

recently found to have the AT1 haplotype conclusively indicate that they are not the “missing” whales from the AT1 group.

Nuclear DNA: Barrett-Lennard (2000) found significant genetic differences in nuclear (microsatellite) DNA, which is inherited from both parents, among AT1s, GOA transients, and WC transients. In particular, the AT1 group sample was found to be the most divergent in its microsatellite allele frequencies because they were more divergent from the nearby GOA Transients and WC Transients than those groups were from each other. The differences between the AT1 group and the other groups would be considered “large” by most population geneticists.

In the case of the AT1 group, the high level of divergence from other transient killer whale groups might be related to the group’s very small size. The average level of heterozygosity in the AT1 group is approximately 60 percent that of the other transient groups, which is consistent with the AT1 group being a small population. For a small population the level of genetic difference seen between AT1 killer whales and other transient groups could occur relatively quickly (perhaps within a few generations; one killer whale generation is 50–100 years). Regardless of how many generations it took to generate, the degree of difference in microsatellite DNA is consistent with current demographic isolation between the AT1 group and GOA and WC transients.

New genetic samples from the northern Gulf of Alaska: Since the analyses documented in Barrett-Lennard (2000), the number of biopsy samples of transient killer whales from the Gulf of Alaska to the Bering Sea has increased substantially. A preliminary analysis of those new data (in combination with existing data) was undertaken to clarify the relationship between the AT1 group and other transient killer whales in Alaska, and these preliminary results were described in the report of NMFS’ status review on AT1 killer whales. The analysis indicated that the Umnak killer whale with the AT1 haplotype is not a member of the AT1 group nor a member of a closely-related population. Furthermore, there was no clear evidence that any of the other transient whales sampled in the Gulf of Alaska are closely related to the AT1 group.

Alternatives to Explain the Genetic Differences

The AT1 group is currently considered part of the eastern North Pacific transient killer whale stock, the only currently identified “stock” of

transient killer whales in the North Pacific. However, the new information described above indicates that the stock structure of transient killer whales should be reviewed, and that the AT1 group is genetically separate from other transient killer whales.

There are at least three possible scenarios that might lead to the genetic differences that are seen between AT1 and other transient groups, though the three scenarios are not necessarily equally plausible given the available information. An assumption that is made when speculating about these scenarios is that a very small population (circa 22 animals) could not persist as an independent population for a very long time.

The first scenario is that the AT1 group represents a remnant of a previously larger population. In this situation, there would have been two separate populations of transient killer whales in Alaska that were genetically and demographically isolated. One of these populations declined in population size, and its remainder is now known as the AT1 group.

The second scenario is that the AT1 group separated from another transient population relatively recently and has never been particularly large. Genetic drift may occur rapidly in a small population so the observed genetic differences could have arisen fairly recently. A small unit like the AT1 group would likely not have had a high probability of persisting as a separate population over a long time period. In other words, if the AT1 group arose from another transient population and was never large in size, it may have been doomed to extinction since its beginning. One problem with evaluating the importance of this possible scenario is that the terms “relatively recent” and “long time” are hard to define. A third scenario is that the AT1 group is part of a larger population of transient killer whales that have not yet been sampled for genetics analysis.

Although the population structure of transient killer whales in the Aleutians, Bering Sea, and in the western North Pacific is not yet fully understood, it is possible to eliminate some of the scenarios above from consideration. The data available are reasonably consistent with the first two scenarios and will be discussed below. However, at this time, there is no evidence to support the third scenario (that the AT1 group are part of a more widespread Alaska transient population that is largely sympatric with the GOA transients from Prince William Sound to the Bering Sea). Substantial sampling along the Alaska Peninsula, the Aleutian Islands, and in

the Bering Sea has failed to find killer whales that are closely-related, genetically, to the AT1 group. Although four individuals have been found with the same mtDNA haplotype as found in the AT1 group, the one individual for which a complete microsatellite analysis was available was strongly assigned to GOA transient whales, rather than the AT1 group.

As stated above, the available data are consistent with the scenario where the AT1 group may be a remnant of a much larger population that has been separate for a long time and are also consistent with the scenario where the AT1 group may consist of a very small number of animals that split off from a larger group in the recent past. Genetic data alone are insufficient to distinguish between these two scenarios. The AT1 group has less genetic diversity than other North Pacific transients, but more genetic diversity than would be expected if they had been at a very small population size for a long time.

In its status review of AT1 killer whales, NMFS included literature on genetic relationships in other species of mammals that live in highly structured societies (e.g., monkeys, lions, wild dogs). Results from the review of 17 studies indicated that strong genetic differentiation between social groups of terrestrial mammals appears relatively rare, occurring in only one of the 17 studies reviewed. The status review cautioned against making strong conclusions based on these other studies because these terrestrial mammals and resident and transient killer whales do not exhibit identical social behavior.

The Depleted Determination

The AT1 Group as a Stock

As discussed above, NMFS’ guidelines for identifying population stocks of marine mammals state that many different types of information can be used to identify stocks, reproductive isolation is proof of demographic isolation, and demographically isolated groups of marine mammals should be identified as separate stocks. These guidelines were based upon the MMPA’s definition of population stock and with the purposes and policies of the MMPA. The biological information discussed above, particularly molecular genetics and associations (distribution and movements), supports a determination that AT1 killer whales are demographically isolated from other groups of killer whales. Therefore, based upon the best available scientific information, NMFS proposes to determine that the AT1 group of