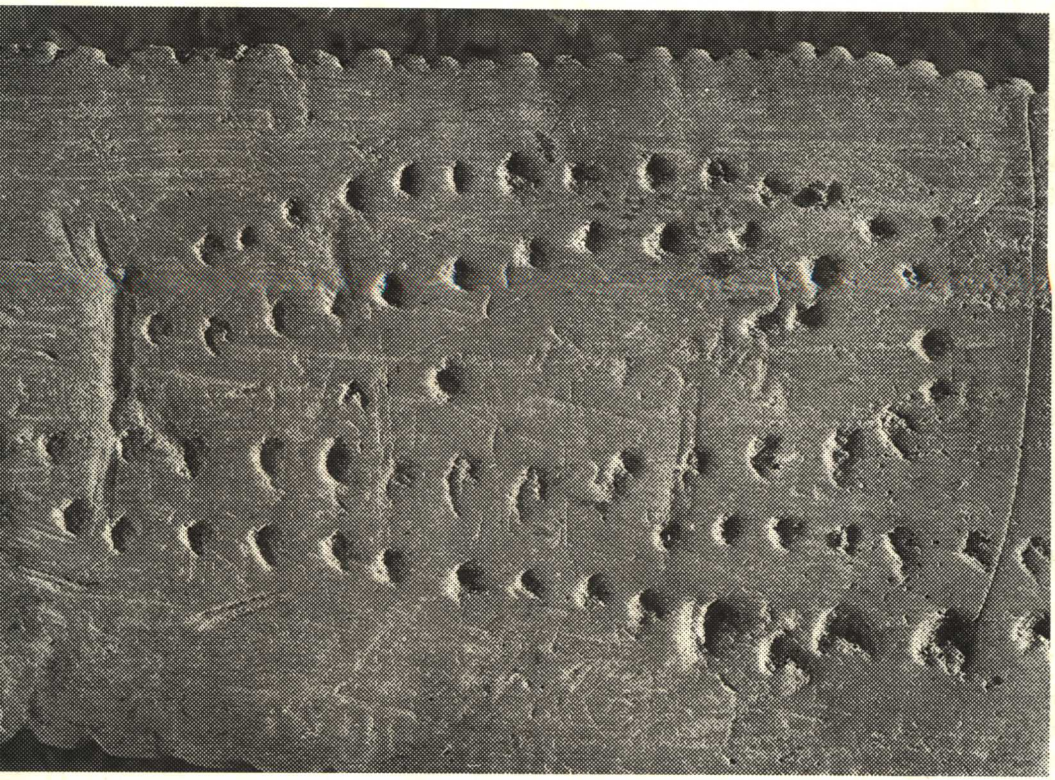
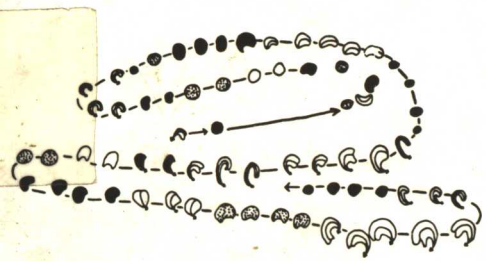
EVOLUTION OF THE BRAIN: CREATION OF THE SELF





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Evolution of the Brain: Creation of the Self

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Preface

It is extraordinary that there has been so little publication on the brain developments during the most important creative process of biological evolution, namely from our hominoid ancestors through some 9 to 10 million years of hominid evolution to the human brain with its transcendent capacity for creativity. The story of hominid evolution to *Homo sapiens sapiens* is the most wonderful story that can be told. It is *our* story. Each of us has to realize that the great success of hominid evolution was the only chance of existence as human beings, if one dares to speak retrospectively. Why then is this story not being often told in the essential features of the coming-to-be of human brains, as has been done in this book? It could be that the brain evolution story appears to be empty of facts and good only for unjustified speculations. While recognizing that much is unknown or only imperfectly known, I have been able to unfold the fascinating story of hominid evolution of the human brain using creative imagination restrained by rational criticism.

At a time when it is fashionable in certain quarters to denigrate Darwinism and even rationality, this book conforms with the Darwinist hypothesis of biological evolution except that phyletic gradualism gives place at intervals to such modifications as the punctuated equilibrium (Section 1.3) and possible chromosomal rearrangements (Section 1.4). The theme of the book goes beyond the materialistic concepts of Darwinism only in the last three chapters, where there is consideration of the most controversial evolutionary happenings. First, there was the emergence of consciousness in the higher animals (Chapter 8) and secondly the much more remarkable transcendence when hominids experienced self-consciousness (Chapters 9 and 10).

Right at the outset of hominid evolution there is mystery. As revealed by albumen dating, the hominoid line split into hominid and pongid evolutionary lines at 9 to 10 million years ago (Section 2.1, Table 2.1). Unfortunately there is an almost complete fossil 'black-out' for 5 million years after this most critical time of hominid evolution (Sections 2.1 and 2.2). Presumably the number of hominids was then extremely small. During those 5 million years there was the evolutionary transformation to bipedal walking as told in Section 3.3. One can assume that there were series of stages between

the arboreal hominoids and the terrestrial Australopithecines. When the 'curtain lifted' 4 million years ago (Section 2.2), the fossil record of a bone and muscle system almost fully transformed for bipedality was disclosed (Figures 3.8, 3.9, and 3.10). Surprisingly there was only a small increase in brain size (Figures 2.4 and 2.6). Yet in the shift from quadrupedality to bipedality there must have been a transformation of the neural machinery of the brain to give the fully evolved bipedal walking that is exhibited in the most wonderful of all fossils, the Laetoli footprints (Figure 3.11).

In the last few decades there have been very rich discoveries of fossil hominids from 4 million years ago to recent times, as briefly told in Chapters 2 and 3. Even the transformation of the brain can be recognized in the endocasts (Figures 2.7 and 2.9). In attempting to appreciate the changes wrought by hominid evolution, it is necessary to utilize a modern pongid brain as a model for the ancestral hominoid brain. The attempt to portray the cerebral changes in hominid evolution has been greatly helped by the exquisite studies of Heinz Stephan and his associates. They have measured the sizes of anatomically identified cerebral structures such as nuclei in a wide variety of primate brains including human brains. The calculated size indices are the basis of many tables in the book.

It must be recognized that only from the higher primates could there have been the evolutionary process leading to beings with the finesse of human perceptual and motor systems. Human evolution was built upon the evolution already accomplished by the higher primates, and so particularly by the hominoids. An excellent example is provided by their superb visual system (Chapter 6) with eyes perfectly adapted for binocular vision. The visual pathways project to the primary visual cortex and thence to the prestriate cortex in a manner that was not appreciably changed in evolution to *Homo sapiens*. Of supreme importance is the cerebral cortex, which in the upper primates is the nearest to the human cerebral cortex (Chapters 8 and 9). Also of importance is the limbic system (Chapter 5) and the learning systems (Chapter 7), which are very similar to the human in general design.

With the cerebral cortex new areas evolved to give the most important functions of the human brain, in particular the speech areas (Chapter 4) that at the most were rudimentary in the pongid brain and non-existent in other primates. As discussed in Chapter 9, these new areas are functionally asymmetrical. Not only were they the last to evolve, but they also are the last to come into function in ontogenesis. In Chapters 9 and 10 there will be special concentration on this distinctively human cortex, which is called the neo-neocortex with its gnostic functions.

In primate evolution there was what we might call conservative wisdom. It can be expressed by an evolutionary adage: never trade a basic inherited feature for seemingly attractive short-term gains, for example the five freely moving digits of the limb for a paw or a hoof or a wing. So hominid evolution took off with the conserved early vertebrate limb with digits and was able to

transform them into the invaluable hand and foot (Sections 3.3–3.5). The hand in particular gave the hominids pre-eminence in evolution, and consequently was continuously perfected, with of course the neural machinery (Section 3.5).

The question is often asked: is our evolutionary line the only one that could conceivably lead to beings with intelligence and imagination matching or even transcending ours? Could for example some super-intelligent apes initiate another evolutionary line matching and even surpassing the hominid line? The answer must be no! Hominid evolution depended on the quantal advances by very small isolates separated from the main genetic pool. Moreover, an immensely long isolation time would be required for each new species – hundreds of thousands of years. Such conditions can never be re-enacted on Planet Earth with its dominance by communication systems and operators! In fact, even in the past, hominid evolution happened only once, and then for millions of years it depended on a minute population with complete extinction as an ever-present danger.

So the story of hominid evolution on Planet Earth that I tell in this book is unique and never to be repeated. *Homo sapiens sapiens* need not fear upstart rivals!

This book has concentrated on the evolution of the human brain with the coming to be of consciousness and self-consciousness. It is recognized that there can be no physicalist explanation of this mysterious emergence of consciousness and self-consciousness in a hitherto mindless world. The philosophical consideration of this problem in Chapters 8, 9, and 10 leads in Chapter 10 to a religious concept of the coming-to-be of the self-consciousness that each of us experiences. It is proposed that at the core of our mental world, the World 2 of Popper (Figures 9.5 and 10.4), there is a divinely created soul. This theme is further developed in the latter part of the Addendum.

Acknowledgements

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I leave to the end a special tribute to my wife, Dr Helena Eccles, who has been deeply immersed in all aspects of the creation of this book – in typing and retyping the whole text and in her wise critical judgements.

A book of this nature is dependent on good illustrations, and I am grateful to the publishers and scholars who generously granted permission for publishing their figures and tables:

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List of abbreviations

ASL	American Sign Language
BoW	body weight
BP	before present
BrW	brain weight
byBP	billion years before present
CBL	cortico-basolateral group of amygdala nuclei
CM	centromedial group of nuclei
CNV	contingent negative variation
DNA	deoxyribonucleic acid
EI	encephalization index
EMG	electromyogram
EPSP	excitatory postsynaptic potential
EQ	encephalization quotient
FSH	follicular stimulating hormone
FSR	functional stretch reflex
HSN	*Homo sapiens neanderthalis*
HSS	*Homo sapiens sapiens*
LGB	lateral geniculate body
LLR	long-loop reflex
LTD	long-term depression
LTM	long-term memory
LTP	long-term potentiation
M1	primary motor cortex
myBP	million years before present
N	newton
NMDA	N-methyl-D-aspartate
PM	premotor cortex
rCBF	regional cerebral brain flow
RNA	ribonucleic acid
SI	size index
SMA	supplementary motor area
STM	short-term memory
STS	superior temporal sulcus
yBP	years before present

Contents

Chapter one

Biological evolution

1.1 The genetic code

In order to be able to present an intelligible story of the essentials of the evolutionary process, it is necessary first to give a much-simplified account of the genetic material of the cell, deoxyribonucleic acid (DNA), and of the mode of its action via the genetic code. The segregation of this essential evolutionary material into the cell nuclei was achieved very early in the evolution of the unicellular eukaryotes that arose about 1.8 billion years ago. This was a very important evolutionary development because it protected the complex machinery that is central to all cell activity including reproduction.

The DNA of the nucleus is a densely coiled and extremely long double helix. As diagrammed in Figure 1.1, each strand is constructed of alternate phosphate (P) and sugar (ribose) moieties. To each sugar there is attached one of the following four molecules: the purine bases, adenine (A) and guanine (G), and the pyrimidines, thymine (T) and cytosine (C). The two helices are effectively cross-linked every 3.4 Å (Figure 1.1). A in one links to T in the other or G in one to C of the other. So a sequence could be:

GTAGCAT
CATCGTA

for the linkage pairs of a very short segment of the two helices. The nucleotide code is thus written linearly along each strand. Figure 1.2a shows the atomic structure of the double helix with below the phosphate (P) and sugar (S) chain and the cross-linkage by the purine and pyrimidine bases through the hydrogen bonding of A with T and C with G. Figure 1.2b illustrates the manner in which the linear code of the DNA is translated to messenger RNA (ribonucleic acid), which effects the segmental building of the amino acid sequences of a protein by means of a three-letter code acting like a machine language in specifying the sequence of the five amino acids in this specimen record.

For a bacterium the code of each strand has about 1.5 million letters. With *Homo* there are about 3.5 billion letters in each DNA strand, which gives the preliminary information for building all of the cells of a human being. Before

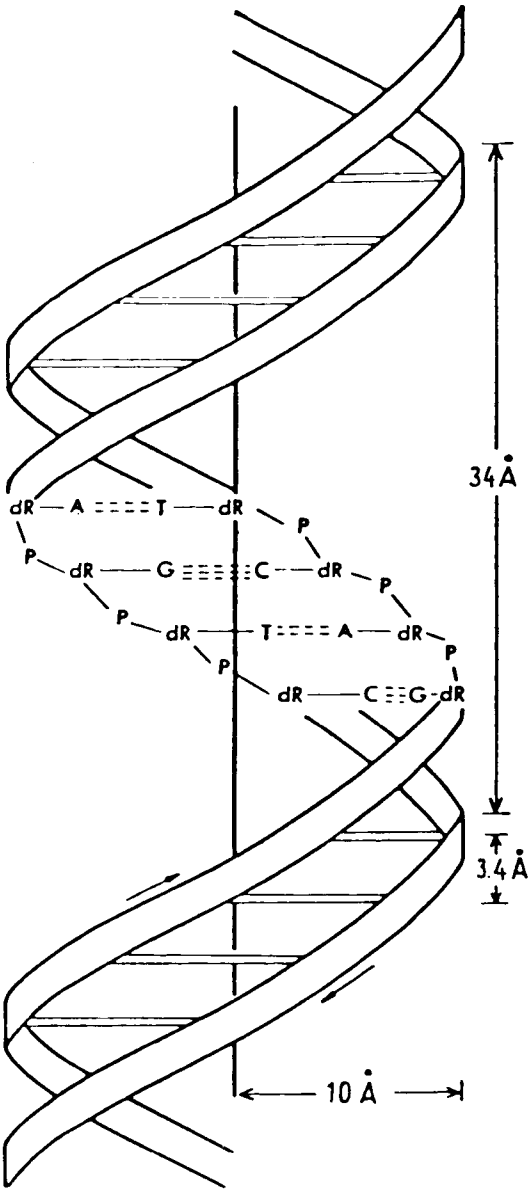

Figure 1.1 The double-stranded helical configuration of the DNA molecule. The two nucleotide strands are held together by hydrogen bonds forming between the complementary purine (A or G) and pyrimidine (T or C) pairs. Note the dimensions given for the spacing, and for width and length of one helical configuration.

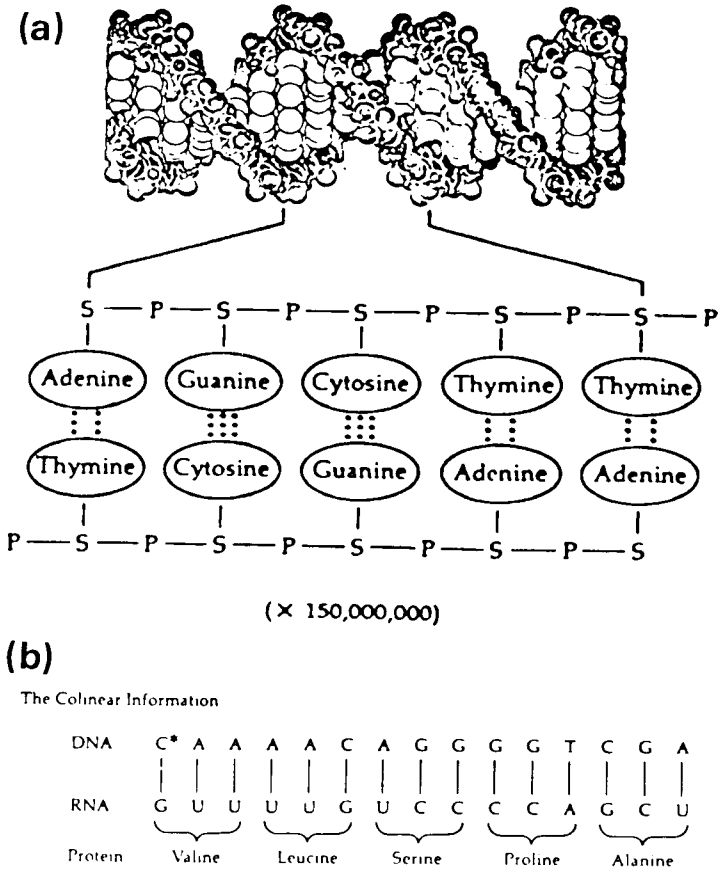

Figure 1.2 **(a)** Above: atomic structure of DNA molecule. Below: diagram of connections in DNA–S, sugar, P, phosphate, covalent bonds as lines, hydrogen bonds as dots. (b) Diagram of a small segment of DNA with the processes of transcription to RNA and translation from RNA to amino acids. From *Darwin to DNA, Molecules to Humanity* by G. Ledyard Stebbins Copyright © WH Freeman and Co. Reprinted with permission.

the cell divides, the two strands of the double helix separate and an enzyme system makes for each the complementary strand. The two double helices that are thus reconstituted are almost always identical copies of the original. The genetic information that builds and controls the cell is coded in the nucleotide sequences, the ATGC letters, along the DNA strands.

It is beyond the scope of this chapter to go into the detailed manner in which, by the precise processes of transcription and translation, this DNA code is read out in the building of the amino acid sequences of a protein (see Figure 1.2b), and so is effective in building the structure of the cell and in the enzymatically controlled metabolism of the cell. Enzymes are proteins.

The code for any such action in building a protein is carried in linear array on the DNA strands, not by a short sequence of letters as illustrated above, but by some thousands of letter sequences, called a *gene*. Genes carry the precise instructions for building the amino acid sequences of particular proteins. It will be recognized that, for building the many species of proteins required for the living processes of a bacterial cell, its DNA chain of about 3 million letter sequences is not extravagant. With our cells the number is more than 1,000 times greater, 3.5 billion. This seems rather extravagant for coding the information required to build the proteins of our cells. It has been estimated by Dobzhansky (personal communication) that the number of human genes is at least 30,000. For an average protein of 500 amino acid sequences, 1,500 nucleotide pairs are required, because three pairs are required for each sequence. So 30,000 genes require 4.5×10^7 nucleotide pairs. However, with redundancies the number could be many times larger, so lifting this low ratio of 1.4 per cent.

Moreover there is the unsolved problem of the 'silence' of at least 30–70 per cent of the mammalian genome. A partial solution is in the DNA spacers, which are sequences separating the active DNA segments.

Normally in reproduction there is an accurate copying of the linear code written in the DNA, and hence there is stability in the genes from generation to generation. However, changes called *gene mutations* do occur in the DNA code. There may be mistakes in copying with the replacement of one nucleotide for another, such as G for A, or there may be more radical changes with deletion or inversion of one or more nucleotide base pairs or even inversion of larger DNA segments. These copying errors may lead to the substitution of one amino acid for another in a protein. The effect of this may be negligible in the functioning of the protein. However, in the great majority these exchanges are deleterious to the survival and reproduction of the individual, which consequently is eliminated in the process of natural selection.

Only on rare occasions is a mutation beneficial for survival and reproduction. Such a mutation will be transmitted to successive generations and will result in enhanced survival of the biological group sharing this mutation. So after many generations by *natural selection* this favourable mutation may come to be incorporated in all members of that species, which consequently reflect a slight change in genotype. Later another mutational selection may be added, and so on.

This is the essential basis of the modern version of Darwin's theory of *natural selection* or *survival of the fittest*. Favourable gene mutations are selected, whereas the unfavourable are eliminated. Hence by an initial process of pure chance, the gene mutation, there can be wrought by natural selection all the marvellous structural and functional features of living organisms with their amazing adaptiveness and inventiveness. As so formulated, the evolutionary theory is purely a biological process involving mechanisms of operations that are now well understood in principle, and it

has deservedly won acceptance as providing a satisfactory explanation of the development of all living forms from some single extremely simple primordial form of life. This theory, stemming from Darwin and Wallace, must rank as one of the grandest conceptual achievements of man. Yet it is in need of remodelling (Sections 1.2 and 1.3 below).

A recent development has been the recognition that many mistakes in DNA copying are virtually neutral. For example, the mutation may result in a changed amino acid sequence in a part of the protein that is not vital for its functioning. Or, again, the mutation may be in a part of the DNA that is not concerned in building protein, so it will be selectively neutral. In time there can be a large accumulation of such neutral mutations that have changed considerably the original DNA of a population. With a changed environment these mutations may no longer be neutral.

The DNA of a cell nucleus does not exist as an enormously long double helix of about 2 m in length, but is subdivided into segments that compose the chromosomes, which become evident when the cell is in the process of meiosis during subdivision. Then the human genome is seen to be packaged into 23 pairs of chromosomes each with its distinctive character (Figure 1.3). In meiosis the chromosomes with their contained DNA subdivide and separate to form the sex cells, and, when there is fertilization, the full complement of DNA is reconstituted, half coming from each sex cell.

The four living species of Hominoidea (Table 2.1) are very similar in their nuclear structure. The three species of pongids – chimpanzees, gorilla, and orang-utan – have 48 chromosomes. In *Homo* two pairs of chromosomes have united by centric fusion to form chromosome 2, hence *Homo* has 46 chromosomes (Figure 1.3). In other respects there is a remarkable similarity, even to the details of the banding patterns along the chromosomes of the respective species.

1.2 The modern synthesis: phyletic gradualism (Mayr, 1963)

Ever since Darwin it has been recognized that biological species play the key role as units in evolution. A species consists of a population rather than of unconnected individuals. The population of a species is reproductively isolated from all other species because of the fertility criterion. Other rather similar species may inhabit the same territory, but despite this *sympatric coexistence* there is no interbreeding. 'Each species is a delicately integrated genetic system that has been selected through many generations to fit into a definite niche in its environment' (Mayr, 1963:109).

In the Darwinian perspective palaeontology accounted for the formation of new species by transformation of the ancestral population by a very slow process with large numbers of individuals in the inhabited territory. It is a process that Eldredge and Gould (1972) called *phyletic gradualism*. Unfortunately this gradualness is not shown in the fossil record. The classical

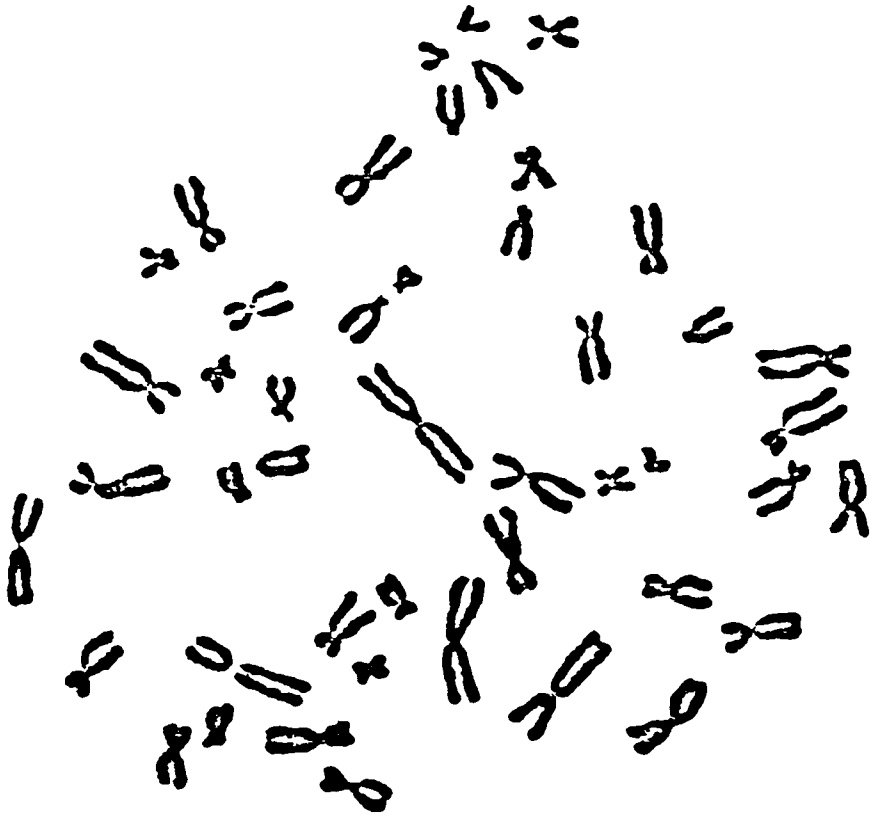

Figure 1.3 A photograph of a normal complement of chromosomes of a human female enlarged 15,000 times. The normal number of chromosomes in the human is 46. (Handler, 1968.)

evolutionists attribute this deficiency to the imperfection of the fossil record. The fossils indicate a story of sharp breaks or saltations in the evolutionary process. The genetic diversity of a species is due to mutations, recombinations, deletions, etc. in the genetic transmission from one generation to the next. However, it is controlled by the collective process of gene flow in the successive generations of a freely breeding population. Nevertheless, no two individuals of a sexually reproducing population are genetically identical (Mayr, 1963), except for identical twins.

Despite the homogenizing effect of gene flow, the modern synthetic theory of phyletic gradualism 'continued this tradition of extrapolation from local populations and used the accepted model for adaptive geographical variation – gradual allelic substitution directed by natural selection – as a paradigm for the origin of species' (Gould, 1982: 134; 'alleles' is used here as a collective