### ANOVA

	<i>d.f.</i>	<i>SS</i>	<i>MS</i>	<i>F</i>	<i>F tabulated</i>
Due to Regression	1	2572186.047	2572186	1360.9871	8.2611E-131
Due to Residuals	400	755976.6099	1889.9415		
Total	401	3328162.657			

	<i>Coefficients</i>	<i>Standard Error</i>	<i>T Statistic</i>	<i>P-value</i>	<i>Lower 95%</i>	<i>Upper 95%</i>
Intercept (a)	73.197714	7.593524939	9.6394908	6.534E-20	58.26950951	88.12591832
Slope (b)	2.1412717	0.058042322	36.891559	8.26E-131	2.027165613	2.255377847

Table 7. Estimated values of intercepts and slopes of linear regressions fitted to dirty meat weight data as a function of % clean meat weights, and minimum and maximum parameter values for samples provided by countries.

Regressions for estimating dirty weight from weights of **100% clean** meat

REGRESSION PARAMETERS	Honduras	Nicaragua	Bahamas	Martinique
Intercept	73.198	107.500	95.150	88.270
<i>95% Lower Confidence Limit</i>	<i>58.270</i>	<i>96.244</i>	<i>71.735</i>	<i>48.812</i>
<i>95% Upper Confidence Limit</i>	<i>88.126</i>	<i>118.764</i>	<i>118.563</i>	<i>127.733</i>
Slope	2.141	2.279	1.994	2.190
<i>95% Lower Confidence Limit</i>	<i>2.027</i>	<i>2.100</i>	<i>1.813</i>	<i>1.983</i>
<i>95% Upper Confidence Limit</i>	<i>2.255</i>	<i>2.358</i>	<i>2.175</i>	<i>2.397</i>

Regressions for estimating dirty weight from weights of **85% clean** meat

REGRESSION PARAMETERS	Honduras	Barbados
Intercept	79.860	64.300
<i>95% Lower Confidence Limit</i>	<i>63.990</i>	<i>3.428</i>
<i>95% Upper Confidence Limit</i>	<i>95.720</i>	<i>125.172</i>
Slope	1.848	1.605
<i>95% Lower Confidence Limit</i>	<i>1.741</i>	<i>1.373</i>
<i>95% Upper Confidence Limit</i>	<i>1.956</i>	<i>1.836</i>

Regressions for estimating dirty weight from weights of **50% clean** meat

REGRESSION PARAMETERS	Nicaragua	Bahamas	Martinique
Intercept	41.360	71.840	66.410
<i>95% Lower Confidence Limit</i>	<i>32.451</i>	<i>43.185</i>	<i>25.035</i>
<i>95% Upper Confidence Limit</i>	<i>50.270</i>	<i>100.500</i>	<i>107.780</i>
Slope	1.681	1.623	1.328
<i>95% Lower Confidence Limit</i>	<i>1.643</i>	<i>1.457</i>	<i>1.203</i>
<i>95% Upper Confidence Limit</i>	<i>1.720</i>	<i>1.790</i>	<i>1.453</i>

The CF estimated following the regression estimation method developed in these analyses for each category of % clean meat and for the countries that provided validated data are given in Table 8.

Fully Developed Example Using the Regression Method to Estimate QC CF



As an example of the application of the regression method to estimate QC CF for any given landing for which average weights of the % clean meat weight is available, we proceed as follows using the parameters for Honduras for 100% clean meat from Table 7:

To estimate the average value of dirty meat weight from the average of 100% clean meat, in a given landing which in this example is 125.38 grams, the linear regression equation is applied with parameters of intercept = 73.198 and slope = 2.141 thus generating:

$$\text{Dirty weight from 100\% clean meat} = 73.198 + 2.141 * 125.38 = 341.67$$

$$\text{Average CF} = 341.67 / 125.38 = 2.72$$

For the lower 95% confidence interval for the CF, the intercept is 58.270 and slope is 2.027 from Table 7 are used to estimate dirty meat weight, which is 312.43 for this case.

$$\text{Lower Average CF} = 312.43 / 125.38 = 2.49$$

For the upper confidence interval, intercept = 88.126 and slope = 2.255 from Table 7 are used., and the resulting dirty weight estimated from regression is 370.905.

$$\text{Upper Average CF} = 370.905 / 125.38 = 2.96$$

The values estimated above are tabulated for Honduras in Table 8 together with the results for the other countries analyzed here.

Table 8. Average Conversion Factors for 100% clean meat to dirty meat weight for fisheries in Honduras, Bahamas, Nicaragua, and Martinique.

		95% Confidence Interval	
	Average	Lower	Upper
Honduras	2.72	2.49	2.96
Bahamas	2.76	2.40	3.13
Nicaragua	3.06	2.80	3.22
Martinique	2.66	2.24	3.08

Average Conversion Factors for 85% clean meat to dirty meat weight for fisheries in Barbados and Honduras.

		95% Confidence Interval	
	Average	Lower	Upper
Barbados	1.73	1.38	2.09
Honduras	2.08	1.93	2.24

Conversion factors for 50% clean meat weight to dirty meat weight for fisheries in Martinique, Bahamas, and Nicaragua.

	Average	Confidence Interval	
		Lower	Upper
Martinique	1.53	1.28	1.78
Bahamas	2.05	1.72	2.39
Nicaragua	1.86	1.79	1.94

#### Objective 4

Analyses for this objective considered estimating an average regional CF with which to estimate live weight (i.e., shell weight + tissue) from CF estimates for countries for which validated information was available. For the estimation of national CF, validated data on live weight and dirty weight for the countries analyzed were used and simple linear regressions were fitted to the data in a manner similar to the method used in objective 3. The estimated values for intercepts and slopes are shown in Table 9.

Table 9. Estimated parameters for intercepts, slopes, and coefficients of determination ( $R^2$ ) for linear functional relationships between live weight and dirty weight, and regression range of the data in dirty weight. Estimates of the 95% confidence intervals of the estimated parameters are shown at the bottom of the table.

	Intercept	Slope	$R^2$	Range
Honduras	789.76	3.3156	0.435	140-600
Nicaragua	862.49	3.3478	0.5197	170-750
Bahamas	1062.83	2.4859	0.3879	200-600
Martinique	1498.54	2.5414	0.2563	300-700
Barbados	816.93	3.0130	0.4136	200-800

	Intercept	95% Lower	95% Upper	Slope	95% Lower	95% Upper
Honduras	789.76	659.059	920.470	3.316	2.946	2.946
Nicaragua	862.49	760.355	964.627	3.348	3.111	3.585
Bahamas	1062.83	928.800	1196.860	2.486	2.107	2.865
Martinique	1498.54	1198.714	1798.363	2.541	1.950	3.133
Barbados	816.93	574.885	1058.965	3.013	2.544	3.482

As an example the case of Honduras is used again for the application of the CF regression method for live weight from dirty weight. In this case the average dirty weight of 341.67 grams previously estimated in objective 3 from the 100% clean meat to dirty meat regression will be used. From Table 9 the intercept and slope of the linear regression fitted to the observed data of live weight and weight of dirty meat are 789.76 and 3.316, respectively. Thus, the average live weight estimated from the regression is given by:

$$\text{Average live weight in Honduras} = 789.76 + 3.316 * 341.67 = 1922.73 \text{ grams}$$

Therefore, the conversion factor from dirty meat to live weight for Honduras will be:

$$FC = \frac{1922.73}{341.67} = 5.63$$

The CF for live weight for the other countries providing validated data are shown in Table 10 with their respective 95% confidence intervals, which were estimated following similar operations as those carried out in objective 3.

Table 10. Conversion factors for dirty weight to live weight (shell weight + dirty meat weight) for fisheries in some countries of the region and for the average of all countries.

	Average	95% Confidence Interval	
		Lower	Upper
Honduras	5.63	4.82	5.64
Nicaragua	5.39	4.91	5.87
The Bahamas	5.58	4.82	6.35
Martinique	5.54	4.35	6.73
Barbados	4.65	3.70	5.60
Regional Average	5.36	4.53	6.04

The 95% confidence interval for the average CF varies among the countries analyzed, being narrower for Honduras and Nicaragua for which there were 406 and 712 pair samples, respectively, while for Barbados there were only 229 pair samples that generated a wider confidence interval for that country. Therefore, the available sample sizes result in estimates of CF for live weight from dirty weight with variable precision due on the one hand to sample size and on the other due to the geographic identity of shell growth in queen conch. It is also noted that the regional average is intended for those countries that do not have a CF available to estimate live weight from dirty weight. The decision to adopt the latter should consider that the regional average has a wide confidence interval indicating lower precision and that it is therefore important that countries should develop their own CF instead of adopting the regional average

to expand dirty weight to live weight as required in the information that countries should submit to FAO.

## CONCLUSIONS AND RECOMMENDATIONS

1. A very significant difference was found between the databases provided by Mexico and Belize even though the QC inhabits the same Mesoamerican Reef coastal ecosystem. The disparity in clean meat weight percentages for the two countries is for the same statistical range of dirty weights. Such disparities were not resolved in discussions with data collectors and therefore it is recommended that Mexico develop a verifiable statistical sampling design to generate new data for the estimation of CF corresponding to the % clean meat categories observed for queen conch in Mexico.
2. The analyses carried out with the two databases available for the estimation of conversion factors provided by Belize, did not achieve statistical validation for their inclusion in this work due to an exact duplication in a significant number of observations in the data, as well as inclusion of unverifiable data that could not be resolved with the institution responsible for the collection of such data. Therefore, it is recommended that Belize develop a verifiable statistical sampling design to generate new data for the estimation of queen conch CF in Belize.
3. The results of the ANCOVA to test the phenotypic characteristics of the QC carried out with the statistically valid samples provided by countries, show that the QC populations in Nicaragua, Honduras, Bahamas, Barbados, and Martinique have slopes that are statistically equal, implying that the linear regressions fitted for dirty weight as a function of shell weight are parallel lines. Such a condition is indicative that the changes in dirty weight due to changes in shell weight observed in the analyzed databases are approximately similar among countries.
4. However, intercepts of the regressions concerning phenotypic characterizations are significantly different between the countries compared, except in the case of Honduras-Bahamas, where the regressions are statistically identical. All comparisons using the QC database from Mexico with those of the other countries, resulted in significantly different linear relationships, adding uncertainty to the origin of the individuals sampled in Mexico. This conclusion indicates that relative to data from other countries, individual weight in the dirty meat samples are significantly larger per unit of individual shell weight observed in the Mexican database. The implication of such result is that QC in Mexico would be phenotypically different from the QC in the other countries, which is an unexpected result.
5. The differences found between the dirty weight data and their relationship to shell weight for Martinique-Barbados, Nicaragua-Honduras, Nicaragua-Bahamas, and Honduras-Barbados were not statistically significant for the slopes of the regressions, but they were for the intercepts. Such differences may be due to possible geographic identity conditions that impact the biology of QC shell growth.
6. The dispersion of dirty weight about regression that is a function of shell weight generated a low degree of association between the two variables, which is indicative that shell weight is not a good predictor of dirty meat weight. This conclusion is supported by

- existing information that total shell volume (i.e., another indicator of shell size) is a very poor indicator of shell cavity volume, while shell cavity volume is a good predictor of dirty weight. Consequently, the results obtained are concomitant with the existing information on the morphometric characteristics of the growth and development of QC.
7. As expressed in the problem identification section, the geographic identity of shell growth in QC, as well as the significant changes in shell structure and shape expected with the advent of sexual maturity, may be significant processes responsible for the low correlations observed between shell weight and dirty weight in the regional data sources available for this study. Such potential differences in growth processes that appear in the analyzed data led to the conclusion that QC conversion factors related to live weight would be more imprecise if one attempts to establish CF for live weight from the various categories of % weight of clean meat.
  8. The results of the analyses show that, while QC is phenotypically very similar among Honduras, Nicaragua and The Bahamas, the difference that exists in intercepts under the condition of statistical equality of slopes between Honduras and Barbados may be due to the fact that the data for these two countries, which are distributed far apart within the habitat range of the species, are significantly different in size but not in growth rates. These differences should reflect considerable differences in the estimated liveweight CF for these two regions which turned out to be 5.63 for Honduras and 4.65 for Barbados. Although such differences may suggest that regional harmonization or standardization of CF for live weight may not be entirely correct, it is also noted that there are very closely similar results among the other countries for which information was available for analysis. Therefore, it is recommended that countries that still lack an adequate CF for estimating live weight should organize work to estimate live weight conversion factors and thus replace the regional estimate with one that is expressly a descriptor of the local QC ecological conditions in each country.
  9. The results of the statistical analyses showed a low statistical significance of shell weight as a predictor of dirty weight. The analyses and results demonstrate that dirty weight data are better correlated with different percentage levels of clean meat processing. These results are important when considering the estimation of conversion factors to live weight (shell weight + meat), which will introduce a large and significant variance due to the greater variance of shell weight relative to the variance of meat weight.
  10. The average total dirty weights reconstructed from the % weight levels of clean meat using the corresponding average CF for the categories estimated in this study always resulted in total weight values that are about 99% of the original dirty weight observed in the samples. This finding supports the validity of the CF estimated by the regression method offered in this study.
  11. An average regional conversion factor for live weight (i.e., shell weight + meat weight) from dirty weight was 5.36, which is similar to that estimated in FAO (2014). However, this regional average has a confidence interval that is wide and therefore it has a lower precision than CF that may be estimated specifically for each country.

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