Chapter 6
Niche Construction Theory and Ethnobiology

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6.1 Introduction

Evolutionary ethnobiology focuses on studying the dynamic relationships between humans and biota and uses evolutionary assumptions to construct models and hypotheses for understanding these relationships. Evolutionary assumptions are used by disciplines other than biology to understand a broad range of natural and social phenomena. Cultural phenomena are also of interest to ethnobiologists, and different researchers have proposed scenarios for the study of cultural evolution based on Darwinian reasoning (e.g., Cavalli-Sforza and Feldman 1981; Richerson and Boyd 1985).

Humans materially and symbolically appropriate nature in a manner unlike any other living organism. In addition to being the dominant species, humans have transformed the planet on a scale that continues to expand. Humans are one of the largest agents of ecological change, and the effects of these changes are still poorly understood. For example, the domestication of plants and animals has produced dramatic global transformations and affected the evolution of domesticated species as well as human populations (Larson and Fuller 2014).

Garrido-Pérez and Glasnovic (2014) argued that human actions can alter the patterns and dynamics of such diversity. When humans collect seeds, they behave as seed predators; and when they hunt animals, they promote top-down changes in the trophic structure (see Garrido-Pérez and Glasnovic 2014). These relationships can be modeled in terms of ecology, culture, and genetics.

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U.P. Albuquerque et al. (eds.), *Evolutionary Ethnobiology*,
DOI 10.1007/978-3-319-19917-7_6

Thus, by altering the environment, humans act as a powerful niche constructor. Niche construction (NC) is a process by which living beings, including humans, modify their own niches or those of other organisms through their activities and decisions. By altering their niches, organisms can also alter the natural selective pressures. The notion of NC is intuitive and there is significant evidence detailing the consequences of organismal activity on the environment (see review in Odling-Smee et al. 2003).

In general, ethnobiological researchers automatically assume that NC occurs. For example, when an ethnobiologist studies the effect of stem bark extraction on the population structure of a plant species, he or she assumes that the extraction action may alter a plant population in one or more aspects. Such assumptions are more explicit when ethnobiologists study the management of species and processes of plant and animal domestication. In the previous examples, the ecological and evolutionary impact of humans on other living beings is clear because it contributes to the creation of selective environments; however, the inference that these same practices may generate selective pressures is not usually made.

NCT is considered an interesting concept for understanding the consequences of changes that organisms produce in environments and how these modifications may have evolutionary implications. The different implications and ramifications of NC are still underestimated and poorly investigated, both theoretically and experimentally (see Laland and Sterelny 2006; Scott-Phillips et al. 2014; Matthews et al. 2014), which may be a result of standard evolutionists not recognizing NC as an essential evolutionary process with the same explanatory power as natural selection (for a discussion of the different viewpoints on the role of NC, see Scott-Phillips et al. 2014).

In this chapter, we explain how NCT can provide scenarios to test the ability of evolutionary and ecological hypotheses to describe the relationships between humans and nature (the interest of ethnobiology) and detail opportunities for further research. We also briefly argue why we believe NCT offers insights that can be useful for approaches in evolutionary ethnobiology. To illustrate how NCT can be an integrating concept in ethnobiology, we focus on classical examples available in the literature on NCT and gene–culture coevolution.

6.2 What Is Niche Construction Theory?

The idea that humans are niche constructors is not recent, and over time, it has been addressed in different ways. Certain organisms have such pronounced NC abilities that they are known as ecosystem engineers. Numerous empirical studies have emphasized the ability of these engineers to create or modify characteristics of ecosystems and generate positive impacts on biodiversity (see the meta-analysis in Romero et al. 2014). One classic example found in many studies on NCT is the ability of beavers to build a dam. Dam building not only creates a lake and affects river flow but also dramatically alters entire local dynamics. Additionally, it affects the propagation of dam-building genes, which can influence the evolution of beavers (Wright et al. 2002). Once a dam is built, future generations of beavers can still benefit from it as a legacy from previous generations. Thus, this example demonstrates an important concept in NCT: *ecological inheritance*. Therefore, niche construction occurs if at least two criteria are present: (1) "an organism (i.e., a candidate niche constructor) must significantly modify environmental conditions; (2) the organism-mediated environmental modifications must influence selection pressures on a recipient of niche construction" (Matthews et al. 2014: 247). This implies that NC can occur without influencing the evolution of an organism, but if it occurs, we have a third criterion pointed out by Matthews et al. (2014: 247): "there must be a detectable evolutionary response in a recipient of niche construction that is caused by the environmental modification of the niche constructor." Note that the niche constructor and the recipient of niche construction can be the same organism (see the above example of a dam built by beavers). Thus, NC differs from ecosystem engineering because the latter meets only the criterion 1 mentioned above.

Thus, in a broad sense, "niche construction occurs when an organism modifies the feature-factor relationship between itself and its environment by actively changing one or more of the factors in its environment, either by physically perturbing factors at its current location in space and time, or by relocating to a different space-time address, thereby exposing itself to different factors" (Odling-Smee et al. 2003: 41). Therefore, changes in time and space and the responses of organisms to these changes are included in the NC concept. The modifications performed by organisms that affect themselves and other species are not always adaptive and do not necessarily have evolutionary consequences.

The effects of NC can be positive or negative. NC effects are positive when they increase the fitness of the niche-constructing organisms, and they are negative when they reduce fitness (Odling-Smee et al. 2003; Barker and Odling-Smme 2014). However, NC does not always increase the fitness of organisms, and the effect is often better characterized by increases in the intrinsic growth and survival rates than reproductive success (see Odling-Smee et al. 2003).

Applying the abovementioned notions to humans, their legacy is observed in changes through space and time and ecological inheritance but also inherited cultural knowledge that is transmitted to future generations, which reinforces culture-mediated NC. Thus, cultural NC can operate by generating genetic changes as well as ecological and cultural changes. For example, the aggregation of people in large communities can lead to the emergence and rapid dissemination of many diseases. Humans can respond to this new selective pressure by building hospitals or developing vaccines (Odling-Smee et al. 2003). Thus, when we build a hospital, we are responding to the effect of a previous NC, and this response may damp out selection on human genetics; such a response is referred to as a counteractive cultural NC. The cultural NC usually responds more rapidly through an adaptive cultural response. However, when a cultural response does not occur, an important genetic response with evolutionary implications may occur if natural selective pressures were modified.

Table 6.1 Examples of the four categories of niche construction

	Perturbation	Relocation
Inceptive	Organisms initiate a change in their selective environment by physically modifying their surroundings e.g., emission of detritus	Organisms expose themselves to a novel selective environment by moving to or growing into a new places e.g., invasion of a new habitat
Counteractive	Organisms counteract a prior change in the environment by physically modifying their surroundings e.g., thermoregulation of nests	Organisms respond to a change in the environment by moving to our growing into a more suitable place e.g., seasonal migration

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Odling-Smee et al. (2003) proposed two basic types of NC: *counteractive* and *inceptive*. The *counteractive* (responses to externally produced changes) form involves all of the activities of niche-constructing organisms that reduce existing selective pressures or oppose changes in environmental conditions, whereas the *inceptive* (produce novel changes) purpose involves activities of the niche-constructing organisms that initiate a specific change, such as dam building by beavers (Odling-Smee et al. 2003; Barker and Odling-Smme 2014). Two other classes of niche construction also require consideration: perturbation and relocation. Perturbation occurs when a niche-constructing organism modifies the environment by either construction or destruction, whereas relocation occurs when a niche-constructing organism moves to a new location (Odling-Smee et al. 2003; Barker and Odling-Smme 2014) (Table 6.1).

Laland and Brown (2011) addressed the question of whether recent human NC is typically adaptive and argued that population growth from the Holocene to the present is strong evidence that many human characteristics remain adaptive. From an ethnobiological perspective, the manner in which humans intellectually and materially appropriate nature could be considered adaptive. Traditional ecological knowledge (TEK) is understood by certain researchers as adaptive knowledge (Berkes et al. 2000). However, despite the claim “that adaptive human behavior will be the norm and maladaptation the exception,” there is evidence that some cultural phenomena are maladaptive cultural traits (Laland and Brown 2011: 126).

Based on the transmission of TEK, many cultures have transferred information (cultural inheritance) to subsequent generations that ultimately modified their local ecosystems (Smith 2011a). However, despite the ethnobiological focus on describing the methods by which cultures have modified their environments, the term NC has not been conceptually employed to describe phenomena or theoretically employed as a framework for understanding these phenomena. There are various terms used by ethnobiologists that essentially describe human NC, including domesticated landscape, anthropogenic landscape, forest management, human-modified environments, indigenous management, traditional resource management, etc. (for additional terms employed in the literature, refer Smith (2011a, b)). According to Smith (2009), all of these terms could comfortably be included under the “general reading of niche construction.”

The adoption of NCT could offer a unifying perspective for ethnobiologists to address the relationship between people and nature. Because many ethnobiologists are interested in the management and conservation of biodiversity, Laland and Boogert (2010: 732) argued that “the properties and dynamics of ecosystems will never be satisfactorily comprehended until it is recognized that organisms do considerably more than compete with each other, eat and be eaten (i.e., engage in trophic interactions) (…). As human are enormously potent niche constructors, understanding how niche construction regulates ecosystem dynamics and affects selection pressures on other species is central to understanding our impact on the environment.”

6.3 Key Concepts of NCT

According to evolutionary biology, adaptation is a process through which natural selection molds an organism to a specific environment (Scott-Phillips et al. 2014). NCT does not focus on the evolution of organisms as an isolated process but rather as a coevolutionary process between organisms and the environment. Thus, NCT views adaptation as a complex, dynamic and reciprocal interaction between the processes of natural selection and NC through which niche-constructing organisms modify the environment (Table 6.2) (Odling-Smee et al. 2003). Therefore, organisms inherit environments through the process of ecological inheritance as well as genes. Compared with the process of genetic inheritance, ecological inheritance is transmitted by organisms through modifications to their environments; in addition, it is not necessarily transmitted by genetically related organisms but rather continuously transmitted by multiple organisms to other organisms within and between various generations (see Odling-Smee and Laland 2011). From a human perspective, the changes made by our species to the environment are not only inherited by parents of the niche constructors but also by an entire unrelated population. However, cultural inheritance must be considered along with the process of ecological inheritance in relation to human populations.

Humans inherit environments as well as information on how to alter (manage or create) and live in these environments. Cultural inheritance differs from genetic inheritance because it is continually transmitted from many people to many people and involves different strategies of information transmission and social learning (see Odling-Smee and Laland 2011). Thus, we can understand cultural NC as a “subset of NC that is the expression of culturally learned and transmitted knowledge (as opposed to individually learned or genetic information)” (Odling-Smee and Laland 2011: 226). According to Laland et al. (2014: 77) “much of human niche construction is guided by socially learned knowledge and cultural inheritance, but the transmission and acquisition of this knowledge is itself dependent on pre-existing information acquired through genetic evolution, complex ontogenetic processes, or prior (a)social learning.”

Table 6.2 Comparing standard evolutionary theory and niche construction theory

Standard evolutionary theory	Niche construction theory
Focus: Organismic evolution in response to environments	*Focus*: The coevolution of organisms and environments
Causation: Primarily unidirectional, with autonomous selective environments shaping organisms. Reciprocal causation is recognized in some "special cases" where the source of selection is biotic (e.g., sexual selection, predator–prey (coevolution)	*Causation*: Primarily reciprocal, with selective environments shaping organisms, and organisms shaping selective environments, either relative to themselves or other organisms
Niche construction: Organisms acknowledged to change environmental states, but this is treated as the product of natural selection and rarely as an evolutionary process in its own right. Focus is restricted to adaptations expressed outside the bodies of the organisms (e.g., extended phenotypes)	*Niche construction*: Treated as an evolutionary process in its own right. Focus is not exclusively on adaptations, but includes changes in environments caused by the byproducts of organisms (e.g., detritus), acquired characters (e.g., learned), or the collective metabolism or behaviors of multiple individuals/species
Inheritance: Primarily genetic, although maternal, epigenetic, cytoplasmic, and cultural inheritances recognized as "special cases"	*Inheritance*: Genetic and ecological inheritance (i.e., legacies of selection pressures previously modified by niche construction). Genetic and ecological inheritance interact to form "niche inheritance." Maternal, epigenetic, cytoplasmic, and cultural inheritances can be examples
Organism–environment complementarity (adaptation): The product of natural selection	*Organism–environment complementarity (adaptation)*: The match between organism and environment results from dynamic interactions between niche construction and natural selection

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Laland and O'Brien (2011: 193–194) list phenomena that when considered from an NCT viewpoint, provide insight into topics of ethnobiological interest:

- "There is selective feedback from niche construction to genes in the constructor other than those expressed in niche construction.
- Niche-constructed effects can persist and act as modified sources of selection for longer than the lifetime of their constructors (ecological inheritance).
- By-products can play an evolutionary role by modifying selection pressures through niche construction.
- Acquired characters can play an evolutionary role by modifying selection pressures through niche construction.
- Evolutionary causality does not always start in the environment.
- Niche construction can drive (diffuse and direct) coevolutionary events.
- Niche construction can modify developmental environments.
- Adaptation (adaptive complementarity) results from two processes (selection and construction), not one."

We are convinced that NCT can be an integrating and unifying concept in ethnobiology because it can accommodate scientists that may or may not feel comfortable with concepts derived from evolutionary biology. Laland and O'Brien (2011: 195) argued that "recognition of the significance of niche construction to developmental and cultural processes does not require any commitment to evolutionary epistemology, and the niche-construction perspective is broad enough to encompass those who regard learning and cultural change as only weakly analogous to biological evolution."

6.4 Interpretations Based on NCT and Its Ethnobiological Implications

6.4.1 Plant Domestication and the Case of Amylase

Plant domestication is a subject that is of interest to ethnobotanical researchers seeking to assess the influence of human management on plant populations either directly (Smith 2007; Parra et al. 2010; Lins Neto et al. 2013) or indirectly by altering the environment. The entire set of archaeological, genetic, and ecological evidence indicates that humans profoundly altered the evolutionary history of many plant and animal species (Larson et al. 2014). By focusing attention on a specific species by artificially selecting phenotypes that are desirable or by altering the environment in which these species live, its frequency may be increased and specific alleles may be propagated. Additionally, the descendants of these original populations can inherit an environment that was generated and/or modified by these actions. However, limited studies have examined the possible effects that domestication, among other cultural practices, can have on the domesticators themselves. In all scenarios, the focus is placed on how humans alter other species, whereas limited studies have examined how these decisions also affect human populations. Human actions can involve different changes depending on the plant or plant part that is the target of interest to the domesticator. For example, many species were selected to increase the size of their tubers or concentration of starch (Smith 2007). In promoting these alterations, however, the domesticators also generated consequences for themselves.

Starch is one of the primary components of foods cultivated throughout the world, and because of its importance, the ability of human groups to digest starch may be associated with the history of agriculture (Perry et al. 2007). Human agricultural populations have a higher proportion of individuals that have a large number of copies of the gene that promotes the expression of the enzyme amylase (*AMY1*) compared with hunter-gatherer, fishing or pastoral populations, whose diets are primarily based on proteins, fats and simple sugars. Additionally, a strong correlation has been found between the number of copies of this gene and expression level of amylase. Because a greater number of *AMY1* copies and the concomitant increase in salivary amylase improve the efficiency of starchy food digestion, the cultural practice of cultivating starch-rich foods increased the frequency of genes responsible for starch assimilation.

High amylase levels enable the rapid absorption of sugars in the mouth. In addition, the activity of salivary amylase continues during digestion in the stomach and intestines (Fried et al. 1987), thus providing a rapid method of obtaining energy that may be crucial to the survival of individuals when they are stricken with diseases of the digestive system, such as inflammation and diarrhea (Perry et al. 2007). Human populations with a poor ability to digest starches encountered various associated problems, such as diseases of the digestive system. From an ethnobiological perspective, these populations most likely had to develop a traditional pharmacopoeia to address these problems. If this hypothesis is correct, differences should be observed in the incidence of specific diseases associated with starch consumption and in strategies for curing these diseases between populations with high or low amylase production.

6.4.2 The Case of Lactase

In the context of this discussion, perhaps the most well-known and discussed case is the dispersal of the lactase persistence allele in the global population. This case is one of the few well-documented cases (genetically as well as ethnographically) of gene–culture coevolution. The ability to digest milk in adults occurs because of the expression of a gene that is responsible for lactase persistence and produces an enzyme involved in the digestion of lactose. The strong correlation between the phenotype of lactase persistence with the history of the cultural practice of cattle domestication and milk consumption suggests that cultural evolution led to the increased frequency of the lactase persistence allele in adults (Fig. 6.1). The distribution of this allele is concentrated in northern Europe and Africa, which are regions where milking practices have historically been performed by human groups (Ingram et al. 2009). According to these authors, this cultural practice acted as a source of selection in humans and produced a higher frequency of specific lactose absorption alleles in people from these regions. However, exceptions to this pattern that are driven by "cultural pressure" have produced a hypothesis wherein other processes could be modulating this phenomenon in certain cultures (for a more detailed explanation, see Ingram et al. 2009).

Feldman and Cavalli-Sforza (1989) suggest that the probability of spreading the allele responsible for lactose absorption in a group depends on the probability that the descendants of a population that consume milk copy this behavior (cultural inheritance) and become milk consumers. If milk consumption is present in the entire generation, there will be an adaptive advantage for the gene that confers tolerance to lactose, and it will become fixed in the population in a few generations. Considering the high incidence of lactose tolerance in the global population, the authors attribute the permanence of this gene to the cultural practice of consuming

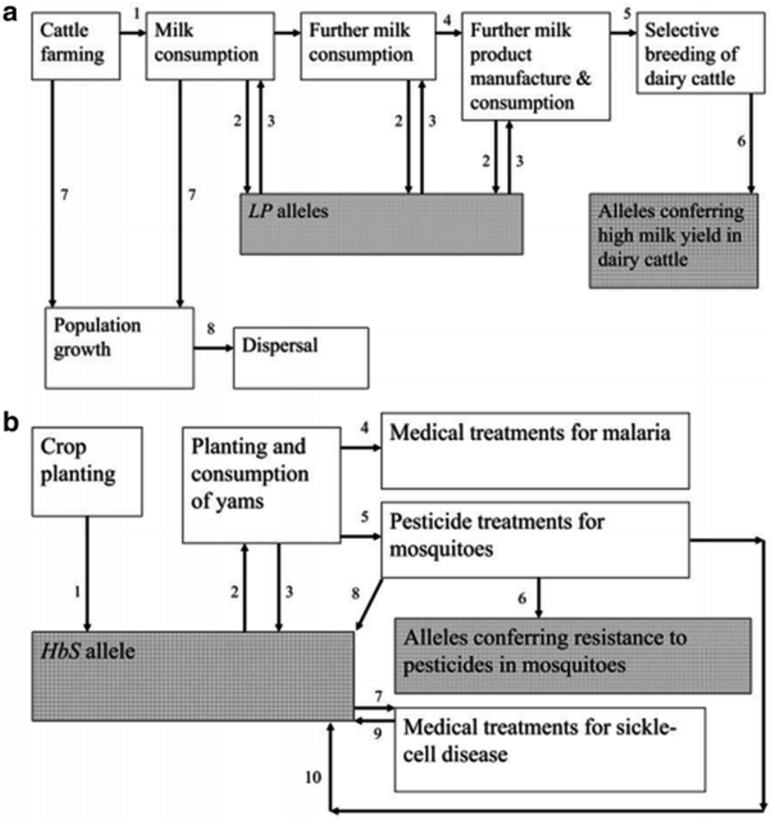

Fig. 6.1 Construction chains, depicting the chain of causal influences following a cultural niche-constructing practice for (**a**) dairy farming and (**b**) crop planting. Cultural processes are shown in *white boxes*, and genetic change is shown in *shaded boxes*. In *panel* (**a**), the domestication of cattle triggers (*1*) milk consumption, which (*2*) favors the spread of lactase persistence (LP), (*3*) promoting further milk consumption, which (*4*) elicits further milk-product manufacture and consumption, which (*5*) leads to selective breeding of cattle, which (*6*) selects for alleles conferring high milk yield in dairy cattle. In addition, cattle farming and dairy-product consumption (*7*) lead to population growth, which (*8*) triggers dispersal into new environments. In *panel* (**b**), crop planting (*1*) inadvertently promotes the spread of malaria, leading to selection for (HbS), and the resulting incidence of sickle-cell disease (*2*) favors the planting of yams and other crops with medicinal benefits, which (*3*) further promotes the spread of (HbS) and (*4*) scaffolds the development and/or application of medical treatments for malaria, as well as (*5*) pesticide treatments for mosquitoes, which (*6*) generates selection for alleles conferring resistance to pesticides in mosquitoes. The spread of sickle cell (*7*) scaffolds the development and/or application of medical treatments for sickle-cell disease. Pesticide treatment of mosquitoes (*8*), medical treatment for sufferers of sickle-cell disease (*9*), and malaria victims (*10*) affect the intensity of selection on the HbS allele. Taken from O'Brien and Laland (2012) with permission of the publisher (Grant number: 108546—University of Chicago Press)

milk for various generations. From the perspective of NCT, lactose tolerance in our evolutionary history was caused by the adoption of the practice of consuming milk, which preceded any genetic modifications (refer to Scott-Phillips et al. 2014). Stated more clearly: "(…) evolution proceeds not because genes that cause dairy farming have higher fitness than those that do not (no such gene exist), but because dairy farming causes a change in the selective environment to favor the lactose absorption alleles, even in societies dominated by lactose intolerants" (Scott-Phillips et al. 2014: 4).

The previous example raises important questions to be addressed in evolutionary ethnobiology studies that adopt an NC perspective. Hypothetically, populations that currently exhibit low frequency of the allele responsible for lactose absorption may use a repertoire of medicinal plants to treat digestive disorders of varying severity caused by the ingestion of milk. However, an extensive medicinal repertoire for these disorders may be not observed in lactose-tolerant human populations, almost certainly because they would not need to develop these medicines. We sought to show that historical decisions made by human populations (adopting the cultural practice involved in the ingestion of milk) affected our resistance to milk products and may have influenced the medical systems studied today. This is a hypothesis that should be investigated in future ethnobiological studies.

6.4.3 The Case of Malaria

Another example of genetic modification caused by cultural practices of a human group is found in the high rates of malaria in agricultural communities in eastern Africa (O'Brien and Laland 2012), which is a robustly documented example of coevolution that has implications for evolutionary ethnobiology. For thousands of years, human groups cultivated edible plants, primarily yams (*Dioscorea* sp.), in eastern Africa (Posnansky 1969). The opening of clearings for the cultivation of yams resulted in the accumulation of water in the soil after rainfall, which formed flooded regions because the removal of trees reduced the soil's capacity to percolate water. This environment favored the reproduction of the mosquito that is the vector for the protozoan *Plasmodium falciparum*, the malaria pathogen (Livingstone 1958), thus generating high rates of malaria in the region. Figure 6.1 illustrates the cascade effect of this cultural practice, which influenced decisions on the use of other natural resources.

Driven by a cultural practice, malaria acted as an evolutionary pressure that increased the frequency of the hemoglobin allele (HbS) and led to a condition known as sickle cell anemia. Individuals that are homozygous for this allele can present with severe anemia, whereas individuals that are heterozygous have sickle-shaped red blood cells, which inhibits the ability of the malaria protozoan to cause infection because the sickle-shaped cells are constantly destroyed by the spleen, which also destroys the parasite. Thus, several years of yam cultivation intensified the selection of the allele responsible for the deformation of red blood cells.

Further evidence that the cultivation of yams acted as an evolutionary pressure is that adjacent communities with distinct agricultural practices did not exhibit an increase in the frequency of this allele (Durham 1991).

However, the practice of deforestation to produce clearings may have generated consequences that have not been investigated. Using traditional medical systems as a reference, we can assume that populations that adopted deforestation as an agricultural practice and show higher resistance to malaria would have developed a much smaller repertoire of plants to treat this disease or its symptoms compared with populations that did not adopt deforestation as an agricultural practice.

Assuming that a specific cultural practice, such as the act of medicating a person for a specific disease, was a result of past decisions that led to a coevolutionary process, then certain cultural differences observed in ethnobiological studies may reflect a cascade of events wherein genes, culture and environment interact (Fig. 6.1). Well-documented examples, such as that of malaria and lactose tolerance, are unavailable to demonstrate how the niche construction theoretical framework can be applied to ethnobiological research. Thus, the interactions between humans and nature may have an even more complex character when considered from an evolutionary perspective.

6.5 Medical Regimens and Local Adaptations

In the previous examples, the consumption of starch and milk were dietary regimes derived from cultural practices that resulted in a coevolutionary process. When our species consumes different plant foods, compounds contained in these plants that can have undesirable effects must be processed. For starch, this process led to an increase in the frequency of the allele that improves digestion of starch. Based on local adaptations, other cultures can reduce these undesirable characteristics by using appropriate food preparation or cooking techniques (see Wollstonecroft 2011). In addition, “medical regimens” of natural products (plants or animals, for example) were developed by humans and added to their cultural systems to treat or prevent diseases.

Pharmacogenetic studies can provide examples of how cultural practices can explain the presence of polymorphisms of specific genes in humans and their implications on evolutionary ethnobiology from the perspective of NCT. Pharmacogenetics studies the genetic variations related to differences in the therapeutic responses of drugs of clinical interest (Ingelman-Sundberg 2001). For example, a dose of a specific drug may have a therapeutic effect on one group of individuals, have no effect on other groups, and be toxic in certain individuals. Thus, pharmacogenetics seeks to investigate genetic explanations of these inter-individual differences (Evans and Relling 2004; Ortega and Meyers 2014).

For example, polymorphisms of the cytochrome *P450* 2D6, also known as CYP2D6, represents a set of enzymes responsible for the metabolism of exogenous substances that protect organisms against toxins (Seripa et al. 2010). Certain individuals have multiple copies of the *CYP2D6* gene, which is responsible for encoding the enzymes of cytochrome P450, and this leads to the high production of CYP2D6 enzymes and high metabolism of exogenous substances, thus compromising the therapeutic response to drugs of clinical interest. In contrast, people that have fewer copies of this gene show lower metabolism of these substances, which can cause adverse effects when administering a small dose of drugs of clinical interest (Ingelman-Sundberg 2005). The distribution of individuals with many and fewer copies of the active gene *CYP2D6* varies in different human populations. Populations in Saudi Arabia and Ethiopia have a low number of inactive copies of the gene *CYP2D6* because of mutations (Ingelman-Sundberg 1997). Variations in the distribution of active copies of the gene in different human populations can be explained through an evolutionary scenario.

The CYP2D6 enzymes have a high affinity for plant alkaloids. Thus, it can be hypothesized that the selection of individuals with many copies of the *CYP2D6* gene in certain human groups is associated with selective pressure caused by previous diet patterns containing large quantities of plant alkaloids, which would be toxic in individuals that have few copies of the gene (Ingelman-Sundberg 2005). Native Ethiopians and a group of migrant Ethiopians living in Sweden were compared to determine their rate of debrisoquine metabolism, a substrate selective for the CYP2D6 enzymes (Aklillu et al. 2002). Individuals with the same genotype were selected from the two groups, and the group living in Ethiopia showed a lower rate of debrisoquine metabolism compared with the group living in Sweden (Aklillu et al. 2002). This result may have been caused by dietary differences between the two groups because the native Ethiopians consume a larger variety of plants, which has resulted in greater ingestion of alkaloids, increased expression of the enzymes and decreased rates of debrisoquine metabolism (Aklillu et al. 2002; Ingelman-Sundberg 2005). Thus, a diet composed of a larger variety of plants requires a greater production of enzymes for the detoxification of alkaloids, which occurs when individuals have multiple copies of the *CYP2D6* gene. Thus, it can be hypothesized that food scarcity suffered by the Ethiopian population 10,000–20,000 years ago generated positive selection in certain individuals that had multiple copies of the *CYP2D6* gene because they could expand their consumption of a wider diversity of plants during periods of food scarcity (Ingelman-Sundberg 2005). Thus, the distribution of individuals with multiple copies of the *CYP2D6* gene in different human groups may reflect a history of food scarcity in each group.

The CYP2D6 enzyme example illustrates how past dietary patterns in human evolution, particularly in relation to cultural decisions in periods of food scarcity, may have influenced the selection of individuals with more copies of the *CYP2D6* gene. Changes in historical dietary patterns in different human populations may also have influenced the presence of polymorphisms of other genes involved in the production of metabolic enzymes (Nebert and Dieter 2000). Moreover, because alkaloids have a broad range of biological activities, it is reasonable to suppose that the presence of individuals with multiple copies of this gene may have affected the therapeutic response of these substances in human populations. If this is true, human groups may have developed their traditional pharmacopoeias according to the severity of their reactions to plant chemicals. The above example of the Ethiopian population suggests a “local food adaptation”; therefore, it is likely that a “local medical adaptation” also occurred in this specific case.

The subject addressed here may have an impact on ethnobiological studies and provide a better understanding of how food resources were used and diseases were treated in different human groups. Let us hypothetically consider the following situation. In a specific group consisting of individuals with many copies of the *CYP2D6* gene, we should expect that a high diversity of plants will be used as food because these people would be less affected by the toxic alkaloids in edible plants. However, the medicinal use of such plants might also be affected because even if a medicinal plant has alkaloids with biological activity, these alkaloids will most likely be degraded by metabolic enzymes. Thus, certain plants may be perceived by a human group as ineffective for medicinal use not necessarily because it does not contain pharmacologically relevant compounds but because a higher dosage, which might be lethal in sections of the population, would be required to exert the desired effect on individuals that exhibit high expression of CYP2D6 enzymes and enzymes responsible for the degradation of exogenous substances. Most likely, adaptive issues caused different cultures to avoid performing adjustments in dosages because of the harm that could be caused at the population level.

Thus, a pharmacopoeia is developed that is adjusted to cultural decisions, genetic variations in the population, and the environment. By adopting a specific “food regimen” or “medical regimen,” genetic and cultural changes begin to mutually reinforce each other. Although limited studies have examined this specific scenario, specific alleles could be selected that would lead to increased or decreased therapeutic responses to specific plant chemicals present in remedies from different peoples. During our group’s field study with the Fulni-ô Indians, which is an ethnic group of northeastern Brazil that has shown a remarkable preservation of their language Yathee (Soldati and Albuquerque 2012), we collected ethnographic evidence that supports our hypothesis. This group frequently stated that allopathic medications did not have the desired effects for certain conditions compared with traditional preparations based on plant resources available in the region.

6.6 Final Considerations

We are still in the early stages of understanding how interactions between human populations and their environments may have been molded by historical decisions; thus, such interactions are open for exploration by ethnobiologists. If the arguments and interpretations from the examples above are accepted, then it becomes clear that NCT can offer a useful conceptual framework for ethnobiology that may strengthen the relationships and dialogue between ethnobiologists with training in the social sciences and ethnobiologists with training in the biological sciences and/or with those scientists who feel comfortable adopting ecological and/or evolutionary concepts in their studies.

NCT can provide ethnobiological insights that may improve our understanding of the relationships between humans and nature, particularly in relation to human actions on the biota, including important information generated from such interactions, and help illustrate the biological and cultural impacts that our actions have had and still have on the environment and our own species.

Acknowledgements We particularly thank Dr. John Odling-Smee (Mansfield College—University of Oxford) and Dr. Kevin Laland (University of St. Andrews) for comments on the manuscript. This work was supported by funding from the National Counsel of Technological and Scientific Development (CNPq—Proc. 471989/2012-6).

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