Summary of the data and information available for the assessment of breeding stock B of the Southern Hemisphere humpback whales

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Summary from 2006 Hobart workshop
- Fair amount of evidence to suggest two sub-stocks B1 (Gabon) and B2 (west South Africa, Namibia, Angola)
- Would make sense to thus try and assess B1 and B2 separately.

SUBSTOCK B1

Abundance Estimates for B1
1) Rosenbaum *et al.* 2004 (SC/56/SH2) – based on aerial surveys
   - 1259 (CV=0.32) for year 2002
   - considered uncorrected and conservative
2) Collins *et al*. 2006 (SC/A06/HW10) based on capture-recapture – gives a number of estimates:
   - lumped Chapmans: 5641 (2002) CV=0.24
   - Schnabel :   5317 (2002) CV = 0.21
   - Chaos':   5766 (2002) CV = 0.20
3) Collins *et al.* (2008) (SC/60/SH28) based on capture-recapture.
   - Photo-ID –   using MARK – Iguela only: 6432 (2003) CV=0.18
   - Genetic data – using MARK – Iguela only: 7196 (2003) CV=0.15

Trend information for B1 (and B2)
The IDCR/SOWER survey estimates (Branch 2006) from the feeding grounds could be used as relative abundance estimates to provide a trend. These estimates correspond to 20ºW – 10ºE, so would cover both the B1 and B2 sub-stocks – but if used as trend information only this is not too important (i.e. the assumption would have to be made that the feeding ground trends are the same for both sub-stocks). Branch could be requested to disaggregate these data further if agreement can be reached on a longitudinal split for B1 and B2 in the feeding grounds.

These data, which have been adjusted to each correspond to all the area south of 60^0S, are:

CPI   1980   692 (CV = 0.84)
CPII   1986   70 (CV = 0.63)
CPIII   1995   595 (CV = 0.51)

Photographic mark-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.

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	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

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	o	
2005					X	

Genotypes – Total sample from all sites (2000-2006)

n							
	2000	2001	2002	2003	2004	2005	2006
	82	155	257	270	188	296	207

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

Genotypes – Iguela only (2001-2005)

n		2001	2002	2003	2004	2005	
		155	170	270	188	137	

$m^{B1,B1}$		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	

The Collins *et al.* (2008) paper suggests the lower and upper estimates for B1 using MARK are:

      lower   6432(CV=0.18) for the 2001-2005 photo-ID Iguela only dataset

      upper   7196 (CV=0.15) for the 2001-2004 genetic Iguela only dataset.

SUBSTOCK B2

Abundance Estimates for B2

Nil

Historic Catch Data (B1 and B2)

The breeding ground catches are split by region so that they could be apportioned into B1 and B2.

The feeding ground catches are reported at 10° longitude intervals. The Core feeding area for BS B (in total) is currently defined as $20^oW – 10^oE$.

Two plausible alternative catch-splitting scenarios are:

      Option 1:   B1 = $20^oW – 0^o$

                     B2 = $0 – 10^oE$

      Option 2:   B1 = $20^oW - 10^oW$

                     B2 = $10^oW – 10^oE$

Prior on the *r* parameter

If some trend information (such as IDCR/SOWER relative abundance estimates from the feeding grounds) or if the mark-recapture data are incorporated, a prior which is uniform between plausible demographic bounds (e.g. [0; 0.106],) could be used i.e. we let the data inform us about the *r* distribution.

If trend information is not available (or is considered unreliable), then a prior on the *r* parameter needs to be specified. One option is to use a posterior distribution from Bayesian assessments of other Southern Hemisphere breeding stocks.

Acknowledgements

References

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