Night-time predation by Steller sea lions

New insight into the feeding habits of these mammals will help conservation attempts.

Measures have been taken to curtail commercial fishing of walleye pollock (Theragra chalcogramma) in Alaska in an attempt to stop the decline of its endangered population of Steller sea lions (Eumetopias jubatus). But our night-time observations of these mammals in Prince William Sound using infrared scanning technology, combined with acoustic surveillance of their prey’s behaviour, reveal that the sea lions feed exclusively on Pacific herring (Clupea pallasi), which are less abundant than pollock but are found closer to the surface at night.

Food limitation is the principal factor in the decline of Steller sea lion populations\(^1\)\(^-\)\(^4\). This decline could be explained by competition with commercial fisheries, as it has coincided with the growth of the pollock-fishing industry, which has become one of the largest fisheries in the world, or it could be related to a change in predator–prey relationships, possibly driven by ocean climate shifts. Central to the uncertainty surrounding the drop in the numbers of Steller sea lions is a lack of observational data on their foraging ecology. There is no quantitative information available that directly relates the foraging behaviour of these animals to the abundance of prey species.

During the winter period, nutritional stress is high. Sonar surveys\(^5\)\(^-\)\(^7\) of the abundance and distribution of adult Pacific herring and walleye pollock in winter have been made in Prince William Sound in Alaska since the early 1990s\(^5\). Steller sea lions were seen during the day near herring schools, but as no foraging activity was detectable, the significance of this occurrence was questionable.

We complemented our sonar surveys during March 2000 with infrared scanning of the Steller sea lions. This technology, which is widely used in night-time military operations and surveillance, enabled us to monitor the animals’ activity during the hours of darkness. Our system had a 27° × 18° field of view and a spectral response of 7–14 μm.

The estimated herring biomass in Prince William Sound in the sonar survey of March 2000 was 7,281 metric tonnes (95% confidence interval, 5,898–8,664). The estimate of pollock biomass was 28,277 metric tons (95% confidence interval, 26,034–30,420). Despite the much greater abundance of pollock, the infrared system revealed that foraging by Steller sea lions was exclusively on herring and was conducted only at night. Foraging activity was intense on dense herring schools (Fig. 1). Steller sea lions were often observed swimming side by side in a row of 50 or more individuals along the edges of a school, suggesting that they were herding the herring. Humpback whales and seabirds were also seen to be feeding alongside the sea lions (Fig. 1). By contrast, no sea lions were coincident with pollock schools.

The sonar records revealed herring schools at depths of 10–35 m at night, but deeper during the day. Walleye pollock, on the other hand, remained at depths of over 100 m during both day and night. Pollock schools were also found in less protected regions and were further offshore. Although Steller sea lions are capable of dives exceeding 250 m (ref. 9), the more accessible distribution of herring at night may be the primary factor in the foraging behaviour of the sea lions. This distribution of herring is characteristic during an extended overwintering period in the North Gulf of Alaska.

Our results indicate that the dependence of Steller sea lions on herring as prey has been underestimated. The infrared scanning technology that has led us to this conclusion should also help in the evaluation of night-time foraging behaviour of other marine mammals and seabirds, with its remarkable ability to detect individual fish flipping on the sea surface at a distance of 5–30 m, as well as sea lions, whales and birds at over 100 m.

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adenyl cyclase in bacteria and vertebrates, but has not been identified in other eukaryotes. Dictyostelium is located in the evolutionary tree between plants and the fungi/animal crown, and sequencing of its genome is approaching completion (see also http://dictybase.org).

We used all 113 listed human genes to screen for homologous sequences in Dictyostelium (27 February 2001; see supplementary information). A TBLASTN screen of the Dictyostelium database yielded 36 sequences with expectation values of less than $10^{-10}$. BLASTX analysis with the obtained Dictyostelium DNA sequences against GenBank identified 11 genes that represent clear Dictyostelium orthologues of human genes: the human sequences share a higher degree of identity with Dictyostelium than with bacterial sequences, and the bacterial sequences score more highly with respect to Dictyostelium than they do to humans (on the basis of BLAST expectation values). A further 17 humans (on the basis of BLAST expectation values). A further 17 human genes: the human sequences share a horizontal gene transfer from bacteria. !Mon ancestor, eliminating the need to invoke Dictyostelium information. Thus, in at least 11 cases, the human orthologues (see supplementary information) can mediate between the bacterial and vertebrate lineages (see supplementary information). Thus, in at least 11 cases, the human orthologues (see supplementary information) can mediate between the bacterial and vertebrate lineages. This is one of the human proteins with an orthologue in Dictyostelium. Phylogenetic analysis of this enzyme reveals a gene duplication late in the vertebrate lineage (MAO-A and MAO-B in Fig. 1). These paralogs seem to share a predecessor with Dictyostelium, indicating that monamine oxidase was present in early eukaryotes, and implying that the gene has been lost in worm, fly, plant, and yeast.

Within the group of 113 genes proposed to have entered the human genome by horizontal gene transfer from bacteria, we have identified at least 11 that probably arose through normal evolution with gene loss in several lineages, suggesting that gene loss is not a rare event. With several ongoing genomic sequencing projects for lower eukaryotes, it will be interesting to see how many genes have truly undergone horizontal transfer.

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**Bone-marrow transplantation**

**Failure to correct murine muscular dystrophy**

Bone-marrow cells have the potential to differentiate into other cell types such as muscle fibres, and can be transplanted into acutely or chronically damaged muscle as a way of delivering normal dystrophin (the protein that is defective or missing in Duchenne's muscular dystrophy) to the skeletal and heart muscle of mdx mice, an animal model for this disease. But the corrective potential of this approach has been hard to estimate against the high background of muscle fibres that spontaneously revert to synthesizing dystrophin, a feature of the original mdx mutation. Here we test the long-term efficacy of bone-marrow transplantation in a different mdx mutant which is free of this problem and find that it has no impact on murine muscular dystrophy.

The mdx4cv mutant (in which a C-to-T nucleotide transition generates a stop codon in exon 53 of the dystrophin gene) has almost no background of revertant fibres in skeletal muscle. We sublethally irradiated (900 Gy) a group of 15 8-week-old mdx4cv mice (C57Bl/6/Ly-5.2 background) and transplanted them with a total of $1.5 \times 10^7$ bone-marrow cells from a pool of 6-week-old, co-isogenic (C57Bl/6/Ly-5.1) animals. We killed the mice at regular intervals from 9 weeks to 10 months after transplantation, and monitored the engraftment of donor cells by cytofluorimetric analysis of the proportion of Ly-5.1 marker compared with Ly-5.2. The degree of chimaerism averaged $85 \pm 2.7\%$ in bone marrow (mean $\pm$ s.e.m.), $93 \pm 1.1\%$ in spleen, $92 \pm 2.9\%$ in thymus and $94 \pm 0.8\%$ in peripheral blood throughout the follow-up study.

We counted dystrophin-positive (dys*) fibres in histological sections of representative muscles (tibialis anterior, quadriceps, diaphragm) after immunohistochemical staining with an anti-dystrophin antibody in transplanted and age-matched, mock-transplanted, control mdx4cv mice. Clusters of dys* fibres were apparent in muscle sections of transplanted animals, averaging $0.23 \pm 0.05\%$ (minimum, $0.06\%$; maximum, $0.54\%$) throughout the 10-month study (Fig. 1a). The proportion of dys* fibres in control animals averaged $0.14 \pm 0.03\%$ (minimum, $0.02\%$; maximum, $0.33\%$), a statistically significant difference ($F = 5.99$, $P = 0.02$). In neither group was there any significant increase in the number of dys* fibres in young (under 5 months) and old (over 12 months) animals. The average number of fibres contained in each dys* cluster varied from 3 to 30, with no significant change with age in either group.

To demonstrate the presence of normal dystrophin in the muscle of transplanted mice (the antibody does not distinguish between corrected and revertant fibres), we developed a polymerase chain reaction with reverse transcription (RT-PCR) assay to distinguish wild-type dystrophin messen-