topic I have ever read. Dennis Venema marvelously explains genetic concepts by using everyday illustrations. Scot McKnight's approach is pastoral. In an awe-inspiring manner, he sensitively leads us into an appreciation of the biblical issues and shows us how theologically rich and intellectually satisfying they are. Because it is so clearly and carefully written, this book will mark a watershed moment in the history of evangelical Christianity. The radical distinction between two seemingly disparate positions ought to disappear forever, these authors show, as each position melds with the other to form one harmonious whole."

—**Darrel Falk**, Point Loma Nazarene University

"This is an unlikely book. Who could imagine a geneticist and a New Testament scholar teaming up to write about Adam and Eve? We are fortunate that they did. Venema and McKnight address in a learned yet accessible way issues about which many of us have little understanding. We are indebted to them for giving us information and insights that enable us to think about human origins in ways that are both scientifically informed and grounded in a carefully nuanced interaction with the biblical text and early Jewish traditions. The church is well served by this sort of interdisciplinary collaboration, which assists us in both adapting and adopting Adam (and Eve) as interpreters have through the centuries."

—**John H. Walton**, Wheaton College

"This is a unique and valuable book: an expert geneticist and a leading New Testament scholar come together to address questions of Adam and Eve. Venema and McKnight guide readers in an in-depth look at the genetic evidence for human evolution and at the views of Adam in the ancient Jewish world. As these two Christian scholars listen to each other, share their personal journeys on origins, and address the questions of evangelicals, their pastoral concern for the church and for students shines through. Not all readers will agree with their conclusions, but the book is essential reading for all who seek an understanding of human origins that respects both Scripture and God's creation."

—**Deborah Haarsma**, president of BioLogos

"Anyone who doubts that Christian faith and evolutionary science can have a peaceful and fruitful relationship needs to read this remarkable book, a shining example of a complementary approach to science and religion in which both enhance, enrich, and complete each other. Dennis Venema offers indisputable scientific evidence for the evolution of living organisms, including humans, in a clear, accessible style. Scot McKnight deals with the challenging issue of whether Adam was a historical person. Drawing upon a wide range of creation accounts from the ancient Near East, and in particular ancient Jewish literature, he demonstrates that biblical passages on human origins and Adam must be read within their ancient milieu and context. I highly recommend this book."

—**Denis O. Lamoureux**, St. Joseph's College, University of Alberta

ADAM AND THE GENOME

Reading Scripture after Genetic Science

DENNIS R. VENEMA
// AND //
SCOT McKNIGHT

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CONTENTS

tetrapod vertebrates, as we have seen, share ancestors with fish; and ultimately all life on earth shares common ancestors dating back over 3 billion years.

But wait, you say: If humans are the product of evolution, what about Adam and Eve? How do they fit in to the story? Are they the sole parents of humanity, even if they had an evolutionary past? When did they live? Were they *Homo sapiens*, like we are, or some other species? We will address these questions—at least from a biological perspective—next.

3

Adam's Last Stand?

In the summer of 2011, my wife and I were in the process of adopting our youngest son. As part of that process, we packed up our family and for a few weeks moved in with the foster family that had cared for him since birth, in a city several hours away from our home. It was a wonderful process, but understandably stressful: Would the transition from a family of four to a family of five go well? Would our new son bond with us as his parents? Would he come to see our biological children as his siblings, and vice versa?[1]

It was in the midst of this process that a controversy rocked the evangelical community and set the phones of my administrators ringing. Earlier that summer, *Christianity Today* had run a cover article titled "The Search for the Historical Adam," replete with art depicting Adam and Eve as Neanderthal-like individuals.[2] The article summary said it all: "The center of the evolution debate has shifted from asking whether we came from earlier animals to whether we could have come from one man and one woman."

The reason my administrators were fielding phone calls was that one of my academic papers, published in the journal of the American Scientific Affiliation (ASA)[3] and featured on the BioLogos website,[4] was prominently discussed in the *Christianity Today* article. Moreover, I had given an extensive interview to National Public Radio (NPR) on the topic, after they

caught wind of the *Christianity Today* article. NPR would edit that interview down to a few sound bites, and the resulting discussion of "my views" led off with this:

> But now some conservative scholars are saying publicly that they can no longer believe the Genesis account. Asked how likely it is that we all descended from Adam and Eve, Dennis Venema, a biologist at Trinity Western University, replies: "That would be against all the genomic evidence that we've assembled over the last 20 years, so not likely at all."[5]

No wonder my administrators were fielding angry calls—according to NPR, I no longer believed the Genesis account. Sigh.

In contrast to the NPR piece, the *Christianity Today* article provided a much more nuanced and accurate presentation of my views. After discussing evidence I had presented supporting common ancestry for humans and apes, the author turns to the primary focus of his article:

> The second—and perhaps more troublesome—issue treated by Venema involves "population genomics." Over the past decade, researchers have attempted to use the genetic diversity within modern humans to estimate primordial population sizes. According to a consensus drawn from three independent avenues of research, he states, the history of human ancestry involved a population "bottleneck" around 150,000 years ago—and from this tiny group of hominids came everyone living today. But the size of the group was far larger than a lonely couple: it consisted of several thousand individuals at minimum, say the geneticists. Had humanity begun with only two individuals, without millions of years for development, says an ASA paper, it would have required God's miraculous intervention to increase the genetic diversity to what is observable today. A BioLogos paper by Venema and Falk declares it more flatly: The human population, they say, "was definitely never as small as two. . . . Our species diverged as a population. The data are absolutely clear on that."

I must admit that the furor over this issue caught me somewhat by surprise—and not merely because of the shock that conservative American evangelicals apparently listen to NPR. Naively I had assumed that people understood that evolution was a population-level phenomenon. If humans evolved, then we did so as a population. Doesn't everyone know that? As I was about to learn, the population genetics data that indicate we descend from a population of about 10,000 individuals rather than a pair in many ways were more inflammatory than the data supporting common ancestry. Our son's foster parents likely didn't know what to make of it all, with me on the phone with

my administrators and constituents calling for my job. What kind of crazy family were we, anyway?

Speciation and Populations

One of the reasons that language change over time is such an apt analogy for evolution is that it clearly illustrates how speciation takes place by incremental changes of average characteristics after two populations separate. No one expects a new language to start because two speakers suddenly start speaking in radically new ways that separate them from their prior population of speakers. Yet this is how many people think speciation works. They assume that *all* species are founded by an ancestral breeding pair that is suddenly and markedly different than the population it arose from. Thus I've encountered many folks who, upon understanding the evidence that humans and other apes share common ancestors, assume that humans—like all other species, in their thinking—got their start when a founding couple "mutated away" in tandem from their ape-like ancestors. These folks then wonder if the Genesis narratives may be portraying this radical shift, with perhaps God intervening to create the necessary, large-scale mutations that made us a biologically distinct species.

While I'll leave the theological questions for Scot,[6] this picture is not based on an accurate understanding of how speciation works. Rather, the process starts when populations are genetically separated in some way, usually through physical separation (though other mechanisms are known). What matters is that two subgroups of what was formerly a continuous population cease interbreeding. This means that as mutations occur in either group, they are not shared across the divide. The incremental process of change is now uncoupled, and the two populations may begin to drift apart in terms of their form and behavior. Eventually, enough change may occur to make the rift permanent, but the process is a gradient over time. Attempting to draw a line on a biological gradient is as nonsensical as deciding what day Old English became Modern English. Any such lines of demarcation are for convenience only, since the processes of language and species formation are continuums.

Lo(o)sing It

To better understand how genetic variability works within a species, let's return to the language analogy for evolution in more detail. As we have seen, languages change over time either through gain or loss of words, meanings,

spellings, and so on. The key is how common such variants are within a language, and their "commonness" is a function of how many individuals employ them. For example, while discussing this analogy with one of my genetics classes recently, I asked them how to spell the English word "lose." A few of the brighter students immediately cracked a smile as they saw what I was up to, and pretty soon the class as a whole had a good laugh. The reason, of course, is that it is depressingly common to see the word "lose" misspelled as "loose," especially on social media. This is a relatively recent "innovation." Ten years ago it was not nearly so common, and (God forbid) ten years from now it may be more common still. Thirty years from now it might be viewed as an acceptable variant spelling, and fifty years from now employing "lose" might be the sure sign of an aging grammarian, comparable to calling a car an "automobile." For better or worse, languages change. (That said, if the words "their," "there," and "they're" ever collapse into a single word determined solely by context, I pray I won't be there to see it. Even evolutionary biologists have their limits.)

Here's where the analogy is once again helpful: the ability of a language to simultaneously "hold" spelling or grammatical variants is dependent on the number of the speakers of that language. Dying languages (for example, the sad case of many indigenous languages of North America) have almost no variation at all since they have so few speakers. Endangered species have the equivalent problem. Languages with large populations of speakers, on the other hand, can hold a large number of variants. Modern English is a prime example; as it increasingly becomes a global language, the opportunity for variation within it increases. The same occurs with species: a large population size allows for maintaining a large number of variants, since each member of a species is able to hold up to two distinct variants (alleles) of any given DNA sequence in its genome.[7] Thus there is a connection between the number of variants present in a population and the size of the population—a connection that scientists can use to estimate one from the other. And since the rate of change over time is slow, it is straightforward to extrapolate backward from the present into the past.

So the baseline expectation *should* be that if humans are the product of an evolutionary process, we arrived at our current state as a population. Now it is technically possible that a species could be founded by a single ancestral breeding pair, just as it is technically possible that a new language could be founded by two speakers. This is not what one would usually expect, however—in fact, it would be highly unusual. If a species were formed through such an event, or if a species were reduced in numbers to a single breeding pair at some point in its history, it would leave a telltale mark on its genome

that would persist for hundreds of thousands of years—a severe reduction in genetic variability for the species as a whole.

Poor Devils

One such species with a profound lack of genetic variability is the Tasmanian devil, a carnivorous marsupial once found across Australia, but now solely on the island of Tasmania off the Australian coast. Tasmanian devils have had very little genetic variability for the last few hundred years: most of them have exactly the same alleles with only rare differences. This suggests that at one point in their past they experienced a severe population "bottleneck."[8] This term derives from imagining a population as marbles in a bottle, with marbles of different color representing gene variants within the population. The bottleneck event occurs when there is a severe reduction in population size; that is, the bottle is tipped over, and only a few marbles escape. The genetic variation of the new population, then, is dependent on which variants happen to pass through the bottleneck. So at some point in their history, Tasmanian devils seem to have suffered a significant reduction in numbers, and they lost a large amount of genetic variation in the process. This has now become a serious issue for conserving this species in light of a new threat: a lethal, transmissible facial cancer. This cancer started in only one devil but was transmissible to others through biting. After a bite, a few cancerous cells take up residence in the new host. Normally, a recipient animal would fight off the cancerous cells, since they would be recognized as foreign. Here's the problem: all devils are so genetically similar to one another that the cancer cells do not trigger an immune response. As a result, this cancer threatens the devil population as a whole, and conservationists are working to save a cancer-free population in captivity that carries as much of remaining devil variation as possible. Should the population in the wild go extinct, they hope to replace it with the captive one.

In humans, on the other hand, tissues transferred between individuals almost invariably produce a strong immune reaction and subsequent rejection, to the point that organ donors and recipients must be carefully screened and matched to each other to minimize their differences. Even when a close match is found, drugs that suppress the immune system must be employed, because no match will be perfect, unless sourced from an identical twin. The reason for this is that humans are genetically highly diverse. In contrast, almost any devil could be an organ donor (or, sadly, a tumor donor) for any other in the population, without drugs. This example also illustrates just how long it takes

a population to rebuild its genetic variation after a bottleneck event occurs. New alleles have to be supplied by new mutations, and as we have seen, the mutation rate is very low. As a result, after a bottleneck event, a species will have reduced genetic diversity for thousands of generations to come. The implications are clear: Tasmanian devils experienced a severe bottleneck in the distant past, but humans did not.

All in the Family

One of the challenges of discussing the data relevant to measuring human ancestral population sizes is that the data are quantitative in nature. It's one thing to describe the remnants of the vitellogenin pseudogenes in humans, and another to start discussing mathematical methods for estimating population size from genetic diversity. Still, given the importance of this question for many Christians—and the strong insistence of many apologists that the science is completely wrong[9]—it is worth at least sketching out a few of the methods geneticists use that support the conclusion that we descend from a population that has never dipped below about 10,000 individuals.

While the story of the beleaguered Tasmanian devil provides a nice way to "see" the sort of thing we would expect if in fact the human race began with just two individuals, scientists have many other methods at their disposal to measure just how large our population has been over time. One simple way is to select a few genes and measure how many alleles of that gene are present in present-day humans. Now that the Human Genome Project has been completed and we have sequenced the DNA of thousands of humans, this sort of study can be done simply using a computer. Taking into account the human mutation rate, and the mathematical probability of new mutations spreading in a population or being lost, these methods indicate an ancestral population size for humans right around that 10,000 figure. In fact, to generate the number of alleles we see in the present day from a starting point of just two individuals, one would have to postulate mutation rates far in excess of what we observe for any animal.

Ah, you might say, these studies require an estimate of mutation frequencies from the distant past. What if the mutation frequency once was much higher than it is now? Couldn't that explain the data we see now and still preserve an original founding couple?[10] Aside from the problems this sort of mutation rate would present to any species, we have other ways of measuring ancestral population sizes that do not depend on mutation frequency. These methods thus provide an independent way to check our results using allele diversity

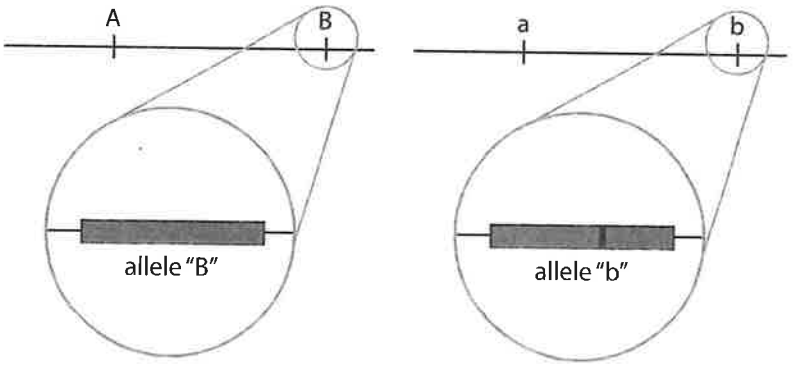

FIGURE 3.1. Geneticists use line diagrams to represent the location of genes and combinations of alleles present on the same chromosome.

alone. Let's tackle one of these methods next: estimating ancestral population sizes using something known as "linkage disequilibrium."

I've often joked with my students that no scientist will choose a simple name when a complicated one will do, and "linkage disequilibrium" ranks right up there as an example of this habit. Despite the name, it is not a difficult concept to grasp. The basic idea is that if two genes are located close to each other on the same chromosome, the alleles present at both locations tend to be inherited together. For example, suppose "gene aye" with possible alleles "A" or "a" and "gene bee" with alleles "B" or "b" are close together.

In figure 3.1, the long line represents a chromosome, and the hash marks across it show us where the two genes in question are located. Geneticists even use the Latin word for "location" (*locus*, pronounced "low-cuss") as a synonym for "gene." (Latin makes us sound smarter, I guess.) If we could zoom in on the diagram, we would see a long DNA molecule with two regions that are translated into proteins (the two genes). The different alleles at either locus would have slight sequence differences, giving us four possible combinations for these two *loci* (plural for "locus," pronounced "low-sigh"). The four possible combinations are "AB," "Ab," "aB," and "ab."

During the cell divisions that make gametes (i.e., eggs or sperm), there is a process of mixing and matching of alleles to make new combinations. For example, suppose an individual had one chromosome with the "A" and "B" alleles, and the other with "a" and "b." During gamete formation, it is possible to produce gametes that are "recombinant"—in this case, ones that have either an "Ab" or "aB" combination. Recombination requires a process of precise

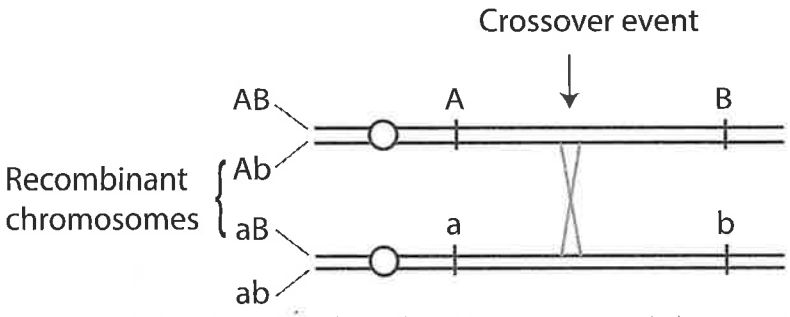

FIGURE 3.2. During the cell divisions that produce gametes (eggs or sperm), chromosomes are replicated and held together at special sequences called "centromeres" (open circles). Replicated chromosomes then pair up with their partner chromosomes, and physical breakage and rejoining occurs along their length at random. If a crossover falls between two loci that have alternate alleles present, a crossover will produce chromosomes with new combinations of alleles. Chromosomes with new combinations of alleles are said to be "recombinant."

chromosome breakage and rejoining called "crossing over"—something you might recall from high school biology (fig. 3.2).

The key point to understand is that the closer together two loci are on a chromosome, the less likely it is that a crossover event will happen between them. The further apart two loci are, the more likely it is that a crossover will recombine them. What this means is that alleles of loci close together tend to be inherited as sets.

Let's work through an example of how this plays out in practice. Consider an extended family represented by a *pedigree*. This is the type of diagram geneticists use to trace alleles through large families. Females are represented by circles, and males by squares. Horizontal lines connecting males and females indicate that they are the parents of the offspring below them (connected with a vertical line). Generations are labeled with Roman numerals (I, II, III, and so on); individuals are labeled with Arabic numerals (1, 2, 3, and so on). In this way we can refer to any individual in the pedigree (fig. 3.3).

Now consider a larger pedigree where we know the allele combinations of everyone represented (fig. 3.4, p. 52). For example, individual I-4 has one chromosome with the "AB" alleles linked together, and one chromosome with the "ab" alleles as a set. We can represent her chromosome set, then, as "AB/ab"—the shorthand that geneticists use. We can then use this convention for other individuals in the pedigree. For example, the daughter of I-1 and I-2 might have an "AB/aB" combination. If these two loci are very closely linked together, it is highly unlikely that crossing over will occur. Thus she would have inherited her "aB" set from her mother, and the "AB" set from her father. Likewise, her husband, II-3, would have inherited "Ab" from his dad, and

"ab" from his mom. Their children (generation III) similarly would inherit these sets without crossing over. Looking at the combinations carried by these children, then, allows us to infer things about their ancestors. If these two loci are very close to each other, we might not expect them to recombine over hundreds of generations or more. Thus it's reasonable to infer that these four combinations come from four distant ancestors. Not exactly rocket science.

The trick is that we can now do this for tens of thousands of loci across the whole human genome. As we have sequenced the DNA of more and more individuals in different people groups around the globe, we've simply been asking the question: Based on the number of allele combinations that we observe in this population, how many ancestors do we need to invoke in order to explain what we observe? In this case, rather than estimating mutation frequency, the calculations require knowing how often crossing over happens between two loci. This is also something we can measure directly in humans and other animals, and there is a well-characterized relationship between chromosome distance between two loci and crossing-over frequency. We've now done this sort of analysis for millions of pairs of loci (yes, millions) for each chromosome pair in our genome (all 23 pairs). And what is the final tally after crunching all that data and counting up ancestors? The results indicate that we come from an ancestral population of about 10,000 individuals—the same result we obtained when using allele diversity alone.[11]

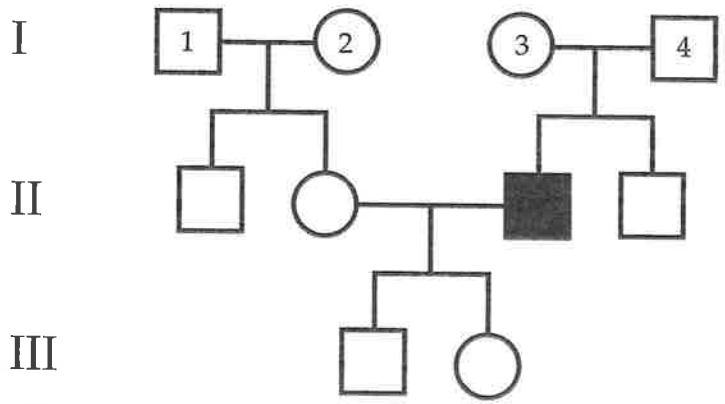

FIGURE 3.3. A pedigree is a diagram showing family relationships. Males are represented with squares, females with circles. Lines connecting individuals represent family groups. Each generation is labeled with a Roman numeral, and each individual within a generation is labeled with an Arabic numeral. Individuals affected with a genetic condition may be represented with a filled-in symbol. In this example, individual II-3 is affected with a genetic condition, though his wife (II-2) and two children (III-1 and III-2) are not affected.

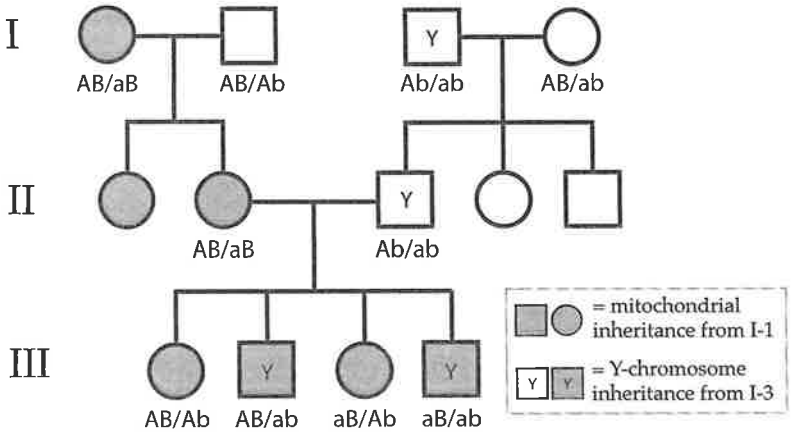

FIGURE 3.4. A pedigree showing how sets of alleles of two closely linked loci are inherited in an extended family. Each set of alleles is called a "haplotype." In the most recent generation, we observe four different haplotypes: AB, ab, aB, and Ab. Since these loci are linked closely to each other, recombination between them is rare.

One interesting feature of this approach is that it allows us to scale how far back in time we want to do the tallying. If we want to examine our distant ancestors, we can pick pairs of loci that are very, very close together. Alleles at these loci require thousands of generations, on average, before a crossover event recombines them. If we're interested in our more recent history, we can select pairs of loci that are further apart from each other. In this way, this approach provides a population "snapshot" at various times in our prehistory. One study using this approach scaled its analysis to investigate our lineage from the present dating back to approximately 200,000 years ago, which, as we will discuss later, is when our species first appears in the fossil record. The researchers found that, during this period, humans living in sub-Saharan Africa maintained a minimum population of about 7,000 individuals, and that the ancestors of all other humans maintained a minimum population of about 3,000—once again, adding up to the same value other methods arrive at.[12]

A more recent and sophisticated model that uses a similar approach but also incorporates mutation frequency has recently been published. This paper was significant because the model allows for determining ancestral population sizes over time using the genome of only one individual.[13] This method is feasible since even one individual, with two copies of each chromosome, will have many regions of her genome where she has allele pairs inherited from different ancestors (just like the children in our example pedigree did). Instead of looking at a given pair of loci in many individuals, this method looks at

many pairs of loci within one individual. Since this was a new method, the authors tested it by creating artificial data sets where they knew the actual population history (since they designed it into the data) and seeing how well their mathematical model would predict what they already knew to be true. The model performed well, and so they applied it to real data from fully sequenced individual human genomes. For sub-Saharan Africans, they observed a population bottleneck down to a minimum of about 5,700 individuals 50,000 years ago. For non-sub-Saharan Africans, they observed a bottleneck down to a minimum population size of about 1,200 between 40,000 and 20,000 years ago. Taken together, this is in good agreement with previous, less powerful methods, with a combined minimum size of around 6,900 individuals. These numbers may shift upward, however, as we sequence more and more individuals from both groups. The authors also extended their analysis back approximately 3 million years and found that the population size of our lineage increases the further one goes back in time, with a prior, less severe bottleneck about 500,000 years ago.

Getting Sorted

One last method to estimate ancestral population sizes that we will discuss has the ability to look back further than 3 million years—back to the common ancestral population we shared with chimpanzees about 4–6 million years ago, as well as back to other common ancestral populations with other great apes. This method, like linkage disequilibrium analysis, is virtually unaffected by varying estimates of mutation rates.

This method exploits the fact that we expect the relatedness pattern of certain genes to sit at odds with what we expect on the basis of species relatedness. While humans and chimpanzees are the closest living relatives of each other as species, we expect that some human genes will be closer matches to those of other great apes, such as gorillas. The reason for this arises out of something called "incomplete lineage sorting," or "ILS."

When a population is undergoing a speciation event, some of the genes/loci in that population will have two or more alleles within the population as a whole. As the population separates, the two new populations will likely both inherit that diversity. We can represent two alleles as shaded boxes on a phylogeny and show how the history of these two alleles may play out within a larger tree of species relatedness (fig. 3.5, p. 54).

In this phylogeny, or "species tree," we see that the common ancestral population of gorillas, chimpanzees, and humans has two alleles of one gene

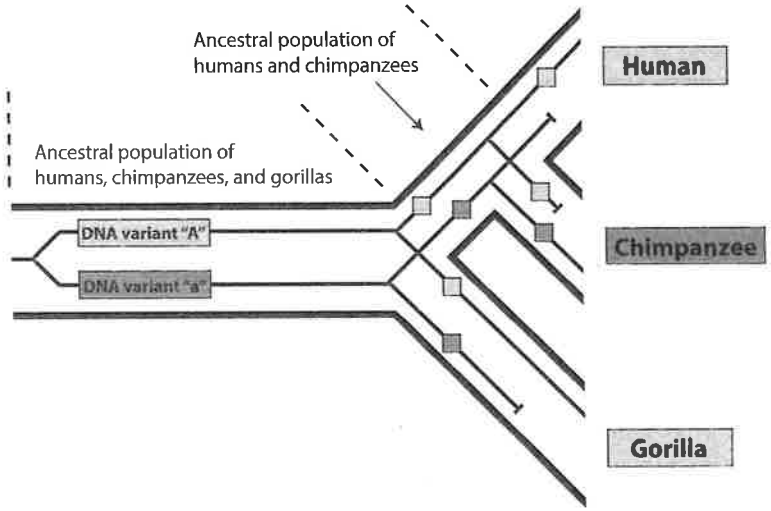

FIGURE 3.5. Alleles in an ancestral population may not sort down completely to every descendant species. In some cases, the sorting pattern produces a "gene tree" at odds with the overall "species tree."

(DNA variant "A" and "a") within the population. As this population separates into the common ancestral population of humans and chimpanzees and the population leading to gorillas, both populations inherit both alleles. In the gorilla lineage, however, variant "a" is later lost, leaving only variant "A" in the present-day gorilla population. The common ancestral population of humans and chimpanzees maintains both variants until after this lineage divides into two, one leading to humans and the other to chimpanzees. In the lineage leading to chimpanzees, the "A" variant is lost, leaving it only with "a" in the present day. Conversely, in the lineage leading to humans, the "a" variant is lost, with only "A" remaining. The final pattern is as follows: humans and gorillas have "A," and chimpanzees have "a." Gorillas and humans, then, have more closely related alleles than either does with chimpanzees. This "gene tree" for the "aye" gene sits at odds with the overall "species tree."

Here's the interesting part: this pattern lets us know that the common ancestral population of humans and chimpanzees had both "A" and "a." It also lets us know that the common ancestral population of humans, chimpanzees, and gorillas had both variants. If you have a way to infer what genetic variants were present in a population, you have a way to estimate its population size. The data here show us that both the common ancestral population of

humans and chimpanzees and the common ancestral population of humans, chimpanzees, and gorillas were large—about 50,000 individuals (effective population size). In fact, based on prior work, scientists predicted in advance how much ILS we should observe with the gorilla genome (estimated at around 25 percent) before we had the gorilla genome sequence to measure it. We observe 30 percent ILS, which is an excellent match to the predicted value. We later made a similar prediction for ILS with the orangutan genome, and once again the predicted value (1 percent) matched the observed value (0.8 percent) very well. These results provide good evidence that our estimates of the ancestral population size leading to humans over the last several million years are accurate. It seems our smallest effective population size over the last 18 million years was when we were already human, at around the time some of our ancestors left Africa.[14]

As our methodology becomes more sophisticated and more data are examined, we will likely further refine our estimates in the future. That said, we can be confident that finding evidence that we were created independently of other animals or that we descend from only two people just isn't going to happen. Some ideas in science are so well supported that it is highly unlikely new evidence will substantially modify them, and these are among them. The sun is at the center of our solar system, humans evolved, and we evolved as a population.

Put most simply, DNA evidence indicates that humans descend from a large population because we, as a species, are so genetically diverse in the present day that a large ancestral population is needed to transmit that diversity to us. To date, every genetic analysis estimating ancestral population sizes has agreed that we descend from a population of thousands, not a single ancestral couple. Even though many of these methods are independent of one another, all methods employed to date agree that the human lineage has not dipped below several thousand individuals for the last 3 million years or more—long before our lineage was even remotely close to what we would call "human." Thus the hypothesis that humans descend solely from one ancestral couple has not yet found any experimental support, and it is therefore not one that geneticists view as viable.[15]

Bones and Contention

While genetics is an excellent way to address the question, How many of us were there at various stages of our evolution?, it is not as well suited to the question, And what were we like? For evidence of physical form and behavior,

we must turn to the fossil record. Once again, we are confronted with the challenge that the fossil record cannot conclusively reveal who our direct ancestors might be, though it will likely be possible to find remains of our close relatives.[16] Just as with whales, however, finding our relatives in the fossil record can give us a good sense of the general trajectory of our evolutionary past.

Though Charles Darwin largely avoided the issue of human ancestry in *On the Origin of Species*, except to briefly muse that "light would be thrown on the origin of Man and his history,"[17] the idea of human descent from ape-like ancestors was obviously a topic of much scientific debate and theological concern following the publication of *Origin* in 1859. Darwin predicted, from the distribution of living great apes, that human origins would be found in Africa; but in the 1860s there were no fossils known that seemed to be intermediate between living apes and humans. A few Neanderthal remains were known, but these were too few and not yet studied well enough to be fully appreciated by the scientific community. They were also so very similar to modern humans that it was thought by many that they were merely ancient human remains.[18]

At this time there was also a widespread expectation within the scientific community that an evolutionary lineage would be a ladder-like progression from one species to the next, culminating in the present-day species. The famous "ape to human" images that look like a police lineup are an example of this expectation. Yes, for any species there should be a lineage that resembles a ladder leading to it, if indeed we had a perfect fossil record to draw from. In reality, fossilization is such an infrequent process that it cannot capture every subtle shift along the way. What the fossil record does capture are common species—species with large population sizes. Thus, when looking in the fossil record, what one will find is biased toward widespread species with large populations. Most of those species will not be direct ancestors of living species, but their relatives. The understanding that evolution was more like a branching bush of related species than an ascent up a linear ladder leading to present-day species would have to be worked out on the basis of paleontological evidence, and much of that work remained to be done in Darwin's time. From Darwin's ideas, scientists and the public expected there to be a series of "missing links" connecting humans and apes that could be found in the fossil record, and that any such species *would* be direct ancestors of humans. Since the most obvious difference between living great apes (for example, chimpanzees and gorillas) and humans was brain capacity and cognitive function, the "ladder" was expected to show a progression from ape, to ape with a bigger brain, to human. In other words, early expectations were that our lineage first evolved from the chin up, and only then from the chin down.

Unfortunately this expectation would hamper research into human evolution for decades. In the 1880s, when the first remains of *Homo erectus* were discovered in Indonesia, they showed a humanlike skeleton with a small, ape-like skull. This, of course, was the complete opposite of the expectations, and so many scientists doubted that the find was in fact a single species. Rather, they suspected, human skeletal remains had been mixed together with an ancient ape skull. Though the discoverer, Eugene Dubois, championed his find as a transitional form linking humans and apes—his original name for the species was *Pithecanthropus erectus*, the "ape-man that stands upright," a choice that was anything but subtle—he was a voice in the scientific wilderness.[19]

Any traction that Dubois did gain would soon be lost in light of a stunning find in the United Kingdom, of all places—a find that fit precisely what was expected of a "missing link" between ape and human. This species had an ape-like jaw and a human-sized skull, suggesting that it had an ape-like skeleton wedded to a human-sized brain. A second find shortly after confirmed that these results were not merely a chance association of ape and human remains. It would be decades before the skulls, belonging to the now-infamous Piltdown Man, would be revealed as frauds. They were constructed using a human skull and the jaw of an orangutan, with the teeth filed to shape them to the expected form for a transitional species. The perpetrator of the fraud has never been discovered, but his handiwork threw scientists off the scent for a long time to come.

Fortunately, paleontological research continued, and data continued to accumulate. These data increasingly showed that Piltdown Man did not, in fact, fit the expected pattern, which was very much pointing to our lineage evolving from the chin down before the chin up, vindicating Dubois. Scientific suspicion of the veracity of Piltdown Man grew, and eventually the remains were carefully reexamined. The evidence of filing on the teeth was uncovered, and the jig was up.

As we have seen for cetaceans, eventually a picture emerged that gives us a good idea of how our lineage changed after we parted ways with the lineage leading to chimpanzees. Though chimpanzees are our closest *living* relatives, a host of species in the fossil record are more closely related to us than chimps. These species are collectively known as "hominins," and we are now aware that there were a lot of hominin species out there.[20] As you might expect, there are different classifications of fossil hominins, and the boundaries between them are fuzzy (fig. 3.6, p. 58). The earliest hominin fossils, grouped together as "probable hominins," include species like *Ardipithecus ramidus*, a species that lived in Africa about 4 million years ago. This species has skeletal characteristics that are intermediate between upright (i.e., bipedal) walking and

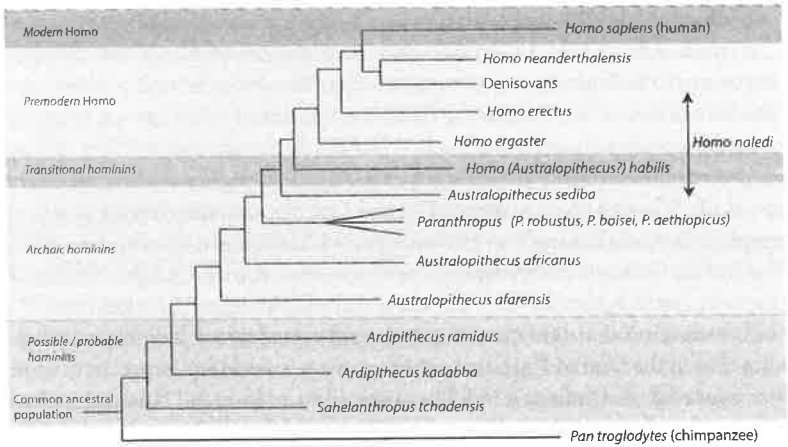

FIGURE 3.6. A phylogeny of hominins—species more closely related to humans than to chimpanzees. The phylogeny is constructed from morphological data, and in some cases genome sequence data. *Ardipithecus kadabba* and *Sahelanthropus tchadensis* may not be hominin species (as indicated by the shaded area at the bottom of the figure). *Homo naledi* has not yet been placed precisely into the phylogeny, though its characteristics place it within *Homo*.

the climbing of trees,[21] and a small cranial capacity of only 300–350 cubic centimeters (cc), or about the volume of a can of soda,[22] whereas modern humans have a cranial capacity of about 1,300 cubic centimeters. Later in the fossil record, we observe various Australopithecine species, of which the famous fossil called "Lucy" is the best known. Lucy's species, *Australopithecus afarensis*, is found in the fossil record between about 4 and 3 million years ago and shows further shifts to bipedal walking,[23] and a larger cranium (between 400 and 550 cc).[24] Later still we observe the earliest members of the genus *Homo*, in a group named "transitional hominins." These hominins have a cranial volume that ranges between 500 and 700 cubic centimeters, and are thought by some paleontologists to be Australopithecines rather than within *Homo*, highlighting their "transitional" features, such as a lack of full bipedalism.[25] Later still we see species within "premodern *Homo*" such as Dubois's renamed *Homo erectus*, a widespread species dating to about 1.8 million years ago with an essentially modern human skeleton but a reduced cranial capacity compared to modern humans. The earliest premodern *Homo* cranial capacities begin at about 700 cubic centimeters and, moving toward the present, eventually reach the present-day human volume of about 1,400 cubic centimeters, and even exceed it in the Neanderthal lineage (Neanderthal skulls with a cranial capacity of 1,600 cc are known). In this group of species we also observe skeletal features indicative of full bipedalism.[26] A recent

fossil find, *Homo naledi*, has been placed within *Homo* but nonetheless has a cranial capacity below that of *Homo erectus* and *Homo habilis* at about 450–550 cubic centimeters. The relationship of this species to other hominins is not yet known, but it has attracted widespread attention because of the evidence suggesting it deliberately placed its dead into the cave in which the remains were found.[27]

Similar to what we discussed regarding whales, we cannot be certain that any of these species is in fact a direct ancestor of present-day humans. What these species can show us, however, is the probable path of our actual lineage, since these species are at least close relatives of our ancestral line. The evidence thus suggests that our lineage over the past 4 million years passed through an Ardipithecine-like species, on to an Australopithecine-like species, and then through various shades of *Homo* until our species is first preserved in the fossil record 200,000 years ago. And as we have seen for languages, the process was a continuous one of average change within a population over time. What we see in the fossil record matches up with what we see in our DNA. Recall just how similar humans and chimpanzees are at the DNA level. These fossil species, then, would have DNA even more similar to us than to modern chimpanzees. In this sense, humans are, biologically speaking, not new—we are the modified descendants of similar species that lived in the past.

National Enquirer, Paleogene Edition

One of the frustrating things about science is that while it is well suited to answer certain questions (and even better at raising questions in the first place), it is not suited to answer others. It's very common, for example, for Christians, when they come to understand this evidence, to naturally wonder where Adam fits in. I sometimes think of this as "pin the Adam on the phylogeny," alluding to the children's game. The main point of such an allusion is that the child is blindfolded, and so are we in this case, so to speak. Science can tell us a few things—we descend from a population rather than a pair; our ancestors likely passed through these sorts of forms; and so on—but it is simply unable to weigh in on the historicity of Adam and Eve as individuals. What we can conclude, however, is that if they were in fact historical, they were not the sole parents of all humanity but part of a larger population. Beyond this, science cannot say.

It should come as no surprise that Christian antievolutionary apologists do feel a need to fit Adam into the fossil record, despite the myriad difficulties—and we will examine some of those attempts in the next chapter.

This task, however, has recently become even more challenging with the advent of *paleogenomics*—the ability to recover and sequence the DNA of extinct organisms. While scientists have been able to recover DNA from the remains of a 700,000-year-old horse that had the good sense to die in the Canadian arctic and be preserved in permafrost,[28] we have yet to stretch the sequencing hominin DNA back that far. The range of hominins does not appear to have included arctic regions until fully modern *Homo sapiens* arrives on the scene, alas—though I hold out hope that one day we will locate a particularly adventurous (and well-preserved) member of *Homo erectus* or a similar species. That said, we have now been able to sequence the DNA of hominins stretching back to about 80,000 years ago, and the results have proved fascinating.

When modern humans first arose in Africa 200,000 years ago, there were other hominin species alive on the planet, some of whom had migrated out of Africa prior to our species coming into being. *Homo erectus*, for example, was already widespread in Africa and outside it. Similarly, the ancestors of Neanderthals had left Africa at least 100,000 years prior to our species evolving, going on to colonize the Middle East and parts of Asia and Europe. Humans left Africa in significant numbers about 50,000 years ago, roughly coinciding with the reduction to our minimum population size; some stayed behind, becoming the ancestors of present-day sub-Saharan Africans, and the rest of us derive from that smaller population that left. As we have seen, the minimum population size within Africa was about 6,000, compared with approximately 1,200 for the emigrating group. As humans left Africa, then, we encountered other hominin species that had left previously.

Scientists have long wondered what the nature of those encounters was like. Some fossils, for example, have long been thought to suggest that Neanderthals and humans had interbred with each other, given their characteristics intermediate between the two species. With the advent of paleogenomics, the opportunity arose to test this hypothesis directly by sequencing Neanderthal DNA. Not surprisingly, Neanderthal DNA is nearly identical to our own, yet it falls (just) outside the range of present-day human variation.[29] This was expected, since Neanderthals are our closest known relatives according to their skeletal morphology. What was noteworthy, however, is that some modern humans do indeed have Neanderthal DNA in their genomes. When our two species encountered each other, there was a limited amount of interbreeding. Some of the offspring of those unions were raised as human, and some of those individuals have passed their DNA down to us in the present day. In part because the group of humans that left Africa was so small, this Neanderthal DNA is present in every present-day human who is not a sub-Saharan African by ancestry. These individuals derive between 1 and 4 percent of their genomes from Neanderthal ancestors.

Of course, this raises the whole "species question" again: If humans and Neanderthals interbred, then aren't we just members of the same species? Recall that attempting to demarcate species is an attempt to draw a line on what is in fact a continuous gradient. So we "sort of" are the same species, because we did interbreed to a limited extent, and some present-day members of our species, yours truly included, descend in part from Neanderthal stock. Are dogs, coyotes, and wolves the same species, or distinct? What about lions and tigers?[30] It's a similar question. As a species, then, we had to shift our Facebook relationship status to "it's complicated" when it comes to Neanderthals. Not long after, however, a second discovery would complicate things even further.

From Russia, with Love

Once it was worked out that ancient DNA could be recovered and sequenced from hominin remains, researchers have been busy sequencing DNA from an increasing number of samples. One such sample turned out to have exceptionally preserved DNA, though it was not previously noted as especially remarkable. The DNA work, however, was a bombshell: this was a previously unknown species of hominin, neither human nor Neanderthal. Found in Denisova Cave in the Altai Mountains of Siberia, the remains would be called the Denisova hominin or, when referring to the species as a whole, Denisovans.[31] Denisovans share a more recent ancestor with Neanderthals than they do with any other known species. We have little sense of their skeletal form, since all that has been found to date are finger bones and teeth—though, in this day and age, that was enough to determine their complete genome sequence. Even more surprising was the finding that we interbred with this species as well. Present-day humans of Asian and Oceanic descent inherit about 3–5 percent of their DNA from this extinct species. A further finding of note was that the Denisovan genome seems to contain stretches of DNA from yet another hominin species. It's tempting to speculate that this DNA comes from *Homo erectus*, since this species was widespread in Asia prior to the Denisovans, or their ancestors, arriving there. There is still no way to test that hypothesis, since we have not (yet) found *Homo erectus* remains that have yielded DNA, though the temporal range of this species in the fossil record (*Homo erectus* persists up until about 100,000 years ago) suggests such a find might be possible given the right conditions.

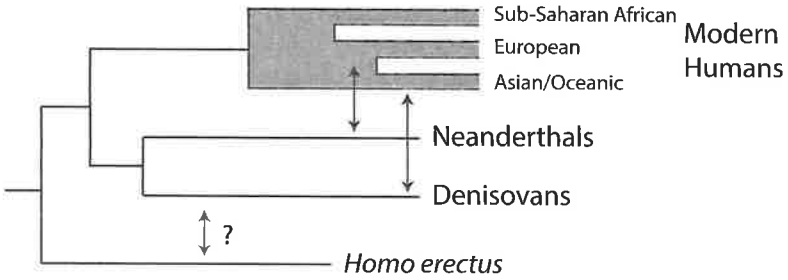

FIGURE 3.7. A phylogeny of modern humans and our closest known relatives. Double-headed arrows indicate interbreeding. Modern humans have diverged from one another slightly as we spread across the globe (gray shading in the expanded human branch). As humans left Africa in large numbers approximately 50,000 years ago, they encountered and interbred with Neanderthals in the Middle East. Humans from this population subsequently expanded into Asia and interbred with the Denisovans, a species related to Neanderthals. Genome sequence data from Denisovans suggests they may have interbred with another hominin species, perhaps *Homo erectus*.

As it stands, then, not only is hominin evolution a branching bush, but there are connections between some of the branches (fig. 3.7). Humans, Denisovans, and Neanderthals share a common ancestral population in Africa dating to around 800,000 years ago.[32] Sometime between 500,000 and 300,000 years ago, the common ancestral population of Neanderthals and Denisovans leaves Africa, later splitting into two species. As humans leave Africa about 50,000 years ago, they encounter Neanderthals in the Middle East and interbreed with them. As this human population expands into Asia, they encounter the Denisovans and further interbreed with them. The result is that present-day sub-Saharan Africans lack Neanderthal or Denisovan DNA, Europeans have Neanderthal but not Denisovan DNA, and Asian and Oceanic peoples have both.[33] Thus there are now even more human ancestors to account for, though they themselves were not members of our species.

The Curious Case of Mitochondrial Eve

When presenting these data to evangelical audiences, I commonly get questions about Mitochondrial Eve (and occasionally Y-Chromosome Adam, her male equivalent). Mitochondrial Eve is an ancestor to every living human, hence the name chosen by the scientific community. Likewise, Y-Chromosome Adam is an ancestor to every living male.

Wait just a minute, you might say. If we all descend from one man and one woman, how is it that scientists can claim we descend from a population of thousands? Well, *both* are true, though it will take a bit of effort to

understand why.[34] It has to do with how mitochondrial and Y-chromosome DNA are inherited, so we'll start there.

Most people are familiar with how the Y chromosome is passed down from father to son, so we need not belabor that here. Mitochondrial DNA, on the other hand, is not generally so well understood. Mitochondria are subcellular compartments that do energy conversion for animals, and they have their own genomes distinct from the usual chromosome set (the so-called nuclear genome, because it is found in the nucleus, another subcellular compartment). In humans, then, we have a nuclear genome consisting of 23 chromosome pairs (thus 46 in all) and the mitochondrial genome. The mitochondrial genome is tiny compared with the nuclear genome, and it is circular (whereas nuclear chromosomes are linear).[35] Mitochondria are passed down only through eggs, not through sperm, since the part of the sperm that fuses with the egg to release its contents does not carry mitochondria. As a result, this tiny circular snippet of DNA is passed down only from mothers to their children, and not from fathers. Mitochondria in males have thus hit a dead end.

Similarly, the Y chromosome has its unique pattern of inheritance: from father to son, and only to sons, since inheriting a Y chromosome determines that the offspring will be male. These two forms of DNA, then, have a pattern of inheritance that is different from that of regular chromosomes, which can be passed on by either mothers or fathers to offspring of either gender. Y chromosomes hit a dead end if a male has only female offspring, and

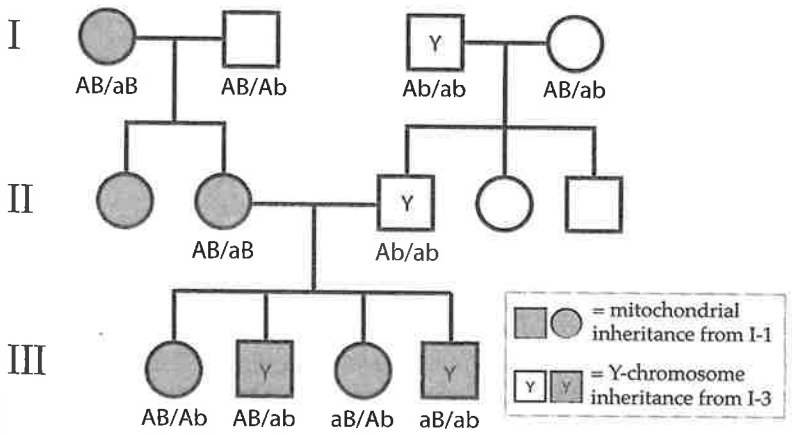

FIGURE 3.8. Inheritance of mitochondrial DNA and Y chromosomes in the same extended family discussed previously. Though the children in generation III must have at least four ancestors for their regular chromosomal DNA, they have only one ancestor for their mitochondrial DNA and their Y-chromosome DNA, respectively.

mitochondria hit a dead end if females have only male offspring. With these two inheritance patterns in mind, let's consider how this might play out in a population over time. Once again, we'll use a pedigree to help us see what may happen—the same pedigree we used to look at inheritance of closely linked alleles previously, but now with a view to tracing mitochondrial and Y-chromosome variation as well (fig. 3.8, p. 63).

With our knowledge of mitochondrial inheritance in hand, we can see that the four children in generation III will inherit the mitochondrial DNA of their mother, who in turn inherited it from her mother (individual I-1). The four children, then, have only one ancestor from generation I for their mitochondrial DNA: their maternal grandmother. Neither their maternal grandfather (I-2), paternal grandfather (I-3), nor paternal grandmother (I-4) contributes mitochondrial DNA to generation III. Similarly, the two boys in generation III have only one ancestor in generation I for their Y-chromosome DNA: their paternal grandfather. The Y chromosome of their maternal grandfather (I-2) has not been transmitted to generation III (nor II, since this man had only daughters).

In contrast, you will recall that all four grandparents contributed regular chromosomal DNA to generation III, and that the DNA diversity in this generation requires that we infer that they have at least four ancestors. These children descend uniquely from one man (for their Y-chromosome DNA), one woman (for their mitochondrial DNA), but from at least four ancestors for their regular chromosomal DNA. This, in microcosm, is exactly the reason why all humans can descend from one Mitochondrial Eve for our mitochondrial DNA, one Y-Chromosome Adam for our Y chromosomes, and 10,000 other ancestors for our regular chromosomal DNA.[36] Both mitochondrial DNA and Y-chromosome DNA are prone to being lost in a lineage over time because of their gender-specific inheritance patterns. The population bottlenecks that we passed through as a species also likely contributed to the loss of many mitochondrial and Y-chromosome lineages. Regular chromosomal DNA, on the other hand, is much more resistant to loss because it can be passed down to offspring of either gender by parents of either gender. Y chromosomes require an unbroken line of male ancestors; mitochondrial DNA requires an unbroken line of female ancestors; but regular chromosomes simply require an unbroken line of ancestors to be passed on.

Now, the elimination of a mitochondrial or Y-chromosome lineage happens not overnight but incrementally over time. Mitochondrial variants and Y-chromosome variants are like any other DNA variation in the sense that they can become more common within a population over time, or less common. Typically, variants that are eliminated have become progressively less

and less common over time, thereby becoming more susceptible to loss. The gender-specific inheritance pattern of these types of DNA does increase the possibility that they will be lost merely by chance, however, once they become rare enough.

Unfortunately, many antievolutionary organizations like to promote Mitochondrial Eve and Y-Chromosome Adam without explaining these issues. Typically, it is enough for them to state that they are respectively the common female ancestor for all women and the common male ancestor for all men, to claim (or merely imply) that these data are consistent with Adam and Eve being the *sole* parents of all humans, and to leave it at that.[37] Thus, for their case to seem plausible, they count on their audience not completely understanding how these types of DNA are inherited—or perhaps they misunderstand it themselves.

Responding to the Evidence

Following that 2011 cover article in *Christianity Today*, a few Christian apologists have attempted to rebut the scientific evidence that humans descend from a population rather than a pair, though without success.[38] Others have merely cast the entire field as "speculative," such as some within the intelligent-design movement.[39]

> Stephen Meyer, a Discovery Institute leader of the intelligent design movement, [claims that] BioLogos leaders are using "an unsubstantiated and controversial claim to urge pastors and theologians to jettison a straightforward reading of Genesis about the human race arising from one man and one woman. They think 'the science' requires such a reinterpretation, but apart from speculative models that make numerous question-begging assumptions, the science does no such thing."[40]

The claim may be controversial to Christians, but it is certainly not controversial to scientists, who are aware of the multiple, independent, converging lines of evidence that support and substantiate the conclusion. Meyer's confident assertions aside, antievolutionary scholars have not yet mounted a convincing response to population genetics evidence, nor is it clear that they will be able to do so, since there does not appear to be anyone in the antievolutionary camp at present with the necessary training to properly understand the evidence, much less offer a compelling case against it. In his critique of one attempt to rebut the evidence, young-earth creationist scholar Todd Wood states the problem clearly:

> The population reconstructions are complex and not easily understood by laypeople right now. So creationist responses lag behind the current science, and the best your typical creationist can do is cast aspersion on the science. Until we have a creationist well-trained in modern theoretical population genetics, I think we will continue to have only unsatisfactory answers to these ancestral population reconstructions.[41]

Several scholars have expended considerable effort on attempting to rebut the evidence for evolution in general, however—and their claims are widely accepted among Christians. In the next chapter, we'll examine two of their key claims: that evolution is unable to produce certain complex biochemical structures, and that it cannot produce the high level of information we observe in DNA.

4

What about Intelligent Design?

> Although I am fully convinced of the truth of the views given in this volume under the form of an abstract, I by no means expect to convince experienced naturalists whose minds are stocked with a multitude of facts all viewed, during a long course of years, from a point of view directly opposite to mine. It is so easy to hide our ignorance under such expressions as the "plan of creation," "unity of design," &c., and to think that we give an explanation when we only restate a fact. Any one whose disposition leads him to attach more weight to unexplained difficulties than to the explanation of a certain number of facts will certainly reject my theory.
>
> Charles Darwin[1]

> Weizsäcker's book *The World-View of Physics* is still keeping me very busy. It has again brought home to me quite clearly how wrong it is to use God as a stop-gap for the incompleteness of our knowledge. If in fact the frontiers of knowledge are being pushed further and further back (and that is bound to be the case), then God is being pushed back with them, and is therefore continually in retreat. We are to find God in what we know, not in what we don't know; God wants us to realize his presence, not in unsolved problems but in those that are solved.
>
> Dietrich Bonhoeffer[2]

In the late 1990s I was a PhD student at the University of British Columbia in Vancouver, studying genetics and development. I had weathered my bachelor's degree with my faith and antievolutionary views intact, and my area of study