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Cod 3M Natural Mortality

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Abstract

This document presents the results of the estimation by different methods of the Natural Mortality (M) of NAFO Division 3M Cod. The methods presented in this document to estimate M are age-independent and agedependent methods that take into account the biological characteristics of this species. The results of M of the GADGET multispecific model that takes into account the trophic relationships between different species are also presented.

With the new input data agreed by the SC in March of 2018 and an assessment model similar to that approved in June 2017 for this stock, the results of three M scenarios has been analyzed: M constant for all ages and years, M variable by age and constant every year and M variable by age and year. Los resultados muestran diferencias significativas cuando se asume variabilidad en M.

Finally, the conclusion of the benchmark on the Natural Mortality that should be used in the 3M Cod assessment is presented.

Introduction

Natural mortality (M) is one of the most influential quantities in fisheries stock assessment and management. The magnitude of natural mortality relates directly to the productivity of the stock, the yields that can be obtained, optimal exploitation rates, management quantities, and reference points. Unfortunately, natural mortality is also one of the most difficult quantities to estimate.

In the current assessment natural mortality (M) for 3M Cod is assumed to be constant in time and age and it is estimated by the Bayesian XSA model. Table 1 present the estimated M values in the assessment for the 2010-2016 period. This table include the new value estimated with a similar Bayesian XSA model approved in 2017 but fit with the new input data and time series decided by the SC in Mars 2018. These new data has substantial changes and the time series are 1988-2016.

On different occasions the NAFO Scientific Council (SC) discussed the low values of M estimated by the model since they did not agree with the biological characteristics and age structure of this stock. This stock has a fairly high growth rate and age composition that is shorter than other stocks of cod.

Preliminary investigations conducted during the Workshop that took place in Vigo in March of 2017 (NAFO, 2017) suggested that M estimation is sensitive to the model configuration. This sensitivity of the estimated M values can also be seen in the gradual change of the estimated M values as new data is included (Table 1).

Due to these problems, the Workshop recommended to estimate M outside the stock assessment model and that the benchmark process further explore this issue.

This document presents estimates of Natural Mortality (M) for NAFO 3M cod based on different methods. The results of M obtained in the updated multispecific model GADGET are also presented.

Age-independent methods

During the 2017 workshop the values of M for the 3M Cod estimated by different methods (ANNEX 1) were presented. These methods are based on fitting regressions through the relationship between estimated and measured M values and a range of life history parameters. The life history parameters were estimated from the FC survey data for the most recent period 2010-2015 (Table 2).

The results with Age-independent methods (average M) for the case of 3M cod are presented in Table 3. These values were estimated using the M.emprirical function of the R package "fishmethods" with the parameters values presented in Table 2.

M.empirical(Linf=140,Winf=26000,Kl=0.121,Kw=0.160,T=3.5,tmax=17,tm=3.9,method=c(1,2,3,4,5))

Size-dependent Methods

Size-dependent models calculate M based on the observation that, in general, natural mortality rate decreases with size due to reduced predation. Whereas some methods use von Bertalanffy growth parameters to estimate size-dependent natural mortality (Chen and Watanabe 1989, Gislason et al. 2010), others calculate natural mortality as a function of weight (Peterson and Wroblewski 1984, McGurk 1986, Lorenzen 1996). It is important to know that both these weight-based methods for estimating M exhibit power relationships consistent with metabolic theory of ecology where biological rates, such as mortality, should scale with body mass to the power of -1/4 (Brown et al. 2004).

The results for M of the size-dependent method and the last approved assessment estimated M is showed in Table 4 and Figure 1. This Table and Figure also include the mean natural mortality at age estimated in the Flemish Cap GADGET model (Pérez-Rodríguez *et al.*, 2016) update with the data until 2016 (Perez-Rodríguez personal communication) and the mean M at age estimated by all the methods.

The results of the updated GADGET model for Flemish Cap indicate a high variability in the 3M cod natural mortality over the period 1988-2016 (Figure 2) mainly for ages 1-3. This high variability is due to the M depending of the predaction. The residual M was estimated constant for all years and ages as 0.35. For ages older than 3 years the predation M seems to be not important. The high inter-annual variability in natural mortality due to predation is probably a frequent issue in the Flemish Cap at least for ages 1-3. Under these conditions, the use of a multispecies model as source of annual values of natural mortality by age, used as input for single species models could be an option.

Possible M scenarios

One of the possible solutions for not estimating M in the assessment model as it was recommended in the 2017 Workshop could be to use a value of M around 0.2. This is a value very similar to that estimated in the last approved assessment (0.19) and is assumed in the assessment of other cod stocks.

But the M results of different models show with certain clarity that the assumption of constant mortality in all years and ages probably does not occur in this case. It seems quite clear in these results that at least ages 1 and 2 and possibly age 3 have a higher natural mortality than the other ages and ages older than three have a fairly similar natural mortality. One solution to take in account this age variability could be to build a vector of natural mortalities by age constant for all years based on the results obtained by size-dependent models. One option is take the median M by age of all methods presented in Table 4.

Age	A1	A2	A3	A4	A5	A6	A7
М	1.26	0.65	0.44	0.35	0.3	0.27	0.24

But the results of the GADGET indicating a high variability in the 3M cod natural mortality over the period 1988-2016 (Figure 2) mainly for ages 1-3. This high variability is due to the M depending of the predation. To include this year/age variability it would be necessary to use the GADGET estimated M matrix (Figure 2), used as input for single species models. This way to estimate M was used in different ICES assessment (Whiting (Merlangius merlangus) in the North Sea (Subarea IV) and the Eastern Channel (Division VIId) and North Sea cod).

Results sensibility to the M scenarios

To test the sensitivity of the assessment results to the different M scenarios described above, it has fit a Bayesian XSA model similar to the last one approved in 2017 for 3M Cod to the new input data approved in March 2018 by the SC for 3M Cod under three different M scenarios:

- 1. M estimated by the model.
- 2. Vector of M variable by constant age for all years (Table 4).
- 3. Matrix of M variable by age and year result of GADGET.

These three scenarios were compared with the last year assessment results. Figures 3, 4 and 5 show these comparisons for the SSB, recruitment and F respectively. It can be observed in these plots that when variability in M is allowed, the SSB results in the last years are much smaller and the Fbar estimated is bigger than when this M is assumed constant. The differences between the scenarios with M variable by age (vector) or M variable by age and year (GADGET matrix) are not very large for SSB and Fbar but are important in the recruitment trajectory. The results show that the confidence limits of SSB estimates in the scenarios with variable M are much narrower than those estimated in the fixed M scenarios.

This big difference observed in the SSB results mainly come from the abundance estimation of ages older than 4 years (Figure 6).

Benchmark conclusion

The previous results were presented during the 3M cod benchmark that took place in Lisbon in April 2018. After analyzing the results, the benchmark concluded that possibly the best option of M to use in the assessment of this stock is to use a vector of M variable by age as a mean prior distribution whit a coefficient of variation of 15% within a Bayesian model.

The reasons for this choice were based on the fact that the results of a vector (M variable by age) and of a matrix of M (M variable by age and years) are quite similar and that the final matrix of M is quite sensitive to the estimate that is made of the residual M. The Benchmark decided to continue estimating M inside of the assessment Bayesian model by providing a prior with enough information that is reflected in the value of the low coefficient of variation (15%). The choice of the final Bayesian model has not yet been made

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Tables

Table 1. Natural mortality estimated by the Bayesian XSA model used in the SC approved assessment of the
3M Cod. The year is the final data time series year. In red is the new M estimation made with the new
input assessment data approved by the SC in Mars 2018.

Year	2010	2011	2012	2013	2014	2015	2016	2016
М	0.15	0.15	0.15	0.16	0.16	0.17	0.19	0.22

Table 2. The life history parameters used to estimate the M in the 3M Cod case. *Linf* and *Kl* are the VonBertalanffy length equation. *Winf* and *Kw* are the Von Bertalanffy weight equation. *T*=meantemperature. *Tmax*=Maximum observed age and *tm*=age of first maturity.

Parameter	Linf	Winf	Kl	Kw	Т	tmax	tm
Value	140	26000	0.121	0.16	3.5	17	3.9
Estimated	No	No	Yes	Yes			

Table 3. The M values estimated with Age-independent methods for the 3M Cod.

Method	М
Pauly (1980) - Length Equation	0.113
Pauly (1980) - Weight Equation	0.136
Hoenig (1983) - Joint Equation	0.261
Hoenig (1983) - Fish Equation	0.246
Alverson and Carney (1975)	0.307
Roff (1984)	0.603

Table 4. The M values estimated with Size-dependent methods for the 3M Cod. This table also include the mean natural mortality at age estimated in the GADGET model (Perez-Rodriguez personal communication) and the mean M at age estimated by all the methods.

Method	A1	A2	A3	A4	A5	A6	A7
M (Gislason)	2.19	0.99	0.56	0.41	0.32	0.25	0.2
M(Charnov)	2.33	1.11	0.66	0.48	0.39	0.31	0.25
M(Peterson and Wroblewski)	0.7	0.48	0.37	0.32	0.29	0.26	0.23
M(Lorenzen General)	0.94	0.61	0.45	0.38	0.33	0.29	0.26
M(Lorenzen Fish)	1.08	0.69	0.5	0.42	0.36	0.32	0.27
M (Chen&Wata)	2.06	0.67	0.39	0.26	0.19	0.15	0.16
M (Gadget) (mean (1988-2016))	0.57	0.48	0.39	0.36	0.35	0.35	0.35
2017 assessment	0.19	0.19	0.19	0.19	0.19	0.19	0.19
Mean All methods	1.26	0.65	0.44	0.35	0.3	0.27	0.24



Fig. 1. Cod 3M natural mortality estimated by different size-dependant methods and the value estimated in the 2017 assessment.



Fig. 2. Total natural mortality (M) estimated by GADGET (Perez-Rodriguez personal communication). Ages older than 7 has the same estimated M (0.35).



Fig. 3. Bayesian XSA Cod 3M SSB results for the different M scenarios. XSA original (blue) is the XSA approved last year. M estimated (black) is a similar XSA original but fit with the new input data. M vector (red) is a similar XSA original but fit with the new input data and with the Table 4 M vector. M matrix (green) is a similar XSA original but fit with the new input data and with the GADGET M matrix. All scenarios with the 90% confidence intervals (dash lines).



Fig. 4. Bayesian XSA Cod 3M recruitment (age 1) results for the different M scenarios. XSA original (blue) is the XSA approved last year. M estimated (black) is a similar XSA original but fit with the new input data. M vector (red) is a similar XSA original but fit with the new input data and with the Table 4 M vector. M matrix (green) is a similar XSA original but fit with the new input data and with the GADGET M matrix.



Fig.5. Bayesian XSA Cod 3M Fbar (3-5) results for the different M scenarios. XSA original (blue) is the XSA approved last year. M estimated (black) is a similar XSA original but fit with the new input data. M vector (red) is a similar XSA original but fit with the new input data and with the Table 4 M vector. M matrix (green) is a similar XSA original but fit with the new input data and with the GADGET M matrix.

8



9

Fig.6. Bayesian XSA Cod 3M abundance at age results for the different M scenarios. XSA original (blue) is the XSA approved last year. M estimated (black) is a similar XSA original but fit with the new input data. M vector (red) is a similar XSA original but fit with the new input data and with the Table 4 M vector. M matrix (green) is a similar XSA original but fit with the new input data and with the GADGET M matrix.

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ANNEX 1

Age-independent methods (average M)

Reciprocal of lifespan: Assuming mortality is similar in each age class, the simplest way of estimating natural mortality M is by relating it to the inverse of the maximum age or lifespan (α max). Beverton and Holt originally suggested that M ~ 1/ α max. This approach has been generalised to:

$$M \approx \frac{C}{\alpha_{max}}$$

Where C is a constant, Hewitt and Hoenig (2005) suggested setting this constant as C = 4.22. In the 3M Cod case, the amax value was take equal 17 years. This data was taken from the commercial catches length distributions samples.

Comparative analysis of longevity and mortality by Hoenig (1983): Hoenig (1983) related M to lifespan (αmax) using least squares regression. When using data from fishes only the equation is:

$$\log M = 1.46 - 1.01 \log \alpha_{max}$$

In the 3M Cod case, the α max value was take equal 17 years.

Comparative analysis of temperature, VBGF, and mortality by Pauly (1980a): Pauly's (1980a) methodology uses the von Bertalanffy growth parameters (k, $L\infty$ or $W\infty$), as well as mean annual water temperature (T, in °C) to estimate natural mortality in fishes. Equations linking growth, temperature to mortality were estimated from least squares regression fits to comparative data spanning 175 fish stocks. The equation for weight-derived growth parameters is as follows:

$$\log M = -0.2107 - 0.0824 \log W_{\infty} + 0.6757 \log K + 0.4627 \log T$$

In the 3M Cod case, $W\infty$ =30000 gr, k=0.16 and T=3.5. These parameters values were estimated from the FC surveys samples information (2011-2015). The equation for length-derived growth parameters is:

$$\log M = -0.0066 - 0.279 \log L_{\infty} + 0.6543 \log K + 0.4634 \log T$$

In the 3M Cod case, $L\infty=130$ cm, k=0.12 and T=3.5. These parameters values were estimated from the FC surveys samples information (2011-2015).

Jensen (1996): By optimization of the tradeoffs between survival and fecundity, Jensen (1996) provided the following equation to calculate M, based on age at maturity (α):

$$M = \frac{1.65}{\alpha}$$

In the 3M Cod case α =3.9, the age of 50% of maturation. This parameters value was estimated from the FC surveys samples information (2011-2014).

Size-dependent methods

Gislason et al.(2010): Another methodology to estimate length-based mortality in marine and brackish water fishes was recently developed by Gislason et al. (2010), which builds upon the comparative analysis developed by Pauly (1980a). Based on a thorough data selection process which eliminated all but the most robust estimates of M the comparative analysis of 168 estimates of M from 70 publications is as follows:

$$\log M_L = 0.55 - 1.61 \log L + 1.44 \log L_{\infty} + \log k$$

where ML is mortality at length L, and k and L ∞ are the von Bertalanffy growth parameters for the stock in question. In the 3M Cod case, L ∞ =130 cm, k=0.12. Mean length at age was taken from the Flemish cap survey information for the period 2010-2015.

Charnov et al.: However, while this equation realistically shows that mortality declines ontogenetically with increasing size, it does not realistically capture the lower overall mortality observed in larger species (compared with smaller ones). This anomaly led to Charnov et al. (in press) to re-analyze the same data but from a more mechanistic basis founded in life history optimality theory. These authors conclude that the coefficients for L and L ∞ are not statistically different and find that a common exponent of 1.5 provides a better fit to the data and conclude that the Gislason et al. (2010) equation can be generalized as:

$$M = \left(\frac{L}{L_{\infty}}\right)^{-1.5} \times k$$

where M is mortality at length L, and k and L ∞ are the von Bertalanffy growth parameters for the stock in question. In the 3M Cod case, L ∞ =130 cm, k=0.12. Mean length at age was taken from the Flemish cap survey information for the period 20103-2015.

Peterson and Wroblewski (1984): Peterson and Wroblewski (1984) created a size-specific equation for estimating mortality in pelagic marine fishes using weight (in grams):

$$M_W = 1.92 W^{-0.25}$$

where MW is natural mortality rate at weight W in grams. Their analysis is based on the idea that predation is the chief process driving natural mortality. However, their model underestimated mortality of the early larval stages of pelagic fishes. Mean weight at age was taken from the Flemish cap survey information for the period 20103-2015.

Lorenzen (1996): Lorenzen derived an equation for estimating M in fish based on their individual weight, using a comparative analysis data from 308 estimates of M from fish in both freshwater and marine ecosystems.

$$M_W = 3.00 W^{-0.288}$$

Where MW is natural mortality rate at weight W in grams. When analysing only values from marine fishes (n = 113), the equation is as follows:

$$M_W = 3.69 W^{-0.305}$$

Lorenzen's (1996) equations explicitly exclude egg and larval stages from their analyses, thus they should not be used to predict natural mortality for those stages. Mean weight at age was taken from the Flemish cap survey information for the period 20103-2015.

Chen and Watanabe (1989): Chen and Watanabe (1989) modelled M based on the von Bertalanffy growth parameters (k and t0) using two separate functions: an age-specific one for the ages prior to the onset of senescence ($t \le tm$) and an age-independent model for ages after the onset of senescence ($t \ge tm$). This model describes a bathtub (U-shaped) mortality curve consisting on decreasing mortality with increasing size which increases at the end of the organism's lifespan due to senescence. The two part model is as follows:

$$M(t) = \begin{cases} \frac{k}{1 - e^{-k(t - t_0)}}, & t \le t_M \\ \frac{k}{a_0 + a_1(t - t_M) + a_2(t - t_M)^2}, & t \ge t_M \end{cases}$$

where the upward mortality trend observable in this model is provided by the following three a coefficients:

$$a_{0} = 1 - e^{-k(t_{M} - t_{0})}$$

$$a_{1} = k e^{-k(t_{M} - t_{0})}$$

$$a_{2} = \frac{1}{2} k^{2} e^{-k(t_{M} - t_{0})}$$

In the 3M cod case the M was estimated for all ages as t>tm formulation.