Introduction of an ecosystem model of the western North Pacific: progress made and future work for its application to multi-species management

Mitsuyo MORI[1)], Takashi HAKAMADA[1)], Koji MATSUOKA[1)], Hiroto MURASE[1)], Tsutomu TAMURA[1)], Hikaru WATANABE[2)], Kenji KONISHI[1)]

Inst. Cetacean Res., Tokyo, Japan[1)], National Res. Inst. Far Seas Fish., Yokohama, Japan[2)]

An ecosystem model based on data collected mainly from the Second Phase of the Japanese Whale Research Program under Special Permit in the Western North Pacific (JARPN II) is introduced. Based on the results from JARPN II, it is known that minke whales feed mainly on Pacific saury and Japanese anchovy, and that Bryde's and sei whales feed mainly on Japanese anchovy. These two fish species support important commercial fisheries in Japan. Thus, the existence and magnitude of interaction between the whales and fisheries on these fish resources is of great interest to fisheries managers. Hence, the purpose of this ecosystem model is to elucidate the role of the cetaceans in the western North Pacific marine ecosystem, and to evaluate both the impact of whaling on the ecosystem and the impact of fisheries on whales. Ecopath with Ecosim was used to develop the model. Uncertainties in input data and functional response curves are taken into account when various harvesting scenarios are evaluated. Further, we discuss the application of such an ecosystem model to future multi-species management, especially as it relates to whales.

Utility of genetic analyses for the management of large whales: applications and limitations

Luis A. PASTENE, Mutsuo, GOTO, Naohisa KANDA

Inst. Cetacean Res., Tokyo, Japan

Recent advances in molecular biology have permitted the application of modern DNA techniques to the study of population genetics of large whale species. Among the most commonly used techniques is sequencing analysis of a portion of the maternal inherited mitochondrial DNA (mtDNA) control region and analysis of bi-parental inherited nuclear DNA (nDNA) using microsatellites. In the context of management of large whales these molecular tools have been applied to i) elucidate population structure, ii) estimates current and historical abundance and iii) investigate the species identity (and populations in certain cases) of whale products in the retail market. These uses are illustrated with case studies conducted at the Institute of Cetacean Research. Limitations of the use of genetic analyses to resolve management issues, and the future work to improve its applications, are identified.