

Mysteries Revealed by Genetic Techniques

Scientists use new technologies to reveal untold mysteries about whales and provide information on whale history that may be crucial to their survival in the future. Genetics techniques provide useful tools for trying to understand the resources of whales, species diversity, population levels, which populations are under threat, and what population histories are. Dr. Stephen Palumbi, a renowned marine biologist and professor at Stanford's Hopkins Marine Station, uses genetic techniques to determine what type of marine species are being sold around the world. He has used these techniques to find out which species are actually in what is sold as Pacific Red Snapper (see microdocumentary, *Cooking with DNA*: www.ggfilms.com/screenings/room7/index.html) and to determine which species are being sold in whale meat markets (see archived webcast, *The History and Future of Whales*: www.esi.utexas.edu/outreach/prevlectures.html). Different DNA sequences can be related to one another evolutionarily and those DNA sequences can be used to draw what is known as a phylogenetic tree (a family genealogy of the relationships of different species to one another). The combination of the DNA sequencing and a known phylogenetic tree for fish and whales gives us the ability to identify a sample out of any market in the world.

When testing DNA from samples, researchers need to decide which loci in the species' genome are going to be tested. Researchers often pick multiple loci and perform a multiple loci analysis of the sample in order to obtain enough markers to sufficiently categorize the sample. The reason behind this is that the most closely related taxa should have the most traits in common. If you did not pick a variety of loci and just tested one, there is an extraordinarily high possibility that every species of whale will have that particular locus in common because most of the genome that they inherit from a common ancestor is the same. Therefore, researchers try to pick a sufficient number of loci to generate enough variability in genotypes to be able to distinguish between species. This allows researchers to match samples with a high enough certainty to already known species, or find that too many of the loci do not match a known species, indicating the possibility of a new species.

Once the researcher chooses the loci that are going to be tested, they need to create large quantities of every locus that is going to be tested. This is accomplished by polymerase chain reaction (PCR). Even though this may sound complicated, the logic behind the process of PCR is fairly straightforward (for a PowerPoint presentation on this topic, see www.esi.utexas.edu/gk12/ret/PCRModeling.ppt#267,2,Modeling_PCR). First, the desired locus is located on its' chromosome and it is cut away from the chromosome by restriction enzymes that recognize a specific sequence (usually repeats; meaning ATATATATAT). Once the desired locus is separated from the entire chromosome, it is then put into a test tube with nucleic acids, the building blocks of DNA, and the enzyme DNA polymerase, which is responsible for DNA replication by pairing the corresponding nucleic acids together. The mixture is then heated and cooled repeatedly. During the time when the mixture is heated, the DNA strands separate and create multiple one-stranded DNA primers. Then the mixture is cooled back down to a temperature where the DNA polymerase enzyme can function. When the mixture reaches the desired temperature, the polymerase uses the single DNA strands as templates and begins synthesizing a complimentary strand of DNA using the nucleotides in the mixture. This process takes

approximately 30 minutes and then is repeated again. This amplifies the DNA exponentially because one original strand will yield 36 strands after two hours. Continuing at this rate after approximately ten hours the result is there is about one million times more DNA than there was at the beginning. After the researcher has used the PCR technique, they have millions of exact clones of the specific sequence they need to test. They can then run multiple tests many times over to ensure that their results are accurate. Genetics doesn't answer every question about marine species, but genetic techniques can help provide a better understanding of marine populations so they can be protected in the future.

Sources:

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