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**Critical Literature Review
(ANTA602)**

A genetic perspective of the recovery and future conservation of the Antarctic blue whale (*Balaenoptera musculus intermedia)* following 20th century exploitation.

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Abstract:

The Antarctic blue whale, *Balaenoptera musculus intermedia*, at over 30 metres long and 150 – 200 tonnes, is considered to be the largest animal to ever have existed. During 20th Century whaling activities in the Southern Ocean, its sheers size made the Antarctic blue whale a prime target. During this period, Antarctic blue whales were reduced to 0.15% of the estimated unexploited population size. In biological terms, such an event is known as a bottleneck, and is considered to have long lasting negative effects on the genetic diversity of the population. In the present study, recent genetic research is reviewed with regards to the genetic status of Antarctic blue whale populations following the 20th Century bottleneck event. The future of Antarctic blue whale conservation and the potential incorporation of genetic information into conservation management and policy decisions is also reviewed.

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INTRODUCTION

Exceeding 30 metres in length and weighing up to 150 - 200 tonnes, the baleen whale *Balaenoptera musculus* is the largest animal known to have ever existed (Clapham *et al.*, 1999; Coffey, 1977; Knox, 2007; Soper, 2008). Residing in the Southern Hemisphere are two of the three recognized subspecies of blue whale; *Balaenoptera musculus intermedia* (Antarctic blue whale) and *Balaenoptera musculus brevicauda* (pygmy blue whale) (Clapham *et al.*, 1999; Knox, 2007). For the purposes of this review the focus will remain on the largest and most exploited subspecies *B. m. intermedia,* hereafter referred to as either blue whale or Antarctic blue whale. I aim to summarize the life history, distribution and exploitation of the Antarctic blue whale, assess the level of genetic diversity within remnant populations, and explore the future use of genetic information as a means of informing conservation strategies and policy relating to the Antarctic blue whale.

LIFE HISTORY & DISTRIBUTION

The Antarctic blue whale is a naturally long-living species with most estimates of average life-span ranging from 70 – 100 years (Coffey, 1977; Knox, 2007). Sexual maturity is generally reached at approximately 24 metres in length which is, depending on sex, between 5 – 10 years of age (Branch & Mikhalev, 2008; Branch *et al.*, 2007; Knox, 2007; Soper, 2008). Being a long lived, large mammal, generation times are also relatively long, with females breeding every three years (Clapham *et al.*, 1999; Soper, 2008).

Current knowledge of Antarctic blue whale distribution, migratory movements and feeding behaviour has been derived primarily from long term passive acoustic monitoring, a method particularly valuable in remote areas of the Southern Ocean where direct sampling methods have proven difficult (Samaran *et al.*, 2013). Although there is limited evidence to indicate exact wintering locations and breeding grounds, it is generally assumed that Antarctic blue whales migrate to temperate oceans of the Southern Hemisphere to mate and calve during winter months before returning to Antarctic waters, generally south of 55°, to feed during the summer (Branch *et al.*, 2007; Knox, 2007; Samaran *et al.*, 2013). The distribution patterns of this filter-feeding mammal are closely correlated to the distribution of the species' primary source of food, *Euphausia,* commonly known as krill (Branch *et al.,* 2007; Knox, 2007). At higher latitudes, Antarctic blue whales are often found to be scattered in bands stretching across the entirety of an ocean basin; this pattern directly reflecting the distribution and sheer abundance of the large Antarctic krill, *Euphasia superba* (Branch *et al.*,

2007; Leonori *et al.*, 2016). The area between the circumpolar belt and Antarctic pack ice is known to be the primary feeding ground for Antarctic blue whales (Branch *et al.*, 2007; Knox, 2007). Lowering in latitude, blue whale pods become progressively more collected and tend to localize themselves along continental margins (Samaran *et al.*, 2013). This grouping and distribution pattern is a mirror of krill density; krill species in temperate oceans tend to concentrate in coastal upwell systems (Branch *et al.*, 2007; Santora *et al.*, 2012).

EXPLOITATION HISTORY

The sheer size of the Antarctic blue whale made it one of the most valuable and therefore one of the most heavily exploited baleen whale species in history (Branch, 2007; Clapham *et al.*, 1999; Samaran *et al.*, 2013; Thomas *et al.*, 2016). Prior to the onset of modern whaling in the Southern Ocean around 1904, estimates put the undisturbed population of Antarctic blue whales at 239,000 individuals (95% CI = 202,000 – 311,000) (Branch *et al.,* 2007; Samaran *et al.,* 2013; Sremba *et al.,* 2012). During the summer season of 1931 – 1932, whaling in the Antarctic peaked. During this time a reported 29,409 Antarctic blue whales were caught and killed (Branch *et al.*, 2004; Clapham *et al.*, 1999). At this point in history, oil derived from Antarctic blue whales accounted for 75% of total whale oil sent back to contemporary civilizations to power settlements (Branch *et al.*, 2004). By 1963, Antarctic blue whale populations had been reduced to levels dangerously near extinction, thus the International Whaling Commission assigned the species a 'protected' status in 1964 (Branch *et al.*, 2004). Illegal whaling conducted by the Soviet Union did not cease until 1972, resulting in the extermination of an additional 872 blue whales (Branch *et al.*, 2004). By 1973 the total Antarctic blue whale population was suspected to be as low as 360 (95% CI = 150 – 840); 0.15% (95% CI = 0.07% - 0.29%) of the pre-exploitation population (Branch *et al.*, 2004). Despite an apparent increase in numbers, primarily based on sightings, the present population is still thought to be less than 1% of the original undisturbed population (Branch *et al.*, 2004; Thomas *et al.*, 2016).

UNDERLYING GENETICS

A high quantity and quality level of genetic diversity is vitally important for the prolonged survival of a species (Mahoney & Springer, 2009; Mousseau *et al.*, 1999). Variability in genetic material means that a species boasts a robust capability to successfully react to changes in its environment and lifestyle (Frankham, 2010; Mahoney & Springer, 2009; Mousseau *et al.*, 1999). Such changes include, but are not limited to, disease, climate change, competition from a novel species or anthropological exploitation. When the size of a population is reduced, genetic variation is

limited to that left in the remaining individuals (Luikart *et al.*, 2012; Mousseau *et al.*, 1999). The chance of further loss of genetic variability is increased in small populations due to the amplified effects of inbreeding depression and genetic drift, which is defined as the random loss of genetic material through natural events (Luikart *et al.*, 2012). Less genetic variance results in a lesser capability of the species to successfully adapt to change, ultimately increasing the chances of extinction of the species through an array of genetic and demographic processes (Frankham, 2010; Luikart *et al.*, 2012).

The Antarctic blue whale has undergone what is referred to as a population bottleneck event, defined as a sudden and severe reduction in the size of a population, typically resulting in the significant reduction of genetic variability (Luikart *et al.*, 2012). Considering that the Antarctic blue whale was once reduced to approximately 0.15% of the presumed pre-exploitation population, the species has potentially lost a significant amount of genetic variability. The evolutionary implications of such a reduction in genetic material could end up being fatal for the Antarctic blue whale, especially given the contemporary context of a rapidly changing environment. It is also important to note that the relationship between population size and genetic diversity is not always linear in that not all devastated populations exhibit reduced genetic diversity (Luikart *et al.*, 2012; Torres-Florez *et al.*, 2014). Life history traits influencing reproduction and population growth are thought to play a role in determining the genetic fate of a declining population (Frankham, 2010; Luikart *et al.*, 2012). Life history traits of the Antarctic blue whale, such as a long life-span, make the species an interesting case study for genetic consequences following an extreme bottleneck event.

GENETIC STUDIES

The process of conducting genetic studies on marine animals, especially the rare and enormous Antarctic blue whale, comes with a host of challenges. Difficulties associated with blue whale genetic studies revolve around limited access to biological samples, ill-defined breeding grounds and restricted access to feeding grounds in the Southern Ocean (Sremba *et al.,* 2012). As such, most genetic studies on the Antarctic blue whale are based on biopsy samples collected by the International Decade of Cetacean Research and Southern Ocean Whale and Ecosystem research cruises (IDCR/SOWER). The IDCR/SOWER program gathered blue whale biopsies from a vast range of locations in the Southern Ocean over no less than 14 years, during which efforts included three circumpolar surveys. The Japanese Whale Research Program is also a frequent provider of biological material from the Southern Ocean.

There are presently two published studies of interest which assess the genetic status of Antarctic blue whales following 20th Century exploitation. Sremba *et al.* (2012), using data provided by the IDCR/SOWER, assessed mitochondrial DNA (mtDNA) diversity and richness within Antarctic whale populations as a means of detecting the effects of the human-induced bottleneck event. Mitochondrial DNA is only inherited from the mother and is a very useful piece of genetic material with regards to population genetics research (Castro *et al.*, 1998). A haplotype, for future reference, describes a specific group of genes which are inherited together from a single parent; namely, particular sequences of mtDNA. From the sample of 183 Antarctic blue whales, 52 unique haplotypes were identified, at a diversity of 0.968 +/- 0.004. This value, which was derived using statistical techniques specific to population genetics (using software package Arlequin v3.1), indicates a high level of mtDNA diversity. Further statistical analysis, including the negative results of both Tajima's D and Fu's F tests, indicated an excess of rare haplotypes and revealed no genetic evidence of a recent bottleneck event. This essentially means that the genetic diversity of Antarctic blue whales is no less diverse than non-threatened mammal species. Sremba *et al.* (2012) went on to analyse haplotype richness within the Antarctic blue whale sample under the justification that haplotype richness, rather than diversity, is perhaps a more sensitive measure of a genetic bottleneck. It was revealed that of the 52 haplotypes identified, most were in very low frequencies within the sample and 15 were represented only by males. Upon the ensuing demise of these males, the 15 mtDNA haplotypes will be lost for good unless they are shared with females not included in the sample. Therefore, although significant genetic diversity still exists in Antarctic blue whales, the probability of diversity loss via genetic drift is increased by that lack of richness of unique haplotypes (Sremba *et al.*, 2012).

The second published study on the genetic diversity of Antarctic blue whales was conducted by Torres-Florez *et al.* (2014) on a population residing at a feeding ground just south of Chile. A total of 52 samples were collected from the Chilean population and diversity of mtDNA was analysed. Similarly to the previously described study, little evidence was found to indicate low levels of genetic diversity of the 12 unique haplotypes identified (Torres-Florez *et al.*, 2014). This study also noted a statistically significant lack of inbreeding, despite the small population size (Torres-Florez *et al.*, 2014).

The results from both studies are unexpected of a species having recently undergone a major bottleneck event. Genetic diversity is expected to be extremely low and ever decreasing due to magnified effects of genetic drift (Luikart *et al.*, 2012). The fact that Antarctic blue whales were reduced to around 0.15% of the original population over a short period of seven decades, with remaining populations still exhibit high levels of genetic diversity, means that demographic factors

must be buffering the genetic effects. To determine the demographic factors at play, the life history characteristics of the species must be considered. Both Sremba *et al.* (2012) and Torres-Florez *et al.* (2014) suggest, nay conclude, that the characteristically long life span and generation times of the Antarctic blue whale are the demographic processes responsible for buffering the adverse genetic effects resulting from the extreme bottleneck event. The long life-span of the Antarctic blue whale grants the possibility that individuals whom lived through the exploitative whaling period are still alive today, carrying with them some of the genetic diversity of the original, unexploited populations. Due to the long generation times of the Antarctic blue whale, it has been suggested that perhaps adequate time has not yet passed to allow for genetic loss via genetic drift to surface; about 40 years since the cease of whaling versus Antarctic blue whale life-span of 70 – 100 years (Sremba *et al.*, 2012). In this instance, the richness of unique haplotypes within the remaining population becomes extremely important for the future evolutionary health of the species. Unfortunately, as indicated by Sremba *et al.* (2012), haplotype richness is very low. Therefore, with time, the older individuals whom account for a great deal of the remaining genetic diversity will die, succumbing significant amounts of unique genetic material. Continued genetic monitoring of the Antarctic blue whale over the next century will elude to the potential fate of the species and reveal the long-term genetic implication of over exploitation.

Although both published studies indicate high levels of genetic diversity in remnant Antarctic blue whale populations, this information must not be taken lightly or relayed out of context due to the risk of prematurely 'down listing' the protected status of the species. Due to the demographic processes at play which are temporarily buffering the genetic implications of the 20th Century bottleneck event, the species appears to be to be genetically healthier than it really is. The low abundance of unique haplotypes combined with very low rates population expansion, not to mention the increasing human-induced shift of environmental parameters, the Antarctic blue whale is a species very much at risk of being ill-equipped to adapt to future alterations to its ecology.

GENETICS AND CONSERVATION

Looking forward, genetic information such as that presented in this review ought to be consulted when considering the future of Antarctic blue whale conservation. Genetic information and research techniques provide vital insights into the biological and evolutionary processes influencing the survival of the Antarctic blue whale. The data presented by Sremba *et al.* (2012) and Torres-Florez *et al.* (2014) should be used as a baseline for future monitoring of the Antarctic blue whale from which future changes to genetic diversity resulting from the bottleneck event can be

derived. Future genetic monitoring of the Antarctic blue whale should be combined with frequent demographic studies, environmental evaluations of localized habitats and assessments of contemporary human impacts (Frankham, 2010). Management strategies and conservation policy regarding the regeneration of Antarctic blue whale populations should thus be based on the genetic, demographic and environmental information gathered.

In general, integration of genetic information into management strategies and conservation policy has been historically futile (von der Heyden *et al.*, 2014). However, with the continual development of efficiency and accessibility of genetic technology, assimilation of genetic information into other fields of conservation will steadily increase. For example, the incorporation of genetic bottleneck tests into evaluations of threatened species is becoming more common (von der Heyden *et al.*, 2014). Even so, there are still significant limitations when attempting to introduce genetic considerations into the management of threatened species such as the Antarctic blue whale. There is an unfortunate lack of theoretical and practical frameworks to guide the multi-disciplinary use of genetic data (von der Heyden *et al.*, 2014). This lack of general guidance reflects genetics as a subject; it is complicated and requires a depth of scientific understanding. There is a need for genetic researchers to clearly communicate their findings to other scientific, management and political communities, as well as to the general public (von der Heyden *et al.*, 2014). The implications of genetic research are often difficult for non-specialists to comprehend. Effectively communicated science, especially where charismatic mammals such as the Antarctic blue whale is concerned, can successfully guide conservation strategies, species protection policy and behaviour of the general public such that the future survival chances of the endangered species are improved.

CONCLUSION

Despite the difficulties associated with conducting genetic studies on rare marine animals, it is promising to see that Antarctic blue whale genetics is becoming a more frequent research topic. It is essential to reiterate that although present studies of genetic diversity show no evidence of a bottleneck event in Antarctic blue whales, the buffering effect of underlying demographic processes means that the species is very much still at risk, with the damaging genetic consequences of 20th Century whaling expected to advance in coming generations.

Ongoing understanding of the genetic processes which underlie population trajectories of remnant blue whale populations will be invaluable when planning future Antarctic conservation strategies and implementing species protection policies. However, for this information to be

implemented as effectively as possible, the biological community must continue to strategize the way genetic information is communicated to the wider population.

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