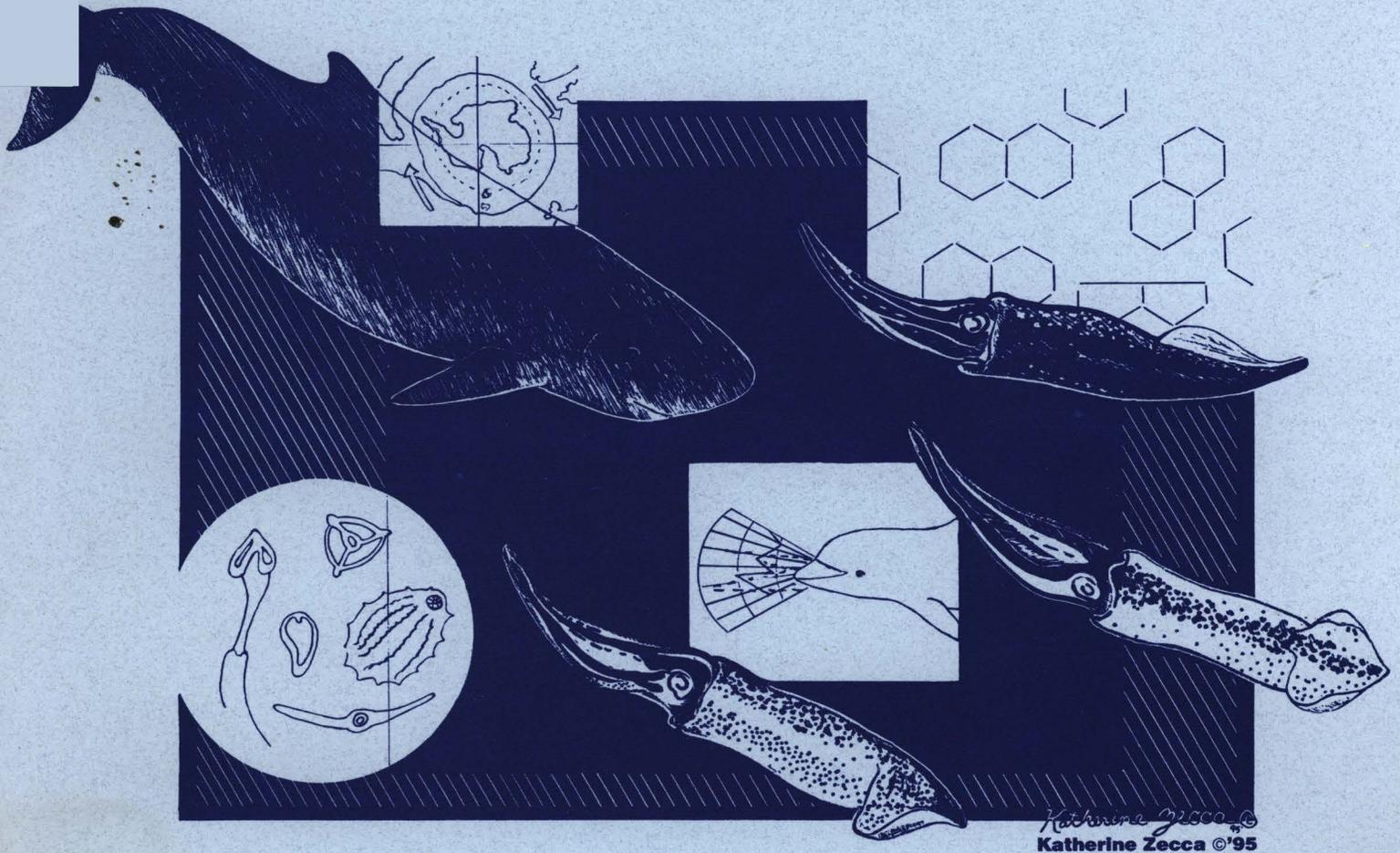


GENETIC STRUCTURE AND BREEDING PATTERNS OF BELUGA WHALES
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Knowledge of intraspecific subdivision and an understanding of the proximate causes of such structure is essential for the effective management of beluga whales. We investigated variation in the mitochondrial genome (mtDNA) and at a number of hypervariable nuclear loci to study intraspecific structure, social organization and breeding patterns of beluga whales in Alaska and northwest Canada. Sequence analysis of over 240 whales revealed that average genetic diversity within mtDNA (D-loop) was low ($\bar{d}=0.002$) in comparison to other odontocetes. Variation at this locus and a number of microsatellite loci indicates that many putative populations of beluga, previously proposed on the basis of disjunct summer distribution in nearshore waters, are genetically differentiated from each other (AMOVA, $\Phi_{st} = 0.32$). The tracking of individual mtDNA haplotypes together with information on gender, age and microsatellite profiles indicate that females in some areas are more philopatric to their natal herds than males and suggest that dispersal in males may be biased towards older animals. Despite limited individual dispersal however, there may be substantial gene flow among some populations. It is hypothesized that the relatively low level of mtDNA variation in beluga reflects a unique evolutionary history in a hostile environment while the high degree of geographical partitioning of this variability is influenced by the summer site fidelity of predominantly matrifocal groupings. Although age and gender bias in dispersal is typical of many vertebrate societies, the occurrence of discrete summering populations in a common wintering area adds a unique dimension to the reproductive and social behaviour of this cetacean.

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ABSTRACTS