# Chapter 14: Human Evolution

## How Humans Evolved

### Protohuman Evolution

Anyone reading this section 50 years from now will laugh at its naiveté, and the reason for his or her bemused state will be justified. The discovery of new fossils, the sequencing of the human genome, and the completion of the Human Genome Diversity Project will provide new insights that alter currently cherished beliefs. This has been the history of science in human evolution, so there is no reason to suspect that the trend will change. Still, we are stuck in the present and must do the best we can with the available data.

Most biologists suspect that humans and chimpanzees (our closest genetic relative) split off from a common ancestor as recently as 4 to 5 million years ago (mya)[1]. The split occurred in Africa. One of the first evolutionary developments that distinguish human ancestors from chimps was upright posture. One of the earliest of the human genera (plural of genus), the Australopithecines (a Latin term for "southern ape"), walked upright and had modified hands, but in many other ways resembled a chimp. They were small (between 3 and 4 feet tall), had curved fingers, and a skull with a protruding jaw, a recessed cranium, and heavy ridges behind what are now the eyebrows.



[1] In terms of biological classification,, the split resulted in the development of the family Hominidae. Hence, the term *hominid* refers to all of our ancient ancestors from this split onward.

The reason for the development of upright posture is unknown, but it certainly permitted the Australopithecines to travel long distances, freed their hands to carry objects, and may even have allowed more efficient thermoregulation. Because of these advantages conferred by upright posture, many anthropologists suspect that the early Australopithecines were adapting to life on the savanna[2] (the open places on the African plains) while the ancestors of today's chimps remained in the forested areas of central Africa. Over the course of 2 million years, several varieties and species of Australopithecines may have cohabited together and possibly even competed with one another in the savanna and woodlands that border the savanna. Little is known about the behavior of the Australopithecines other than they probably used tools and were a highly social species as chimps and we are today.

About 2 mya, fossils begin to appear from our own genus, *Homo*. Although several species of *Homo* are recognized, we will lump them all together for didactic purposes and refer to them as *Homo erectus*. The most striking feature of evolution in *h. erectus* (i.e., striking for this book's purpose) is the change in the brain. Instead of the skull increasing in size as a function of increased body size, the very *form* of the skull changed. The upper cranium of the skull expanded and assumed a more rounded shape, permitting brain size to increase from about 450 cc to between 800 and 1200 cc. Other evolutionary trends continued—the protruding jaw receded a bit, teeth became smaller, and height increased. Two behavioral phenomena are striking—(1) tool use is now well documented in the form of flint and stone deliberately fashioned to act as chopping,



[2] Preoccupation with the savanna environment may be a classic case of looking for the keys under the lamppost because the light is better there. Bones in humid, forested areas decay rapidly while those in drier climates can fossilize.

scraping and cutting tools; and (2) *Homo erectus* migrated out of Africa. Fossils of *erectus* have been found in China, Southeast Asia, and southern Eurasia. It is assumed that *erectus* retained the sociality of their ancestors.

As time progressed these trends in skeletal evolution continued—the cranium and brain size increased, the jaw receded, the thick brow ridges shrank, and teeth became smaller. In more recent times (c. 100,000 of more ya) anatomical variants[3] are evident in the fossil record. One of these, the Neandertals[4], were a heavy boned hominid whose fossil remains stretch from Western Europe to the Middle East. A second variant, with a more gracile (i.e., slender) skeletal form, also appeared between 100,000 and 200,000 ya. By 50,000 ya the gracile form lived side-by-side with Neandertals in some areas.

Who were these variants and how did they relate to anatomically modern humans (amh) and *Homo erectus*? This is a matter of considerable debate among anthropologists and evolutionary geneticists. Two main theories (along with numerous offshoots) have been proposed.



**Theories of Recent Human Evolution**

The first theory is termed the *multiregional hypothesis* (AKA *regional continuity hypothesis*) and is espoused by some physical anthropologists (Wolpoff & Caspari, 1997). This view holds that *Homo erectus* populations in Africa, Europe, and Asia underwent convergent evolution and with sufficient gene flow among the geographically

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[3] I use the term *variant* loosely. It does not necessarily imply a different species, although that might indeed be the case.

[4] Named after the Neander Valley in Germany where their fossils were first discovered. Although the term Neandertal today carries the connotation of a brutish and stupid barbarian, Neandertals had the noble qualities of esthetics and respect for the dead evident in their careful burials. Why they disappeared has not

separated populations, jointly evolved into amh. Convergent evolution occurs when different populations face similar selection pressures that lead to the same adaptive response. Development of the fin in fishes and in whales is a classic example in which two very different types of organisms evolved a similar mechanism for swimming through water. Applied to humans, the need to seek shelter from temperature extremes is the same the world over and could—in theory at least—lead to selection for the increased cognitive skills to build those shelters.

Few, if any, advocates of the multiregional hypothesis hold that convergent evolution alone is responsible for the worldwide anatomical similarity of modern humans. Some gene flow is required among geographically separated populations. Theorists posit that there was a sufficient amount of human migrations and mate exchanges between adjacent populations to permit *H. Erectus* populations to evolve in similar directions. In this way, mutant but beneficial alleles that originated in Africa could eventually spread to other regions of the Old World.



The multiregional hypothesis holds that the descendants of *Homo erectus* are our direct ancestors. Anatomically modern humans are the result of some beneficial mutations that caused an increase in population size. Subsequent migrations and interbreeding with extant groups of *Homo erectus* in different regions of the world spread these mutations. According to this view, Neandertals were not a different species of hominids that became extinct. Instead, generations of matings between the Neandertals and the more gracile variant, coupled with a selective advantage for the genes of the

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been clearly established. They may have interbred with a more numerous variant of *Homo* and lost their distinctive anatomy and/or been driven towards extinction by competition.

gracile variant, resulted in a change in the mean of a continuous distribution of skeletal dimensions.

**[? ADD EXAMPLE HERE]**

The second theory has been dubbed the *Garden of Eden* or GOE hypothesis (Harpending & Rogers, in press) **[GET CORRECT CITE].** The name of this theory has little to do with the accounts of creation given in the Judaic-Christian tradition. Instead, the term is a slightly perverse—but humorous—extension of early reports from the genetic literature of a "mitochondrial Eve" (Cann, Stoneking, & Wilson, 1987) and later a "Y-chromosome Adam" (see Cavalli-Sforza, 2000). Mitochondrial DNA and the Y chromosome are in many ways ideal for studying human evolution because they are passed intact from mother to child (mitochondria) or from father to son (Y chromosome) and do not recombine as the DNA on the autosomal chromosomes do[5]. This form of transmission has the mathematical implication that in some very ancient ancestral population, all but one of the mitochondrial variants (or Y chromosome variations) will eventually die out. After all, the mitochondria of a mother who has only sons will die out as will the Y chromosome of a male who has only daughters. By examining today's mtDNA and today's Y chromosome, one can work backwards to arrive at an approximate date for these ancestral populations.



Today's estimates are between 100,000 and 200,000 ya. Somewhere in this time period, a single woman lived from whom all current mtDNA is derived. A man also lived during this time and gave rise to all variants of the Y chromosome seen today.

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[5] There is, however, a small section of the Y chromosome, called the pseudoautosomal region, that recombines with a homologous region on the X chromosome.

Contrary to popular misconception, this Eve and Adam are *not* the ancestors of all modern humans. (In fact, they may not have been anatomically modern humans at all.) They are the ancestors of *only* our mitochondrial DNA and the DNA on the Y chromosome. Many other individuals contributed to the DNA in our autosomal chromosomes.

According to the GOE hypothesis, amh originated somewhere in Africa between 50,000 and 150,000 ya. The African origin is suggested by the observation that genetic variation is greatest in contemporary African populations. This ancestral population was possibly a new species of *Homo* that grew in size and migrated—possibly more than once—out of Africa and into the Middle East.

One hallmark of the GOE theory is *population replacement*. Advocates of this speculate that early *Homo sapiens* was a completely different species that did not interbreed with the populations of *H. erectus* and Neandertals with whom it came into contact. Instead, they competed with those populations and eventually replaced them[6].



Two types of data are used in support of the GOE theory. First, archeological investigations show noticeable skeletal differences between Neandertals, recent *Homo erectus* populations and the gracile form that is assumed to be our direct ancestor. In parts of Eurasia, the emergence of these fossils also coincides with a marked advancement in technology stretching from Europe to Siberia. The second line of evidence consists of the molecular genetic data. Estimates of the time frame for human origins from these data fit very well with the archeological data.

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[6] Note that the ideas of replacement versus interbreeding are *not* mutually exclusive. Both phenomena may have occurred.

**Human Evolution into the Historical Era**

Irrespective of whether amh replaced and/or interbred with *Homo erectus* and Neandertals, there is considerable agreement on the particulars of very recent human evolution (i.e., evolution from 100,000 ya to 50,000 ya). The slanted forehead of *H. erectus* gave way to the large, vertical forehead of modern humans, permitting the brain to increase in size. The skeletal structure attained a gracile form very close to modern humans. Tool use—or at least the evidence of tool use—suggests that it developed into an art. Spearheads were invented, bone instruments were fashioned to sew, pictorial drawings appear in caves, and some implements show evidence of engraving. But human evolution was not finished by 50,000 ya. The skeleton continued its gracile development and cranium capacity still increased to give its present day range of 1000 to 2000 cc, the average today being somewhere between 1300 and 1400 cc.

Most scientists believe that early amh were foraging hunter-gathers. They lived in small, cooperative groups that would settle in a single location and hunt, dig roots, pick fruit, and possibly harvest grain until the immediate resources were depleted. Then they would move on. Many hypothesize strong sex-role differences during this period—the guys hunted, the gals gathered. The small human groups—like virtually every other mammalian omnivore—adapt to seasonal change, migrating to areas of optimal foraging and hunting at the appropriate time of year. Somewhere in the history of this—and whether it started 2 mya or 20,000 ya is anybody's guess—the mating structure changed. Some form of *Homo* eventually recognized a relative permanence in mating that said something to the effect that this guy (or these guys) have a recognized relationship with this gal (or these gals) that permits them to mate, call them "their own," and transfer

property and prestige to their offspring. Early *Homo* also became cognizant of genealogy. Barak was not just Barak. He was also Thrug's and Amalog's son.

Everyone agrees that the increasing human cranial capacity was accompanied by an increase in intellect—memory, symbolic manipulation, learning capacity, etc. The largest anatomical differences between human and chimp brains are in the frontal lobes—those areas associated with executive functioning, evaluation, and reason. The increase in frontal material permitted our hominid ancestors to develop culture beyond the simple social learning cultures of macaques, chimps, and bonobos. Our monkey and ape cousins have only the "monkey see—monkey do" cultural transmission. *Homo*'s ability to transmit culture includes simple imitation but expands into symbolic instruction. At some point *Homo* could communicate the idea "don't do it that way, do it like XYZ" without ever physically demonstrating the "XYZ" behavior. Barak is no longer just Barak and is no longer just Thrug's and Amalog's son. He is also Gortog's grandchild, even though Gortog, dead for several years, is a person unknown to the listener.



The reasons behind the evolutionary increase in brain size are not known, although there is no shortage of speculation. The need to fashion better tools, the requirements for sophisticated social interaction with conspecifics, the benefits of symbolic thought and language for competition between human groups have all been postulated as reasons for the intelligence of hominids. It is also possible that the causes for increased brain size shifted over time, say from social communication to symbolic and rational thought to competition. Whatever the reason(s), they must have been quite important. Metabolically, the brain is a very expensive organ. Although it comprises

only 2% of body weight, it consumes about 20% of the body's metabolic resources. Such an expense does not come without important evolutionary trade offs. Also, the increased brain size posed (and still does pose) difficult problems for mothers who must squeeze such a large structure through the pelvis and vagina during childbirth.

Two cultural inventions altered the environment for amh. The first (i.e., the first to be explained here, not necessarily the first temporally) was the domestication of certain animal species. A few human populations no longer had to hunt for meat. They could simply tame the "meat," lead it to green pastures, slaughter it at will, and use its milk, wool, etc. The second invention was agriculture. It is thought that agriculture was developed sometime around 10,000 ya, probably independently in several different areas of the world. But the pattern of its discovery and diffusion is unclear. No matter. The end result was the same—agriculture limited the nomadic wandering of some human populations. They had to stay in a single geographical area to plant, tend, and harvest crops.



It is assumed that agricultural populations increased in number. This had two important effects. First, some agricultural populations migrated into the adjacent areas occupied by hunter-gatherer societies. Because the agriculturists grew in size while the population size of their hunter-gatherer neighbors remained stable, the number of agriculturists would eventually overwhelm the hunter-gatherers. Through interbreeding, population growth, cultural assimilation, and/or competition, the agricultural societies would become dominant in many fertile areas of the world.

The second effect of population growth under agriculture was an elaboration of social roles. As the technology of raising crops improved, it was no longer necessary for

everyone to toil in the fields. Some people could become what today's economists call service and manufacturing employees while others became supervisors. The result was an integrated web of codependent roles and occupations, leading to the development of cities and what we now call civilization[7], the first evidence of which appeared 5,000 ya.

The archeological record clearly shows that civilization did not start in one place and then spread unchecked throughout the world. Civilization appeared here and there in a series of starts and stops and not from a slow, inexorable diffusion from a single central origin. In a manner still obscure to science, civilizations develop in an area, flourish, and disappear. To the best of our knowledge, the actual humans do not change, at least in any dramatic way—the cranial capacity of those who start and develop a civilization appear to be no different than those who disperse and engage in less sophisticated social, political, and occupational roles after the civilization's demise. Indeed, the reasons for change in civilizations are some of the greatest mysteries facing social science.



## Genetics and Human Races

So far, we have examined humanity as a whole. Yet it is quite clear that over the course of history, humans have lived in different groups that have evolved different languages, cultures, and physical traits. What does genetics tell us about how individuals relate to a group and how different groups relate to one another? We being discussion by considering orangutans and jaguars.

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[7] The term "civilization" has several meanings. Here, it is meant as an elaborate system of interacting social, political, and occupational roles that coincides with the development of cities. It is not meant to imply "cultural refinement" in either a moral or esthetic sense, nor is it meant to imply that nonagricultural societies are "uncivilized." *All* human populations have a culture, but not all human populations have a culture that involves cities.

Orangutans live in two large islands in Southeastern Asia, Borneo and Sumatra. By visual inspection, the orangs inhabiting Sumatra are indistinguishable from their cousins on Borneo. Yet genetically, the two populations are quite different. They are two different races of orangutan.

Most jaguars have conspicuous orange, tan, and black sports. Yet occasionally a jaguar is born with a dark, black coat that makes the spots impossible to see from a distance. Despite the glaring visual differences, these two types of jaguars are *not* different races.

To the geneticist race need not imply visual morphological differences and visual morphological differences need not imply race. Clearly, there are important differences between how geneticists define race and societies define race. The social definition is *absolute* and *categorical*. It is the type of box that we check when filling out a form; it is how demographic statistics are broken down; it is often how we think of someone that we have seen but never met simply on the basis of that person's appearance; and it is based on clear, visual morphological differences.



Geneticists define race as a population with a characteristic set of allele frequencies and whose ancestors have tended to mate among themselves for an appreciable amount of time. Geographical separation prevented the orangs on Borneo from freely mating with those on Sumatra and evolutionary forces resulted in different allele frequencies on the two islands. The orangs qualify as genetic races. Only a few genes are responsible for the differences between black and spotted jaguars. The ancestors of spotted jaguars have freely mated with those of black jaguars. They fail to meet the genetic definition of race.

The genetic definition is *relative*, not absolute[8]. For this reason, some geneticists eschew the term "race" in favor of the term "genetic population[9]." The Irish, Scots, and Welsh could be considered three different "races" of Celts or they could be combined into a Celtic "race" if they were being compared to Greeks. The Zulus in South Africa, the !Kung in the Kalahari Desert, and Ibo in Nigeria could legitimately be compared as three different "races."

The genetic definition can also be dimensional. Genetically, human populations do not fall neatly into categories. Instead, they tend to blend into one another often as a function of geographical proximity. The gradual expansion of humans throughout the Old World resulted in *some* geographical isolation, but many populations grew, expanded, and migrated to merge with other populations. As a result, when one color codes populations according to allele frequencies and then paints them onto a map of the Old World, the result resembles subtle changes in hue as one moves from one area to another. It does *not* resemble an Impressionist painting with dabs of quite different colors placed adjacent to one another**. [CAN GET FIGURES FROM CAVALLI HERE?]** The majority of human populations—or "races" if you prefer that term—genetically resemble the people geographically closest to them.



Note how the genetic definition of race mentions nothing about those visual and morphological characteristics that highlight the social definition. Genes for skin color; hair texture, etc. are only a small part of the tens of thousands of loci in the human genome. Furthermore, the population geneticist, Mashitoshi Nei suspects that genes for

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[8] A relative term has meaning only when it is compared to something else. Philadelphia is north of Baltimore, and Boston is north of Philadelphia. Hence, Philadelphia can be north and south at the same time—it all depends on which city Philadelphia is compared to.

external morphology can give misleading impression of genetic distance because they change at a different evolutionary tempo than the rest of the genome (Nei, 1987). This is an important point, so let us further explore it.

Consider the following: the proverbial Martian biological anthropologist visits earth and is asked to pick the "odd ape out" from the following collection of great apes—gibbons, orangutans, gorillas, chimps, and humans. Which would you pick? Then answer the following multiple-choice question:

The chimpanzees in the Bronx zoo most closely resemble:

(a) gorillas

(b) orangutans

(c) gibbons

(d) the author of this book



If the criteria for similarity were based on genes, then the odd ape out is the gibbon and the answer to multiple choice question is (d) the author of this book. Despite all the obvious morphological differences between humans and the other great apes—density of hair, gracile skeleton, upright posture, etc.—we are genetically more similar to an orangutan than an orangutan is to a gibbon. Our closest genetic cousins are chimpanzees. Hence, a chimp is genetically more similar to us humans than to a gorilla or an orangutan. In short, external morphology is not always a good indicator of genetic distance among closely related populations or species.

The phenotype of human skin color follows the same lesson that we learned in discussing sickle-cell anemia. The primary correlate of gene frequency differences for

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[9] Be careful not to confuse the term *population* as used in genetics with the same term used in statistics.

sickle cell anemia is malarial ecology, not race. Similarly, the primary correlate of skin pigmentation differences is *distance from the equator*. Dark skin is an evolutionary adaptation that has something to do with exposure to the sun and is found among the majority of Old World populations living in equatorial areas[10]. Many people in southern India and Sri Lanka are more darkly pigmented than some African populations, yet they are genetically closer to Scandinavians than they are to sub-Saharan Africans. Similarly, some populations in Papua New Guinea are visually indistinguishable from equatorial Africans, but are genetically closer to current-day Japanese and Chinese than they are to Africans. **[? GET A PICTURE OF THESE THREE TYPES OF PEOPLE FROM GOLDSBY]**.

In summary, geneticists define "race" quite differently from social scientists and stress *all* genes, not simply those for skin color and other visible morphological differences. Because the vast majority of human genes result in "invisible" phenotypes (blood groups, kidney functioning, etc.), they are much more important for defining concepts like race or population than are loci for visible phenotypes. The old phrase "you can't judge a book by its cover" describes very well the geneticists' view of human population differences. Concepts like "black," "white," and "people of color" are very useful and valid for the social scientist studying prejudice. They are not particularly helpful to the geneticist.



[10] The reason(s) for differences in human pigmentation are not completely known. The best guess is that our very early ancestors were lightly pigmented with a dense covering of hair much like today's chimps. Loss of hair was accompanied by darkening of the skin to prevent damage from ultraviolet (UV) radiation. As humans migrated from equatorial regions, selection pressure for UV protection diminished and was replaced by a greater need for UV light to assist in the synthesis of vitamin D, something better accomplished by lighter pigmentation.

In fact, the difference between the genetic and the social definitions of race becomes even more striking when one examines the actual types of data used by population geneticists to measure similarities and differences among populations. The simplest way to measure genetic distance between two individuals is to sequence a section of their DNA and then count the number of nucleotides that differ between the two[11]. However, to avoid the problem that natural selection may have created these differences, scientists prefer to study *neutral* genes. Neutral genes are those that have no selective advantage or disadvantage and are most often found among the "junk" part of the human genome[12]. We can corrupt the English language—and logic—by saying that these are the most invisible of the invisible phenotypes.

## Genetic Differences among Human Populations

Just how genetically different are human populations from one another? The short but correct answer is "Not very much." The same types of genetic studies that pointed to our recent African origins also imply that we are a very new species that has not had time for strong genetic divergence. Templeton (1999) compared genetic diversity among human populations to that of other large mammals and showed that coyotes, wolves, deer, gazelles, and elephants have anywhere from three to nine times the genetic diversity between their respective populations than we humans do among ours. He went on to argue that the term "race" should not be applied to human populations



[11] Naturally, there are other ways in addition to this oversimplified example. For repeated nucleotide sequences, one could the number of repeats in person one and person two and then take the absolute value of the difference.

[12] Neutral alleles are also helpful in constructing evolutionary clocks. Because mutations that cause nucleotide substitutions occur at a fixed rate, one can obtain crude estimates of the time of population divergence by studying neutral alleles. Alleles subject to selection cannot perform this task as easily as neutral alleles can.

because no population is sufficiently different from any other one as to warrant the use of the word as it is typically used in population biology.

A full accounting of human genetic differences must await the results from the Human Genetic Diversity Project, a massive research project with two major aims: (1) the detection and cataloguing of allelic differences among the quickly-disappearing indigenous populations of the world; and (2) using these data to reconstruct human evolution and migration. Nevertheless, smaller studies over the past 50 years have been so consistent in their findings that the broad conclusions are known (e.g., Cavalli-Sforza, Menzonni & Piazza, 1994; Hartl & Clark, 1997; Nei & Roychoudhury, 1974; Nei, 1987). Somewhere between 10% and 15% of all human genetic variation differs between populations. The vast majority of human genetic variation—fully 85% to 90%--is found *within* human populations[13].

The statistical jargon of between and within group differences is very abstract, so let us try to depict it in picture. Figure 14.1 gives three normal curves with the same mean but different variances. The curve with the solid line has a variance of 1. This is analogous to the genetic diversity in the whole species. The curve with the short dashes gives the within-population genetic variance when it accounts for 85% of all genetic diversity. The curve with the longer dashes denotes the between-population genetic variance. Notice how similar the "total" curve is to the "within-population" curve. This demonstrates how the genetic variation *within* any human population—or "race" if you prefer that term—almost captures *all* the genetic diversity of our species.



[13] Technically, 5% to 15% of all genetic variance is due to mean differences in allele frequencies between populations. The remaining 85% to 95% is within-population genetic variance.

[Insert Figure 14.1 about here]

A second way of picturing genetic diversity is to assume that we had the nucleotide sequence for a large stretch of human DNA and tabulated all the nucleotide differences in the human species. Let us scale these differences so that the total variance is 100 units and let 15% of these differences be due to between population (or between races) differences. Now let us pick two individuals at random from the whole human species (regardless of race) and count the number of nucleotides at which they differ in this DNA stretch. Suppose that we repeat this an infinite number of times—selecting two random people and counting the number of nucleotide differences. We then tabulate the percent of our pairs who have no differences, the percent with one or fewer differences, the percent with two or fewer differences, etc. The solid line in Figure 14.2 gives a plot of these hypothetical data[14]. To interpret these data, pick a figure on the horizontal axis—say 5 for example—and then read the value on the vertical axis for the solid curve. For 5 nucleotide differences, the value of the vertical axis is 30.3. This means that 30.3% of the pairs of randomly chosen individuals differed by 5 or fewer nucleotides. Hence 69.7% of them differed by more than five nucleotides.



[Insert Figure 14.2 about here]

Suppose we now select two individuals *within the same race* and count their differences. Again, we repeat this an infinite number of times and tabulate the percent of pairs who have a certain number of nucleotides (or fewer) different. This curve is depicted in the short dashed line in Figure 14.2. Notice how this curve differs very little

[14] These hypothetical curves in the figure were generated from Monte Carlo simulations assuming that the original distribution was normal.

from the one from two randomly selected people from the entire species. This implies that two individuals within the same race are almost—but not quite—as different from each other as two individuals selected from the whole species. Most of human genetic diversity is found *within* a race.

The long dashed curve in Figure 14.2 pictures what would happen if we calculated the *mean* nucleotide sequence for each race. We then picked two races at random and then compared the *mean* nucleotide sequence of the first race with the *mean* nucleotide sequence of the second race. Again, by repeating the sampling a very large number of times and tabulating the differences, we would arrive at a curve similar to the long dashed one in Figure 14.2. Notice how this curve departs markedly from the other two. Over two-thirds of the racial means differ by five nucleotides of less, about one third of the comparisons within a race differ by five or fewer nucleotides, while 30.3% of the comparisons made at the species level differ by five or fewer nucleotides. Of the racial means, 99.9% differ by 17 nucleotides or less while this cutoff captures 82% of the within-race comparisons and 79% of the species comparisons.



If this hypothetical example were applied to, say, the ABO gene, the results would suggest that the majority of human populations have the A allele, the B allele, and the O allele in them. Although the populations differ in the *frequency* of the A, B, and O alleles, these differences in frequency are usually relatively minor compared the fact that almost all human populations have the three alleles in them.

A final thought experiment could also illustrate the concept of between and within population genetic diversity. Suppose a grand catastrophe occurred (e.g., a large asteroid struck Earth) that resulted in the extinction of all of humanity except for a population of

Eskimos living on the Arctic Circle. After many years, this population expands and migrates to eventually resettle the entire planet. From such limited origins, humanity would now have fully 85% to 95% of its pre-cataclysmic genetic diversity. That is, we would go from the solid-line normal curve in Figure 14.1 to the short-dashed curve in Figure 14.1. Or, if we wanted to select two randomly chosen survivors and compare them to randomly chosen people before the event, then the differences would be in the range of the short-dashed curve and the solid curve in Figure 14.2. People on different corners of the planet may *look* more similar to one another than they did before the calamity, but the genes for visible morphology are only a very small—and inconsequential—part of the totality of human genetic diversity.

**[? ADD SECTION ON HUMAN TREES]**

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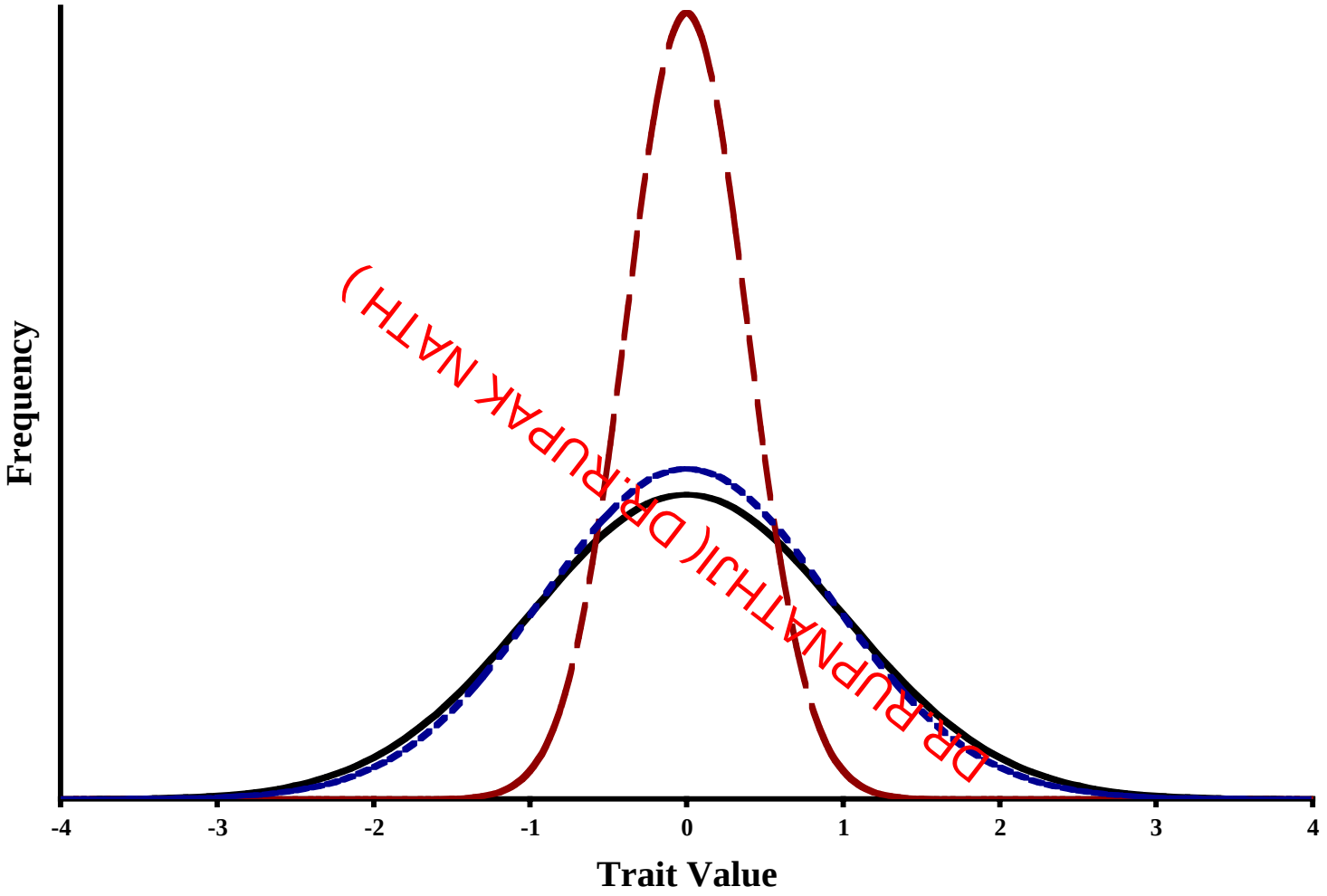


Figure 14.1. An illustration of total phenotypic variance (solid line), 15% of which is due to between-group variance (long-dashed line giving the curve with the high peak), and 85% to within-population variance (short-dashed curve).

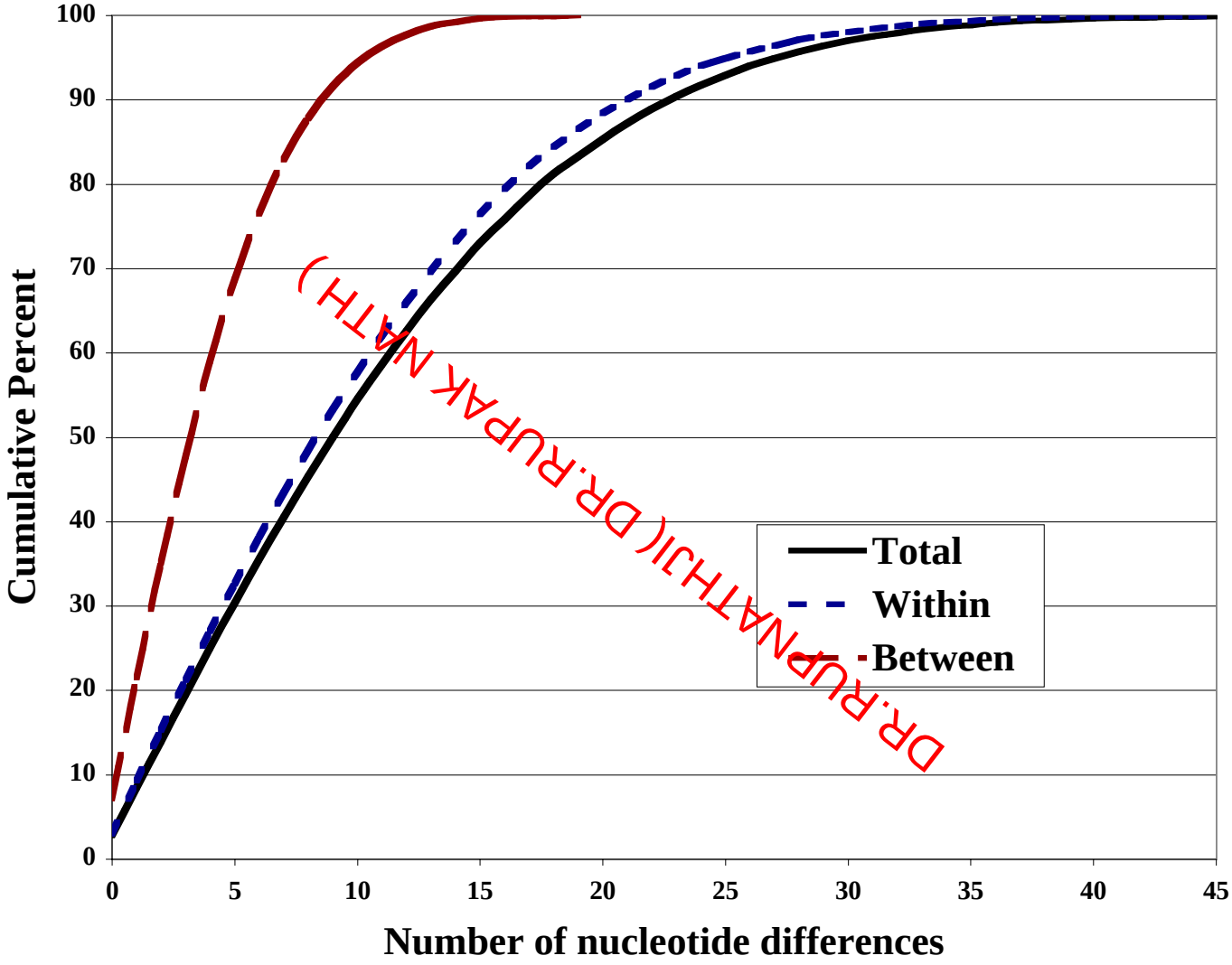


Figure 14.2. Relationship of total phenotypic variance, between-group variance, and within group variance (see text)