Chapter 23
New Ecological Directions: Isotopes, Genetics, Historical Ecology, Conservation

This chapter provides an overview of three areas of research collaboration for zooarchaeologists. The first is stable isotope analysis, which began as a way to reconstruct ancient climate, evolved into investigating ancient human diet and mobility, and more recently entered zooarchaeology and conservation biology. The second is animal genetics, which has revolutionized the study of plant and animal domestication, and has also been applied to understanding ancient foragers' relations with wild species. The third is use of zooarchaeology in the conservation and management of animal species.

Both isotopic and genetic materials can be considered to be strong proxies for specific processes in the past. Certainly, isotopic "signatures" are checked for the effects of situationally variable causes of sample contamination. However, such possible chemical influences on isotopic ratios are *understood* within a systematic causal framework. Likewise, archaeogeneticists' concern with specimen contamination with modern DNA stems from understanding of the biomolecular processes by which the proxy is related to the object of investigation. The next sections outline principles of these methods and offer examples of their applications.

23.1 Bone Stable Isotopes, Diet, Mobility

Isotopes are variants of an element that have the same numbers of protons but differing numbers of neutrons, and hence different atomic masses (Sulzman 2007). Stable isotopes are non-radioactive variants, for example, ^{12}C and ^{13}C versus radioactive ^{14}C. These generally behave similarly in forming molecules and compounds with other elements, but they do display subtle divergences in how they function in chemical processes according to their differences in atomic mass. These subtle divergences in isotope uptake during geochemical, meteorological, and physiological processes form the basis of stable isotope analysis. Pioneering research used the ratios of stable oxygen isotopes ^{18}O to ^{16}O to investigate long-term changes

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in ocean temperatures and, by extension, global paleoclimate (Emiliani 1958; Shackleton 1967, 1968). Shells of Foraminifera, protozoan plankton that grow calcium carbonate ($CaCO_3$) exoskeletons, preserve the oxygen isotope ratios in the seawater surrounding them when they build their shells. Researchers found variations in the ratio of ^{18}O to ^{16}O (the most common stable isotope) in foram shells from deep sea cores, when compared to a modern ocean water standard. Shackleton (1967) detailed the relationship of the proxy to its context of production: the varying ratios reflected the differentially greater uptake of lighter ^{16}O over ^{18}O via evaporation from the sea and other waters and its precipitation into ice sheets, where it was sequestered during glacial maxima, leaving proportionately more ^{18}O in the oceans where the forams were building their shells. Thus, relatively less ^{16}O in the $^{18}O/^{16}O$ ratio in foram shells would reflect colder, glacial conditions, whereas relatively more would reflect warmer seawater conditions. Systematic coring of marine sediments and glacial ice, radiometric and geomagnetic reversal chronology, and analysis oxygen isotope ratios has enabled a chronology of global climate change millions of years long (see Wright 2000 for Marine Isotope Stages).

In the 1970s, advances in mass spectrometry combined with findings on stable carbon isotope ratios in major plant groups to provide new insights into ancient human diet. Archaeologist and geochemist van der Merwe proposed that the prehistoric introduction of cultivated maize, a tropical grass with a distinctive carbon isotope ratio, into temperate North America should produce a shift in carbon isotope ratio "signatures" in the bones of people who up to that time had consumed mainly temperate woodland products. Diachronic analyses of cemetery populations from the Midwest confirmed a shift in $\delta^{13}C$ values – and hence diet – about the time archaeobotanical evidence indicated the introduction of maize (van der Merwe and Vogel 1978).

This led to a proliferation of carbon and nitrogen isotopic analyses of human bones from many temporal and geographic settings (Lee-Thorp et al. 1989, 1994; Ambrose and DeNiro 1986; Lambert et al. 1979; Schoeninger 1979; Schwarcz et al. 1985; Tauber 1981; Walker and DeNiro 1989), as well as refinement of the technique. Bone is more liable to chemical alteration by diagenetic processes Chap. 16), and dental enamel is preferred (Koch 2007). Initially, one sample per individual was considered the norm. However, researchers later began exploring the possibilities of constructing individuals' "osteobiographies." This approach juxtaposes isotopic analysis of teeth and bone with data on deciduous and permanent tooth formation with different bone tissue turnover rates – ribs, for example, replace bone tissue more quickly than do femora – to sample across the body, charting changes in diet and place of residence from childhood through a few years before an individual's death (Sealy et al. 1995; Schroeder et al. 2009).

Stable isotope ratios are measured as R, where R is the heavy/light isotope ratio for a particular element, against the R of a standard reference sample for the element, times 1000.

$$\delta(‰) = ((R_{sample}/R_{standard}) - 1) \times 1000$$

This ratio is written ‰, or "parts per mil."

23.1.1 Carbon Isotope Analysis

Like radioactive radiocarbon (^{14}C), stable carbon isotopes enter plant tissues from atmospheric CO_2 through photosynthesis, then moving into tissues of herbivores and ultimately to carnivores (Koch 2007). Carbon-12 (^{12}C) is the most common (98.9% of stable carbon) stable carbon isotope; ^{13}C comprises 1.1% of stable carbon. Carbon isotope dietary research is based on the recognition that three major groups of terrestrial plants fix carbon into their tissues differently during photosynthesis, in the process incorporating divergent proportions of the two stable carbon isotopes (O'Leary 1981). The C3 physiological pathway includes trees, shrubs, and temperate grasses and is thought to be ancestral to the C4 photosynthetic pathway (Ehleringer and Monson 1993). C4 plants are primarily tropical grasses. The third photosynthetic pathway, the CAM (Crassulacean Acid Metabolism), is typical of succulent plants.

The first step of building plant tissue in the C3 (Calvin-Benson cycle) photosynthetic pathway gives the pathway its name. Atmospheric carbon dioxide is taken in by the plant and fixed, via reaction with a catalyst, into phosphoglyceric acid, a *three-carbon* acid. The first step of the C4 (Hatch-Slack cycle) chemical uptake of atmospheric CO_2, results in oxaloacetate, a *four-carbon* acid (Ehleringer and Monson 1993). In physical and biological reactions involving atmospheric carbon dioxide, a bias against uptake of heavier $^{13}CO_2$ molecules plays out because this molecule has slightly stronger chemical bonds than do $^{12}CO_2$ molecules (O'Leary 1981). This disproportionate uptake of stable isotopes, relative to their abundances in a source – in this case the air – is called *fractionation*. Plants using the C3 pathway discriminate relatively more against ^{13}C, resulting in tissues with proportionately less ^{13}C, than do C4 plants. Thus, C3 plants have less ^{13}C in their issues than do C4 plants, which in turn affects their stable carbon isotope ratios. C3 plants have $\delta^{13}C$ values averaging −28‰, while C4 $\delta^{13}C$ values average −13‰. CAM photosynthesis somewhat resembles that of C4 plants, but, because these plants are seldom part of the human food chain, these will not be detailed here (see O'Leary 1981 for details; Ehleringer and Monson 1993). Persons working with human dietary reconstructions in areas known for consumption of cactus leaves and fruit should be aware of the effects of CAM foods on isotopic signals. The standard for $^{13}C/^{12}C$ ratio was Carolina PeeDee Belemnite, which is now exhausted, so the Vienna-PDB is used instead (Koch 2007).

For stable carbon isotopes, the calculated ratio is written as $\delta^{13}C$. As a proxy for plant diet, $\delta^{13}C$ is clearly defined because the pathways of carbon isotopes in plants are well understood, as well as are the processes that transfer plant food carbon isotopes into tissues of primary and secondary animal consumers, or through the longer trophic chains of marine consumers, which are also relatively well understood (Koch 2007). Primary producers in marine environments vary in their concentrations of ^{12}C and ^{13}C, depending upon the overall productivity of the marine environment, on the specific ocean current regime, and on their location in the nearshore–offshore spectrum (Koch 2007). If these factors can be controlled, the locations of primary, secondary, etc. consumers' foraging relative to land masses can be reconstructed (Clementz and Koch 2001).

In human dietary analysis, as with analysis of any omnivore's diet, the signal becomes somewhat more ambiguous, because each food provides its own carbon ratios, and proportionate inputs from different foods can vary. An extensive literature now exists on how best to deal with admixture of foods in the diet (e.g. Newsome et al. 2004; Pilot et al. 2012). Carbon isotope ratios have been shown to fractionate up trophic levels but only about 1‰ in bone collagen with each trophic level (DeNiro and Epstein 1978; Schoeninger 1985). This increment is too small to be accurately used to evaluate consumers' trophic levels, however, nitrogen isotopes can be used to do so.

23.1.2 Nitrogen Isotope Analysis

Proportions of stable nitrogen isotopes, ^{15}N and ^{14}N, have been used to specify animal food inputs and terrestrial versus marine foods (Sealy and van der Merwe 1988; Schoeninger and DeNiro 1983; Schoeninger and Peebles 1981; Walker and DeNiro 1989). Nitrogen enters the food chain at the level of plant primary producers, which obtain it from the soil in which they grow. Levels of nitrogen, especially ^{15}N, vary with overall soil chemistry, as well as with the presence of nitrogen-fixing plants, such as legumes, and their bacterial symbionts. Therefore, local baseline values must be obtained for local terrestrial environments. Nitrogen enters primary producers in marine environments via a different pathway, which produces a distinctive $\delta^{15}N$ marine signature.

Animals obtain nitrogen almost exclusively from the protein they ingest. The proteins are then broken down into amino acids, complex molecules that include carbon, oxygen, and hydrogen (carboxyl groups) bonded with nitrogen and hydrogen units (amino groups), as well as "side chains" of carbon and hydrogen. Animals' physiological breakdown of proteins and use of amino acids differentially fractionates the two nitrogen isotopes. In this case, fractionation in animal tissues takes up more of the lighter ^{14}N isotope than the heavier ^{15}N, the lighter isotope being differentially excreted in urea. This process enriches the proportion of ^{15}N in an organism's tissues, compared to that in its protein intake. As the proportion of ^{15}N in the body consistently increases, $\delta^{15}N$ at each trophic level increases by about 3‰. This permits researchers to assess trophic levels occupied by extinct organisms or the amount of animal protein in an omnivorous organism's diet. In marine ecosystems, a latitudinal gradient in nitrogen isotopes at the level of primary production also exists, which permits estimation of the latitude where an animal foraged, if other parameters can be controlled. Animal species with high-protein diets use amino acids and the nitrogen they contain differently than do animals with low-protein diets (Koch 2007). Therefore, some knowledge of the actual physiological linkages of this proxy in "target" species is necessary.

Nursing mammals display a $\delta^{15}N$ isotopic signature 3‰ above that of their lactating mothers, given that they are literally consuming her tissues, in the form of breastmilk. Biological anthropologists interested in the weaning ages of different

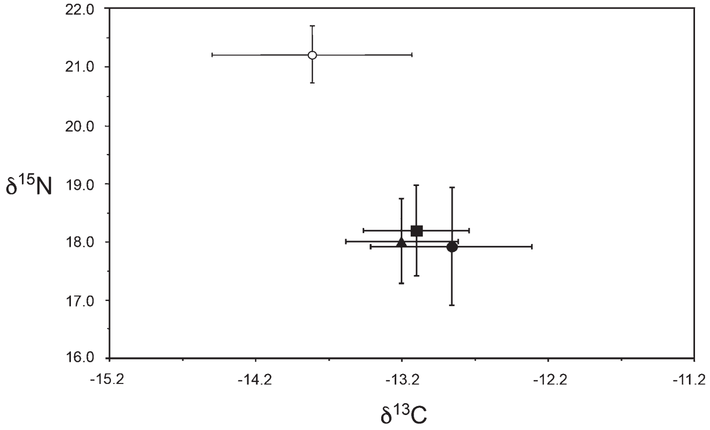

Fig. 23.1 δ15N plotted against δ13C values for northern fur seal (*Callorhinus ursinus*) specimens recovered from CA-MNT-234, the Moss Landing Hill Site showing nursing pups (open circles) are 3‰ higher in δ15N than are adult females (closed squares). Also depicted are juveniles a little over a year old (closed circles) and older subadults (closed triangles). (Redrawn by the author from Burton et al. (2001:111, Fig. 1), with permission of the R. Burton and Springer)

human populations and pre-modern hominins have analyzed $\delta^{15}N$ isotopic signatures of teeth that typically develop during early childhood (Richards et al. 2009; Oelze et al. 2011). Using the same analyses zooarchaeologists have examine livestock (Balasse and Tresset 2002) or other species' weaning patterns (Newsome et al. 2007, Fig. 23.1).

Analyses of human bones have combined stable carbon and nitrogen isotope analysis in surveying cemetery samples to assess whether elite versus lower-ranking individuals had different diets, as has Gerry (1997) with elite versus commoner diet among the Classic Maya (see also White and Schwarcz 1989) and Ambrose et al. (2003) with diets of those interred in Mound 72 at the Mississippian metropolis of Cahokia. At Cahokia, researchers saw clear gender differences in estimated proportions of maize to animal inputs in diet according to gender, and presumably, the rank of the individuals.

23.1.3 Oxygen Isotope Analysis

The standard for oxygen isotopes is a global O^{18}/O^{16}ratio, the Vienna Standard Mean Ocean Water (the Vienna Pee Dee Belemnite limestone is also used). More positive fractional ratios have proportionately more of the heavier and rarer isotope, while those more negative ratios have proportionately more of the lighter and more common isotope. For a clear summary of the actual technological analysis by which samples are assayed for their isotopic ratios, see Sulzman (2007). The same oxygen isotopes used in marine paleoclimate research have been used in different contexts, albeit with some complications, to characterize dietary intake, climate, seasonality, and, by extension migration to habitats characterized by different $\delta^{18}O$ regimes. In purely geological-meteorological systems, processes of isotopic fractionation are well understood, with evaporation leaving relatively more ^{18}O than ^{16}O behind in the evaporating water, although the water vapor in clouds does contain another, relatively predictable amount of ^{18}O in its molecules (Gat 1996). *Meteoric water*, that is, water deriving from precipitation, can vary in $\delta^{18}O$ values, depending upon a complex set of interactions: the initial condensation of water vapor into precipitation favors heavier water molecules, so that the first rain, snow, or sleet to fall is relatively enriched in ^{18}O, while later precipitation in the same event is isotopically lighter. Rainfall patterns are not random and somewhat predictable: land, especially mountains, close to the first landfalls of water-rich air masses moving in from large bodies of water will, by virtue of their lower temperatures, provoke condensation and precipitation, whereas zones farther inland will receive less, and relatively isotopically lighter, precipitation (Gat 1996). Thus, it is possible to predict to some degree where isotopically heavier versus lighter precipitation is likely to fall. Seasonal variations are also relatively clearly reflected in $\delta^{18}O$ values of precipitation collected at weather stations, and researchers have identified at least some of the major drivers of these variations in the marine evaporative and precipitation cycles (Gat 1996).

Notwithstanding these variations in the $\delta^{18}O$ composition of precipitation (see Gat 1996 for more details), by virtue of its evaporative origins, meteoric water is generally lighter in ^{18}O than is seawater. Gat (1996) points out that ^{18}O enrichment of meteoric water can occur if it travels through dissolvable bedrock enriched in that isotope, such as phosphate-rich rocks. Meteoric water in lakes where evaporative processes have outpaced fresh meteoric inputs will display heavier $\delta^{18}O$ values, as more ^{18}O is "left behind" in the unevaporated water. However, all of these geological and meteorological processes are stable enough that $\delta^{18}O$ ratios can be used to monitor past variations in cooler/moister versus warmer/drier phases in geological history (e.g. Ricketts and Johnson 1996). In other words, the functional linkages between the "target" of interest and the proxy are reasonably well understood.

When oxygen isotopes are taken into animal tissues, an additional fractionation is added. Oxygen isotopes are taken up into bioapatite phosphate, as well as carbonate and calcium carbonate, all of which derive from body fluid (Koch 2007). Experimental observations have stipulated some of the sources of variation. Oxygen isotope fractionation in homeothermic mammals' phosphates in bioapatites remain consistent at about 18‰, while that in carbonates in bioapatite is lower 8‰ (Koch 2007). Thus, the *physiological* aspect of isotopic uptake of environmental oxygen isotopes in mammal bodies is relatively well understood. As with other isotopic signatures in vertebrates, dental enamel is the most stable record of ambient conditions.

The proportionate transfers of oxygen isotopes into the mammalian body depend on the sources of $\delta^{18}O$. Over half of oxygen uptake by terrestrial mammals is through drinking water and the water in foods, and no fractionation occurs during uptake. Inhalation of atmospheric oxygen and water vapor during respiration does result in fractionation, with differential uptake of ^{16}O, while exhalation, sweating, and excretion take oxygen from the body, with the first two fractionating in favor of loss of ^{16}O (Koch 2007). Meteoric water is the main source of drinking water most modern mammals, and, as noted above, $\delta^{18}O$ values will be expected to vary geographically and seasonally. The larger the body of fresh water from which they drink, the less seasonal variation will be recorded in $\delta^{18}O$ values. Thus, archaeologists interested in using $\delta^{18}O$ values to reflect seasonality must know a good deal of the physical geography and hydrology of the target region.

Finally, the habitual dietary water sources of herbivore species will affect $\delta^{18}O$ values. Leaf water $\delta^{18}O$ values are higher in C3 plants than in C4 plants, and among C3 plants, higher in dicot plants than in grasses (Koch 2007). This means that interspecies variations in browsing versus grazing habits of the primary consumers (herbivores) may be considerable. Prudent studies of seasonality based on $\delta^{18}O$ therefore focus on a single species within a restricted region, where drinking and plant sources of water can be controlled, as was the case with studies by Balasse et al. (2003).

Given all these considerations, oxygen isotopic analysis of terrestrial vertebrate remains best proceeds with a thorough understanding and explicit description of the boundary conditions for its application within the geographic, temperature, precipitation, forage and other influences on the samples under study.

In an application of oxygen isotope analysis to humans, White et al. (2002) used $\delta^{18}O$ in dental enamel to explore the regions of origin of persons exhumed from under the Temple of the Feathered Serpent in Teotihuacán's Citadel area. Their analysis built upon known $\delta^{18}O$ values for bioarchaeological dental enamel in humid lowland regions of Mesoamerica, which display relatively lower $\delta^{18}O$ values, in comparison to relatively higher $\delta^{18}O$ values in persons from the drier highlands, including ancient inhabitants of Monte Albán and Teotihuacán. White et al. found that most warriors, so identified from their body decorations and associated weaponry, interred in the mass inhumation had formed their teeth in humid lowlands and moved to Teotihuacán as adults. By contrast, most of the women put into the mass burials displayed local $\delta^{18}O$ values, reflecting their having lived in or near Teotihuacán their entire lives. Male individuals from the central part of the temple, assumed to be high-ranking personages, were much more variable in their personal histories of mobility.

23.1.4 Isotope Analysis and Zooarchaeology

Isotopic analysis of human tissues can reveal what a person actually ate, in contrast to the coarser resolution supplied by archaeofaunal and archaeobotanical evidence available at a site, but which may not have been equally accessible to all. One may well ask, why go to all the trouble of zooarchaeological analysis, if we can just find out what people ate by analyzing their bone chemistry? Amidst sorting a 10,000-specimen faunal assemblage, this question may seem particularly compelling. Some good reasons exist why isotopic analysis does not supersede zooarchaeological analysis. Most importantly, human skeletons are not that readily encountered nor used for stable isotope analysis. Not all archaeological sites that yield faunal remains also have burials. Not all burials can be used for isotopic analysis: descendant communities may be in the position to ban the destructive analysis involved in isotopic research, if they believe that it treats ancestral remains disrespectfully. Although bone isotope analysis can reveal, for example, proportions of terrestrial and marine animal foods in the diet, it cannot specify the species actually taken and processed. Finally, isotopic studies cannot shed much light on the handling of animal bodies prior to their death or after. Only zooarchaeological analysis of pathologies, bone modifications, and refuse disposal practices can elucidate these topics.

Ideally, archaeofaunal data can be read in a dialogue with the bone isotope data, to ask if there are radical departures from expectations generated by one dataset in the results of the other. Zooarchaeologists may note varying taxa in different houses' trash, but seldom can determine the extent to which social or economic barriers restricted members of specific social or gender classes from regularly consuming animal products or plant products they processed, but bone isotope analysis can do so. Stable isotope analysis of *archaeofaunal* samples has proliferated as a normal practice in zooarchaeology, and only a few cases will be discussed here. Noe-Nygaard (1988) assayed isotopic composition of domestic dog bones from Danish sites spanning the transition from Mesolithic hunting-gathering subsistence to food-production. Because of dogs' commensal relation with humans, she used them as proxies for human diet, in effect substituting for human bone not recovered from the middens. Stable isotope ratios in dog bones changed diachronically, reflecting subtle dietary shifts in the transition to domesticates not definitively indicated by other evidence. White et al. (2001) examined dog and deer bone isotopes from refuse at the Classic Maya site of Colha. Results showed that dogs ate a predominantly C4 pathway plant food diet (probably maize), reflecting both their intimate dependence on human provisioning, and, since most died at about 1 year of age, that they seem to have been raised as a meat source. By contrast, deer bones from Colha reflected a C3 pathway diet, typical of deer's natural wild browsing. Later research distinguished a few deer at other Maya sites that appear to have been heavily provisioned with maize or that were set to feed heavily on cultivated land, perhaps in preparation for religious ritual in which they were sacrificed (White et al. 2004).

A research group of which I was a member used bone stable isotope ($\delta^{13}C$, $\delta^{15}N$) analysis to explore why northern fur seal (*Callorhinus ursinus*) remains were common in central coastal California sites up to about a thousand years ago, then vanish from the region's archaeological record. Many present-day female *Callorhinus* forage about 8 months year at middle latitudes off Oregon and California, never coming ashore unless ill or injured. They go north to breed in the Pribilofs and Siberian islands, where they feed offshore for the 4 to 6 months they nurse their young. Though most *Callorhinus* today follow this pattern, in 1968, the species re-established a breeding colony on San Miguel Island, off Santa Barbara, California, having been wiped out there by commercial sealing in the 1800s (Peterson et al. 1968). In the early twenty-first century, fur seals re-established a breeding colony on South Farallon Island, due west of California's Golden Gate, where they had been extirpated in the 1820s (Pyle et al. 2001; Martin 2006).

Using modern stable carbon isotopes from reference samples of modern fur seals and near-shore foraging harbor seals (*Phoca vitulina*), Koch and Burton established that archaeofaunal fur seals displayed an offshore carbon signature, and like modern conspecifics, they foraged far from land (Newsome et al. 2007). Koch and Burton also sampled harbor seal and California sea lion (*Zalophus californianus*) museum specimens from points between Alaska to Mexico to assess whether pinniped $\delta^{15}N$ values reflected foraging latitude, establishing that isotopic variation exists (Burton et al. 2002). Female archaeofaunal specimens showed divergent $\delta^{15}N$ values from those of modern, Pribilof-breeding females, with values closer to those of Miguel Island females, which do not feed or breed in the far north Pacific. The $\delta^{15}N$ values implied that the archaeological females from central Californian coastal sites came ashore to breed in the region, placing them and their pups at risk of predation by hunters. Measurements of central Californian *Callorhinus* young-of-the-year suggested these were below weaning age (Etnier 2002), which was confirmed by their 3‰ enrichment of $\delta^{15}N$ above maternal values (Fig. 23.1). Newsome and Etnier expanded isotopic studies of archaeofaunal *Callorhinus* samples to far northern California, Oregon, Washington, British Columbia, and Alaska, where northern fur seals were present later than in central California. Isotope values suggested the past existence of two fur seal populations, one foraging and breeding along the California and Oregon coast, and one circulating north from the Olympic Peninsula with multiple breeding sites south of the Aleutians (Newsome et al. 2007). A study of the fall-off in 3‰ $\delta^{15}N$ enrichment in weaned young suggested that young at the latter sites were weaned later than do those in the far northern islands do today.

Summing up, stable carbon and nitrogen isotope ratios indicate that northern fur seals formerly had a different biogeography ago than in any historically recorded time, and that something changed around a millennium ago for animals along the coast of California. Explanatory hypotheses for this shift include human overcropping (Whitaker and Hildebrandt 2011), effects around the time of the Medieval Climatic Anomaly, when California was subject to prolonged drought (Jones et al. 1999), or termination of the mid-Holocene Neoglacial and reopening of the higher-productivity Bering Sea for breeding colonies (Crockford and Frederick 2011; Gifford-Gonzalez 2011).

23.2 Genomics, Domestication, Biogeography

While not without its own interpretive controversies (see Marshall et al. 2014), genomic analysis offers another strong set of proxies to zooarchaeologists investigating the evolutionary and biogeographical history of wild or domestic species. DNA analysis has greatly improved zooarchaeological research on actual genetic affinities of morphologically similar species, patterns of intraspecific population replacement from past to present in various regions, and animal domestication. Before examining applications of genomics to zooarchaeologically relevant questions, a review of basic terms, processes, and analytic approaches is useful.

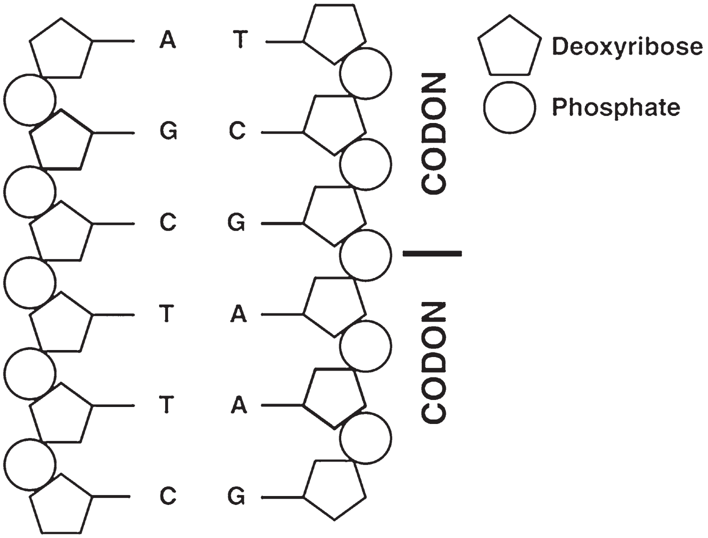

Fig. 23.2 DNA strand, showing an "unzipped" double row of nucleotide bases and the possible pairings of the bases and two three-base pair codons. The nucleotide bases consist of a deoxyribose sugar, phosphate, and a nitrogenous base. Key: A-adenine; T-thymine; G-guanine; C-cytosine. The first two only bond with each other, as do the second two (From Campana et al. (2013):24, Fig. 1). Used with permission of the D. Campana and Springer)

23.2.1 Terms, Processes, and Analyses

The famous "double helix" of DNA, or deoxyribonucleic acid, is made up of made four nucleotide bases, each comprising a deoxyribose sugar and a phosphate, plus a nitrogenous base. In DNA, these four nucleotide bases are cytosine, guanine, adenine, and thymine, abbreviated as C, G, A, and T, respectively (Fig. 23.2). Each of these bases bonds with only one of the others, forming "bridges" between the two spiraling strands of the double helix: adenine bonds with thymine, and guanine bonds with cytosine (Hartwell 2011). Eukaryote cells, including those of mammals, have a nucleus, which contains the DNA (*nuclear* or *nDNA*) comprising most of the DNA in the organism. Nuclear DNA contains the codes, three base pair units called *codons*, which direct specific amino acid and protein synthesis, building living tissue and determining its function. These are flanked by "start" and "stop" codes that regulate the syntheses (Matisoo-Smith and Horsburgh 2012). Some codons are promotor regions, which regulate lower-order tissue synthesis and function (Hartwell 2011). Much nuclear DNA seems to serve neither function and is often called "junk DNA," although this term may reveal more of our ignorance of gene function than the non-functional role of these codons. Nuclear DNA is considered to be the focus of selection, and mutations at the regulatory level are seen as key to the rapid morphological changes seen during domestication (Zeder et al. 2006). Nuclear DNA is "packaged" into dense bodies called chromosomes, which, except for the X and Y sex chromosomes, exist in pairs (homologous chromosomes), one derived from each parent. Numbers of chromosome pairs vary with species.

Nuclear DNA replicates itself with ribonucleic acid as messenger RNA (mRNA), via *transcription,* in the process traditionally called *mitosis*. In transcription, the double helix unzips the bonds between the bases, and RNA builds on the open bonds with the same bases, except that uracil substitutes for thymine. Transcription produces the mRNA copy of the gene replicated, which then structures the assembly of new amino acids in the order of the original DNA, in a process known as *translation*. Translation is facilitated by ribosomes in the cell's cytoplasm and another form of RNA, ribosomal RNA (rRNA). In contrast to one-celled organisms, eukaryote translation is more complex because cell walls separate the nuclear DNA from the ribosomal bodies that synthesize the proteins coded by mDNA (Hartwell 2011). The processes involved are intricate, involving sequences of triggering and dampening chemical reactions. During these multiple steps, errors in transcription or translation can occur, which may produce mutations.

Transcription errors transmitted to later generations are those that occur during *meiosis*, the unique process leading to specialized sex cells called *gametes*, the sperm and ova. In meiosis, the cell nucleus first divides in two, somewhat like with mitotic division, producing two cells with the full (diploid) complement of chromosomes in their nuclei. In contrast to mitosis, the two daughter cells divide again, partitioning halves of each homologous chromosome pair into separate nuclei and cells containing half the normal complement of chromosomes, the *haploid* condition. Genetic diversity can emerge two ways during the initial phase of meiosis. First, *crossing-over* can occur, as a section of one parent's homologous chromosome swaps with the corresponding section of the other parent's chromosome. This *recombination* produces a novel set of codons on each chromosome. Second, nonhomologous chromosomes sort independently of one another, that is, a single daughter cell can include some halves of chromosomes pairs from the mother and other halves from the father. With the second cell division into four haploid cells, one gamete could thus include some maternal and some paternal chromosomes.

Another type of DNA important in genetic research is located outside the eukaryote cell nucleus, in mitochondria. This is referred to as mitochondrial DNA or *mtDNA*. While passed from a mother to both her male and female offspring, it is only transmitted through the female line. Mitochondria are quite numerous in most eukaryotes' extra-nuclear cytoplasm and have been called the powerhouses of the cell, because they use glucose to produce adenosine triphosphate (ATP), the energy source for cell activity. They are considered *endosymbionts*, having originated as independent aerobic bacteria that were engulfed by early cells with nuclei (Hartwell 2011). DNA of a single mitochondrion replicates itself in a way more like that of one-celled organisms and is highly diverse. Mitochondrial DNA is not thought to be directly under selection, a trait that makes it advantageous to use in studies of evolution (Bruford et al. 2003). In mammals, the control region of the mtDNA's roughly circular, D-loop mutates more swiftly than does nuclear DNA, which allows the relatively short-term evolutionary changes on the scale of mammal domestication to be monitored. Analyses of mtDNA initially used segments of the D-loop, but whole-genome of mtDNA analysis is now possible.

Several terms commonly used in genomic analysis also require definition. A *single-nucleotide polymorphism* (SNP) is a codon in which one of three base pairs – G-C, C-G, A-T, T-A – differs from codons of other members of the same species. It is the simplest form of polymorphism. It may code for different amino synthesis, but most SNPs have no such effect. They are useful in tracing relationships of common descent and differentiation (Hartwell 2011).

A *haplotype* is a string of related codons at a specific place, or locus, on a single homologous chromosome that function as a "gene," that is, they code for a specific protein or function. They can be as small as a one locus, single-nucleotide polymorphism (SNP), or as large as an entire chromosome. Haplotypes are transmitted as units during replication processes. The term is a contraction of "haploid genotype" (Hartwell 2011). A species may have only one haplotype for a trait, or, due to base pair changes, there may be variants for the trait, called *alleles*.

A *haplogroup* (or *clade*) is a group of similar haplotypes that derive from a common ancestor with a single nucleotide polymorphism mutation.

Nuclear *microsatellites*, or tandem repeats, are short sequences of nucleotides that are both paternally and maternally inherited and repeat variable numbers of times in the DNA sequence of base pairs. Over time, these may increase or decrease in number, apparently neutrally with relation to selective forces. They can be distinctive to regional populations and thus are particularly useful in tracing the domesticated animal movements from their regions of origin to other areas.

A *genome* is the sum total of a given species' genetic information. Genomics is the study of all aspects of such information.

Y-chromosome analysis involves comparisons of the diversity in the male sex chromosome, which passes through the father's line. Because the Y-chromosome is nuclear DNA, it is relatively rarely retrieved from ancient tissues. As noted earlier, it is complemented by *mtDNA* analysis to assess similarities, differences, and common descent through the paternal and maternal lines, respectively. This has proved especially useful in tracing introductions of domestic animal males or females into new areas (see next section).

Ancient DNA (*aDNA*) analysis provides insights into animals' genetic diversity in the past, allowing study of now-extinct ancestral populations and sometimes revealing now-extinct branches of extant species. It relies on analysis of genetic material extracted from bones, teeth, or eggshells. Ancient DNA research suffers from several impediments. DNA degrades over time, shortening the lengths of the fragments of recoverable bases, and thereby challenging base pair amplification in the laboratory. Varied environmental conditions, can hasten DNA deterioration, and arid zones are generally unfavorable for DNA preservation (Campana et al. 2013). Various contaminants can enter DNA samples, in both field and the laboratory, including penetration of fungal and bacterial DNA into archaeological specimens in their depositional contexts (Chap. 15) and contamination by modern DNA during retrieval and laboratory preparation.

Ancient DNA analysis relies on *amplification* of genetic materials. Until recently, this involved variants of the *polymerase chain reaction* (PCR) method, developed in the mid-1980s (for a history of this and earlier methods, see Matisoo-Smith and

Horsburgh 2012 or Hartwell 2011). PCR made it possible to isolate small segments of DNA and reproduce numerous copies of them in a gel, using artificial heat cycles to instigate replication and providing the chemical raw materials for the replications. Over time, the PCR process became more intensively automated, but it always required a substantial amount of human labor in the transfer of the original DNA segments to their replication matrix. It has been widely used in forensic investigations, where DNA is often recovered in degraded form, as well as in research on the genetics of disease and the phylogeny of species. PCR allowed researchers to extract degraded DNA from ancient bone or other biological tissues and to determine the genetic sequences present. The first “targets” of such ancient DNA research were shorter nucleotide strands such as SNPs and microsatellites, as these would often be preserved in short lengths of degraded DNA.

By the late twentieth and early twenty-first centuries, laboratories experimented with reliably sequencing and reading entire genomes of common lab organisms such as *Escheria coli*. The Human Genome Project pioneered “high throughput” laboratory instrumentation, with computer programming suited to reading masses of biochemical sequencing output and constructing coherent digital versions of it. In the early 2000s, such sequencing took months of complete, even with entire DNA samples, and was intensive of labor and resources and hence expensive. The high-throughput approach did permit, for example, sequencing the Neanderthal genome (Green et al. 2010). Emergence of a range of next-generation sequencing (NGS) methods in the late 2000s rendered whole-genome sequencing of relatively cheap and reliable (Matisoo-Smith and Horsburgh 2012), and permitted swift study of targeted parts of genomes in biomedical research. NGS techniques involve recovering, labeling, and amplifying DNA on a massive scale, largely automatically after preliminary sample preparation. Some approaches continue to use PCR. Others use newly devised biochemical means of isolating target DNA within much larger assemblages of genetic materials (Koboldt et al. 2013). Presently, many different commercial technologies are available, with high degrees of reliability in controlled tests, but considerable variance in cost. The next few years will doubtless see more standardization in these approaches. Koboldt et al. (2013) stress that NGS methods all rely upon the prior existence of reference sets of species genomes, with which genetic segments can be identified.

23.2.2 Animal Domestication Research in Zooarchaeology

Research on animal domestication has benefited tremendously from the emergence of genomics and a truly global approach to the genetics of modern, economically important species and breeds. Genomic research has focused on domestic species because of their commercial uses, while wild species have been less well studied. Data derived from modern breed research provides insights into early domestication, and aDNA of the same species has refined ideas derived from surviving lineages. This section provides some examples of how genomics has revolutionized zooarchaeological research on domestication.

Formerly, animal domestication was the sole research province of zooarchaeological, and most frequently, European archaeozoological, research. Investigations relied upon osteometrics and distinctive non-metrical morphological traits thought to be distinctive of certain regional populations. However, many problems attended these efforts (Zeder 2001; Zeder and Hesse 2000). Analysis of living domesticates' mtDNA and Y-DNA has produced a clearer picture of where and how many times members of a wild species moved into domestication. Results of this research have prompted rethinking of initial assumptions about domestication processes. For example, domestic animals of any given species were expected to have only one or two mitochondrial lineages. Yet horses, goats, sheep, llamas, and alpacas have multiple maternal lineages, and substantial interbreeding of domestic llamas with alpacas is evident (Naderi et al. 2008; Meadows et al. 2007; Bruford et al. 2003; Barreta et al. 2013).

Multiple mtDNA lineages were initially interpreted as reflecting independent, geographically distinct domestications that later coalesced as agrarian systems expanded. It was more recently proposed that this results from intentional recruitment of wild females into early domestic herds (Marshall et al. 2014), challenging the long-held idea that domestication occurs only under reproductive isolation from wild conspecifics. Marshall et al. also propose that, rather than a one-size-fits all model for domestication, zooarchaeologists and archaeogeneticists must understand how the behavior of specific classes of domesticates affect domestication trajectories, a point also raised by Zeder (2012). Dogs and cats, also displaying multiple mtDNA lineages, may have come to domestication as commensals rather than prey (O'Brien et al. 2008; vonHoldt et al. 2010; Ottoni et al. 2017).

Mitochondrial and Y-chromosome DNA of living domestic breeds and, in fortunate cases, aDNA (thus far, nearly always mtDNA) from archaeofaunal specimens can be used to trace the history of domestication in space, and through time (*phylogeography*). Haplotypes indicate that cats came under domestication twice, once in Southwest Asia around 10,000 years ago and millennia later, in Dynastic Egypt (Ottoni et al. 2017). Ancient DNA has the advantage of revealing lineages of wild or domestic species that no longer exist. For example, aDNA from the palaeolithic dogs noted above showed these were not related to any living dog population. Donkeys comprise two mtDNA lineages, one of which represents the Nubian wild ass and the other an extinct population most like, but not identical to, the Somali wild ass (Kimura et al. 2011).

Genetic evidence can offer insights into livestock management (Marshall et al. 2014). Ottoni et al. (2017) argue that maritime trade in the Classical Mediterranean world, and that between the Roman Empire and South Asia, facilitated the spread of domesticate cats, probably as ship's cats as well as in their more traditional role in farm pest control. DNA analysis significantly revised the history of pig management in Europe. The wild ancestors of domestic pigs were widespread across Eurasia and North Africa, and haplogroups indicate a least six local domestications from regional Asian and European populations (Larson et al. 2005). Pigs were domesticated in the Southwest Asia 13,000–15,000 years ago and were introduced to Europe as part of the "Neolithic package" of domesticates. Archaeologists initially assumed European domestic swine descended from this stock, but modern European domestic pigs uniformly lack Southwest Asian haplotypes, instead bearing those of native European boar . Archaeogenetics shed light on this issue: the oldest, sixth-fifth millennium BC domestic pig specimens in Europe display only Southwest Asian haplotypes (Larson et al. 2007). However, a millennium later, some specimens testify to emergence of indigenous domestic pig stock alongside imported swine (Larson et al. 2007). By the mid-fourth millennium BC, all European domestic swine sampled display European haplotypes, suggesting that European stock increased from around 5% to 100% in less than 500 years. This may suggest European pigs' greater fitness in their ancestors' native environments, but their rapid spread from the British Isles to Eastern Europe also reflects human interaction at a continental scale. Thus, genomics of domestic animals and plants can be a reasonable proxy for human interaction and exchange.

23.2.3 Applications of DNA Analysis to Wild Species

The use of wild species has also been explored with aDNA analysis. Salmon aDNA from archaeological sites along the Northwest Pacific coast was able to identify species with greater accuracy than did zooarchaeological analysis across a range of sites (Cannon et al. 2011). Cannon and Yang (2006) combined aDNA analysis with the archaeology of Namu, a long-occupied village facing the Inside Channel. Based on archaeological evidence for salmon storage plus aDNA evidence for dominant use of pink salmon (*Oncorhynchus gorbuscha*), they argued that occupational disruption may have been due to interruptions in the abundance pink salmon in the region. Speller et al. (2012) used SNP's in aDNA to explore the hypothesis that ancient herring populations in the British Columbia region were more regionally specific than recent ones subject to heavy harvesting, finding no demonstrable differences from modern populations.

Our investigation of ancient fur seal biogeography and feeding ecology showed via archaeofaunal evidence that *Callorhinus* was once more densely distributed from San Miguel Island to Unalaska Island, and, via stable carbon and nitrogen isotope analyses, that a northern and a southern foraging population existed at that time. We asked Malin Pinsky, from Liz Hadley's Stanford University aDNA laboratory to explore whether ancient northern fur seals were of a different genetic stock than modern ones, and if the northern and southern foraging groups were genetically distinct. aDNA results indicated that, like their modern relatives, archaeofaunal *Callorhinus* were part of one, heterogeneous pool of haplotypes ranging from the far north to the far south of their ranges, without geographic distinctions (Newsome et al. 2007). Individual tagged *Callorhinus* have shifted breeding sites from Pribilof and Siberian Islands to the Santa Barbara Channel and Farallon Islands. Pinsky et al. (2010) argued that the great dispersal abilities of these marine mammals have probably contributed to the species' resilience in the face of heavy local extirpation over the last few centuries. This research leads into the final topic discussed in this chapter, zooarchaeology as it can be applied to species conservation.

23.3 Zooarchaeology and Conservation

"Applied zooarchaeology" (Lyman 1996) aims to support conservation biologists in managing endangered or economically valuable taxa, by synthesizing and conveying data on species ancient biogeography and population dynamics. It emerged in the 1990s as a practical means to contribute to the field of *historical ecology*, which studies human interactions with species and landscapes over time, using all types and scales of evidence, from written documents and photographs to geological and climatic data. Jackson et al. (2001) noted that written records cover a few thousand years, and usually much less, and, to understand evolution and ecology of species with which humans have interacted for millennia, only archaeological and paleontological records offer relevant records. Several excellent sources on applied zooarchaeology exist. Lauwerier and Plug's *The future of the past: Archaeozoology in wildlife conservation and heritage management* (2004) provides a global perspective on similar matters. Lyman and Cannon's *Zooarchaeology and conservation biology* (2004) and Wolverton and Lyman's *Conservation biology and applied zooarchaeology* (2012a) offer thoughtful contextualizing analyses of the field's challenges as well as a range of case studies.

This section reviews basic themes in applied zooarchaeology, with examples from the literature and my own research experience. While applied zooarchaeology seems a worthy way of making zooarchaeology relevant to present-day problems, three issues face zooarchaeologists who wish to use archaeofaunal data in this way. One is largely methodological, another theoretical, and the last and most critical is sociopolitical. As will be seen, these issues blend into one another, so that that all communications between zooarchaeologists and conservation biologists are imbued with more political aspects than the former may initially assume.

Some definitions are useful at the outset. First, I follow Wolverton and Lyman's (2012a) use of the term *conservation biologist* to refer to persons who manage wild species or habitats. As outlined in Lyman and Cannon's introduction (2004), this group actually includes the more senior generation of "wildlife managers," who worked to conserve species that were valued economically or aesthetically, and who executed their tasks largely without recourse to an ecosystems approach. More recently credentialed conservation biologists tend to view their role as applying ecosystems-based approaches to management of species under threat from economic exploitation, pollution, and other factors. Lyman and Cannon point out that, the more interest managers have in species' long-term adaptation and ecological history, the more relevant zooarchaeological data are to them. However, as Reitz and Wing (2008:331–334) note, the differences between archaeofaunal datasets and those to which conservation biologists are accustomed require some mutual education and negotiation of expectations.

23.3.1 Requisites for Effective Applied Zooarchaeology

To give conservation biologists the information they need requires regional-scale data, drawn from multiple, well-dated and well-recovered sites. Reitz and Wing (2008:316–334) offer a nuanced discussion of a range of methodological and interpretive issues to be considered when producing reliable information for conservation biologists, as well as offering insights into why applied zooarchaeology emerged relatively late in the history of the field. Zooarchaeologists must also apply rigorous standards when assessing historical documents regarding species of interest in the region. Applied zooarchaeologists thus judiciously abstract and synthesize from ecological, historical, and archaeological literatures as well as from their own research findings.

Another major consideration is how well certain archaeofaunal samples were recovered, especially if one is dealing with smaller taxa, such as fishes, birds, and smaller mammals (e.g. Butler and Delacorte 2004; Grayson 2011). If ¼" mesh was used to screen site materials for animal remains, one's ability to tell managers about the presence, absence, or relative abundances of small taxa is compromised (Chap. 8). Some well-recovered archaeofaunas from a region could be used in conjunction with less well-recovered ones from the same regions, to provide general outlines of species representation, as has been the intention of the Arizona State Museum's FaunaAZ database (Pavao-Zuckerman et al. 2006).

Regional samples can be used to tell conservation biologists whether a species that is not present in a region now existed there earlier, when it did, and with some informed opinions on climatic or human impacts with which its disappearance coincided. Stable isotopic analysis can shed light on whether individuals of a species moved considerable distances during their lifetimes, or whether their diets diverged from what is known to characterize the modern species. With well-recovered archaeofaunal samples, or with coordinated aDNA data, zooarchaeologists might be able to offer an opinion on whether the species was abundant in an area. For some species, zooarchaeologists might use mortality profiles or presence of young-of-the-year to assess whether the species bred in the region.

A few cases can illustrate these applications. After decades of controlled sampling of Great Basin microfauna and critical synthesis of radiometric dates from many sites, Grayson (2011) could chart the fortunes of two lagomorph species, the alpine pica (*Ochotona princeps*) and big sagebrush-adapted pygmy rabbit (*Brachylagus idahoensis*), as well as various rodent taxa closely associated with specific vegetation communities. He was thus able to track a range of temperature and humidity regimes at different altitudes and various regions of the Great Basin since the Last Glacial Maximum to historic times. Grayson supplemented and contextualized his voluminous archaeofaunal data with supplemental environmental records from published pollen spectra, dated macrobotanicals from packrat middens, and other sources. Tracking the biogeography of these microfaunal species, along with larger taxa, including deer, antelope, and bison, through changing climate and patterns of human land use, Grayson (2011) was able to comment with substantial empirical support on present-day management issues. This included his inference that decline in sagebrush, widely attributed to historic overgrazing by introduced domesticates, was in fact already underway before the arrival of Euro-Americans.

Bovy (2012) used historic records and archaeofaunal remains of sandhill crane (*Grus canadensis*) to argue that early historic observations of dense aggregations of the cranes on the Strait of Juan de Fuca (northwestern Washington State) actually were breeding colonies. She placed her research findings the context of current management issues regarding the species. Rosania (2012) used bone stable isotopes to compare the diets of modern black bears (*Ursus americanus*), which are extending their range from the state of Arkansas into Missouri, where the species was extirpated in historic times. With black bear specimens recovered from a pre-Contact Missouri cave, she found no isotopic differences between ancient and modern bear diets in the same region. Crowley et al. (2012) used intensive radiocarbon dating and stable isotopic analysis to track the patterns of extinction of Madagascar megalemurs in the last 2000 years, coinciding with human colonization of the island. Among their most interesting findings is that all lemurs, including surviving ones, lived in more arid environments than those set aside as reserves for these threatened species, with management implications for sustainability of these populations.

23.3.2 Defining the Target Baseline: A Collaborative Exercise

The second major issue in applied zooarchaeology is that of the target state to which managers wish to restore ecosystems and the species within them. Most can agree that the desired state is one that existed before degradation by over-exploitation, agricultural practices, invasive non-native species, and other forms of habitat destruction. But what – and when – should that target "baseline" be, and how can zooarchaeologists collaborate in deciding this? In the Americas and Africa, for example, it is becoming increasingly clear that native peoples managed landscapes more intensively than previously assumed by biologists and ecologists. In California, for example, the open, flower-rich grasslands praised by such naturalists as John Muir may largely have been created and maintained by Native Californians, who used repeated, small-scale burning to maintain the vegetational succession at stages most useful to them for food and basketry materials (Anderson 2013; Lightfoot et al. 2013; Williams 2002). Wildlife ecologists and environmental historians now recognize African pastoralists' role in grassland maintenance by consistent application of fire as benefiting not only their herds but also wild savanna grazers (Kjekshus 1996[1976]; Homewood and Rodgers 1984; Lamprey and Waller 1990).

Given such considerations, do habitat restorers want to reset plant and animal communities toward the states in which foreign explorers encountered them? Such a goal presents its own conceptual issues and reveals how value-laden this enterprise is. Evidence from the Americas and Africa suggests that many indigenous populations crashed because of foreign diseases transmitted from colonizers along exchange systems, well *before* the first entry of European explorers into their region. This probably permitted a “rebound” in taxa formerly heavily cropped by humans, such as salmons and the wild ungulates that so impressed European explorers in western North America (Broughton 1999; Butler 2000) or in eastern and southern Africa (Kjekshus 1996[1976]; Percival and Cuming 1925). Should conservation biologists and applied zooarchaeologists aim for the “explorer encounter” state as the baseline state, or should they aim for an earlier, humanly managed landscape? If the latter, should it be the one immediately preceding disease impacts? Grayson (2011) noted that, *as the norm*, arid and semiarid regional ecosystems undergo major shifts in state within longer-term trends in climate and vegetation, probably rendering it unrealistic to aim for a very tightly defined “steady state” in such areas.

23.3.3 Conversations About Conservation: Exercises in Cross-Cultural Communication

Decisions about baselines are not simply objective, scientific ones, but rather imbued with values and preexisting views of nature, indigenous people, and even human nature. Zooarchaeologists tend to assume that defining baselines would require either paleontological or zooarchaeological data, even if historic records are available. This may be true, but they should not assume that conservation biologists, especially those tasked with the actual management of fisheries or terrestrial ecosystems, necessarily share their perspective. Lyman (1996) argued that zooarchaeologists should provide wildlife managers with rigorous standards of empirical information regarding the presence or absence of certain species in the past, to help them develop historically informed management plans. However, Lyman’s own (1998) account of trying to convince Olympic National Park wildlife managers to incorporate zooarchaeological and ethnohistorical information into their mountain goat (*Oreamnos americanus*) management policies noted that this is may not be an easy road.

Reitz and Wing (2008:333) state, “Responding to management questions requires us to teach first.” But resource managers often must respond quickly to policy initiatives and might have little patience for instruction in the classic sense.

Zooarchaeologists wishing to engage productively with conservation biologists must recognize several facts. If they do not, this is poor social science research and a recipe for ineffectuality. First, those responsible for conservation management decisions exist in an often-contradictory web of administrative directives and popular pressures from industry, indigenous, and environmental interest groups. Wolverton and Lyman (2012b:9) called this *political ecology*, “the social, political, economic, ecological, and any other sort of human-interest context in which conservation biology, restoration ecology, and landscape management occurs.” Effective communication begins with understanding their day-to-day concerns, persisting constraints, and hot-button issues.

Second, if conservation biologists have any narratives about premodern resource use, these come from popular publications that many professionals find problematic. For example, the idea of the "tragedy of the commons" publicized by Hardin (1968), argued that any resource, but especially land, held in common is inevitably overexploited and degraded. This was uncritically assimilated into many fields, including rangeland and fisheries management and used to justify radical "reforms" of East African pastoralists' land tenure and grazing systems, traditional fishing practices in the European Atlantic, and other resource uses, without empirical research into local management systems. Research by human ecologists, anthropologists (McCabe 1990), historians (Johnson 1993) and economists (Ostrom et al. 1999) found very few cases of environmental degradation within *traditionally* managed land or fisheries, where access to "commons" is often governed by complex, culturally enforced, unwritten policies. Reitz (2004) shared her own insights on this topic with regard to fisheries.

Third, zooarchaeologists in North America, and perhaps other settler colonies, must acknowledge that conservation biologists might have images of Native peoples either as natural conservationists or unbridled extirpators. Some books in the 2000s held Native Americans responsible for massive wildlife depopulation, from extinction of Pleistocene megafauna to wiping out large mammal communities during colonial times (e.g. Kay 2002; Martin 2002). Zooarchaeologists have used documented declines or presence/absence of species in regional archaeofaunal samples, and critically assessed fundamental assumptions of such arguments (for judicious examples of these approaches, see Lyman 2010; Nagaoka 2012). Yet, the influence of one spate of popular books or another may have to be negotiated.

Finally, because their training in biological sciences stressed other areas of knowledge, conservation biologists might not believe that osteological elements, even if well preserved, can be identified to species. Zoological experts have asked me, sometimes with genuine curiosity, sometimes in a more challenging way, whether I could really tell the bones of one species from those of another. Deep breathing, tactful responses and supporting documentation are helpful.

An example of potential difficulties comes from our team's research on the occurrence of northern fur seals in central California and farther north. We contacted experts who managed the United State stocks of the species because we hoped their knowledge would help us understand aspects of *Callorhinus* ecology could have allowed the biogeographic variation we saw in the archaeofaunas. We assumed that managers would think our findings were interesting. We were cordially welcomed to use facilities and younger male collaborators were invited to visit fur seal colonies, perhaps to test of their "fiber." But then ensued a decade of challenging interactions. Informal questions were not responded to at all or dealt with on the fly without follow-up data. Critical reviews of our submitted manuscripts and grants – we suspected by these experts – referenced largely unpublished data and recommended against publication or funding. Some criticisms forced us to be more rigorous, but we did not grasp the source of the problem until submitting a manuscript that summarized our zooarchaeological, isotopic, and genetic findings (Newsome et al. 2007). One review stated the study is important because it could set a "historical benchmark" for a top predator in the north Pacific ecosystem and complimented our thorough and appropriate application of analytical techniques – yet recommended against publication. The review stated our conclusions were not justified, nor was the work of "suitable quality." The paper's biggest problem in the reveiwer's eyes appeared to be the possible harm that our research could do if "certain groups" used our data that the species was abundant along the Pacific coast of North America in pre-Columbian timessto advocate for imprudent species restoration or other actions in the present. We were urged to "search our souls" about whether we wanted this to happen. Only then did we realize that our findings were being read through the political ecology of pinniped management, in an increasingly depleted North Pacific fishery, amidst multiple and contradictory pressures from government, industry, and interest groups. We never set out to undermine managers working in such situations, but I suspect this is how our findings and questions were perceived: as potentially destabilizing "facts" from ivory tower academics ignorant of management realities.

However, this was a learning experience for everyone. Within 3 years, perhaps associated with a changing of the guard among senior conservation biologists, members of the same management unit coauthored an article with members of our research group (Pinsky et al. 2010). It discussed management implications of ancient and modern *Callorhinus* DNA and the archaeofaunal evidence for the species' past distribution. In the wake of this experience, I realized that a more culturally and politically informed approach to conservation zooarchaeology was required. When the head of a fisheries research lab on our campus invited my graduate student researching mid-latitude Pacific fish archaeofaunas to join his lab group, I strongly encouraged her to do so. She "learned the language" and became a credible actor with her graduate student peers in fisheries research. Hopefully, with this start, she will have success in discussing the fate of fishes past and present with that community. Beyond specific examples, the take-away message for aspiring applied zooarchaeologists is to understand conservation biology takes place in a sociopolitical context, and that a bit of ethnography of "one's people" can facilitate productive conversations.

Summing up this diverse chapter, stable isotope analysis and genomics offer strong proxies for past human diet, mobility, and exchange, as well as the emergence of mutualist relations in domestication, and the place of wild species in regional ecosystems – if used with care. Using archaeofaunal data in conservation biology is possible, laudable, and at the same time makes novel demands on zooarchaeologists to grasp and negotiate mutually satisfactory communication within the "political ecology" of that community's practices.

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