DNA fingerprinting and 'scientific' whaling

SIR—We would like to report that the collection of small (200–300 mg) skin biopsies from free-ranging whales and their subsequent analysis by molecular genetic techniques is an alternative to 'scientific' whaling for addressing several important questions, including stock identification and population census.

Skin biopsy samples can be collected at a range of 10 to 30 m or more by firing a dart-tipped arrow from a cross-bow or compound-bow, air gun or rifle. As we have described previously[1], our dart is a metal cylinder 7 mm in diameter and 20 mm long. The arrow is tethered to a fly-casting reel and fired from an adjustable compound bow. Sample collection at sea is not dependent on refrigeration as the biopsy can be stored for extended periods in a salt-based preservative at ambient temperature.

Each sample yields 0.5–1.0 mg DNA, which is ample for many experimental analyses. The figure shows a 'DNA fingerprint' pattern and mitochondrial DNA (mtDNA) restriction digest from killer whale (*Orcinus orca*) DNA extracted from a skin biopsy collected at sea by the method described above. Human polycore minisatellite probes donated by Dr Alec Jeffreys (University of Leicester)[2] and a dolphin mtDNA probe donated by Dr Sarka Southern were used. DNA fingerprints from similar-sized skin samples taken from seven additional cetacean species are also shown, indicating a wide applicability for the technique.

One critical database for the conservation of cetacean populations is the census data currently gathered by sighting surveys, photographic identification of individuals, and marking studies where 'discovery tags' are fired into the whale to be recovered if the animal is later killed. DNA fingerprinting biopsy samples offers a minimally intrusive method with greater potential for accurate population census than current methods, although logistical considerations may make sighting surveys more practical for some species. Most vertebrate species show sufficient DNA fingerprint variation to allow individuals to be identified with vanishingly small probabilities of misidentification[2,3].

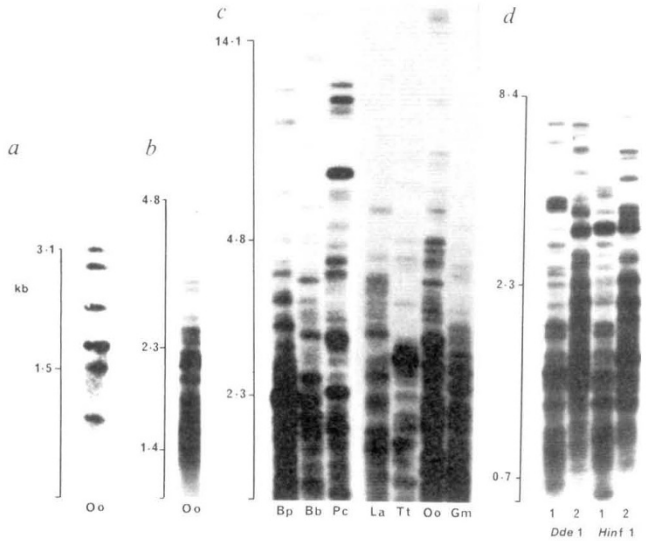
A fundamental concern for the long-term survival of these species is the maintenance of genetic variation, which is dependent on maintaining population numbers at a viable level. The impact of reduced variation on fitness for normally outcrossing species has been discussed extensively elsewhere[4]. Biopsy sampling has the potential to identify the genetic structure of populations and the dispersal and reproductive behaviour that contributes to the observed patterns of genetic variation. This can be achieved through paternity matching[5] and the examination of various genomic components useful for describing variation at the population level, such as mtDNA and the ribosomal DNA gene family[1].

In a news article[6] written at the time of the International Whaling Commission (IWC) meeting in Bournemouth last spring, Kathy Johnston described the controversy that arose when three member nations indicated their intention to take whales for scientific research in accordance with the IWC Convention, after agreeing to a three-year moratorium on whaling. There was disagreement within the IWC Scientific Committee over the feasibility of the scientific aims of Japan's intended catch, the size of which was later reduced to 300 minke whales before the fleet set sail in December. (A subsequent postal vote by the IWC delegates on a UK resolution that Japan refrain from allowing the catch to proceed registered 19 votes in favour, 6 against and 8 abstentions.)

For some time it has been a caveat of whale conservation and research that some aspects of cetacean biology can be investigated only using tissue samples from stranded animals or from a commercial or scientific catch. Indeed, the whaling industry has in the past provided the means to acquire important baseline data on age of sexual maturity, recruitment, population age structure, and various aspects of physiology. Given this database, however, our new priority should be to characterize accurately the size of populations and their genetic status. The technology needed to determine these fundamental population parameters without killing animals is at hand. This means that management policies and conservation measures may now be determined without the need to kill whales.

A. RUS HOELZEL
WILLIAM AMOS

Department of Genetics,
University of Cambridge,
Downing Street,
Cambridge CB2 3EH, UK



Mitochondrial DNA restriction pattern (*a*) and DNA fingerprint (*b*) from DNA extracted from a skin biopsy collected in the field, DNA fingerprints from five additional species (*c*) and variation in DNA fingerprint patterns with DNA from two individuals of the same species digested with two different enzymes (*d*). *a*, *O. orca* (Oo) mtDNA digested with *Hin*d III and *Xba* I and probed with a *Cephalorhynchus commersonii* mtDNA probe labelled with ^{32}P. *b*, *O. orca* DNA digested with *Hin*f I and probed with a ^{32}P-labelled polycore human minisatellite clone (33.15)[3]. *c*, *Balaenoptera physalus*, *B. borealis*, *Physeter catadon*, *Lagenorhynchus acutus*, *Tursiops truncatus*, *O. orca*, and *Globicephala malaena* DNA digested with *Hin*f I and probed with the 33.15 clone. *d*, *Delphinus delphus* DNA from two individuals (1 and 2) digested with *Dde* I or *Hin*f I and probed with the 33.15 minisatellite clone.

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Supernova 1909A: a precedent for SN1987A?

SIR—The unusual light curve and the low peak luminosity of the type II supernova 1987A in the Large Magellanic Cloud (LMC) are attributed to the fact that the stellar progenitor, Sanduleak −69 202, was a blue supergiant, rather than a red one, when it exploded[1]. The blue-supergiant nature of the progenitor is thought to have been connected with the relatively low abundance of heavy elements (low metallicity) in the LMC[2,3]. Here we note the resemblance of the light curve of supernova 1909A to that of SN1987A. SN1909A appeared in the outskirts of the