

UPDATED ASSESSMENTS OF SOUTHERN HEMISPHERE HUMPBACK WHALE BREEDING SUB-STOCK B1

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ABSTRACT

Updated Bayesian stock assessment results for humpback breeding sub-stock B1, which take into account recently advised capture-recapture data, are presented. These suggest this population presently to be within the range of 65-90% of its pre-exploitation size in terms of posterior median estimates. However, alternative options for inputs to this assessment are possible, and need to be discussed by the Scientific Committee.

KEYWORDS: HUMPBACK WHALES, BAYESIAN ASSESSMENT

INTRODUCTION

The Southern Hemisphere humpback whale stock B, which winters off west Africa, is currently divided into two sub-stocks:

Sub-stock B1 – Gabon

Sub-stock B2 – west South Africa, Namibia, Angola.

The exact boundaries between these two sub-stocks is unclear. This report aims to provide updated stock assessment results for sub-stock B1 whales in the interests of advancing discussion. As there is as yet no abundance estimate available for sub-stock B2, this is not assessed here.

The Bayesian assessment methodology used is essentially identical to that used for results presented in Johnston and Butterworth (2007a), except that the assessments now incorporate either capture-recapture data or alternatively the updated abundance estimates estimated therefrom, which have been recently provided by Collins *et al.* (2008).

DATA

Historic Catch data

There are two sources of historic catch data that relate to breeding sub-stock B1.

- i) Catches north of 40°S - those from “Congo” and 50% of “Congo/Angola” categories from Allison’s database (Allison pers. commn).
- ii) Catches south of 40°S - this series refers to catches recorded for 20°W-10°E and will thus include both B1 and B2 whales. Table 1a and Figure 1 report these three historic catch series. Three possible simple options are explored here for splitting this combined catch series. These are that to assume that either 25%, 50% or 75% of this combined series can be attributed to sub-stock B1.

Absolute abundance data

The absolute abundance data used in these analyses are presented in Table 1b. These are the upper and lower abundance estimates suggested by Collins *et al.* (2008), which result from the MARK program estimates when fitted to the photo-ID capture-recapture data from Iguela only (lower estimate of 6432 in 2003) and the genetic data from Iguela only (upper estimate of 7196 in 2003).

Trend information

No trend data (other than in the form of information implicit in the capture-recapture data) are available for the breeding grounds. IDCR/SOWER survey estimates provided by Branch (2006) are available for feeding ground II (20°W-10°E) for 1980, 1986 and 1995 – see Table 1c. These trend data clearly relate to both B1 and B2

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animals and the estimates have very large associated CVs. Sensitivity results to omitting these data are presented.

Capture-recapture data

The capture-recapture data used here are those reported in Collins *et al.* (2008). These consist of both photo-ID and genotypic mark-recapture data from Gabon. The data span the period 2000-2006 and are reproduced in Appendix 1. The data are reported both for all data sites, and for Iguela only (for which the data cover the years 2001-2005 only).

METHODS

Simple population modelling approach

A simple Bayesian stock assessment modelling approach is used here to assess sub-stock B1. This modelling approach is identical to that used for other breeding stocks and is described fully in Johnston *et al.* (2007), and applied to breeding stocks A (Zerbini *et al.* 2006), G (Johnston *et al.* 2007), and sub-stocks C1 and C2+3 (Johnston and Butterworth 2007). When the capture-recapture data are used directly as input instead of an abundance estimate derived from them, the term in the negative log likelihood for the abundance estimate is replaced by the negative log likelihood for the basic data as given by equation (5) of Johnston and Butterworth (2008).

Here the catches from the feeding grounds (catches south of 40°S) are apportioned either 25%, 50% or 75% to sub-stock B1. The IDCR/SOWER survey data are either used as trend data. The prior for r is $r \sim U[0; 0.106]$, although sensitivity to using $r \sim \text{post (BS A)}$ where the posterior of the r parameter from breeding stock A (Zerbini *et al.* 2006) is explored. Capture-recapture data for both photo-ID and genotypic sources are used combined, either for all data sites (Models 1-6) or for Iguela only (Model 7). Results for a total of seven alternate models are reported.

N_{\min} Constraint

An N_{\min} constraint of 368 whales is imposed. This value is 4 times the number of haplotypes (92) identified by Rosenbaum *et al.* (2006) for this stock.

RESULTS AND DISCUSSION

Table 2a reports a numbers of assessment results for breeding sub-stock B1, where the capture-recapture data for all data sites is incorporated. Table 2b reports the sensitivity to using capture-recapture data from Iguela only (Model 7). These results are shown as variations on a Reference Case (Model 1) based upon using the post (BS A) prior for r , and the use of all capture-recapture data and the IDCR trend information. Generally these suggest a resource currently increased to within the range of 80-90% of its pre-exploitation size in terms of posterior median estimates (Models 1-7), although Model 7 which uses capture-recapture data from Iguela only suggests the current population to be around 65% of its pre-exploitation level.

These results are, however, intended as initial only for the purposes of promoting further discussion. Clearly further alternative choices for input options can be motivated, and these need further discussion in the Scientific Committee.

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ACKNOWLEDGEMENTS

Support from the National Research Foundation, South Africa, and the International Whaling Commission is gratefully acknowledged.

Table 1a: Historic catches from sub-stock B1 from the breeding grounds and for the combined B1+2 sub-stocks from the feeding grounds (source Allison, pers. commn).

Season	B1 Breeding ground catches	B1+2 Feeding ground catches	Season	B1 Breeding ground catches	B1+2 Feeding ground catches
1900-1911	0	0	1951	1105	428
1912	418	0	1952	265	202
1913	2227	0	1953	0	102
1914	1843	0	1954	0	318
1915	0	0	1955	0	144
1916	0	0	1956	0	96
1917	0	0	1957	0	62
1918	0	0	1958	0	88
1919	0	0	1959	161	62
1920	0	0	1960	0	118
1921	0	0	1961	0	18
1922	613	0	1962	0	14
1923	685	0	1963	0	2
1924	519	0	1964	0	0
1925	756	0	1965	0	892
1926	321	0	1966	0	148
1927	0	0	1967	0	366
1928	0	0	1968	0	0
1929	0	18	1969	0	0
1930	578	64	1970	0	0
1931	0	4	1971	0	0
1932	0	18	1972	0	2
1933	0	86			
1934	362	38			
1935	894	300			
1936	595	250			
1937	150	188			
1938	0	0			
1939	0	0			
1940	0	242			
1941	0	0			
1942	0	0			
1943	0	0			
1944	0	0			
1945	0	0			
1946	0	2			
1947	0	2			
1948	0	84			
1949	1356	466			
1950	1404	228			

Table 1b

Absolute abundance estimates used for sub-stock B1 assessments.

Year	Breeding Stock B	
		Source
2003 upper estimate	7196 (CV = 0.18)	Collins <i>et al.</i> (2008)
2003 lower estimate	6432 (CV = 0.15)	Collins <i>et al.</i> (2008)

Table 1c

IDCR/SOWER estimates for the breeding grounds over 20°W-10°E (Branch 2006) for breeding stock B, adjusted to correspond to the same northern boundary for comparability, that are used to provide information on population trend.

Year	Breeding Stock B (20°W-10°E)
1980	692 (CV = 0.84)
1986	70 (CV = 0.63)
1995	595 (CV = 0.51)

Table 2a

Breeding sub-stock **B1** model estimates. Posterior medians with the 5th and 95th percentiles (in parentheses) are reported. Specifications that differ from those of the RC are shown in bold.

	RC: Model 1	Model 2
Historic Catch	50% of feeding ground catches	25% of feeding ground catches
Recent abundance	None	None
Trend information	IDCR	IDCR
<i>r</i> prior	$r \sim U[0; 0.106]$	$r \sim U[0; 0.106]$
capture-recapture data	All data sites – photo-ID and genotypic	All data sites – photo-ID and genotypic
<i>r</i>	0.042 [0.008; 0.097]	0.042 [0.007; 0.096]
<i>K</i>	10720 [8010; 20085]	10241 [7957; 19257]
<i>N_{min}</i>	3559 [1602; 7807]	4113 [1915; 8260]
<i>N₂₀₀₆</i>	8559 [7525; 9757]	8534 [7518; 9733]
<i>N_{min}/K</i>	0.286 [0.181; 0.865]	0.323 [0.211; 0.923]
<i>N₂₀₀₆/K</i>	0.805 [0.429; 1.000]	0.831 [0.447; 1.000]
<i>N₂₀₂₀/K</i>	0.940 [0.475; 1.000]	0.950 [0.490; 1.000]
<i>N₂₀₄₀/K</i>	0.992 [0.548; 1.000]	0.993 [0.555; 1.000]
	Model 3	Model 4
Historic Catch	75% of feeding ground catches	50% of feeding ground catches
Recent abundance	None	None
Trend information	IDCR	IDCR
<i>r</i> prior	$r \sim U[0; 0.106]$	$r \sim \text{post (BS A)}$
capture-recapture data	All data sites – photo-ID and genotypic	All data sites – photo-ID and genotypic
<i>r</i>	0.044 [0.009; 0.095]	0.055 [0.024; 0.086]
<i>K</i>	10926 [8195; 20637]	9431 [7915; 14128]
<i>N_{min}</i>	3040 [1344; 7300]	2838 [1359; 7398]
<i>N₂₀₀₆</i>	8555 [7545; 9734]	8462 [7453; 9694]
<i>N_{min}/K</i>	0.249 [0.149; 0.778]	0.265 [0.160; 0.819]
<i>N₂₀₀₆/K</i>	0.785 [0.418; 1.000]	0.911 [0.613; 1.000]
<i>N₂₀₂₀/K</i>	0.937 [0.468; 1.000]	0.986 [0.754; 1.000]
<i>N₂₀₄₀/K</i>	0.992 [0.541; 1.000]	0.999 [0.896; 1.000]
	Model 5	Model 6
Historic Catch	50% of feeding ground catches	50% of feeding ground catches
Recent abundance	6432 in 2003 (CV=0.15)	7196 in 2003 (CV=0.18)
Trend information	IDCR	IDCR
<i>r</i> prior	$r \sim \text{post (BS A)}$	$r \sim \text{post (BS A)}$
capture-recapture data	None	None
<i>r</i>	0.065 [0.027; 0.088]	0.065 [0.027; 0.088]
<i>K</i>	8411 [7060; 13045]	8525 [7124; 13158]
<i>N_{min}</i>	1156 [467; 5447]	1639 [582; 6551]
<i>N₂₀₀₆</i>	6858 [5536; 8854]	7447 [6168; 9301]
<i>N_{min}/K</i>	0.132 [0.064; 0.637]	0.180 [0.079; 0.776]
<i>N₂₀₀₆/K</i>	0.830 [0.500; 1.000]	0.895 [0.564; 1.000]
<i>N₂₀₂₀/K</i>	0.981 [0.680; 1.000]	0.989 [0.720; 1.000]
<i>N₂₀₄₀/K</i>	1.000 [0.855; 1.000]	0.999 [0.893; 1.000]

Table 2b

Further breeding sub-stock **B1** model estimates, showing sensitivity to replacing the use of capture-recapture data from all sites to using those data from Iguela only (Model 7), or to excluding the capture-recapture data and using the lower of the abundance estimates of 6432 in 2003 (Model 8). Posterior medians with the 5th and 95th percentiles (in parentheses) are reported. Specifications that differ from those of the RC are shown in bold.

	RC: Model 1	Model 7
Historic Catch	50% of feeding ground catches	50% of feeding ground catches
Recent abundance	None	None
Trend information	IDCR	IDCR
<i>r</i> prior	$r \sim U[0; 0.106]$	$r \sim U[0; 0.106]$
capture-recapture data	All data sites – photo-ID and genotypic	Iguela – photo-ID and genotypic
<i>r</i>	0.042 [0.008; 0.097]	0.053 [0.008; 0.091]
<i>K</i>	10720 [8010; 20085]	9172 [6870; 18259]
<i>N_{min}</i>	3559 [1602; 7807]	1053 [405; 4335]
<i>N₂₀₀₆</i>	8559 [7525; 9757]	6000 [5102; 6959]
<i>N_{min}/K</i>	0.286 [0.181; 0.865]	0.114 [0.057; 0.241]
<i>N₂₀₀₆/K</i>	0.805 [0.429; 1.000]	0.650 [0.312; 0.942]
<i>N₂₀₂₀/K</i>	0.940 [0.475; 1.000]	0.901 [0.350; 0.998]
<i>N₂₀₄₀/K</i>	0.992 [0.548; 1.000]	0.992 [0.408; 1.000]

Figure 1: Historic catch series for sub-stock B1 feeding ground and the B (i.e. B1+B2) feeding ground catches.

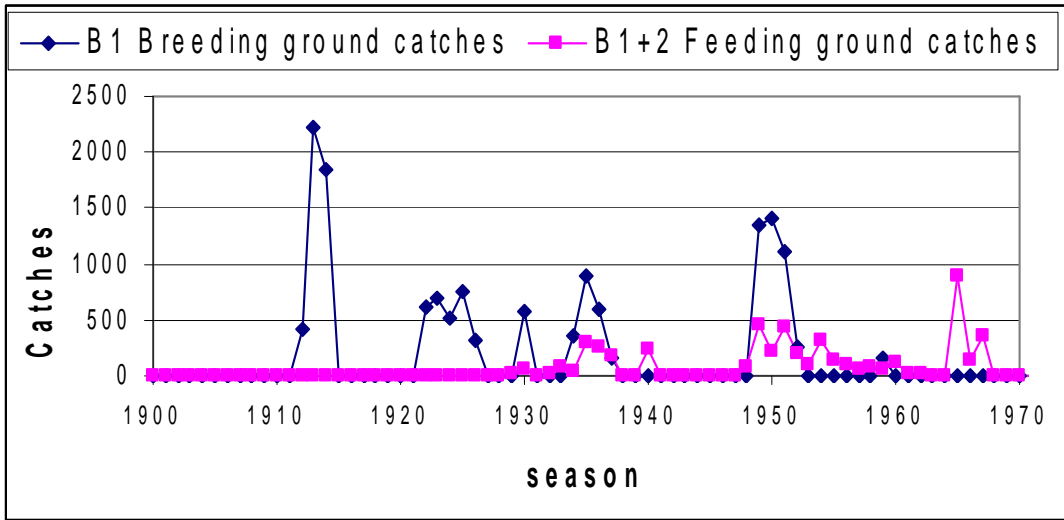
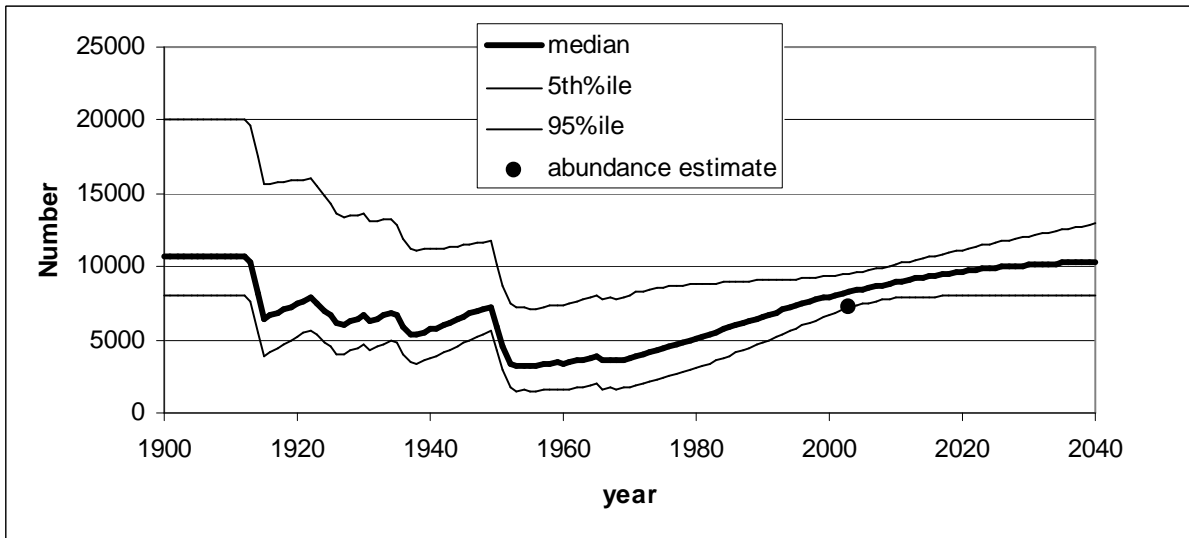


Figure 2: Reference case (Model 1) population abundance estimates for sub-stock B1. Medians with 5th and 95th percentiles shown. The Collins *et al.* (2008) preferred upper abundance estimate is shown as a circle on the plot for comparison.



Appendix 1: Data from Collins *et al.* (2008) used in these analyses

Photographic capture-recapture data from B1 – from SC/60/SH28 (Collins *et al.* 2008) [n = number of different individuals sighted each year, m = total recaptures between pairs of years]. Note $m^{B1,B1}$ refers to individuals captured in B1 and recaptured in B1.

Table A1.1: Photo-ID Dataset – Total sample from all sites (2000-2006)

N	2000	2001	2002	2003	2004	2005	2006
	24	111	233	161	138	216	99

$m^{B1,B1}$	2000	2001	2002	2003	2004	2005	2006
	2000	X	0	1	0	0	0
2001		X	5	6	5	3	2
2002			X	12	2	2	4
2003				X	7	2	1
2004					X	2	2
2005						X	6
2006							X

Table A1.2: Photo-ID Dataset – Iguela only (2001-2005)

N		2001	2002	2003	2004	2005	
			111	143	161	138	121

$m^{B1,B1}$		2001	2002	2003	2004	2005	
	2001		X	4	6	5	1
2002			X	6	6	1	
2003				X	7	1	
2004					X	0	
2005						X	

Table A1.3: Genotypes – Total sample from all sites (2000-2006)

<i>N</i>	2000	2001	2002	2003	2004	2005	2006
		82	155	257	270	188	296

<i>m^{BI,BI}</i>	2000	2001	2002	2003	2004	2005	2006
	2000	X	1	1	4	2	3
2001		X	6	8	6	3	2
2002			X	6	6	6	4
2003				X	8	7	1
2004					X	3	3
2005						X	11
2006							X

Table A1.4: Genotypes – Iguela only (2001-2005)

<i>N</i>		2001	2002	2003	2004	2005	
			155	170	270	188	137

<i>m^{BI,BI}</i>		2001	2002	2003	2004	2005	
	2001		X	6	8	6	0
2002			X	4	2	6	
2003				X	8	4	
2004					X	6	
2005						X	