CHAPTER 19

Using Humans as a Central Example in Teaching Undergraduate Biology Labs

Craig E. Nelson and Martin K. Nickels

Craig E. Nelson
Department of Biology
Indiana University
Bloomington, IN 47405-3700
nelson1@indiana.edu
(Note: 1 in nelson1 is the number 1)
812-855-1345

Martin K. Nickels
Anthropology Program
Campus Box 4660
Illinois State University
Normal, IL 61790-4660
mnickels@ilstu.edu
309-438-7745

Craig E. Nelson received his PhD from the University of Texas in 1966. He is Professor of Biology and of Public and Environmental Affairs at Indiana University in Bloomington, where he has been since 1966. Dr. Nelson's research has focused on questions in evolutionary ecology and on college teaching. He has taught undergraduate and graduate courses in biology and in interdisciplinary fields and a graduate course on teaching college biology. He has received awards for distinguished teaching from IU as well as nationally competitive teaching awards from Vanderbilt and Northwestern Universities and has been a Sigma Xi National Lecturer. He was named Outstanding Research and Doctoral University Professor of the Year for 2000 by the Carnegie Corporation for the Advancement of Teaching and the Council for the Advancement and Support of Education (CASE) and is a Carnegie Scholar for 2000-2001.

Martin K. Nickels received his PhD from the University of Kansas in 1975. He is Professor of Physical Anthropology and Adjunct Professor of Biology at Illinois State University. His research interests include the history of human evolutionary studies, hominid paleontology and prehistory, human evolution education, primate behavior and the biological bases of human behavior. He has twice been selected as the Outstanding University Teacher at Illinois State University and has been a Sigma Xi National Lecturer.

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General Introduction

These three activities (one using amino acid sequence data and two skull comparison exercises) illustrate two different aspects of human biology and underscore the immense pedagogical value and appeal of emphasizing humans as a central example when discussing the evidence for evolution in college biology courses. The combined use of skeletal morphological data with biochemical data is especially effective with students. All three activities are intended to provide students the opportunity to utilize *real* data, some of it self-determined.

Introduction for the Primate Molecular Sequence Comparison Lab

This activity has two goals. First, it takes students through the transformations from sequence data to cladograms and molecular clocks. This hands-on analysis greatly facilitates the students' understanding of these concepts. Second, it applies these concepts to the relationships of humans with other primates. Using primates, and emphasizing the great apes (including humans), helps students focus on what is otherwise a major difficulty for many —understanding the strength of the evidence that humans have indeed evolved. Using this activity in conjunction with one of the hominoid skull exercises will substantially enhance the effectiveness of each activity in addressing the latter goal. Note that the molecular sequence activity can be done either in a laboratory setting or in small groups in a lecture room.

Materials and Notes for the Instructor for the Sequence Lab

Materials, Time and Procedures: The only materials needed are the handouts. Time: One to two 45-55 minute periods, depending on the amount of analysis you want to have the students engage in. (Some or all of the analyses can be done outside of the classroom as homework.)

Discussion of the activities, concepts and results will foster both deeper and more enthusiastic learning. Ideally, students work in groups of 3-5. Some classes will benefit from noting the species key earlier in the exercise. However, its current placement allows them to analyze the similarities among the sequences without interference from preconceived ideas about the relationships. It sometimes may be helpful to withhold Cladistic Tree B until the students have completed Cladistic Tree A. Tree B could be shown on an overhead, made a separate handout or given as a part of a take home exercise.

Comments on Individual Working Boxes

Box A: Diagonal values compare a sequence with itself (thus no differences are possible). Remind the students to count DIFFERENCES on BOTH DATA PAGES. It is best to have at least two different groups do each of the counts to ensure accuracy. A good technique is to put the matrix on an overhead and fill in the blanks as the class goes. *The completed matrix should be:*

Species	I	II	III	IV	V	VI	VII	VIII
I	s	0	1	2	8	8	25	24
II	x	s	1	2	8	8	25	24
III	x	x	s	3	7	9	24	25
IV	x	x	x	s	6	6	23	24
V	x	x	x	x	s	11	22	27
VI	x	x	x	x	x	s	25	24
VII	x	x	x	x	x	x	s	33
VIII	x	x	x	x	x	x	x	s

Box B: We would have to move the columns and rows into whatever order made the numbers show the simplest patterns within columns and across rows. The first two columns would contain the two most similar species. The third the species that was most similar to the first two, etc. And, yes, it gets more complicated if you add several species from each group.

Box C: The two most similar species share all 146 amino acids (i.e., NO differences between species I and II). The two least similar species share 146 – 33 = 113 (for species VII with VIII). Patterns are a stepwise decrease along each row (least clear between columns V and VI) and relative uniformity within each column. This suggests that every species to the left of a given species is approximately equally divergent in sequence (and hence evolutionarily) from that species. This is counter-intuitive as most students expect a ladder. See Box D for more.

Box D: Prosimians are the least similar to the others and are about equally divergent from each of the others species (i.e., the pattern is NOT ladder-like, with gorillas half way to humans from gibbons, etc.). Gorillas are equally distant from humans and from chimps. Gibbons are almost exactly equally distant from chimps, humans and gorillas (as expected if these three shared common ancestry after the gibbon lineage diverged. Humans thus fall *within* the Great Ape clade. Thus, humans have to be viewed as great apes IF clades are to be monphyletic and not paraphyletic (see e.g., Freeman and Herron, 2000, Evolutionary Analysis, for terminology).

Box E: The two most similar species are chimpanzees and humans. They go on the two shortest branches of Tree A (in the middle of the tree). It makes no biological difference which one goes on the left—and indeed the form of Tree A is designed to emphasize that fact (thereby allowing a contrast with the conventional, more human-centered presentation in Tree B.) Gorillas are next, then the gibbon. The similarities in values for the Gibbon when compared with each of the Great Apes suggest that these three are all about equally distant from Gibbons, presumably because they had the same, shared common ancestors for a while after their lineage diverged from that of the gibbons. The left to right order in the matrix is the same as the top to base order of branching.

Box F: #33 is V (valine) in all species except the Old-World monkey, which has L (leucine). The straight-forward interpretation is the incorporation of a new mutation to Leucine in the OW monkey lineage after it branched from the ape lineage. African apes (including humans) differ from Gibbons at positions **#87** and **#125**. In both cases the change is from Q (glutamine), found widely across the lower primates at these two positions, to T (threonine) at 87 and P (proline) at 125. The most parsimonious interpretation is that the two mutations occurred in the great ape lineage before any of the three species diverged from the others. **#50** and **#104** both require either convergent substitutions or back-mutations and the data here does not allow these two alternatives to be differentiated (the DNA sequences might allow an unambiguous interpretation). Be sure to ask WHY the more parsimonious interpretations should be preferred.

Box G: The age data on Tree B are new. The biological information in Trees A and B is identical.

Box H: The general relationship is more changes over longer times since separation. This pattern is the basis for the idea of molecular clocks--total mutations increase fairly regularly with time. However, nothing makes the clocks tick exactly at the same rate (the extra mutation in the gorilla, for example). With more time, convergences and back-mutations begin to reduce the differences to fewer than expected from a simple clock. This acts to slow the rise in the curve with time. This is especially evident in the comparisons of apes and monkeys first with the lemur and then with the horse. The differences with the horse are much fewer than the 1.5 times the differences from the lemur (the expectation from a linear clock, given the differences in divergence times).

Extensions and Additional Comments

Deeper mastery of the concepts and more confirmation of the strength of the evidence for human evolution (as well as for evolution generally) can be achieved by searching out and comparing other molecules. Recent, especially helpful guides to doing this include:

R.P. Hershberger. 2000. What I could teach Darwin using "Darwin 2000," an interactive web site for student research into the evolution of genes and proteins. Tested Studies for Laboratory Teaching 21:4-32 Association for Biology Laboratory Education. See also his site www.bioactivesite.com.

R.Moss.1999. The molecular evidence for evolution. Journal of College Science Teaching 29:111-113. Also features student use of public, on-line databases.

S.D. Brewer. 1997. Constructing Student Problems in Phylogenetic Tree Construction. Paper presented at the Annual Meeting of the American Educational Research Association (Chicago, IL, March 24-28, 1997). EDRS DOCUMENT LINK: http://orders.edrs.com/members/sp.cfm?AN=ED407227

See also the lessons, tutorials and advanced resources directly available through the "Biology Workbench" homepage http://glycine.ncsa.uiuc.edu/educwb/index2.html.

Introduction for the Hominoid Skull Comparison Labs

These skull comparison exercises introduce students to the skull and dental morphology of hominoids: modern apes, modern humans and fossil hominoids. The goal is to provide 1) experience for understanding the basis for taxonomic classification of apes and humans and 2) a referential set of attributes for interpreting the taxonomic placement and probable evolutionary relationships between prehistoric hominid forms and modern humans. As one element of teaching about the nature of the evidence for human evolution, our experience validates the unusually high pedagogical value of having introductory-level biology students work with skull casts and/or drawings in order to generate their own classificatory data set. The actual handling of skull casts of apes, humans and fossil hominids is unequaled in conveying to students the nature and value of the morphological evidence for a close ape-human evolutionary relationship and the pattern of hominid evolutionary change over time.

We provide two different variations of this exercise to illustrate a range of approaches that the instructor may use in dealing with this subject matter. The amount of time one devotes to this activity primarily depends upon the number of specimens the students work with.

Materials for the Hominoid Skull Comparison Labs

1. Casts of modern apes, humans and fossil hominids. Preferably two chimpanzee or gorilla specimens, male and female are ideal. A modern human skull may be available from the skeleton standing in the corner of your lab, but, if not, the 25,000 year old Predmost fossil cast will serve, as well. Good first choices for fossil casts are:

    a) A Neandertal (50-60,000 year old La Chapelle is commonly available);
    b) *Homo erectus* (the 450,000 year old "Peking” is widely available and least expensive);
    c) A "robust" australopithecine (preferably the 1.8 million year old Olduvai number 5 = “Zinjanthropus”) which shows a “mosaic” mixture of ape-like and human-like features; and
    d) "Lucy" (*A. afarensis*) which shows a terrific mosaic of ape and human features.

Our recommendation is to use as many specimens as possible, but realize that the availability of skull casts is the prime determiner of how much time the instructor can give to this exercise. The comparisons work much better when each group has an ape and human for comparison with each of the other forms (which can be rotated among groups). Our specific suggestions for expanding your collection and some sources are given in Appendix A. Scale drawings of a number of specimens are provided in Appendix D and can be substituted for some of the actual casts. (If you want the students to measure the figures, use a photocopy machine to enlarge them to life size -- ruler on each figure will allow you to tell when the size is right.) However, we strongly recommend that casts be used whenever possible.

2. Sliding calipers and/or rulers with metric scales (optional for Lab 2-A, required for Lab 2-B). Preferably a hinge caliper. (Extremely inexpensive plastic sliding calipers may be purchased at hardware stores. Hinge calipers can be cut-out of cardboard.)
3. Carpet squares (preferably) or similar table padding, such as old computer mouse pads, to set the casts on at each student grouping or “Skull Station.”
4. For Lab 2-A: Individual copies of the worksheets. For Lab 2-B: Individual copies of the Hominoid Cranium Comparison Checklist. Blank sheets of paper that students draw columns on are sufficient for recording data and observations in Version B.

Hominoid Skull Comparison Labs: Notes for the Instructor
Time: One to two 45-55 minute periods, depending on the amount of analysis you want to have the students engage in. (Some or all of any student analysis can be done as homework.)

Procedures:

1. Have students work in groups of 3-5. Discussion of the specimens and worksheets will foster deeper and more enthusiastic learning. This is a logistical necessity when one has fewer cranial casts than students.
2. Students may either work in stationary groups (in which case the specimens are passed from one group to another) or in groups that move from one “Skull Station” to another. Where the number of specimens will allow, it is helpful for the groups to be able to compare two or three skulls simultaneously.
3. Each student should have a copy of either the Skull Comparisons (Version A) or the Hominoid Cranium Comparison Checklist (Version B) because the details of each measurement and observation are spelled out on it. Each student should also have her/his own data worksheet for recording descriptions and measurements.
4. In Version B, have each student label the columns on their data worksheets with the name of each specimen. Have them simply number the left-hand edge of the worksheet 1 through 18 to correspond to the 18 items on the checklist. (This will put all entries for a single checklist item on the same line across the page to facilitate comparisons.)
5. Have students take turns being responsible for the items or questions on the checklists in order to keep everyone involved as much as possible.
6. If appropriate, remind students to record all measurements in millimeters (not inches).
7. Ask students to hold each specimen in the palms of their hands and not like bowling balls with their fingers stuck into the eye orbits and nasal cavity!
8. After the students have measured and described the specimens, have them determine and describe the patterns represented by their findings. This can be done in a variety of ways:

Simply list those features that all of the specimens have in common;

a) Identify those features which are most useful for distinguishing between the specimens;
b) Describe the changes that occur in only the hominid crania over time; or
c) Plot their data on graphs using the geological dates listed above.

9. Following their efforts to summarily describe the patterns they perceive in the specimens, engage the students in a discussion and/or consideration of the evolutionary significance and adaptive benefits of the changes they have just described in the hominid specimens. Here are some sample questions: Why do you think the canine tooth reduced in size so much from earlier to later hominids? Why do you think the face flattens over time in hominids? How does the position of the foramen magnum relate to the body posture and locomotor pattern of the animal? What areas or portions of the brain case enlarge first and which ones enlarge later in the hominids? What behavioral and cognitive functions are associated with these cerebral areas? Have we really lost the brow ridge?

Debriefing Information: Anatomical Trends In Hominid Evolution

Based on examination of fossil specimens spanning the last four million years, the most basic changes in the appearance of the hominid skull include:

BRAIN CASE: In addition to becoming larger overall (essentially tripling in size since the earliest hominids), the shape of the brain case became higher and more rounded. This is especially notable in humans in the shape of the forehead (frontal bone), which now rises more vertically above the eye orbits and is expanded laterally (as reflected in greater minimum frontal breadth measurements behind the eye orbits), and in the absence of any distinct postorbital constriction. The brow ridge is reduced considerably overall, but often still remains larger in males than in females. The bottom of the brain case also became more flexed or curved downward and less flat over time.

FACE AND JAWS: The face and jaws became shorter or flatter in profile. However, primarily as a result of the maxilla (upper jaw) reducing or shrinking, the nasal bones actually became more prominent forming an arch over the nasal opening. The mandible (lower jaw) lost much bony mass at the front as the front teeth (including their roots) shrank. But, in order to be able to provide sufficient structural resistance to the chewing stresses that focus at the front of the jaw, there is still a slight massing of bone at the front bottom edge of the jaw. This produced the formation of a slightly concave or curved appearance in the front of the mandible when it is viewed from the side. The concavity was the result of bone loss with the lower front edge of the mandible left “sticking out” as a chin--widely regarded as a distinctive skeletal trait of modern humans and rarely, if ever, seen in other hominid forms.

DENTITION: Basically, all of the teeth became much smaller over time, although this is more obvious with respect to the front teeth. The 8 incisors became somewhat thinner front to back and narrower from side to side. The 4 canines reduced to the point that they seldom project much, if at all, above the chewing surface of the other teeth. The shrinking of the front teeth was largely responsible for them becoming more clearly vertical or upright in the jaws when viewed from the side. The verticality of the front teeth is the principal contributing factor to the overall flattening of the face described above. The so-called “cheek” teeth (the 8 premolars and 12 molars together) also shrunk in overall size. It is noteworthy that modern humans still retain the same number of teeth both as adults (typically 32) and as juveniles (typically 20) that is characteristic of all Old World monkeys, apes and prehistoric hominids.

MOLECULAR SEQUENCES & PRIMATE EVOLUTION: AN AMINO ACID EXAMPLE

Martin Nickels, Craig Nelson, Doug Karpa-Wilson, Steve Freedberg and Nathan Murphy

WORKING BOX A – From a Set of Sequences to a Matrix of Differences.

There are 146 amino acids in the beta chain of hemoglobin. The sequences on the data sheets (TWO PAGES at end of handout) include ONLY the positions where the sequences are NOT identical across all eight species. You only need to fill in the upper right half of the matrix below because the same number would go in the corresponding positions (i.e., row I--column II and row II--column I, etc.). We have put an "x" in each redundant position. Each of the values in the matrix below is the number of differences between the amino acid sequences two species.

1. What species comparison is represented by the first "s" in the matrix (i.e. species 1 is compared with which species)? How many differences can there be for this comparison? Why?

2. Why would the values along the diagonal (I vs I, II vs II, etc.) each be zero? We use S (for Self) to avoid confusing these values with the values for differences between species.

3. Count the differences among the sequences for species I, II and III on BOTH DATA PAGES and enter the results in the three appropriate blanks in the matrix below. Do your group members agree? If so, count the differences for each remaining pair of sequences, compare results, and complete the matrix.

4. Calculate the average values for each column (ignoring S and X).

MATRIX: DIFFERENCES AMONG AMINO ACID SEQUENCES

Species	I	II	III	IV	V	VI	VII	VIII
I	s	__	__	__	__	__	25	24
II	x	s	__	__	__	__	25	24
III	x	x	s	__	__	__	24	25
IV	x	x	x	s	__	__	23	24
V	x	x	x	x	s	__	22	27
VI	x	x	x	x	x	s	25	24
VII	x	x	x	x	x	x	s	33
VIII	x	x	x	x	x	x	x	s
Average:	--	__	__	__	__	__	__	__

WORKING BOX B – Organizing Data

The rows and columns in the matrix above were arranged to make the similarities apparent. When researchers first get actual molecular data, the data are not organized. What would we have to do if (as in the matrix below) the data were not already organized for us? How would we do this? What would determine what two species we put in the first two columns? In the next column?

	IV	VII	VI	I	II	V	III
IV	S	23	6	2	2	6	3
VII		S	22	25	25	22	24
VI			S	8	8	11	9
I				S	0	8	1
II					S	8	1
V						S	7
III							S

WORKING BOX C – From Differences to Similarities [Use Matrix in Box A.]

1. How many of the 146 amino acids in the beta chain of hemoglobin do the two most similar sequences **share**? How many do the two least similar sequences **share**?

2. Note that the values within each species' column are those for that species compared with each of the species to its left. What is the general pattern of differences among the column averages from left to right across the table? Are the values within each column usually more similar to each other than they are to the values in the other columns? What does this suggest about the biological relationships of each species to the species on its left?

WORKING BOX D–Primate Similarities

THE FIRST SEVEN SPECIES IN THE DATA TABLE AND MATRIX ARE PRIMATES:

I: Human
II: Chimpanzee (a Great Ape)
III: Gorilla (a Great Ape)
IV: A "Lesser" Ape: Common Gibbon
V: An Old World Monkey: Rhesus Monkey
VI: A New World Monkey: Squirrel Monkey
VII: A Prosimian: Ring-tail lemur

1. Which group of primates is least similar to the others? (Prosimians, Old World Monkeys, New-World Monkeys, Lesser Apes, Great Apes or Humans?) Are the differences between this least similar group and the other groups all about equal **or** are the differences suggestive of a ladder of progress? (An example of a ladder would be if gorillas were half way between gibbons and humans).

2. Are Gorillas more similar to Humans or to Chimpanzees on the sequence data? Which species are most similar to Gibbons on the sequence data? Chimps and Gorillas are Great Apes. Should Humans be thought of as Great Apes as well? How could you explain these patterns in terms of common ancestry?

WORKING BOX E – Building a Cladistic Tree

1. Using the species list, write names of species I through VII on the side and top of the data matrix in working boxes A.

2. Which are the two species have the most similar sequences (fewest differences)? Put these two species in the blanks indicating closest similarity on Cladistic Tree A. Does it matter which one you put on the left? Why?

3. What third species is most similar to the first two species? Put it in the appropriate place on Tree A. Select the next most similar species and put this fourth species appropriately on the tree. Why does this fourth species have nearly the same number of differences with each of the first three species? How would this relate to the time since the line leading to the first species diverged from the line leading to the fourth species?

4. Now put the remaining species on Tree A.

WORKING BOX F – Identifying Evolutionary Events from the DATA

1. Consider position #33 on the DATA page (not the tree). What amino acid did the common ancestor of old-world monkeys and apes probably have at this position? How can you tell from the sequence data along which branch (of Tree A) the amino acid sequence changed?

2. At what two positions does the Gibbon sequence (IV) differ from the African Great Ape sequences (II, III)? Given both the entire tree and the primate sequence data (I-VII), what mutation (s) happened at position 87 and along which branch(es)? At position 125?

3. What mutation(s) happened at position 50 and along which branch(es)? At position 104? (Note the ambiguity in each case!)

WORKING BOX G – Cladistic Trees and Evolutionary Relationships

We've rearranged Cladistic Tree A into Cladistic Tree B. What is the difference in biological information between the two trees? (Ignore the dates in answering this question.)

WORKING BOX H – Introduction to Molecular Clocks

The dates (in Millions of Years Ago = MYA) by each node (branching point) of Cladistic Tree B represent the divergence dates based on fossil evidence and radiometric dating (not on molecular evidence).

1. Fill in the average number of molecular differences for each node on Tree B (using your

numbers from the appropriate columns in the table on the first page).

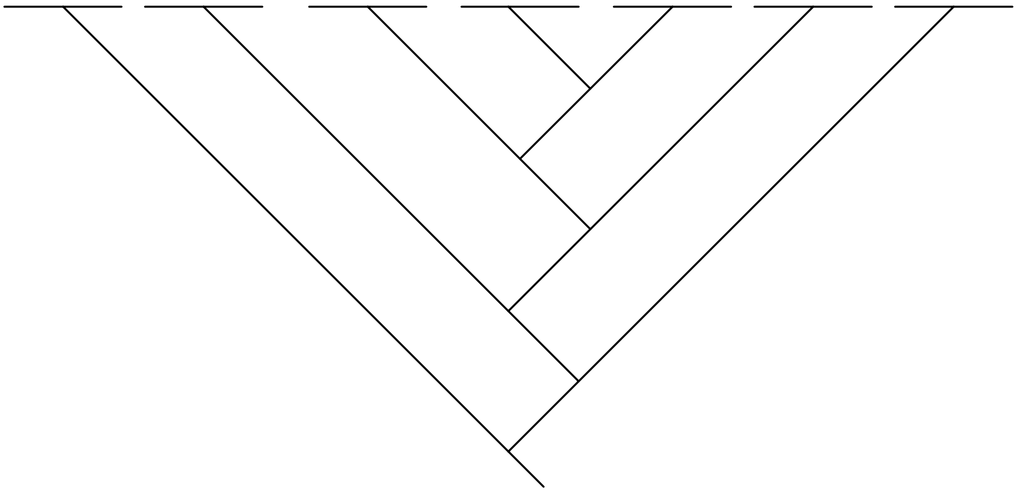
2. What is the general relationship between the geological ages of the nodes and the average numbers of molecular divergences? How could you explain this pattern?

3. On the graph of Differences vs. Time, plot the data for the relationship between the average number of amino acid differences and the time since divergence.

4. What is the general relationship between the time and average number of differences? Why isn’t this relationship perfectly linear (i.e. why don’t the points all fall on a straight line)?

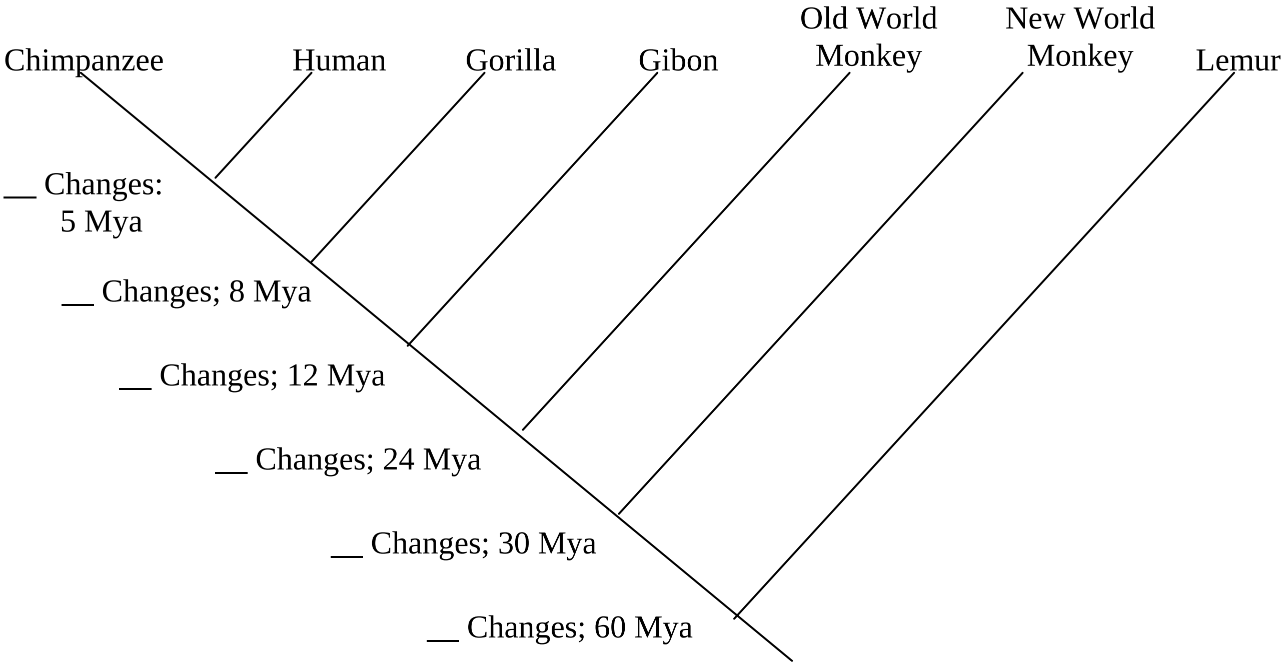
5. Species VIII in the data table and the matrix of differences is the horse. Based on these molecular data, where would horses fit on a cladistic tree (such as Tree B) with the primates examined above? Horses are not primates and are not especially close to primates. The group that includes horses diverged from the primates lineage around 90 million years ago. Add this point to the graph of Difference vs. Time (you will have to extend the graph onto another sheet of paper). What does this do to the shape of the curve? What would back-mutation have to due with the shape? Explain.

CLADISTIC TREE A

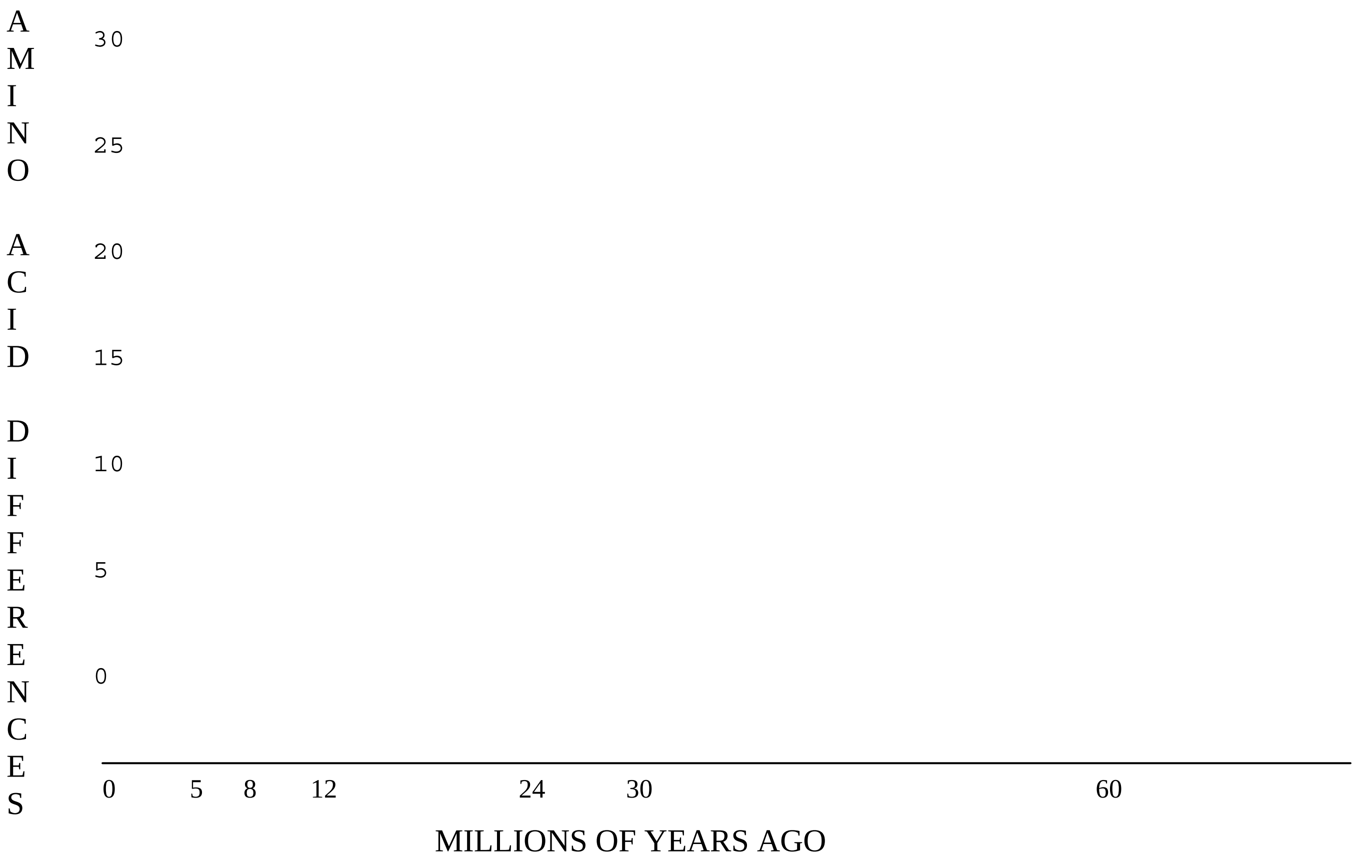


CLADISTIC TREE B

Mya = Million years ago



GRAPH OF SEQUENCE DIFFERENCES VS TIME



COMPARISON OF THE AMINO ACIDS IN THE BETA CHAIN OF THE HEMOGLOBIN MOLECULE IN EIGHT SELECTED SPECIES

Of the 146 amino acids positions in the beta hemoglobin molecule, only the 41 positions showing any <u>differences</u> between any of these eight species are included in this table. The other 105 positions do not vary across these eight species. The key to the amino acids is at the end. (You do not need to learn these for this exercise.) **The data continue onto the next page!**

	SPECIES							
AMINO ACID POSITION	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**
1	V	V	V	V	V	V	T	V
2	H	H	H	H	H	H	F	Q
4	T	T	T	T	T	T	T	S
5	P	P	P	P	P	G	P	G
6	E	E	E	E	E	D	E	E
8	K	K	K	K	K	K	N	K
9	S	S	S	S	N	A	G	A
10	A	A	A	A	A	A	H	A
12	T	T	T	T	T	T	T	L
13	A	A	A	A	T	A	S	A
16	G	G	G	G	G	G	G	D
20	V	V	V	V	V	V	V	E
21	D	D	D	D	D	E	E	E
22	E	E	E	E	E	D	K	E
33	V	V	V	V	L	V	V	V
43	E	E	E	E	E	E	E	D
50	T	T	T	T	S	T	S	N
52	D	D	D	D	D	D	D	G
54	V	V	V	V	V	V	I	V
56	G	G	G	G	G	N	G	G
69	G	G	G	G	G	G	S	H
70	A	A	A	A	A	A	A	S
72	S	S	S	S	S	S	S	G
73	D	D	D	D	D	D	E	E

POSITION	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**
75	L	L	L	L	L	L	L	V
76	A	A	A	A	N	A	H	H
87	T	T	T	Q	Q	Q	Q	A
94	D	D	D	D	D	D	V	D
95	K	K	K	K	K	K	A	K
104	R	R	K	R	K	R	K	R
112	C	C	C	C	C	C	I	V
116	H	H	H	H	H	H	H	R
120	K	K	K	K	K	K	N	K
121	E	E	E	E	E	E	D	D
123	T	T	T	T	T	T	S	T
125	P	P	P	Q	Q	Q	Q	E
126	V	V	V	V	V	V	T	L
129	A	A	A	A	A	A	A	S
130	Y	Y	Y	Y	Y	Y	F	Y
135	A	A	A	A	A	A	T	A

KEY TO THE ABBREVIATIONS FOR THE AMINO ACIDS:

A: alanine
G: glycine
T: threonine
C: cysteine
F: phenylalanine
E: glutamic acid
S: serine
D: aspartic acid
K: lysine
P: proline
N: asparagine
L: leucine
V: valine
R: arginine
H: histidine
Y: tyrosine
Q: glutamine

SOURCES*:* Morris Goodman (1992). Reconstructing human evolution from proteins. In: Steve Jones et al. (1992). *The Cambridge Encyclopedia of Human Evolution.* Cambridge University Press. pp. 307-312. *and* GenBank, National Center for Biotechnology Information. http://www.ncbi.nlm.nih.gov

HUMAN ORIGINS: HOMINOID SKULL COMPARISONS

C. Nelson, M. Nickels, D. Karpa-Wilson, S. Freedberg and N. Murphy

ROUND 1: Humans & Apes. *Compare the morphology (form) of the ape and human skulls. In groups, carefully write out the relative differences you observe in each of the features listed below.* (Hominoids = Humans + Apes + Related Fossils).

1. How are the differences in **brain-size** between humans and apes reflected in the length and width of the **brain-case** relative to rest of skull? In the **forehead slope** (more vertical or flat)?

2. The jaw muscle (**temporalis muscle**) runs through the large opening just behind and lateral to the orbit (eye opening).

   a) How is the size of the jaw muscle reflected in the sizes of these openings?

   b) How is the size of the jaw muscle reflected in the relative sizes the **post-orbital constriction** (width of skull across forehead just behind the brow ridges)?

   c) How is the size of the jaw muscle reflected in where it anchors on the skull and in the size of the attachment areas? On the side of the brain case **or** on the **sagittal & nuchal crests** (respectively: the bony ridges on top and at back of some hominoid skulls)?

3. How do the relative size of the **brow ridges** compare on humans and apes? How are these related to the sizes of the brain case (including the forehead slope) and of the jaw muscles?

4. Where is the **foramen magnum** (hole for spinal cord) located relative to the rest of the skull? What direction did the spinal cord (and vertebral column) probably run? What does

this suggest about posture? *Keep the upper jaw horizontal and the eyes oriented straight forward in this and the following comparisons.*

5. **Facial "prognathism":** How much does the skull project forward from eye orbits to the front of teeth? Shape of **chin area** (sticks out or slopes back)? What is the main reason for these differences? How do these features relate to the relative size of the set of teeth?

6. **Teeth: Shape of tooth row** (straight sided or parabolic)? **Angle of incisors** (slanted out or vertical)? Size of the **upper canine** tooth compared with adjacent teeth? **Gap ("diastema")** between upper incisors and canines? What is the function of this gap?

7. **Dental formula**. Number of Teeth in *one half of one jaw*? Incisors (front teeth)? Canines? (1) Cheek teeth (Molars + Premolars)? Do modern and early *Homo sapiens* differ? What would wisdom teeth have to do with any of these differences?

ROUND 2: Now compare "Lucy" *(Australopithecus afarensis)* **with humans and apes.** For each feature from round 1, above decide whether *A. afarensis* is more like humans, more like apes or distinctly intermediate.

HUMAN ORIGINS: HOMINOID SKULL COMPARISONS--MORE FOSSILS

C. Nelson, M. Nickels, D. Karpa-Wilson, S. Freedberg and N. Murphy

Skull casts are available for a number of species that are thought to be closely related to human ancestors that existed after the split from chimps. *A. afarensis* is the oldest of these.
In round 2 you compared a number of features of the skulls of apes, *Homo sapiens* and *Australopithecus afarensis.* Now, you'll use your newfound skills in skull anatomy to characterize at least two other fossil species. Those available include:

Species	Approximate ages
Homo sapeiens	0-0.15 My
Homo sapiens steinheimensis	0.2 My (?)
Homo erectus (Sinanthropus pekingensis)	0.3- 2 My
Homo habilis (small)	1.6-2.2 My
Australopithecus "gracile" (*A. africanus*)	2.5-3Mya
Australopithecus afarensis	2.5-4Mya

For at least two of these, rate each of the traits in the table below on a scale from 1 to 5 where:

1 – Just like *Australopithecus afarensis*
2– Mostly like *Australopithecus afarensis*
3 – About halfway between *Australopithecus afarensis* and *Homo sapiens*
4 – Mostly like *Homo sapiens*
5 – Just like *Homo sapiens*

Trait	**Specimen**			
	Sp #1	**Sp #2**	**Sp #3**	**Sp #4**
Brain case size				
Brow ridge size				
Forehead slope				
Jaw muscle size (Hole under zygomatic arch)				
Canine size/Diastema size				
Molar width				
Facial prognathism				
Foramen magnum location (How close to the middle of the skull is it?)				

1. Did these eight traits all evolve evenly and gradually across this time, or were there large changes in some of the traits between particular forms? Which ones did what?

2. Do the traits all evolve together or do different traits evolve at different times? Which ones evolved sooner and which later?

3. Extra difficulty! We have discussed something about the functional significance of these traits. Pick four traits and discuss whether they evolved at the same times or at different times. If they evolved at different times, what does that tell you about the different selective pressures experienced at different times in human history? Note: "Mosaic evolution" refers to different traits often evolving at different rates.

HOMINOID CRANIUM COMPARISON CHECKLIST

Martin K. Nickels

PLEASE READ THESE 5 STATEMENTS **BEFORE BEGINNING** THIS ACTIVITY:

1. Work in groups of 3-4 students so that everyone can be involved in the activity.
2. BE SURE (!) TO TAKE TURNS doing different measurements and observations.
3. When taking a measurement, use the SLIDING CALIPERS (except for #11 & #12 which may require the HINGE calipers) and remember:
4. ALWAYS MEASURE IN MILLIMETERS [mm] and round off to whole numbers.
5. PLEASE DO NOT ADD ANY PENCIL OR PEN MARK "TATTOOS" TO THESE CRANIA OR STICK YOUR FINGERS IN THEIR EYE ORBITS OR NOSES!

I. BRAIN CASE: (7 items)

1. Does the FOREHEAD (frontal bone) look more vertical OR flatter when the skull is held in normal anatomical position [NAP] (i.e., with the eyes oriented straight forward)?

2. Is a SUPRAORBITAL BROW RIDGE present?

3. If present, is the BROW RIDGE DIVIDED in the middle or CONTINUOUS?

4. What is the SHAPE OF THE BRAIN CASE (front to back) when viewed from above?

5. Is a SAGITTAL CREST present?

6. In NAP, is the FORAMEN MAGNUM oriented more downward OR more to the rear?

7. Is the MASTOID process relatively flat OR does it noticeably protrude (project)?

II. FACE: (5 items)

8. Are the NASAL BONES raised (arched) OR flat?

9. Measure the MAXIMUM BREADTH (width) of the NASAL OPENING [mm].

10. Measure the MAXIMUM HEIGHT of the NASAL OPENING [mm].

11. Measure the LENGTH of the MAXILLA (the upper jaw) [mm]. (Measure down the middle of the palate from the front edge of the foramen magnum to either between or just in front of the two central incisors to determine how much the face projects forward.)

12. Measure the BIZYGOMATIC BREADTH using the hinge caliper if necessary [mm]. (This is the width or breadth of the face from the widest part of one zygomatic arch to the widest part of the other zygomatic arch.)

III. DENTITION: (6 items)

13. SHAPE OF THE DENTAL ARCADE: Do the tooth rows diverge towards the back OR are they more straight-sided and parallel to one another?

14. When viewed from the side, are the INCISORS angled out OR are they vertical?

15. Measure the COMBINED WIDTH or BREADTH of the 4 INCISORS together.

16. Does the CANINE tooth project above the chewing surfaces of the other teeth?

17. Is a CANINE DIASTEMA present?

18. Measure the COMBINED LENGTH of the LEFT 2 PREMOLARS and 3 MOLARS together by measuring from the back of the last molar to the front of the first premolar to determine the length of the chewing surface of the "cheek teeth". [mm]. (NOTE: Measure the right side if the left side is missing any of these 5 teeth.)

APPENDIX A SELECTING SKULL CASTS & MODELS

Most of these are now available in materials that are extraordinarily sturdy and resistant to the most concerted student abuse--except for students "tattooing" them with pen/pencil marks! Bone Clones is introducing new "sculptures" that make available forms not included below that were impossible to obtain or very expensive. These sculptures are very satisfactory.

Humans

If you do not already have a modern human skull available, we suggest getting the fossil form found at PREDMOST, Czechoslovakia because it can serve double duty as a modern but also prehistoric version since it is about 25,000 years old. It also has the advantage of not having a sectioned skull (sectioning can be a real detriment to long term use by students).

Apes

In order to establish a baseline for interpreting fossils, you need a modern human skull and at least one ape form. Each ape form has advantages and disadvantages:

CHIMPANZEE: Closest to humans in many respects but not quite as useful when examining fossil forms like the robust australopithecines. The Bones Clones male chimp skull is nice.

MALE GORILLA: Most dramatic form as far as student interest goes but provides an exaggerated contrast to both modern humans and the australopithecines.

FEMALE GORILLA: Less dramatic comparison for modern humans but the best comparison for the best australopithecine cast to have (the robust "Zinjanthropus," see below) to illustrate the clearly hominid but still ancestral attributes of these early forms.

Recommended Hominid Fossils

1. "Lucy" (*A. afarensis*) which shows a terrific mosaic of ape and human features;
2. Robust australopithecine (Olduvai Hominid 5 ["Zinj"] is best);
3. *Homo habilis* (the best specimen is Olduvai Hominid 23);
4. *Homo erectus* (Zhoukoudian is best); and
5. Neanderthal (La Chapelle or La Ferrassie is best).

Some Sources for Ape and Fossil Hominid Skull Casts:

Bone Clones boneclones.com
Carolina Biological Supply Co. carolina.com
Skulls Unlimited   Skullsunlimited.com
Ward's   wardsci.com

APPENDIX B ANNOTATED BIBLIOGRAPHY FOR TEACHING HUMAN EVOLUTION

Boyd, R. and Silk, J. B. 2000. How humans evolved. Second edition. W. W. Norton, New York, 652 pages. (Excellent and up-to-date paleoanthropology textbook.)

Johanson, D. and Edgar, B. 1996. From Lucy to Language. Simon and Schuster Editions, New York, 272 pages. (Spectacular full-size photographs (by David Brill) are the highlight of this book with commentary Johanson and Blake.)

Lewin, R. 1998. Principles of human evolution. Malden, Massachusetts, Blackwell Science, 526 pages. (Up-to-date treatment of the major topical areas.)

Nelson, C. E. 2000. "Effective Strategies for Teaching Evolution and Other Controversial Subjects." Pp. 19-50 in: The Creation Controversy and the Science Classroom**.** National Science Teachers Association. (Suggests ways to reduce conflict with religion while teaching human evolution.)

Nickels, M. 1987. Human evolution: a challenge for biology teachers. American Biology Teacher 49:143-148. (Provides more detailed information regarding the skeletal features, measurements and observations on the Hominoid Cranium Comparison Checklist.)

Wolpoff, M. H. 1999. Paleoanthropology. Second edition. Boston, McGraw-Hill, 878 pages. (Invaluable: Detailed discussions of almost all the known hominid fossils.)

APPENDIX C HOMINOID (Apes and Humans) SKULL TERMINOLOGY

For locations see drawing B in Appendix D

BONES:	FEATURES:
1. Frontal (single bone)	A. Brow ridge B. Post-orbital constriction (minimum frontal breadth)
2. Parietal (right & left) (temporalis muscle)	C. Temporal line D. Sagittal crest (some apes)
3. Temporal (left & right)	E. Mastoid process F. Auditory meatus G. Zygomatic arch
4. Occipital (single bone) (nuchal muscles)	H. Foramen magnum I. Nuchal area/line/crest J. External occipital protuberance
5. Malar (right & left): forms zygomatic arch with part of the temporal bone (masseter muscle)	
6. Nasal (right & left)	
7. Maxilla (right & left) (Upper jaw)	K. Dental arcade L. Canine diastema (gap)
8. Mandible (single bone = Lower jaw)	M. Chin (in some humans)

Facial Prognathism = The projection or protrusion of the face from the eye orbits to the front of the jaws.

Dental Formula = The number and types of teeth from front to back in ONE HALF of ONE JAW. Example 2:1:2:3 = 2 incisors, 1 canine, 2 premolars and 3 molars.

APPENDIX D HOMINOID SKULL DRAWINGS

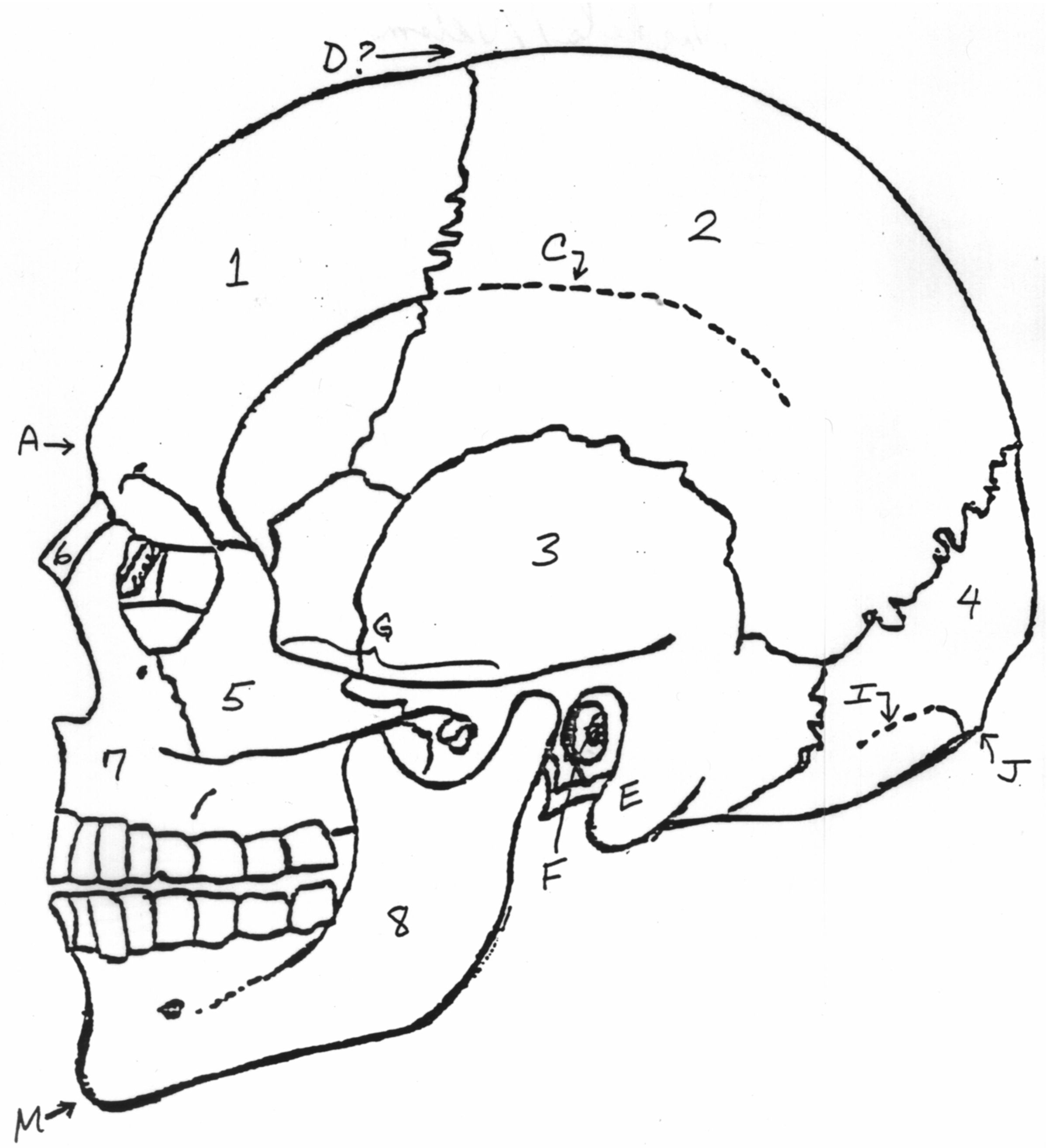


Figure A. Modern human skull with bones and features indicated.

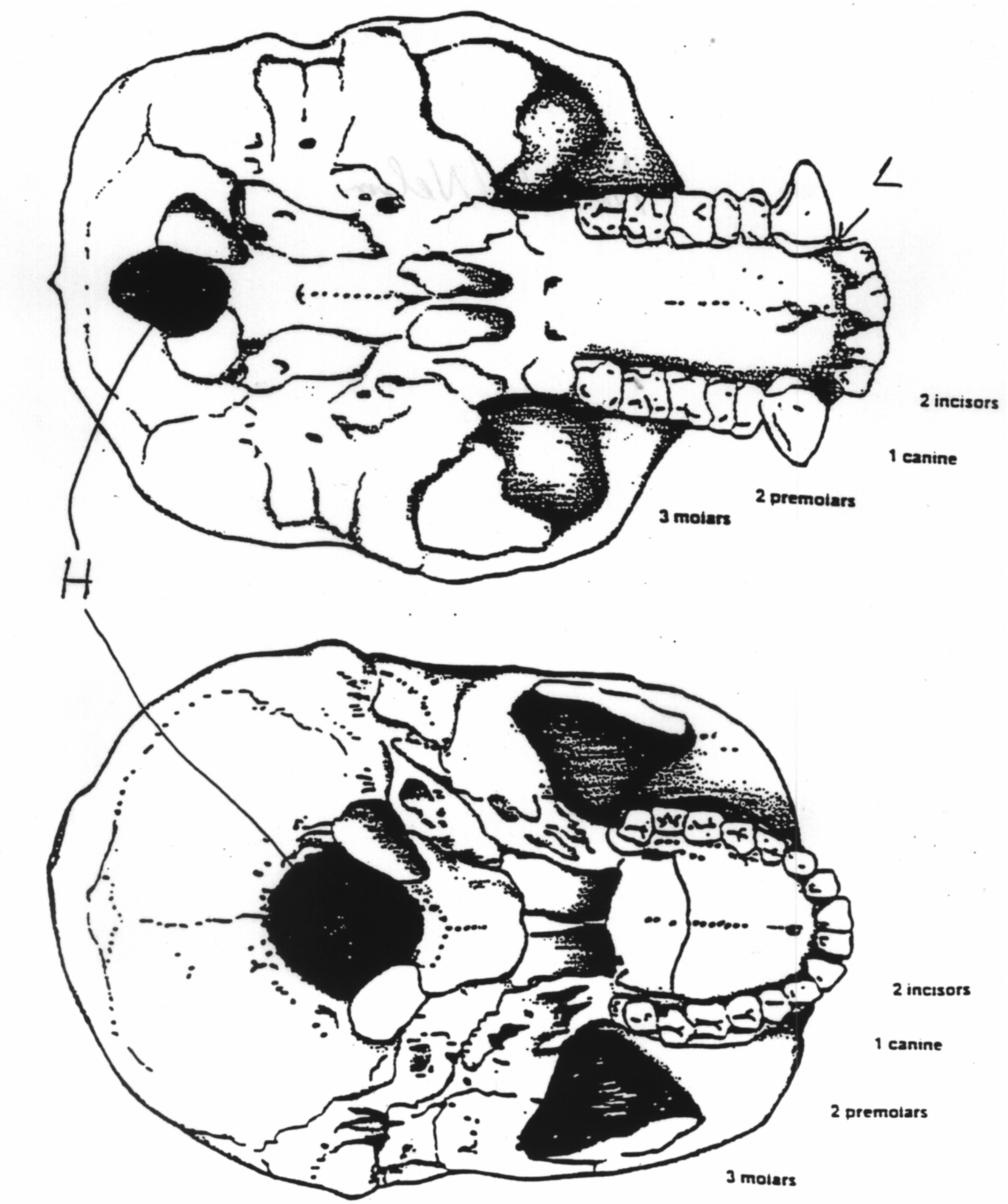


Figure B. Basilar view of chimpanzee (top) and modern human (bottom) crania.

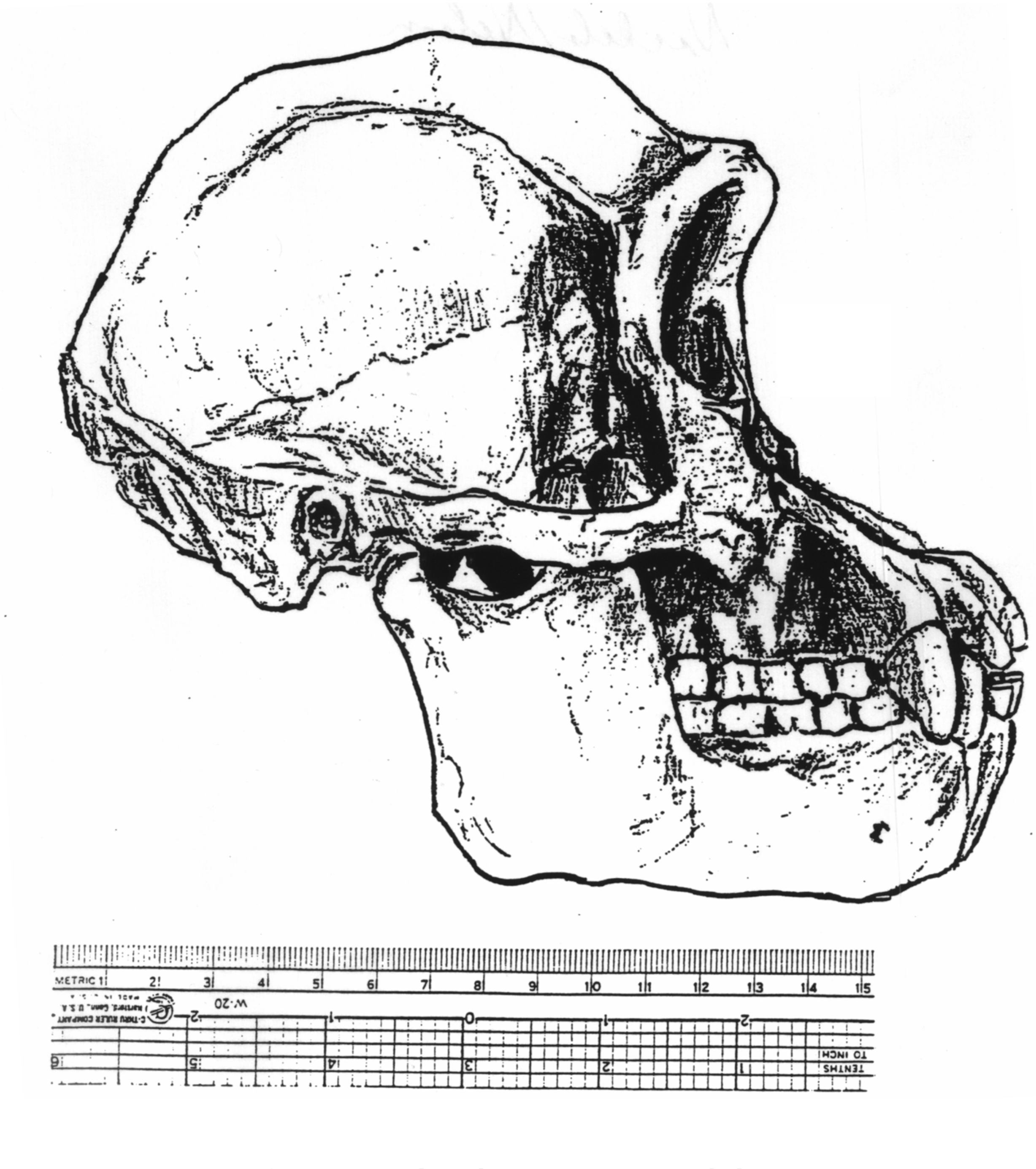


Figure C. Modern chimpanzee *(Pan troglodytes*).

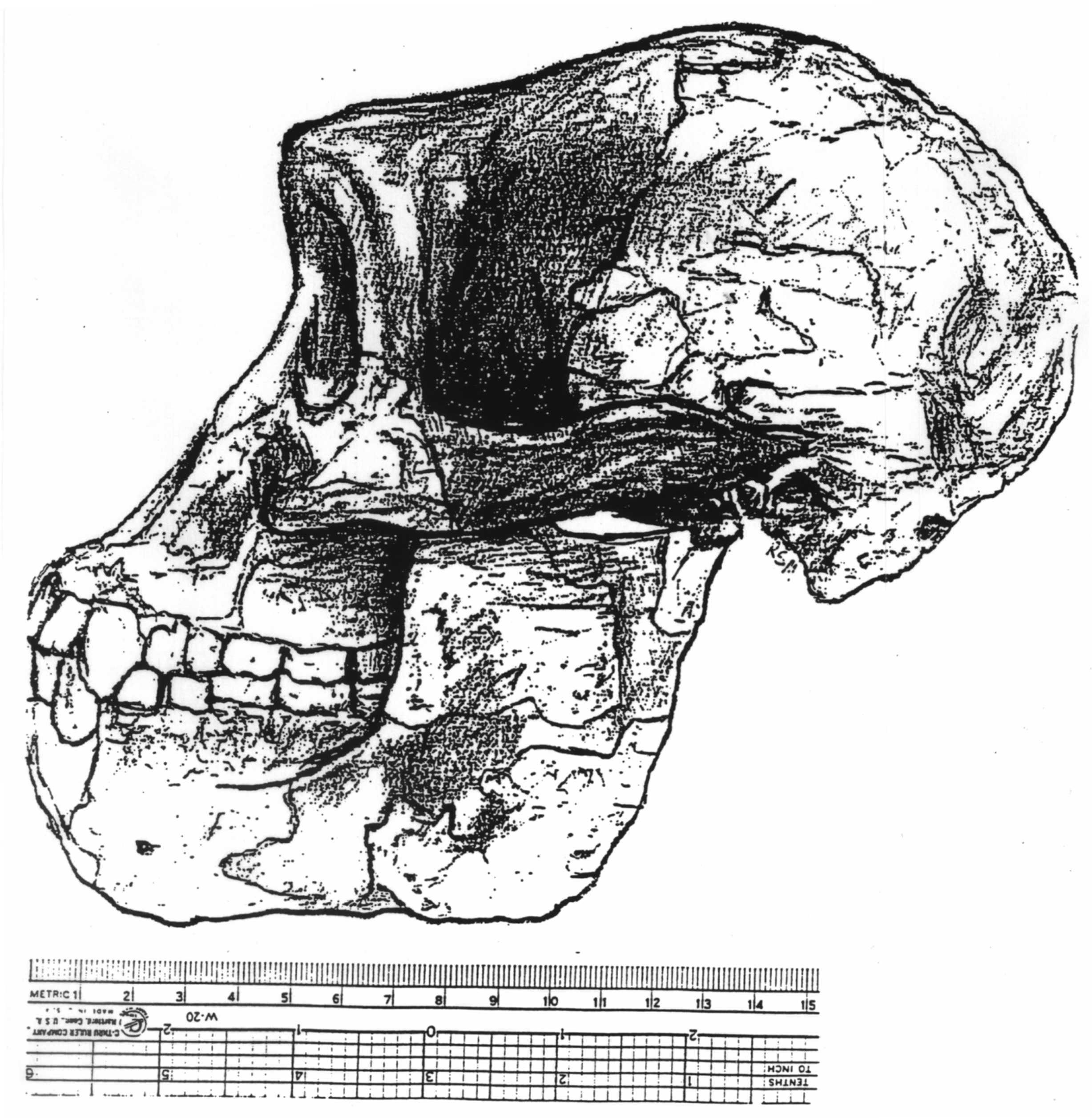


Figure D. *Australopithecus afarensis* (“Lucy”) composite reconstruction, c. 3.0 mya*.

* mya = million years ago

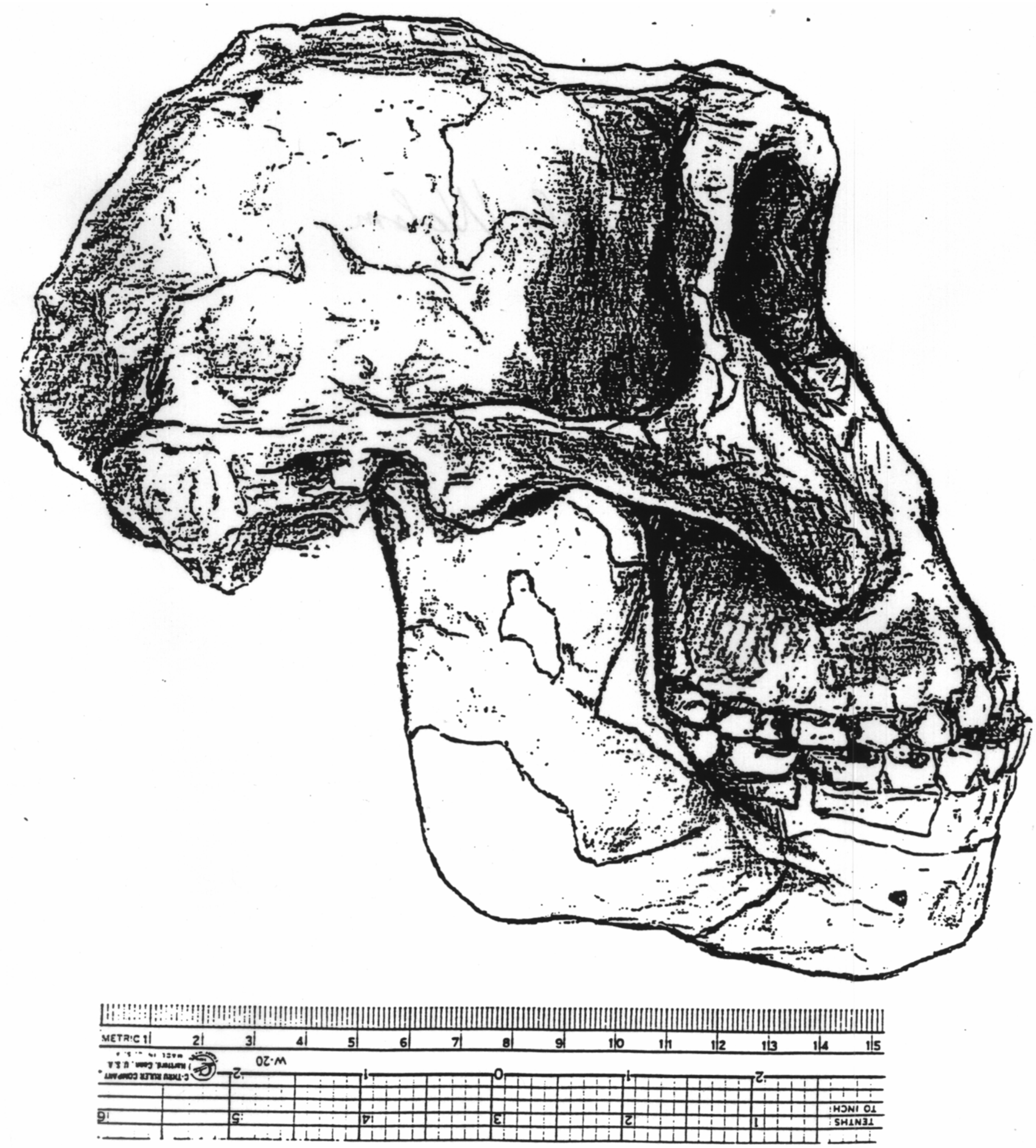


Figure E. *Paranthropus boisei* (“Zinjanthropus”) [robust australopithecine], c. 1.8 mya.

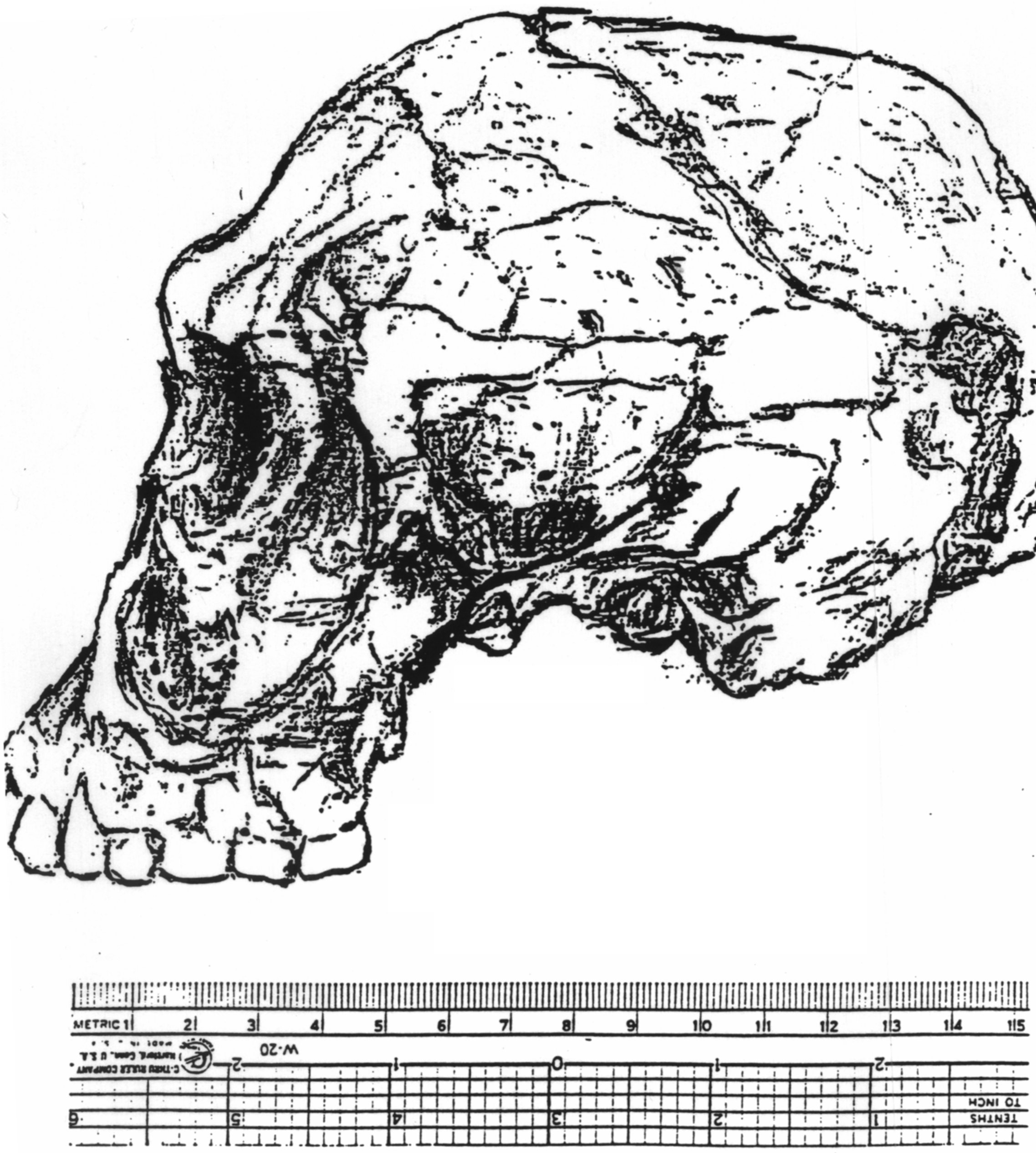


Figure F. *Homo habilis* (KNM-ER 1813), c. 2.0 mya.

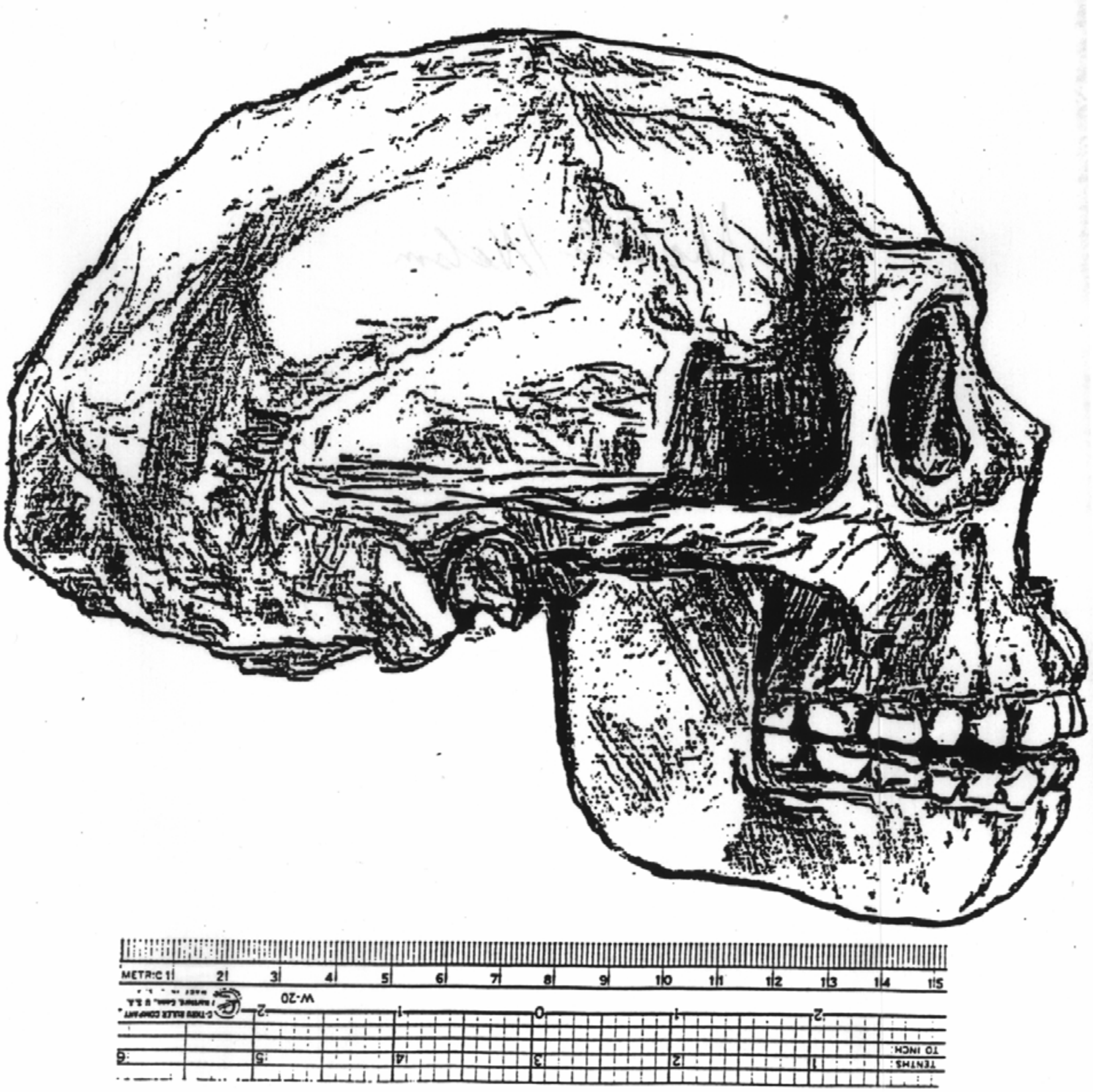


Figure G. *Homo erectus* (“Sinanthropus”), c. 450,000 years ago.

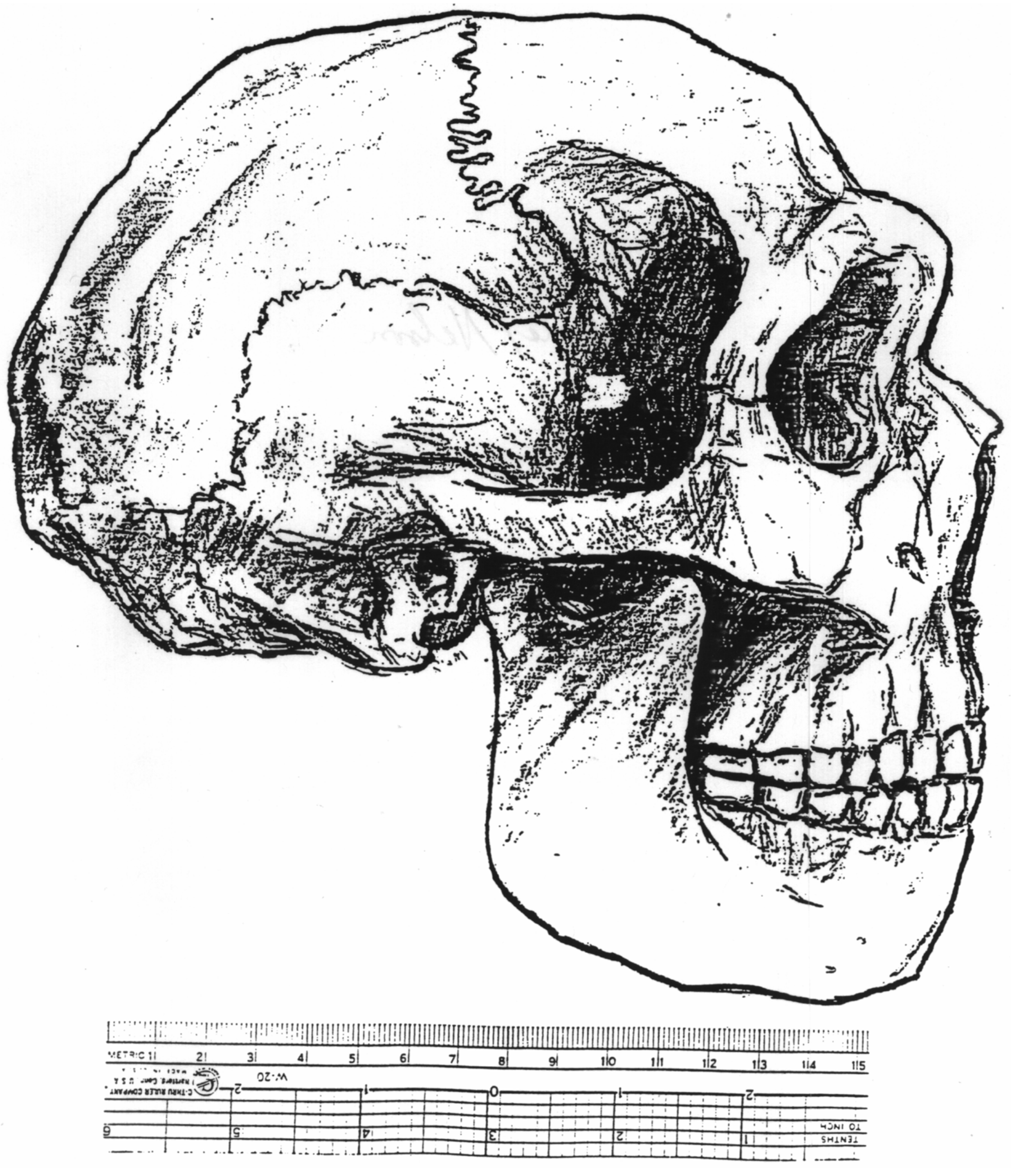


Figure H. Neanderthal (La Ferrassie), c. 60,000 years ago.

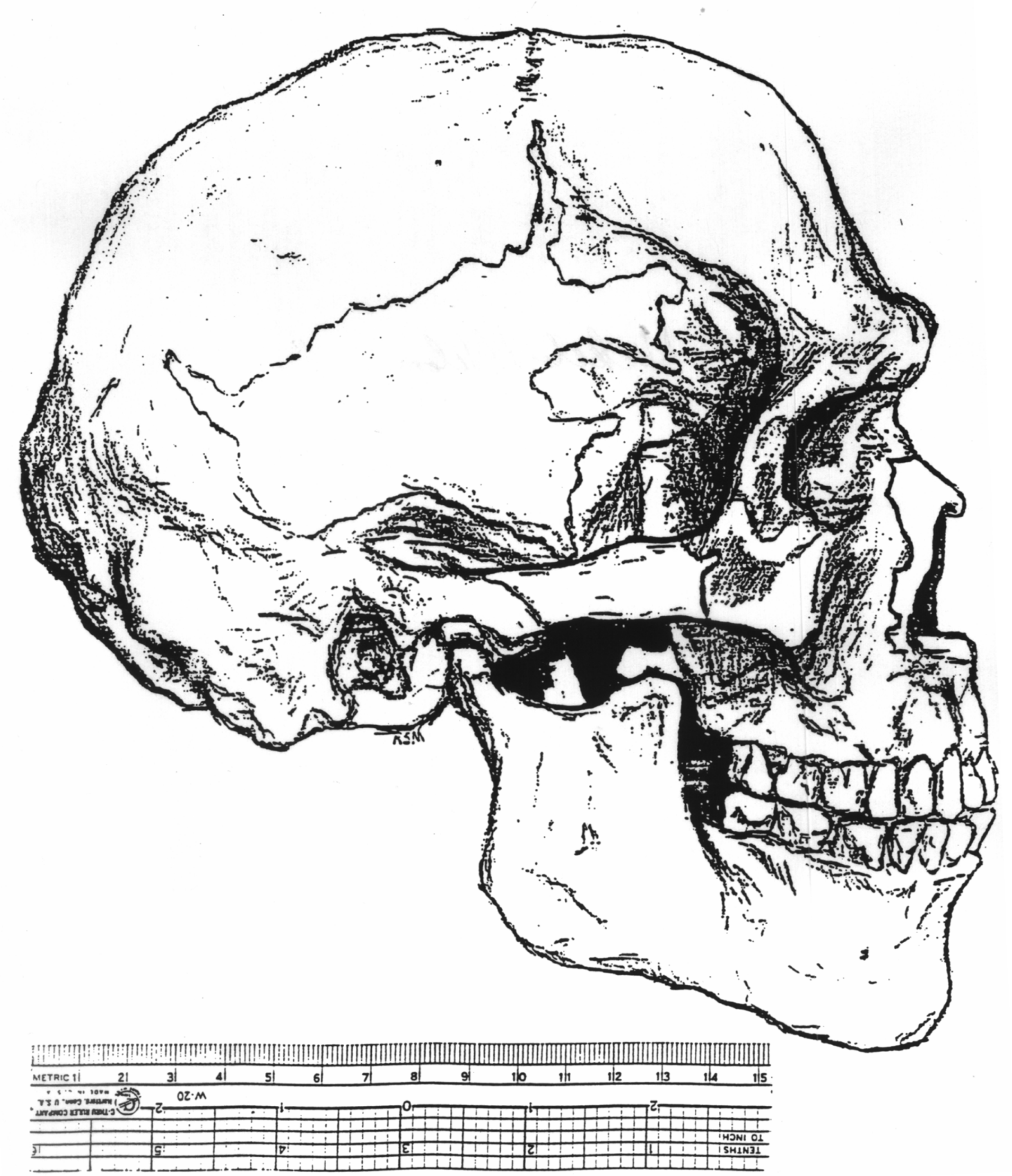


Figure I. Prehistoric modern *Homo sapiens* (Predmost), c. 25,000 years ago.

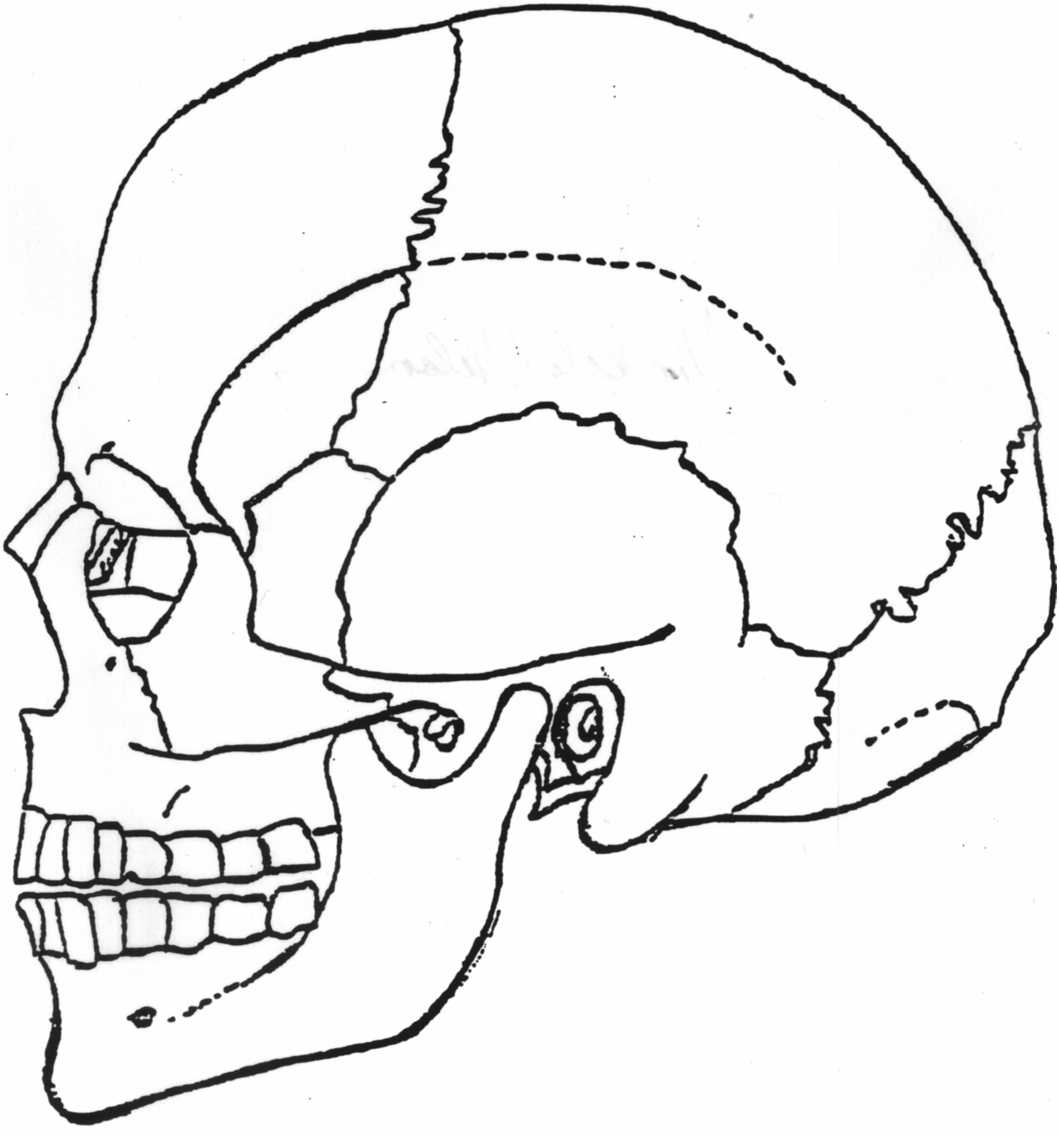


Figure K. Modern *Homo sapiens.*