Evolution of Brain Structures and Adaptive Behaviors in Humans and Other Animals: Role of Polymorphic Genetic Variations

GEORGE D. BITTNER and BARRY X. FRIEDMAN

One important goal of neuroscientists is to eventually understand complex behavioral adaptations of humans and other animals as explained by the structure and function of their brain tissues and principles of evolutionary biology. To this end, the dominant model in evolutionary psychology assumes that complex adaptations involving brain or any other tissue are precisely crafted for a specific function and are produced by genes whose alleles all have equal fitness (genetic monomorphism) because sexual recombination would disrupt adaptations produced by genes whose alleles have unequal fitness (genetic polymorphism). This genetically monomorphic model maintains that humans and other animals have evolved universal neuronal circuits and behavioral adaptations, which in their sum constitute a species-typical nature (a universal human nature for Homo sapiens), and that almost all variation in adaptive behavior among *same-sex* individuals is due to environmental effects. Alternatively, we assert that a review of currently available data in neuroscience, biology, and psychology strongly suggests that complex adaptations involving brain and other tissues have many imperfections, different functions in different environments, and much polymorphic genetic variation. Our genetically polymorphic model accounts for all these data and predicts that humans and other animal species have evolved many nonuniversal complex behaviors (multiple species-typical behaviors or "human natures") that differ genetically between males and females, as well as within males and within females. Variability in same-sex behavior is therefore due to both environmental *and genetic variation.* Our genetically polymorphic model reconciles fundamental assumptions of evolutionary psychology with basic principles of evolutionary biology, behavioral genetics, and neuroscience. NEUROSCIENTIST 6(4):241–251, 2000

KEY WORDS *Behavioral evolution, Individual differences, Evolution of brain structures and functions, Adaptive genetic variation, Evolutionary psychology*

School of Biological Sciences (Neurobiology Section), College of Pharmacy (GB), Department of Psychology (BF), and Institute of Neuroscience (GB), The University of Texas at Austin, Austin, Texas.

Address correspondence to: Dr. George D. Bittner, Department of Zoology, The University of Texas, Austin, TX 78712 (e-mail: bittner@mail.utexas.edu).

This article reviews data and current concepts on the evolution of brain structure and behavior in the fields of neuroscience, evolutionary biology, and evolutionary psychology. We propose that such data can best be explained by assuming that genetic polymorphisms are responsible for much of the past and present phenotypic variation in brain structures (brain circuits) and functions (behaviors) of humans and other animals. That is, biologists and psychologists commonly observe that members of noninbred populations of a species (including Homo sapiens) exhibit much phenotypic diversity (Box 1). Phenotypic diversity can arise from variations in the environment and/or from variations in the genetic composition of different members of a species. When different members of a noninbred species possess different alleles at many gene loci, such genetic diversity can be responsible for much of the phenotypic diversity.

However, genetic diversity does not necessarily produce adaptive phenotypic diversity. If the diversity for each gene is monomorphic (all alleles produce a phenotype having exactly the same adaptive function and fitness in all environments), then this "nonadaptive" (i.e., nonfunctional, neutral fitness, genetic noise) form of genetic diversity (see Box 1) will not produce adaptive phenotypic diversity. Any phenotypic variation in complex adaptations (e.g., behaviors) observed under monomorphic genetic conditions is necessarily due to environmental variation (see Boxes 2 and 3). Specifically of interest to neuroscientists, monomorphic genetic variation in one given environment would produce the same brain structures yielding the same behavior in all humans (or in all members of another animal species) that all had the same environmental experiences. Different behaviors in different humans would be produced only through plastic changes in brain structures elicited by different environments (Fig. 1).

In contrast, if much of the maintained genetic diversity for many genes in Homo sapiens (or any other animal species) is polymorphic (such that some alleles for many genes each produce a different phenotype having a different adaptive function with different fitness), then much of the phenotypic variation in complex

ISSN 1073-8584

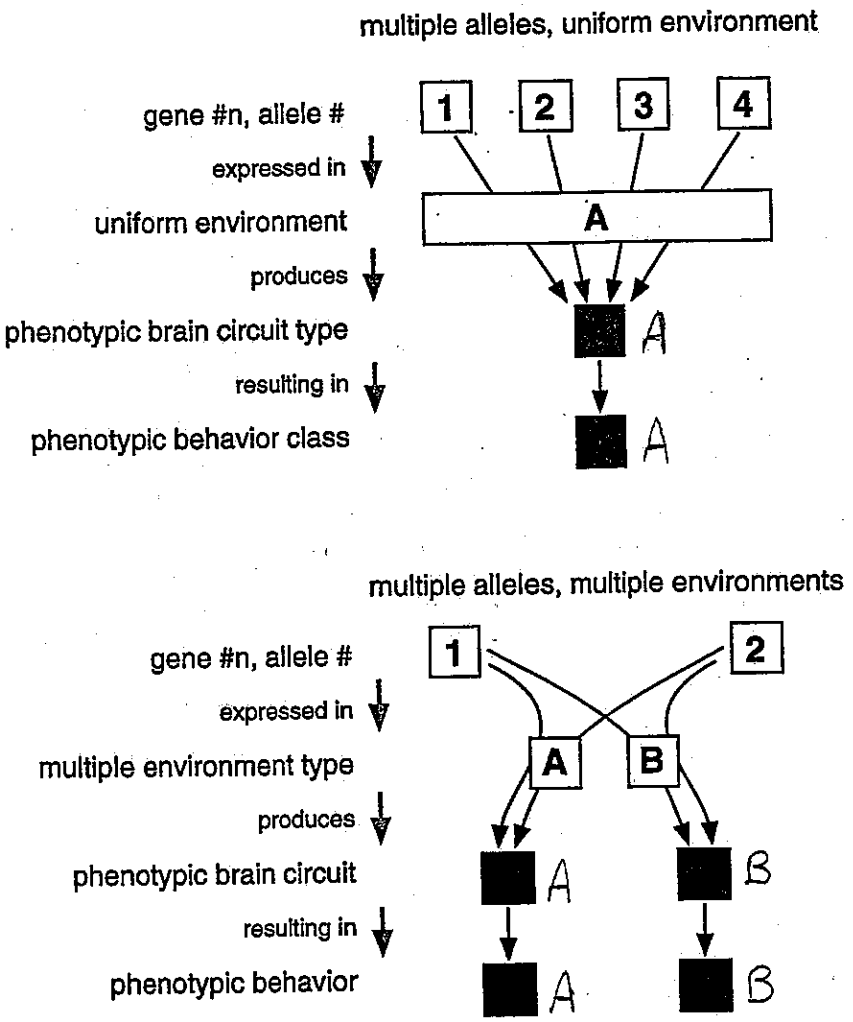

Fig. 1. Schematic diagram showing that brain circuits and behaviors are determined by the environment, and not by allelic differences, in a genetically monomorphic model.

adaptations for different humans would have a genetic basis that has been shaped by natural selection. Specifically of interest to neuroscientists, adaptive polymorphic genetic variation in one environment would produce different brain structures yielding different adaptive behaviors in different members of the same species who had the same environmental history. Different adaptive behaviors in different environments would result from a complex mosaic of genetic and environmental effects on the structure and function of brain tissue in humans and other animals (Fig. 2).

In this assessment of current data and models that might explain the evolution of behavior in humans and other animals, we first review the rationale for concluding that all Homo sapiens (or any other species) of the same sex have the same set of complex brain circuits and behavioral adaptations (a species-typical or universal "human nature") based on a genetically monomorphic model of complex adaptations originally developed by the evolutionary psychologists John Tooby and Leda Cosmides (7–9). This influential model is accepted explicitly or implicitly by others in the field (e.g., 10–13). We then explain why it is not necessary or appropriate to assume that genetic monomorphism is the basis for complex adaptations (neuronal or nonneuronal in structure or function). Finally, we present a rationale for concluding that Homo sapiens (and other animal species) do not have the same set of complex brain circuits or behavioral adaptations (i.e., they have different circuits and multiple human natures or multiple species-typical natures) based on a genetically polymorphic model of complex adaptations. We believe that this alternate model of genetically polymorphic adaptations is in agreement with some recent publications relevant to evolutionary psychology (14–18). Our model of genetically polymorphic adaptations also integrates much available data in evolutionary psychology, individual differences psychology, behavioral genetics, ethology, evolutionary biology, cognitive neuroscience, and neurobiology.

A Genetically Monomorphic Model of Complex Adaptations (e.g., brain structures and behaviors) and Its Consequence: Species-Typical Behaviors and Universal Human Natures

In the current monomorphic model of complex adaptations (Fig. 1, Boxes 2–4), quantitative (e.g., stomach size, threshold for aggression, and differences in jealousy thresholds) and other genetic differences in morphological structures or behaviors (e.g., bone color) are all assumed to be irrelevant with respect to fitness (7–9). The alleles that give rise to these variations in adaptations (structures or functions, including brain circuits and behaviors) are assumed to be monomorphic (that is, to produce no differences in fitness) and to exist primarily as a defense against pathogens (19). In this model, heritable variation in a trait is generally taken a priori to mean that such a trait is not an adaptation. A small amount of genetic diversity that is not monomorphic is assumed to produce functionally different phenotypes and is exposed to natural selection, but almost all of this diversity is assumed to be in noncomplex adaptations (adaptations

Box 1: Some Terminology and Concepts in Evolutionary Biology

Phenotype refers to the observable characteristics of an organism and results from the interaction of its genes (genotype) with the environment, where the environment includes events that occur within, and exterior to, the organism. The genetic code produces neuronal and nonneuronal structures that have multiple functions (many neuronal functions are termed behaviors). These structures and their functions are termed adaptations if they increase the ability of the organism or the relatives of that organism to leave more offspring, relative to other members of the same species. Hence, an adaptation may be defined as a phenotypic characteristic having a genetic basis that positively affects the reproduction of individuals or their relatives (1, 2). Natural selection usually acts on the whole organism and not on specific complex adaptations. Finally, evolutionary forces and principles are the same for neuronal and nonneuronal structures or functions (behaviors).

In this paper, the following sets of terms, which are used by different disciplines to express essentially the same concept, will be taken as synonymous:

"adaptive function, selective advantage, adaptive significance, adaptation, fitness"
"genetic noise, neutral fitness, nonadaptive structure or function"

Historically, adaptation and fitness are terms that have been used interchangeably. However, an adaptation is almost always subjectively described, whereas fitness is often used as a quantifiable measure (3). Qualitative descriptions of adaptations might benefit from the more rigorous analyses that have been made for fitness. For example:

1. Fitness is relative and context specific and is defined for a given phenotype (complex adaptation) relative to other phenotypes (4). Killing all your same-sex contemporaries is a behavior that reaches the pinnacle of quantifiable fitness (3) but is not subjectively regarded in most human societies as a highly adaptive behavior.
2. The fitness of a phenotype can be defined and measured only for a particular ontogenetic stage in a specific environment. Dark adult moths are more fit in industrialized areas and peppered adult moths more fit in other areas (5).
3. Fitness shows much covariance among complex adaptations, for example, body size, bill width, and behavior in ground finches (6). The recognition of such covariation helps make the point that natural selection acts on the whole organism and not on specific complex adaptations.

Box 2: Some Fundamental Tenets of Monomorphic and Polymorphic Models of Complex Adaptations

Common Assumptions

1. All organisms have evolved by natural selection (including sexual selection).
2. The structure and function of brain tissue at any point in time in the life of an organism (its ontogenetic history) is due to the genetic makeup of its brain cells (determined by natural selection, genetic drift, and, perhaps, somatic mutations), which interact with the internal and external environment.
3. Interactions within brain tissue and among brain tissue, other body tissues, and the external environment have evolved by natural selection according to the same rules as have the structures, functions, and interactions of all other tissues in humans and all other animals.
4. The structures and functions of the brains of humans and all other animals result from environmental interactions with the genetic substrate (genomic DNA), the latter having been evolutionarily determined by natural selection and genetic drift acting over time. (NB: There are no special rules that apply only to brains or only to humans.)

Differing Assumptions

1. Complex adaptations have a single function and are analogous to finely machined devices (e.g., car engines) in which much variation in their components would yield a nonfunctioning device.

versus

Complex adaptations do not have a single function and are very imperfect devices that function despite many imperfections. Organisms with imperfect adaptations survive, reproduce, and successfully compete in evolutionary history because they are in competition with other organisms that also have imperfect adaptations. In fact, there is no such thing as a perfect adaptation, because it could be "perfect" only for one life stage in a particular environment.

2. Complex adaptations are almost always monomorphic. Although many loci that contribute to an adaptation may be polyallelic, the alleles all have a neutral fitness with respect to each other and hence are not exposed to the forces of natural selection.

versus

Complex adaptations are almost always polyallelic. Many (most?) alleles have different fitness values in different environments or life stages and are exposed to natural selection.

3. All members of the same sex in a species have a "species-typical nature," and there is a universal brain circuitry responsible for a universal human nature.

versus

All members of the same sex in a species do not have a species-typical brain circuitry or nature, and there is no universal human nature. Rather, complex adaptive behaviors in Homo sapiens or other long-lived outbreeding species are coded for by sets of genes having various probabilities for alleles at different loci. Differing sets of complex behaviors with differing genetic bases produce multiple human natures that differ between males and females, as well as among males and among females.

Box 3: Assumptions of a Genetically Monomorphic Model of Complex Adaptations

1. Complex adaptations are intricate machines that require complex "blueprints" at the genetic level. This means that they require coordinated gene expression involving hundreds or thousands of genes to regulate their development.
2. Sexual reproduction automatically breaks apart existing sets of genes and randomly generates in the offspring new, never before existing combinations of [alleles of] genes at those loci that vary from individual to individual.
3. If [alleles of] genes differed from individual to individual in ways that significantly impacted the developed design of the component parts of complex adaptations, then existing genetic combinations whose developed expressions had fit [precisely] together into complex adaptations would be pulled apart by sexual recombination. Equally, new combinations [of alleles exposed to natural selection] would be thrown randomly together, resulting in phenotypes whose parts were functionally incompatible. This is because parts in any complex machine are functionally interdependent: If you tried to build a new car engine out of a mixture of parts from a Honda and a Toyota, the parts would not fit together. To build a new car engine whose component parts fit together, you would have to salvage parts from two "parents" that were of the same make and model.
4. Because sexual recombination is a random process, it is improbable that all of the [alleles of] genes necessary for a complex adaptation would be together in the same individual if the [alleles of] genes coding for the components of complex adaptations varied substantially between individuals.
5. Therefore, it follows that humans, and other complex, long-lived, outbreeding organisms, must be very nearly uniform [monomorphic] in [the alleles of] those genes that underlie our complex adaptations.
6. By the same token, sexually reproducing populations of organisms freely tolerate genetic variation to the extent that this variation does not impact the complex adaptive organization shared across individuals. To return to our car engine example, the color of the parts is functionally irrelevant to the operation of the car and so can vary arbitrarily and superficially among cars of the same make and model, but the shapes of the parts are critical to functional performance and so cannot vary if the "offspring" design is to function successfully. (7, pp. 78–9)

that require the coordinated action of a very small number of genes). Consequently, almost all of the differences in the phenotypic expressions of adaptations are assumed to result from differing environmental influences experienced by different members of the species. (In this and other models, different brain tissues [neuronal circuits] are interposed between the genomic DNA and the complex behavioral adaptations. See Fig. 1.) However, males and females are regarded as different morphs of the same species, having a shared genetic basis for many complex behavioral and nonbehavioral adaptations, but a different genetic basis for other complex adaptations, which are typically activated by genetic switches such as those associated with the Y chromosome. Hence, this model assumes that all species members of the same sex are (largely) genetically monomorphic and share universal male or universal female brain circuits and natures (defined as

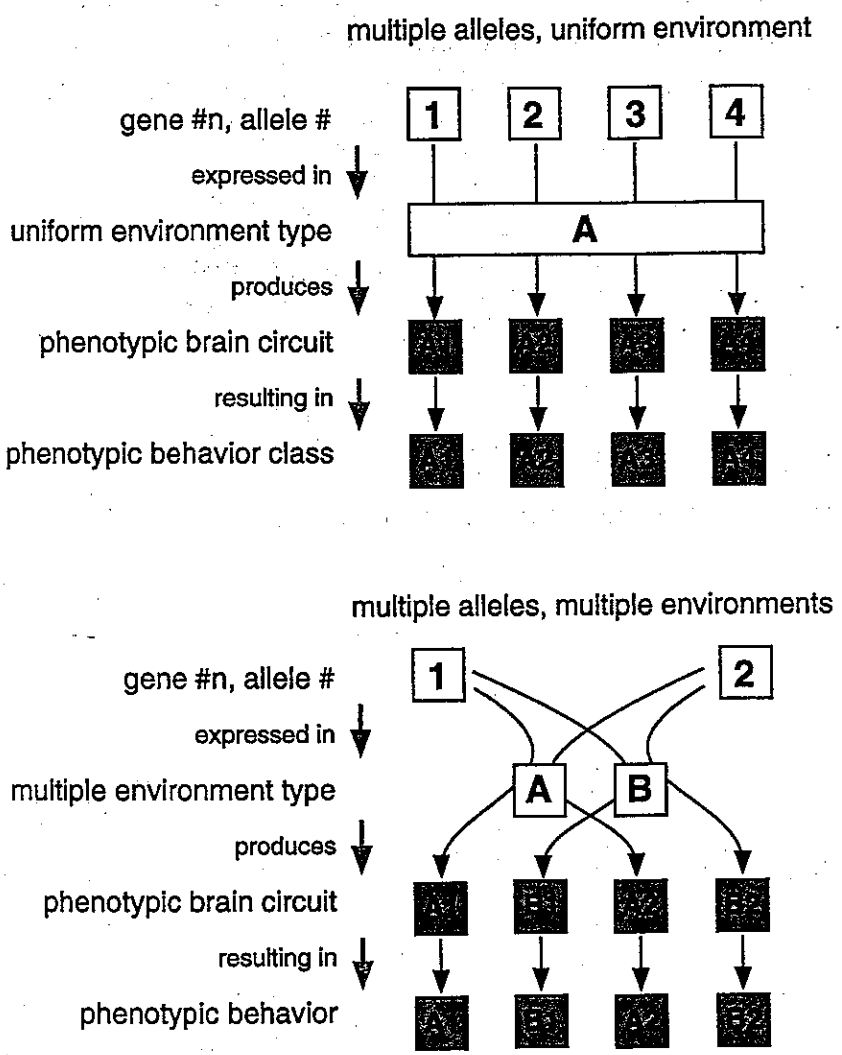

Fig. 2. Schematic diagram showing that brain circuits and behaviors are determined by the environment and by allelic differences in a genetically polymorphic model.

a set of innate psychological mechanisms and developmental programs that are exactly the same in all members of the same sex of a given species, including Homo sapiens). From these suppositions, the current model (8, p. 18) concludes the following:

> A human nature composed of uniform psychological mechanisms may produce individual differences as a result of different individual experiences. It is the existence of genetic differences between individuals that poses problems: It renders the study of causation of individual differences difficult, and more important, it calls into question the very idea of a universal [genetically male or genetically female] human nature.

Genetically Monomorphic Models of Complex Adaptations Are Not Tenable

Complex Adaptations Are Imperfect Solutions to a Set of Functions

In the current genetically monomorphic model (Fig. 1, Box 2), complex adaptations are generally assumed to be exceptionally well-designed and well-engineered (if not necessarily optimal) solutions to a particular function when considering broad aspects of their structures (including brain tissues) and functions (including behaviors). (Note that many of the examples given in this review describe complex nonbehavioral adaptations, but no distinctions are made in current evolutionary theory between evolutionary forces that act on behavioral as opposed to nonbehavioral adaptations, or on humans compared to other animals.) However, complex adaptations are influenced by many factors and compromises that lead to suboptimal functioning in different environments (e.g., shell color in *Cepaea*: 20; copper tolerance in *Agrostis tenuis*: 21). A careful evaluation of the detailed components of a complex adaptation often reveals its suboptimal and nonuniform nature (18) and that the phenotypic relationship between form and function is a continuum of imperfection (22). Furthermore, inferring past selective pressures from phenotype alone is exceedingly difficult, because many components of a complex adaptation have more than one function, many components have been subjected to multiple selection pressures, selection may not have been responsible for some components in the first place, and selection may not have acted directly on a particular component but rather on structures correlated with the component in question. Recognizing all these factors and those outlined in Box 1, most evolutionary biologists (e.g., 3, 23–25) now regard complex adaptations as sufficient or adequate solutions to a set of functions that are difficult to quantify, and that structure-function relationships and past selection pressures are not intuitively inferable, as is ostensibly assumed by the current monomorphic model (Box 3).

Complex Adaptations Are Genetically Polymorphic

Many data in evolutionary biology do not support two key assumptions of the current monomorphic model (Box 3): 1) adaptive phenotypic variation in complex adaptations does not have a genetic basis and 2) polymorphic (alleles having different fit-

Box 4: A Paradox in Evolutionary Theory: Rapid Short-Term Change, yet Slow Long-Term Change

Evolutionary biologists acknowledge that selection over microevolutionary time can be very powerful in particular cases and many orders of magnitude larger than that seen on average over macroevolutionary time (3). A fundamental theory in population genetics (29, 30) states that the change in the mean of a quantitative trait or adaptation in one generation is determined by the amount of phenotypic variation exposed to selection (often about 10% [31]), the amount of such variation that has a genetic basis (typically ranging from 0.3 to 0.7 [32]), and the intensity of directional selection (which can be as great as 0.43 [33]). For this last factor, such selection pressures mean that individual ground finches one phenotypic standard deviation above the mean are more than twice as fit as individuals one standard deviation below the mean. Such data show that natural selection sustained in a particular direction can produce evolutionary changes of greater than 1% in each generation, that is, capable of taking an animal the size of a mouse to that of an elephant in less than 1200 generations (3). Current data suggest that such microevolutionary rates are not sustained in macroevolutionary time because the direction of selection is not sustained, rather than because polymorphic genetic variation is used up (as assumed by Tooby and Cosmides [7–9]).

ness) genetic variation is eliminated by natural selection. That is, polymorphic genetic variation for complex adaptations is the norm, rather than the rare exception, in part because even very favorable mutations have a very low probability of becoming fixed (monomorphic) in a population (26), and because selection at other loci usually impedes the spread of advantageous alleles (27, 28). Furthermore (as outlined in the previous section), particular alleles have different fitness in different environments, resulting in different allele frequencies in different environments. Polymorphic genetic variations that produce spatial patterns of phenotypes are maintained by local selection, migration, genetic drift, linkage between traits, frequency- dependent selection, and sexual selection. Natural selection does indeed reduce polymorphic genetic variation (a result emphasized by genetically monomorphic models). However, polymorphic genetic variation is constantly reintroduced and maintained in the population by mutation, migration, sexual recombination, genetic drift, and so on. (A result generally not emphasized by genetically monomorphic models. See also Box 4.) This polymorphic genetic variation is necessary for evolutionary change and produces scatter around fitness peaks in a particular environment (Box 1), that is, produces imperfect adaptations. This fitness load due to genetic variation is nontrivial (34, 35), but organisms with imperfect adaptations are competing with other organisms that also have imperfect adaptations. In other words, it is relative fitness that is acted on by natural selection and individual complex adaptations can be very suboptimal.

Many findings in evolutionary biology suggest that much phenotypic variation in complex adaptations results from polymorphic genetic variation (Fig. 2), rather than solely from different environmental experiences (Fig. 1), as would be predicted by the current genetically monomorphic model (Box 3). For example, the physiological functions of allozymes for alcohol dehydrogenase (ADH) in *Drosophila* correlate with adaptive explanations for their distribution (36, 37), behavioral studies correlate with alcohol tolerance, enzyme kinetics, and habitat (38–40), and allelic variations correlate with adaptive functions in lab conditions (37, 41). Furthermore, genetic variation in ADH interacts with alleles at other loci to determine fitness (42, 43). This adaptation is very complex as evidenced by the variety of enzymatic, physiological, and behavioral mechanisms that are used to cope when the organism is challenged by alcohol (44). Similar complexities in genetic determinants are also seen in *Cepaea nemoralis*, whose shell patterns are influenced by predator preferences, temperature, altitude, frequency-dependent selection, genetic drift, and linkage disequilibria (20). A significant polymorphic genetic basis for phenotypic variation at the biochemical level is also seen in leucine aminopeptidase variants in *Mytilis edulis* (45), lactose dehydrogenase in *Fundulus heritoclitis* (46), phosphoglucose isomerase in *Colias* butterflies (47–49), and hemoglobin variants in *Peromyscus* (50–52). A significant polymorphic genetic basis for complex anatomical variation has been extensively documented for body size and life history in sailfin mollies and guppies (4) and for the beaks of Galapagos finches (6, 53).

Of particular relevance to the evolution of brain structure (circuitry) and function, behavioral geneticists have extensively described a genetic basis for phenotypic variation in various complex behaviors, at least some of which almost certainly are complex adaptations. Most behavioral traits are reported to be moderately heritable, with typical values ranging from 0.25 to 0.75. (Heritability is the proportion of phenotypic variance attributable to genetic differences between individuals [14, 54].) Phenotypic variation in such diverse traits as intelligence (55), extraversion (56, 57), schizophrenia (58), and alcoholism (59, 60) has consistently been found to

be due (in part) to polymorphic genetic differences between individuals. Indeed, "appreciable genetic variation underlying behavioral variation is the rule, not the exception" (14, p. 219).

Finally, a growing minority of evolutionary psychologists is beginning to interpret individual differences in complex behaviors as possibly resulting from complex adaptations. For example, Gangestad and Simpson (61) propose that individual differences in the mating strategy of women have been produced and maintained by frequency-dependent selection. The success of women adopting a "restricted" mating strategy, marked by prolonged courtship and the delaying of intercourse, depends on the frequency of other women pursuing an "unrestricted" strategy in which intercourse occurs relatively sooner and in the absence of a strong attachment to the man. Gangestad and Simpson (62) also propose that the ability to feign emotion and expressive behavior (i.e., the ability to hide one's true emotional states—a heritable trait) may result from frequency-dependent selection. As the frequency of individuals in the population able to feign emotion increases, vigilance should increase, resulting in selection for individuals who do not posses the ability to feign emotion. Although evidence that the variation in the mating strategy of women and expressive control in either sex was produced (and has been maintained) by frequency-dependent selection is still accumulating, the possibility that polymorphic genetic variation is responsible for other behavioral traits is beginning to receive serious consideration (14–18).

In summary, polymorphic genetic diversity is maintained among different members of noninbred species (including Homo sapiens) and this genetic variation affects the fitness and function of complex adaptations. Hence, many data external to the dominant monomorphic model in evolutionary psychology to explain complex adaptations (7–9) suggest that some key assumptions of that model are not valid, for example, that adaptations are well-designed and well-engineered solutions to a single functional problem and that complex adaptations are genetically monomorphic. Most important, if polymorphic genetic diversity underlies the phenotypic expression of brain circuits and behaviors (complex adaptations), then the conclusion of species-typical brain circuits and a universal human nature is almost certainly not valid, as recognized by Tooby and Cosmides in their passage quoted above (8, p. 18).

A Genetically Polymorphic Model of Complex Adaptations (e.g., brain circuits and behaviors) and Its Consequence: Multiple Human Natures

We now propose a genetically polymorphic model of complex adaptations that incorporates the observations cited above and that relates the evolution of brain structures and function to the evolution of complex behaviors (Fig. 2, Boxes 2 and 5). In developing our genetically polymorphic model, we explicitly make a set of assumptions that are also implicitly made by monomorphic models (7–9) (see Box 2). Our genetically polymorphic model also makes assumptions 1 and 2 made in the genetically monomorphic model of Tooby and Cosmides (7) (see Box 3): 1) complex adaptations require the coordinated expression of many hundreds or thousands of genes during development, and 2) sexual reproduction breaks apart different sets of genes and randomly generates combinations of alleles that are different for each individual that does not have an identical sibling. However, our genetically polymorphic model differs in large or small part from the current genetically monomorphic model as follows (summarized in Box 2).

Complex adaptations have more than one function and have many imperfections. Neuronal and nonneuronal adaptations are not like a single model car engine in which parts are precisely machined and cannot be interchanged. Eukaryotic organisms such as humans have survived with imperfect adaptations, sexually reproduced, and have successfully competed over evolutionary history because they were in competition with other organisms that also had imperfect adaptations. In fact, there is no such thing as an optimal adaptation, because it could be "optimal" only for one life stage in a particular environment. For example, limb length is correlated with both climate (shorter limbs having advantages in colder climes and longer limbs in warmer climes) and locomotive ability (shorter limbs having advantages for rapid changes of direction over irregular terrain and longer limbs for long-distance travel over level terrain). Both body plans function with different amounts of fitness in any combination of climes or terrain (63).

Complex adaptations have a polymorphic genetic basis in which many alleles have different fitness in different environments. Complex adaptations have different phenotypic functions that are acted on by natural selection. Many genes code for proteins that are often expressed in a wide variety of cell types (including neurons), and within nervous tissue by different subsets of neurons. A particular protein often does not affect a single adaptation but rather many adaptations (e.g., some potassium channels have multiple alleles and are in many cell types in many organs), and a particular adaptation (e.g., the heart, kidney, hand, jealousy, aggression, etc.) has many functions. Hence, a particular allele will often affect many different adaptations having different selective value in different environments. Therefore, new combinations of alleles having different fitness are thrown randomly together by sexual recombination. Many, perhaps most, of these combinations are deleterious. However, many of these combinations are not functionally incompatible (much less lethal), in part because polymorphic complex adaptations are

Box 5: A Summary of Our Genetically Polymorphic Theory of Brain Structure, Brain Function (Behavior) and Mind

The functional states of brain tissues as they interact with the state of the other body tissues are referred to as "mind states" or as "mind" in the common vernacular; the externally observable results by humans of all these interactions that are occurring in a given organism are commonly termed "behaviors." Even the most complex mind states and behaviors are an emergent property of biological organisms dependent on currently known physical laws. We now have some good insights (but nowhere near complete knowledge) about which brain tissues are important for various mind states or behaviors such as sensory perceptions, memory, learning, emotions, language, higher conscious thought, and so on. We also have some insight into how the polymorphic genome interacting over time with the internal environment (including embryological development) and the external environment during the life of an organism can alter brain-plus-rest-of-body states (mind states and behaviors). If the functional state of brain tissue (membrane voltages due to action potentials, synaptic potentials, pacemaker activity, receptor potentials, biochemical properties, etc.) together with the functional states of other tissues (blood glucose levels, hormonal release, etc.) constitute a mind state, then there is basically no greater problem in explaining brain-brain function-body-external environmental interactions (which constitutes what is often called mind) than there is in explaining liver-liver function-body-external environmental interactions (which constitutes what is often called homeostasis, a very complex set of interactions that, to our knowledge, no one has yet invoked the paranormal to explain).

There are no "special rules" for the actions/effects of natural selection on brain tissue as opposed to any other tissue or for human tissues. The structure and function of brain tissues and other tissues are both encoded by a polymorphic genome. In fact, the same polymorphic gene can be expressed in both neuronal and nonneuronal tissues. The structure and function of nonneuronal tissues also affect mind states and animal behaviors; brains evolve with hips, feet, livers, and so on, in an organism whose complex adaptations are all imperfect. Natural selection does not act on brains independently of the rest of the organism. Successful sexual reproduction breaks up and transmits part of the entire polymorphic DNA package of an organism. The DNA in the organism interacting with the internal and external environment during ontogeny determines the phenotype of the organism. Organismic phenotypes are acted on by natural selection, producing changes in average frequencies of alleles in a species.

From the fossil record, we have reasonable knowledge about the evolution of hard tissues (bones, etc.). We have much less knowledge about the evolution of any soft tissue, much less the function of any soft tissue, much less the function of a soft tissue like brain whose very function depends on the precise nature of connections between its nonfossilized cells. Nevertheless, we do now have some insight into the evolution of many brain structures and functions and how developmental and environmental processes can interact to alter brain and other body structures and functions (mind states and behaviors) in evolutionary history.

All mind states and behaviors (including complex conscious ones) in organisms are the end result of natural selection of brain and other tissues in previously existing organisms that reproduced. The behavior of an organism at a given point in time depends on the exact states of the brain, other tissues in the body, and the environment at that time. That is, nature provides the knobs and nurture determines the settings of those knobs of brain structures, and hence of brain functions and behaviors. The brain, other tissues in the body, and the environment constantly interact and change each other with time. (Hence, in the text that follows, for "brain" read "brain plus rest of body.") Consequently, the structure and function of the brain of a particular organism at a given point in time are uniquely different from the brain of that same organism at other points in time and from the brain of any other organism at all points in time, thereby in theory accounting for the differences in behavior of the same organism at different points in time and among different organisms at any point in time. In fact, if two organisms—say two genetically identical members of an invertebrate species or human monozygotic twins—had exactly the same number and type of nerve cells but bodies that were not exactly the same, then the function of their two nervous systems and mind states and behaviors would not be exactly the same. However, the functional and structural state (array of action potentials, synaptic contacts, transmitter release, etc.) of the brain of a given organism at a given point in time is usually very similar to its state in nearby time, thereby accounting for similarities in behavior at different points in time and for the continuity of consciousness and other mind states. The brain of a particular organism is also closely related to the brains of other organisms of the same species because of similarities in their genetic histories (DNA), developmental histories, and environmental histories, thereby accounting for the similarities of behavior among organisms of the same species. The greater the differences in these four variables (polymorphic genetic composition, developmental history, internal environmental history, external environmental

history), the greater the differences in brain structure and function among the brain states of a given organism at different points in time, different organisms of the same species, and different organisms of different species.

Given our current knowledge of evolution and natural selection, it is highly unlikely that a trait will appear in a particular species (much less a particular organism) fully developed de novo with no similar trait in related species. Hence, behaviors such as language, nonverbal symbolic manipulations, higher conscious thought, emotions, and so on, in humans are found, or will surely be found, in some form in primates (and perhaps in other mammals, vertebrates, or even some invertebrates)—as are (or will be) found the brain structures whose functioning is largely responsible for those behaviors. The brain structures whose function is largely responsible for those behaviors will have many similarities in organisms that are closely related in phylogenetic history. (Analogous functions having different structural bases may independently evolve in unrelated species/phyla.) As one specific example, humans have a particularly well developed ability for spoken language and nonverbal symbolic manipulations (music, math, etc.) that probably provides much of the basis for what we commonly call "higher conscious thoughts," including self-awareness, logical reasoning, and so on. All of these behaviors (and hence brain structures that produce those behaviors) are present in many other animals, in many cases to a lesser degree than in humans, but in a greater degree than is currently part of the dogma of much of cognitive neuroscience, in part because other animals with high cognitive abilities (e.g., primates closely related to humans) do not have a sufficiently complex vocal apparatus to mimic human speech patterns and those with a sufficient vocal apparatus (e.g., parrots, mynah birds, etc.) do not have the cognitive abilities of higher primates.

imperfect devices that function in a sufficient manner despite many imperfections. Furthermore, natural selection works on the finest scale of adaptations whose functional differences can be quantitative or qualitative. The existence of even a small functional difference in a complex adaptation between different members of a species (including Homo sapiens) means that the adaptation has variation that will be operated on by natural selection.

The more complex the adaptation, the more polymorphic its genetic basis is likely to be. Complex monomorphic adaptations are rare. Polymorphic genetic variation in a species is not necessarily reduced in evolutionary time by the action of natural section because polymorphic genetic variation is reintroduced in each generation by sexual recombination and mutation. Some variants do become more common but are rarely monomorphically fixed in the gene pool, in part because different alleles have different selective value in different environments (both ancestral and present). That is, genetic variation introduced by mutation and sexual recombination is maintained by balanced polymorphisms, hybrid vigor, frequency-dependent selection, geographical isolation followed by nonisolation, temporal pleiotropy (alleles with different fitness values in a given environment at different stages of an organism's development/ontogeny), and environmental pleiotropy (alleles with different fitness values in different environments at a given stage of an organism's development/ontogeny), as discussed in the previous section. Defense against pathogens is only one of many reasons for the common existence of polyallelic genes. In brief, humans—like other complex, long-lived, outbreeding organisms—are decidedly not monomorphic in the alleles of those genes that underlie complex adaptations. Rather, complex adaptations in Homo sapiens and other species are the phenotypic expression of sets of genes with various probabilities for alleles at different loci, and many of these alleles have different fitness. As presented in greater detail in Box 5, the phenotypic expression of these genes in brain tissues whose circuits are determined by both (polymorphic) genetic and environmental factors produces complex adaptive behaviors that differ between individuals in a given species.

Because humans and other animals have many complex behavioral and nonbehavioral adaptations and most complex adaptations are genetically polymorphic, it follows that individual members of Homo sapiens or other species probably have genetically different circuits and multiple natures, rather than genetically universal circuits or species-typical natures (including a universal human nature). Specifically for humans, this genetically polymorphic model is consistent with much available evidence that Homo sapiens are a polytypic species that occupies many ecological niches with genetic specialization in those niches combined with much gene flow between niches (64). Complex adaptations are phenotypically polymorphic in humans and are produced by differences in the environment as well as by differences in the polymorphic genetic composition of different individuals (Fig. 2), rather than produced almost exclusively by differences in the environment, as would be predicted by

genetically monomorphic models (Fig. 1).

Advantages of a Genetically Polymorphic Model

As discussed above, our genetically polymorphic model for complex adaptations (Boxes 2 and 5) can account for data from evolutionary psychology, individual differences psychology, behavioral genetics, ethology, evolutionary biology, and neurobiology showing that complex adaptations 1) are nonoptimal in any environment, 2) have different functions and fitness in different environments and in different ontogenetic stages, and 3) have a genetically polymorphic basis in which many alleles are acted on by natural selection. In contrast, the current genetically monomorphic model (Boxes 2 and 3) is in conflict with all of these observations. (Any other genetically monomorphic model could not, in theory, account for the last two observations.)

In addition to better accounting for a mass of currently available data from many subdisciplines of neuroscience and/or biology for many species of animals, our genetically polymorphic model would also reconcile data and theories that dominate current research by behavioral geneticists and evolutionary psychologists—and reconcile both with the assumptions of many (most?) neuroscientists. That is, most behavioral geneticists have studied the heritability of variable behaviors in humans, assuming a genetic basis and multiple human natures, and have not concerned themselves with the evolutionary origins of those behaviors. In contrast, most evolutionary psychologists have studied the possible evolutionary origins of behavioral differences (and the psychological mechanisms regulating those behaviors) between males and females—assuming such behavioral differences have a genetic basis representing a universal male or female human nature—and have not much concerned themselves with genetically specified individual differences among males or among females. Most humans, including scientists, do not find what they do not look for. If our model is accepted, behavioral geneticists would have a theoretical basis for considering evolutionary origins for behavioral differences and evolutionary psychologists would have a theoretical basis to investigate polymorphic genetic bases for differences among females or among males. Our genetically polymorphic model of complex adaptations would provide a heretofore missing theoretical bridge to reconcile the disciplines—and bring both into the mainstream of neuroscience. At the very least, in such an instance, behavioral geneticists and evolutionary psychologists would no longer have only their detractors in common.

Furthermore, according to our polymorphic model of complex adaptations, the environment and genes produce phenotypic diversity in brain circuits and adaptive behaviors (Fig. 2), instead of the environment acting alone to produce adaptive phenotypic diversity of behavior (Fig. 1), as predicted by genetically monomorphic models (see Boxes 2 and 3). Indeed, heritability would no longer be prima facie evidence that a trait is not an adaptation, as predicted by monomorphic models. Moreover, universality would no longer be required as evidence that a trait is an adaptation, as is the case when genetically monomorphic models are accepted. As properly inferred by Tooby and Cosmides (8, p. 18, quoted above), the existence of polymorphic genetic differences between individuals of the same sex "calls into question the very idea of a universal human nature." Indeed, our model predicts that polymorphic genetic variations underlying complex adaptations in Homo sapiens produce (in their terminology) multiple human natures.

Finally, rigorous searches for polymorphic genetic variation using theoretical constructs that account for the evolution of complex adaptations should one day give us a better understanding of the structure and function of different brain circuits that produce different adaptive behaviors exhibited by individuals of each sex in humans and other animals. Only with this level of eventual knowledge can we begin to understand how natural selection has produced different brain circuits responsible for multiple human natures (beyond that of "male" and "female") in evolutionary history.

Acknowledgments

We thank Dr. Sandra Tanner for insightful input at all stages of the development and writing of this model. We thank Dr. Robert Dudley, Dr. David Hillis, Dr. Mark Kirkpatrick, and Dr. Michael Ryan for their comments on drafts of this article.

References

1. Hamilton WD. The genetical evolution of social behavior. I and II. J Theor Biol 1964;7:1–52.
2. Williams GC. Adaptation and natural selection. Princeton, NJ: Princeton University Press; 1966.
3. Kirkpatrick M. Genes and adaptation: a pocket guide to the theory. In: Rose MR, Lauder GV, editors. Adaptation. New York: Academic Press; 1996. p. 125–48.
4. Reznick D, Travis J. The empirical study of adaptation in natural populations. In: Rose MR, Lauder GV, editors. Adaptation. New York: Academic Press; 1996. p. 243–90.
5. Kettlewell HBD. Selection experiments on industrial melanism in the Lepidoptera. Heredity 1955;9:323–42.
6. Grant PR, Grant BR. Predicting microevolutionary responses to directional selection on heritable variation. Evolution 1995;49:241–51.
7. Tooby J, Cosmides L. Psychological foundations of culture. In: Barkow J, Cosmides L, Tooby J, editors. The adapted mind. New York: Oxford University Press; 1992. p. 19–136.
8. Tooby J, Cosmides L. On the universality of human nature and the uniqueness of the individual: the role of genetics and adaptation. J Pers 1990;58:17–68.
9. Tooby J, Cosmides L. The past explains the present: emotional adaptations and the structure of ancestral environments. Ethol Sociobiol 1990;11:375–424.
10. Brown DE. Human universals. New York: McGraw-Hill; 1991.
11. Pinker S. How the mind works. New York: Norton; 1997.
12. Symons D. If we're all Darwinians, what's all the fuss about? In: Crawford C, Smith M, Krebs D, editors. Sociobiology and psychology: ideas, issues and applications. Hillsdale, NJ: Lawrence Erlbaum; 1987. p. 121–46.

13. Thornhill R. The concept of an evolved adaptation. In: Bock G, Cardew G, editors. Characterizing human psychological adaptations. Chichester, UK: Wiley; 1997. p. 4–13.
14. Bailey JM. Can behavioral genetics contribute to evolutionary behavioral science? In: Crawford C, Krebs DL, editors. Handbook of evolutionary psychology. Mahwah, NJ: Lawrence Erlbaum; 1998. p. 221–34.
15. Buss DM, Greiling H. Adaptive individual differences. J Pers 1999;67:209–43.
16. Gangestad SW. Evolutionary psychology and genetic variation: non-adaptive, fitness-related and adaptive. In: Bock G, Cardew G, editors. Characterizing human psychological adaptations. Chichester, UK: Wiley; 1997. p. 212–30.
17. Mealey L. The sociobiology of sociopathy: an integrated evolutionary model. Behav Brain Sci 1995;18: 523–99.
18. Wilson DS. Adaptive genetic variation and human evolutionary psychology. Ethol Sociobiol 1994;15:219–35.
19. Tooby J. Pathogens, polymorphism and the evolution of sex. J Theor Biol 1982;97:557–76.
20. Jones JS, Leith BH, Rawlings P. Polymorphism in Cepaea: a problem with too many solutions? Annu Rev Ecol Syst 1977;8:198–43.
21. McNeilly T. Evolution in closely adjacent plant populations: III. *Agrostis tenius* on a small copper mine. Heredity 1968;23:99–108.
22. Dudley R, Gans C. A critique of symmorphosis and optimality models in physiology. Physiol Zool 1991;64: 627–37.
23. Latter BDH. Natural selection for an intermediate optimum. Aust J Biol Sci 1960;13:30–5.
24. Lauder GV. The argument from design. In: Rose MR, Lauder GV, editors. Adaptation. New York: Academic Press; 1996. p. 55–92.
25. Seger J, Stubblefield JW. Optimization and adaptation. In: Rose MR, Lauder GV, editors. Adaptation. New York: Academic Press; 1996. p. 125–48.
26. Fisher RA. The general theory of natural selection. 2d ed. New York: Dover; 1958.
27. Hill WB, Robertson A. The effect of linkage on limits to artificial selection. Genet Res 1966;8:269–94.
28. Felsenstein J. Sex and the evolution of recombination. In: Michod RE, Levin BR, editors. The evolution of sex: an examination of ideas. Sunderland, MA: Sinauer; 1988. p. 74–86.
29. Falconer DS. Introduction to quantitative genetics. 2d ed. London: Longman; 1986.
30. Lande R, Arnold SJ. The measurement of selection on correlated characters. Evolution 1983;37:1210–26.
31. Yablokov AV. Variability of mammals. New Delhi: Amerind; 1974.
32. Mousseau TA, Roff DA. Natural selection and the heritability of fitness components. Heredity 1987;59:181–97.
33. Price T, Turelli M, Slatkin M. Peak shifts produced by correlated response to selection. Evolution 1993;47:280–90.
34. Muller HJ. Our load of mutations. Am J Hum Genet 1950;2:111–76.
35. Schluter D, Nychka D. Exploring fitness surfaces. Am Nat 1994;143:597–616.
36. Henistra PWH, Thorig GEW, Scharloo W, Drenth W, Nolte RJM. Kinetics and thermodynamics of ethanol oxidation catalyzed by genetic variants of the alcohol dehydrogenase from *Drosophila melanogaster* and *D. simulans*. Biochem Biophys Acta 1988;967:224–33.
37. Freriksen A, De Ruiter BLA, Groenenberg H-J, Scharloo W, Heinstra PWH. A multilevel approach to the significance of genetic variation in alcohol dehydrogenase of *Drosophila*. Evolution 1994;48:781–90.
38. Mercot H, Defaye D, Capy P, Pla E, David JR. Alcohol tolerance, ADH activity, and ecological niche of *Drosophila* species. Evolution 1994;48:756–7.
39. Hougoto N, Lietaert MC, Libion-Mannaert M, Feytmans E, Elens A. Oviposition-site preference and Adh activity in *Drosophila melanogaster*. Genetica 1982;58:121–8.
40. Hoffman AA, Parsons AA. Olfactory response and resource utilization in *Drosophila*: interspecific comparisons. Biol J Linn Soc 1984;22:43–53.
41. Chambers GK. The *Drosophila* alcohol dehydrogenase gene-enzyme system. In: Caspari EW, Scandalois JG, editors. Advances in genetics. Vol. 25. New York: Academic Press; 1988. p. 39–107.
42. Cavener DR, Clegg MT. Evidence for biochemical and physiological differences between enzyme genotypes of *Drosophila melanogaster*. Proc Natl Acad Sci U S A 1981;78:4444–7.
43. Van Delden W, Kamping A. The association between the polymorphisms at the Adh and Gdph loci and the In(2L)t inversion in *Drosophila melanogaster* in relation to temperature. Evolution 1989;43:775–93.
44. Geer BW, Heinstra PWH, McKechnie SW. The biological basis of ethanol tolerance in *Drosophila*. Comp Biochem Physiol B Biochem Mol Biol 1993;195B:203–29.
45. Koehn RK, Hilbish TJ. The adaptive importance of genetic variation. Am Sci 1987;75:134–41.
46. Powers DA, Di Michele L, Place AR. The use of enzyme kinetics to predict differences in cellular metabolism, developmental rate, and swimming performance between LDH-B genotypes of the fish, *Fundulus geteroclitus*. Isozymes: Curr Topics Biol Med Res 1983;10:147–70.
47. Watt W. Adaptation at specific loci: I. Natural selection on phosphoglucose isomerase of Colias butterflies: biochemical and population aspects. Genetics 1977;87:177–94.
48. Watt W. Adaptation at specific loci: II. Demographic and biochemical elements in the maintenance of the Colias PGI genotypes are predictable from in vitro biochemistry. Genetics 1983;103: 691–724.
49. Watt W, Cassin RC, Swan MS. Adaptation at specific loci: III. Field behavior and survivorship differences among Colias butterflies: biochemical and population aspects. Genetics 1983;103: 725–39.
50. Chappell MA, Snyder LRG. Biochemical and physiological correlates of deer mouse a-chain hemoglobin polymorphisms. PNAS 1984;81:5484–8.
51. Chappell MA, Hayes JP, Snyder LRG. Hemoglobin polymorphisms in deer mice (*Peromyscus maniculatus*): physiology of beta-globin variants and alpha-globin recombinants. Evolution 1988;42:681–8.
52. Snyder LRG, Hayes JP, Chappel MA. Alpha-chain hemoglobin polymorphisms are correlated with altitude in the deer mouse, *Peromyscus maniculatus*. Evolution 1988;42:689–97.
53. Weiner J. The beak of the finch. New York: Vintage; 1994.
54. Plomin R, DeFries JC, McClearn GE. Behavioral genetics: a primer. 3d ed. New York: Freeman; 1997.
55. Hernstein RJ, Murray C. The bell curve: intelligence and class structure in American life. New York: Free Press; 1994.
56. Loehlin JC. Genes and environments in personality development. Newbury Park, CA: Sage; 1992.
57. Loehlin JC, Rowe DC. Genes, environment, and personality. In: Capara G, Van Heck, GL, editors. Modern personality psychology: critical reviews and new directions. New York: Harvester Wheatsheaf; 1992. p. 352–70.
58. Gottesman II. Schizophrenia genesis. San Francisco: Freeman; 1991.
59. Cloninger CR. Neurogenetic adaptive mechanisms in alcoholism. Science 1987;17:410–15.
60. Kendler KS, Heath AC, Neale MC, Kessler RC, Eaves LJ. A population-based twin study of alcoholism in women. JAMA 1992;268:1877–82.
61. Gangestad SW, Simpson JA. Toward an evolutionary history of female sociosexual variation. J Pers 1990; 58:69–96.
62. Gangestad SW, Simpson JA. Development of a scale measuring genetic variation related to expressive control. J Pers 1993;61:133–58.
63. Steudel K. Limb morphology, bipedal gait, and the energetics of hominid locomotion. Am J Phys Anthropol 1996; 99:345–55.
64. Cavalli-Sforza LL, Menozzi P, Piazza A. The history and geography of human genes. Princeton, NJ: Princeton University Press; 1994.