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Updated November 16, 2026

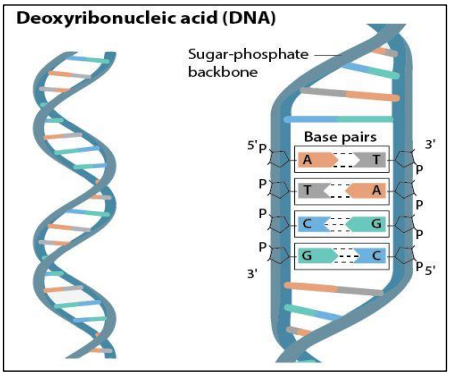
DNA Methylation: Applications to Living Marine Resource Management

Deoxyribonucleic acid (DNA) is a molecule that contains the genetic information of an organism (**Figure 1**). It consists of two linked strands of alternating sugar and phosphate groups, which make up the "backbone" of the DNA. The two strands are connected by chemical bonds between the bases: adenine, cytosine, guanine, or thymine. The sequence of these bases encodes the biological information for the development and function of an organism (e.g., instructions for making a protein).

DNA methylation refers to a chemical modification of the DNA chain through the addition of a methyl group, which is composed of one carbon and three hydrogen atoms. DNA methylation (**Figure 2**) occurs when the 5-prime (5') carbon of the cytosine nucleotide (i.e., the fifth position carbon atom of cytosine bonded to the deoxyribose sugar molecule) is modified by the addition of a methyl group, becoming 5'-methylcytosine. As organisms age, changes in DNA methylation occur. These changes may have utility as a nonlethal biochemical test to measure an organism's age, along with other traits and factors (e.g., disease risk).

Congress has included funding and directives to federal agencies in appropriations legislation regarding the use of molecular and genomic technologies for a variety of applications (e.g., disease detection, genome sequencing). With its interest in ocean and marine resources management, Congress may consider the utility of technologies such as DNA methylation and environmental DNA (eDNA) in biological surveys and assessments to enhance the characterization and monitoring of living marine resources (LMRs).

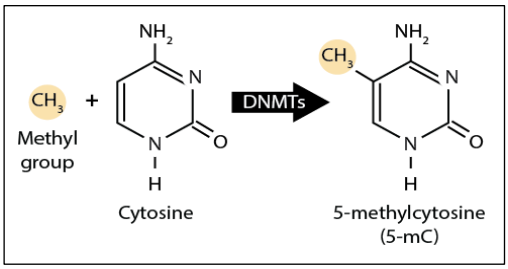
Figure 1. Structure of Deoxyribonucleic Acid (DNA)



Source: CRS, modified from National Human Genome Research Institute, "Deoxyribonucleic Acid (DNA)," 2025.

Notes: Each strand of DNA consists of alternating sugar (2-deoxyribose) and phosphate (P) groups that comprise the "backbone" of the DNA molecule. Attached to each sugar molecule is one of four nitrogenous bases: adenine (A), cytosine (C), guanine (G), or thymine (T), which are connected by chemical bonds to form a base pair (either A-T or C-G linkages).

Figure 2. Schematic and Pathway of DNA Methylation



Source: CRS, modified from Ana Valente et al., "The Effect of Nanomaterials on DNA Methylation: A Review," *Nanomaterials*, vol. 13, no. 12 (2023).

Notes: The figure represents the methylation pathway that can occur on the cytosine base pair in a DNA molecule. CH_3 = methyl group; DNMTs = DNA methyltransferases, a type of enzyme that mediates DNA methylation; H = hydrogen; N = nitrogen; O = oxygen (together with carbon, indicated with the hexagons, these three elements are components of the cytosine and 5-mc molecules). A double line indicates a double bond of carbon to a given element.

DNA Methylation in Living Marine Resources

Scientists have discovered that the amount of methylated DNA increases in certain cells, tissues, and organs as an individual ages. Studies find that the level (i.e., quantity) of methylated DNA in an organism can produce an accurate estimate of an individual's age. Experts have proposed using methylated DNA as an accurate, novel, and less invasive sampling technique for biological surveys to inform the management of living resources. For example, DNA methylation could be used to age certain LMRs, including vertebrates (e.g., fishes, reptiles, mammals, seabirds) and invertebrates (e.g., shellfish, including lobster). Currently, the ageing of LMRs is often performed by examining the hard parts (e.g., vertebrae, ear bones, scales, shells) of animals that are sacrificed during sampling. DNA methylation also may allow for greater sampling and ageing of threatened, endangered, and protected marine species, for which the use of lethal approaches is generally undesirable. Additionally, the use of DNA methylation applied toward understanding species' life histories could complement efforts by federal agencies that incorporate other molecular techniques in scientific investigations. For example, the National Oceanic and Atmospheric Administration's National Marine Fisheries Service (NMFS) has made progress in using eDNA, in LMR surveys and for estimating population abundance, in addition to other genetics-based (e.g., molecular) techniques to investigate LMRs and their ecologies

(including some DNA methylation studies). Like eDNA, DNA methylation techniques may provide additional information regarding LMRs, such as age composition. CRS has not identified examples where agencies have used DNA methylation for LMR surveys and assessments.

Applications to Fishery Species

Studies find that the amount of methylated DNA in fishes can be used to non-lethally determine sex (i.e., not require death of an individual for gonad examination) and biological age; examine environmental influences on size and growth; detect spawning activity; and account for other elements of fish species' life histories (e.g., timing of sexual maturity). Further studies find that DNA methylation may be a useful tool for fisheries and aquaculture management, helping indicate reproductive health, viability of offspring, or resistance to disease and stress. Together with other biological information, data on the age, growth, sex, and maturity of individuals in a fishery population (or *stock*) are used in stock assessments to determine the status of that population (i.e., whether it is being harvested sustainably). For example, age-based fisheries models typically are used to determine the amount of *fishing mortality* that a population is experiencing, which can be applied toward setting sustainable harvest levels. Additionally, information on a species' timing of maturity can be used to confine harvest to specific size limits to prevent fishing for juveniles or certain mature breeding individuals.

Experts have found that changes in DNA methylation correlate with age across multiple fish species and certain other vertebrates, enabling the development of an *epigenetic clock* (i.e., one related to gene functioning) that can be used to estimate the age for commercially or recreationally important fish species. For example, recent studies have determined accurate epigenetic age estimations for Atlantic cod, cownose rays, deepwater scorpionfish, and European seabass, along with potential estimations for other fishes and shellfish. Studies also suggest an epigenetic clock would perform similarly for shorter- or longer-lived fish species. However, the same experts recommend further testing for fishery species of differing morphologies (e.g., larger versus smaller fishes) or life histories (e.g., fishes that spawn once versus fishes with multiple spawning events). They also recommend a greater examination of how environmental factors such as temperature changes, hypoxia, salinity, and diet may affect the rate of DNA methylation in different populations of the same species, which some studies have observed. Others suggest that methylation may predict chronological age (i.e., time lived since birth) independent of environmentally driven perturbations in certain species.

Applications to Marine Mammals and Other LMRs

DNA methylation may show utility for determining the age and sex of other marine vertebrates. Studies indicate that nonlethal small tissue biopsies can be used to age various long-lived cetaceans (e.g., killer whales), pinnipeds (seals, sea lions, and walruses), and polar bears, and to determine age and sex in beluga whales and certain bottlenose dolphin species. Utilizing DNA methylation techniques may further inform assessments of marine mammal populations, potentially aiding in their conservation and management.

DNA methylation techniques have detected epigenetic changes associated with age and other factors in some seabird and sea turtle species. Scientists found that short-tailed shearwaters, a long-lived seabird, showed increased methylation with estimated age in most cases. This finding may be useful, as experts note that most seabirds do not have external identifiers of chronological age, traditional estimates of which generally require additional analysis, including long-term studies. Other studies have investigated the use of genomes to predict sea turtle age (e.g., for predicting leatherback sea turtle lifespans). Researchers note that DNA methylation may be a promising method to determine a sea turtle's *relative age* (i.e., the time between two events), but not its *absolute age* since hatching, and that developing an epigenetic clock for all sea turtles would require more investigation. Other studies show that the amount of methylated DNA in sea turtles also can assist with early sex determination and in detecting thermal stress.

Issues for Congress

Some stakeholders and experts note the utility that "less invasive" molecular techniques, including quantifying DNA methylation, may have for assessing and managing a variety of LMR populations. Experts and federal agency representatives have testified during congressional hearings about how molecular techniques can inform wildlife conservation and management. Experts find that molecular approaches often complement or supplement data taken by traditional sampling methods for determining age, sex, and maturity of LMRs (e.g., analysis of hard parts and gonads), given limitations in applying certain molecular approaches across species. Experts also note ongoing knowledge gaps in developing universal approaches for broader application.

Congress continues to recognize and support advancements in biotechnology and genetics-based techniques for LMRs and other purposes. Congress has seen legislation (e.g., S. 5273 in the 119th Congress) to direct NMFS to evaluate and validate the utility of eDNA and emerging technologies for use in federal fishery stock assessments, and for informing about federally managed fisheries, which may be interpreted to include DNA methylation. Congress may evaluate the utility of incorporating molecular techniques into LMR surveys and assessments to determine if they are less invasive and more cost effective than traditional survey approaches. Congress may evaluate whether agencies' resources are sufficient to include such approaches in LMR surveys or whether molecular or traditional sampling methods may independently provide sufficient information for assessing and managing LMRs (e.g., including DNA methylation data in marine mammal *unusual mortality event* examinations to determine age and potential disease). Congress may consider directives to federal agencies about the use of these approaches and whether agencies should make management decisions using these techniques. Congress may examine how other emerging technologies (e.g., artificial intelligence) might complement or provide alternative benefits to molecular approaches and how agencies should consider them.

Anthony R. Marshak, Analyst in Natural Resources Policy
Todd Kuiken, Analyst in Science and Technology Policy

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