

HUMAN EVOLUTION, PAST CLIMATES AND STATISTICS

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DEDICATION

CHARLES ROBERT DARWIN, 1809-1882



Darwin aged 7 in 1816.
Source: Wikipedia.



Darwin as a young man.
Source: Wikipedia.



Darwin aged 7 in 1816.
Source: Wikipedia.



Darwin as a young man.
Source: Wikipedia.

Lachenalia, Cape cowslip

Charles Darwin

In 1836, Darwin visited South Africa for three weeks (Cape Flats, May/June). Diary records: “a dull and un-interesting country”.

In *The Voyages of The Beagle*, he speculated about past environments and the impact of major changes of climate on large habitats and large ungulate fauna. Mentions Pleistocene extinctions (Cuvier): Siberian woolly rhinoceros known from fossils.

Darwin referred to reports of modern rhinoceri in the South African Karoo where vegetation is sparse (Andrew Smith) . Considered that “there is no place in the world such as South Africa for its large quadrupeds”.

He questioned the nature of a relationship (if any) between habitat and fauna (South Africa as compared to South America) with regard to biomass.

Charles Darwin

In 1851, 1854 Recognised that there are not clear boundaries between species (based on barnacles)

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220.

Trophi; 1, 2, 3, 4, 6
cirri.



220

Chthamalus
stellatus
Swanage

C. Darwin Coll.
Mon. Balanidae, p. 455
Feb. 20, 1897

224.

Twofold Bay
[New South Wales]



224

Chthamalus
antennatus

C. Darwin Coll.
Mon. Balanidae, p. 460
Feb. 20, 1897

235.

Trophi; 1, 2, 3,
4, 6 cirri.



235

Verruca
strömia

Red Sea

C. Darwin Coll.
Mon. Balanidae, p. 518
Feb. 20, 1897

239.

Trophi; 1, 2, 3,
4, 6 cirri.



239

Verruca
laevigata

C. Darwin Coll.
Mon. Balanidae, p. 520
Feb. 20, 1897

240

Edg
etc.

240

Alcip
lar

C. Darwin
Mon. Bal

Charles Darwin

In 1851, 1854 Recognised that there are not clear boundaries between species (based on barnacles)

In 1859 Darwin stated that “light will be thrown on the origin of man”, and emphasised in *The Origin* that there was a need to quantify “the amount of difference” between species. (Darwin was not inclined towards statistics but recognised the need).

In 1871 In *The Descent of Man*, he recognised that the “progenitors” of humankind must have originated in Africa (based on comparative anatomy)

HUMAN “PROGENITOR” FROM AFRICA



THE TAUNG CHILD

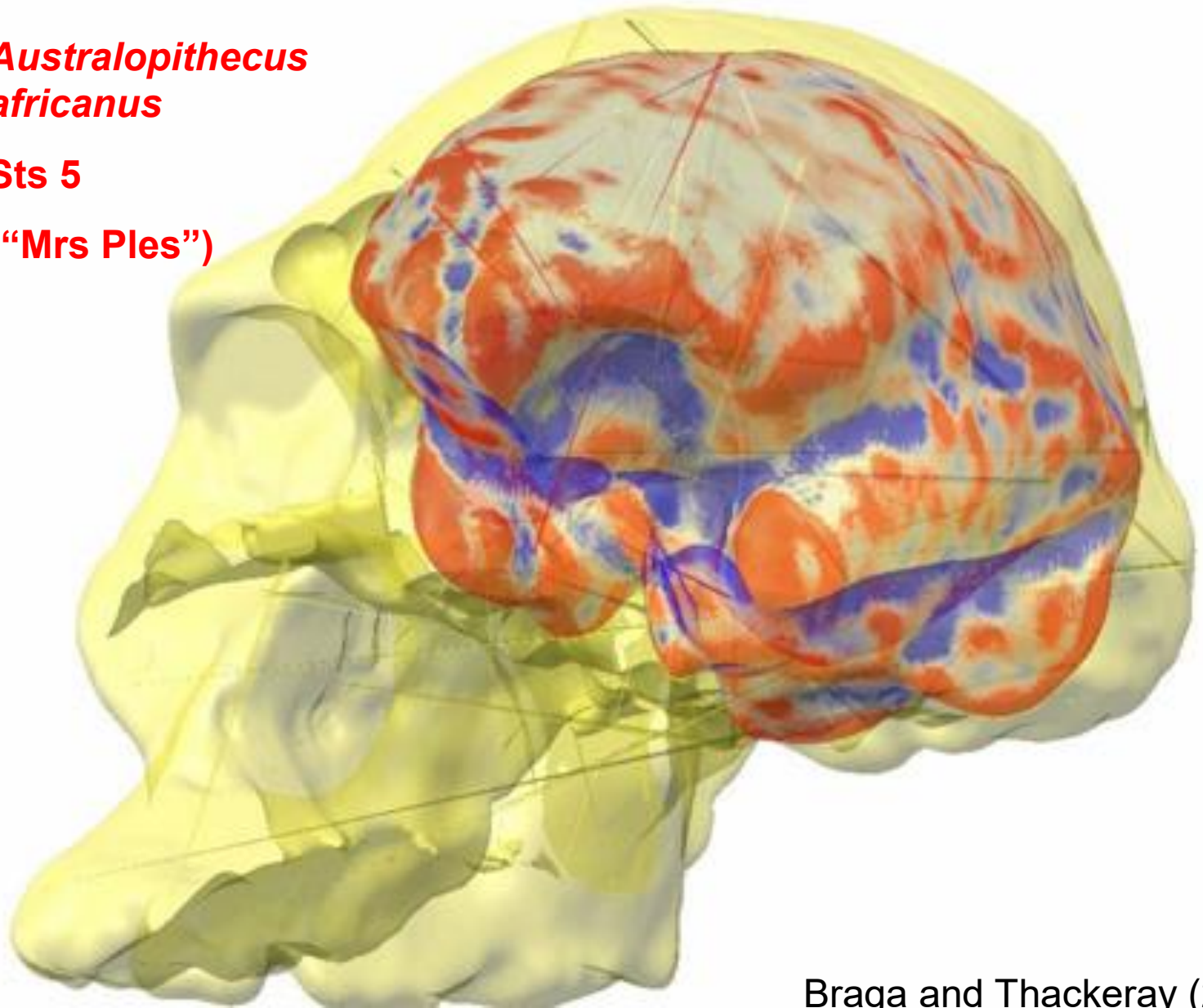
AUSTRALOPITHECUS AFRICANUS (Dart, 1925)

Photographs: David Brill

*Australopithecus
africanus*

Sts 5

(“Mrs Ples”)



Braga and Thackeray (2007)

Australopithecus sp
Stw 573
(“Little Foot”)

**Discovered by Ron
Clarke
Nkwane Molefe
and Stephen Motsumi**

Photograph:

F. Thackeray (2000)



AUSTRALOPITHECUS SEDIBA

(Berger *et al*, 2010)

ANOTHER

HUMAN

“PROGENITOR”



Photograph: L. Berger

DARWIN'S FIRST SKETCH OF AN EVOLUTIONARY TREE (1837)

FROM NOTEBOOK B, ON "TRANSMUTATION OF SPECIES"

Reprinted from "99% Ape: How evolution adds up", Edited by
J. Silvertown (2008), Natural History Museum, The Open
University

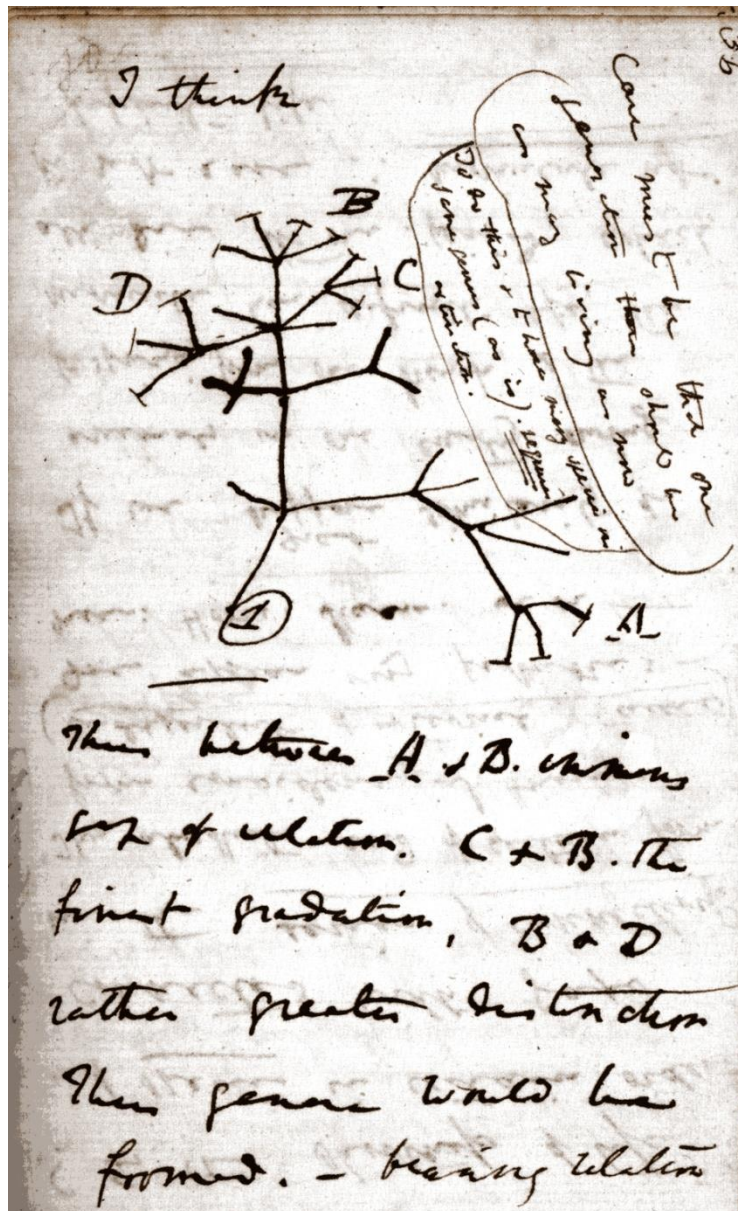
**"THUS BETWEEN A AND B, IMMENSE
GAP OF RELATION.**

C AND B, THE FINEST GRADATION.

**B AND D RATHER GREATER
DISTINCTION. **THUS GENERA WOULD
HAVE FORMED"****

**HOW DOES THIS RELATE TO
HOMO**

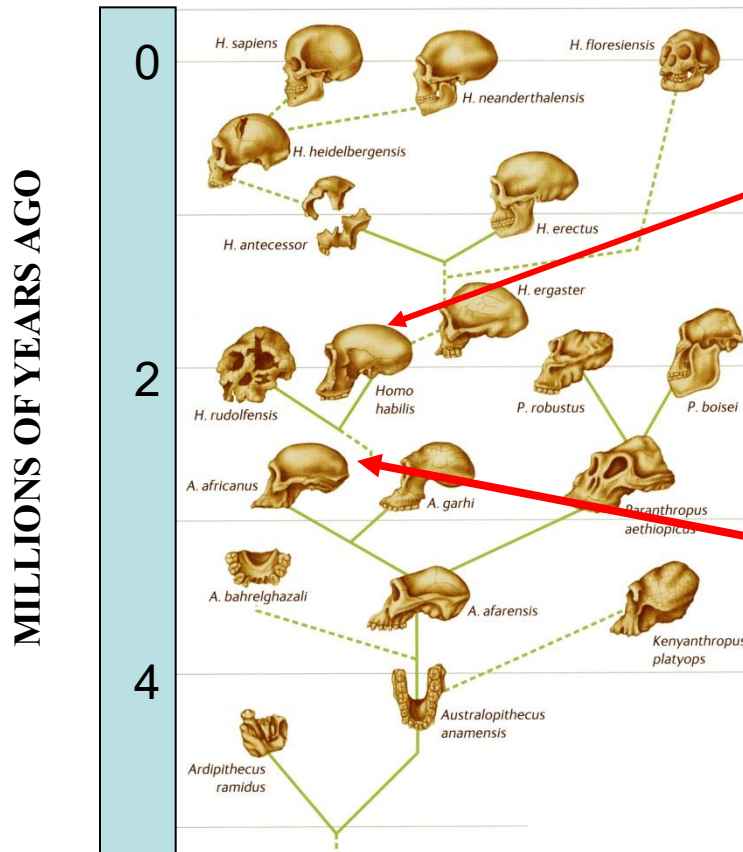
AND AUSTRALOPITHECUS ?



POSSIBLE PHYLOGENY

Reprinted from "99% Ape: How evolution adds up", Edited by J. Silvertown (2008), Natural History Museum, The Open University

I think....



HOMO HABILIS

(Leakey, Tobias and Napier, 1964)

AUSTRALOPITHECUS

AFRICANUS (Dart, 1925)

QUESTION: WHERE IS THE BOUNDARY BETWEEN AUSTRALOPITHECUS AND HOMO ?

Orrorin

Sahelanthropus

WHERE ARE THE BOUNDARIES BETWEEN SPECIES ?

e.g. Between *Australopithecus africanus* and

Homo habilis ?

WHERE ARE THE BOUNDARIES BETWEEN SPECIES ?

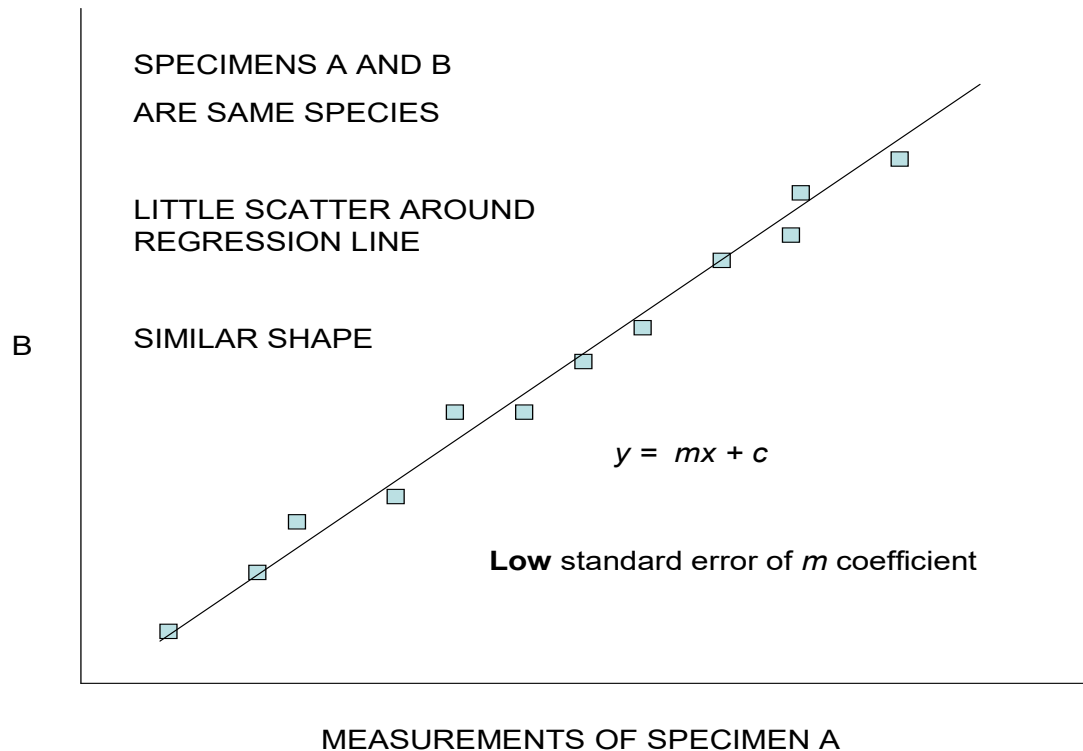
e.g. Between *Australopithecus africanus* and

Homo habilis ?

Or between *Australopithecus africanus* and

Australopithecus sediba ?

NEEDED: A NEW LOOK AT THE CONCEPT OF A SPECIES, RECOGNISING THAT DARWIN (1859) HAD EMPHASISED THAT IT IS NECESSARY TO QUANTIFY THE “AMOUNT” OF DIFFERENCE BETWEEN SPECIMENS THAT MAY BELONG TO THE SAME SPECIES (“VARIETIES”), OR WHICH MAY OTHERWISE BE DIFFERENT SPECIES



PROBLEM:

HOW TO DEFINE A SPECIES IN A WAY WHICH IS EASILY APPLICABLE TO PALAEO-ANTHROPOLOGY ?

POTENTIAL SOLUTION:

MORPHOMETRIC ANALYSES OF MODERN SPECIMENS WHICH ARE KNOWN TO BELONG TO THE SAME SPECIES, USING LEAST SQUARES LINEAR REGRESSION ANALYSIS

ULTIMATE OBJECTIVES:

1. TO FIND A WAY TO DEFINE A SPECIES
STATISTICALLY

2. TO ASSESS

“PROBABILITIES OF CONSPECIFICITY”
(THE PROBABILITY THAT TWO SPECIMENS
REPRESENT THE SAME SPECIES)
WHEN TWO SPECIMENS ARE COMPARED

ULTIMATE OBJECTIVES:

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(THE PROBABILITY THAT TWO SPECIMENS
REPRESENT THE SAME SPECIES)
WHEN TWO SPECIMENS ARE COMPARED

RECOGNISING THAT
BOUNDARIES BETWEEN SPECIES
ARE NOT NECESSARILY ALWAYS CLEAR

**APPLICATION TO FOSSILS FROM
THE “CRADLE OF HUMANKIND”
WORLD HERITAGE SITE,
SOUTH AFRICA,**

**AND TO FOSSILS FROM OTHER AREAS OF
AFRICA, THE CONTINENT FROM WHICH
“PROGENITORS” OF HUMANKIND EVOLVED**

ALGEBRAIC BIOLOGY

SKULL MEASUREMENTS

or

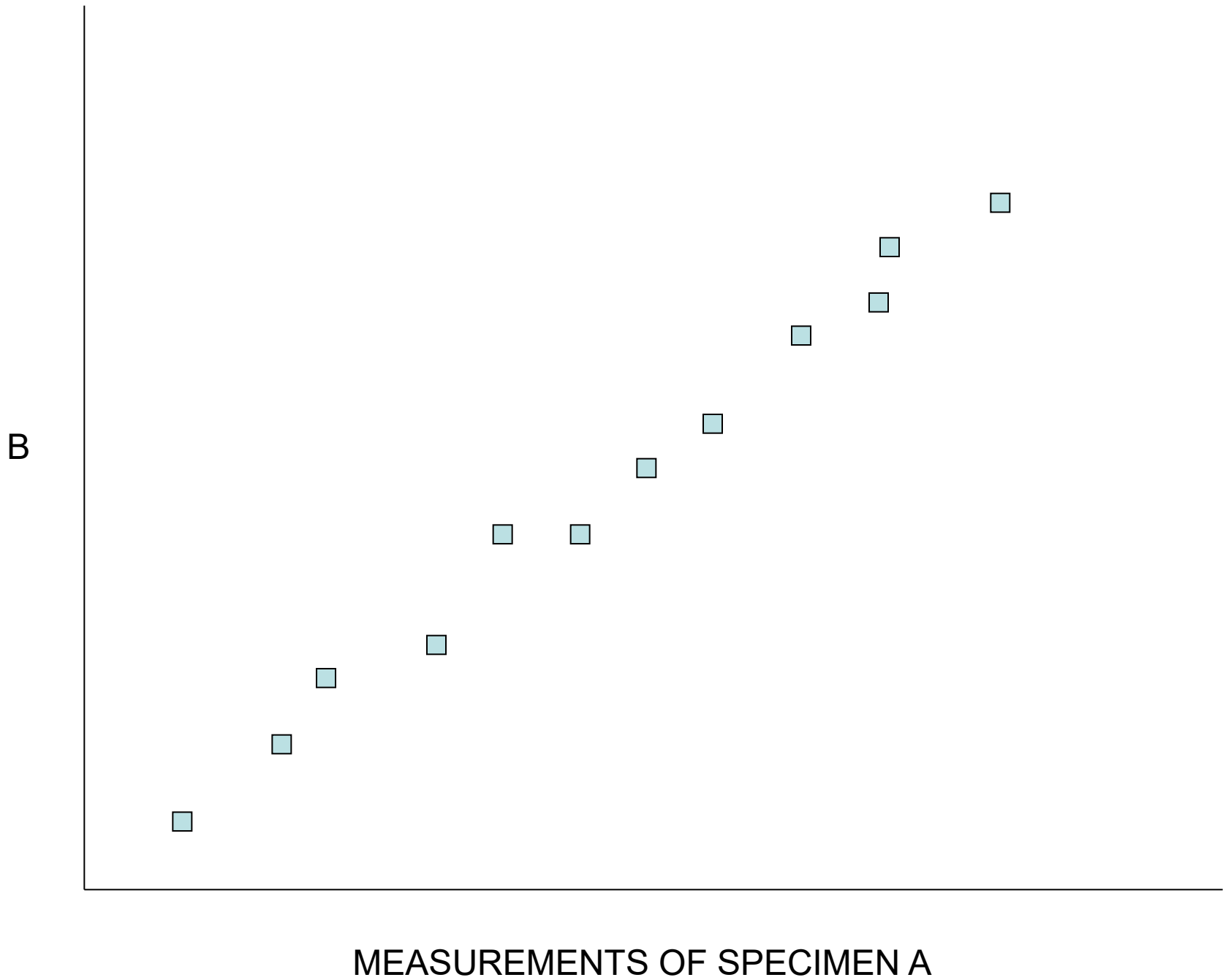
TOOTH MEASUREMENTS

or

SKELETAL MEASUREMENTS

B

MEASUREMENTS OF SPECIMEN A



Y AXIS

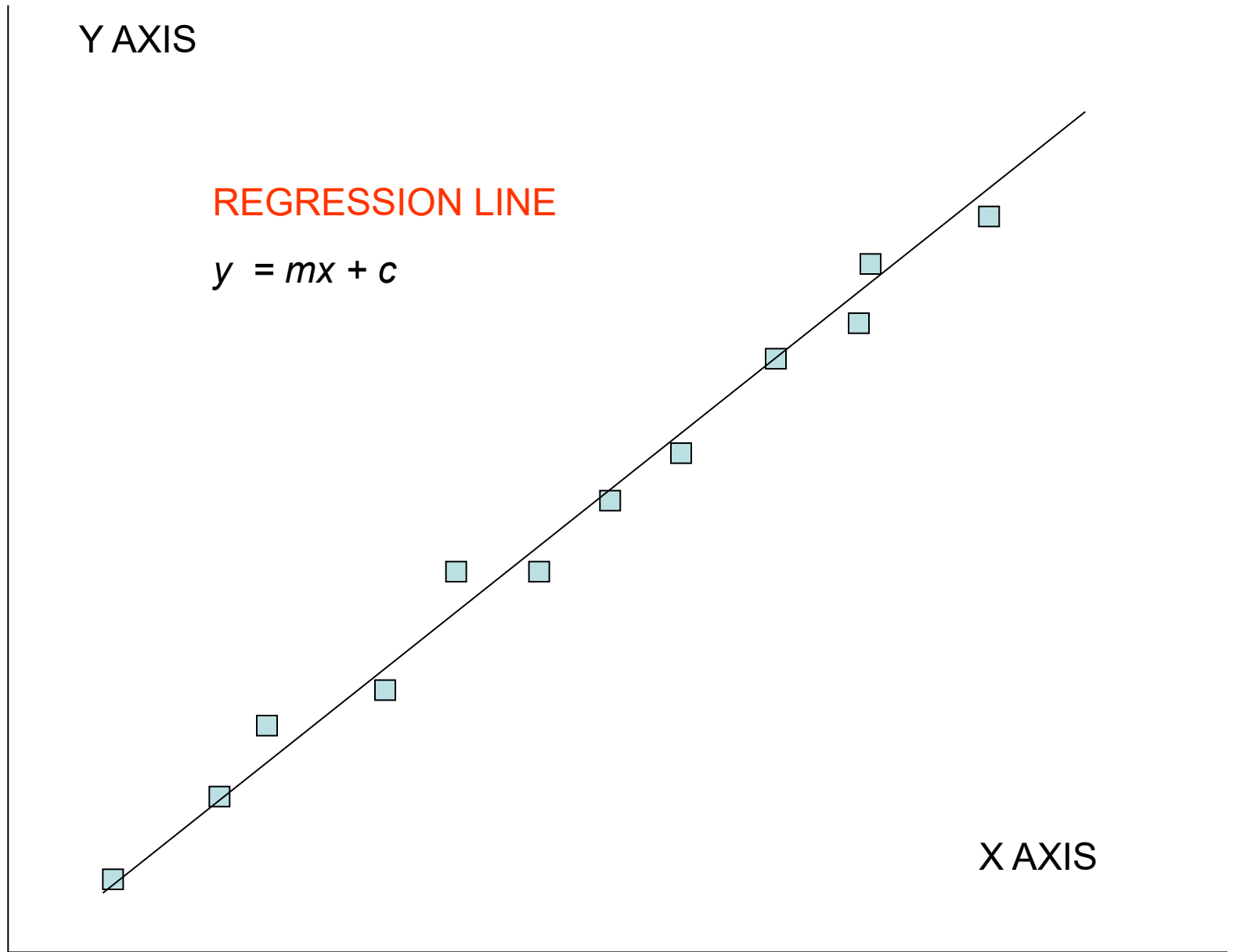
REGRESSION LINE

$$y = mx + c$$

B

X AXIS

MEASUREMENTS OF SPECIMEN A



SPECIMENS A AND B
ARE SAME SPECIES

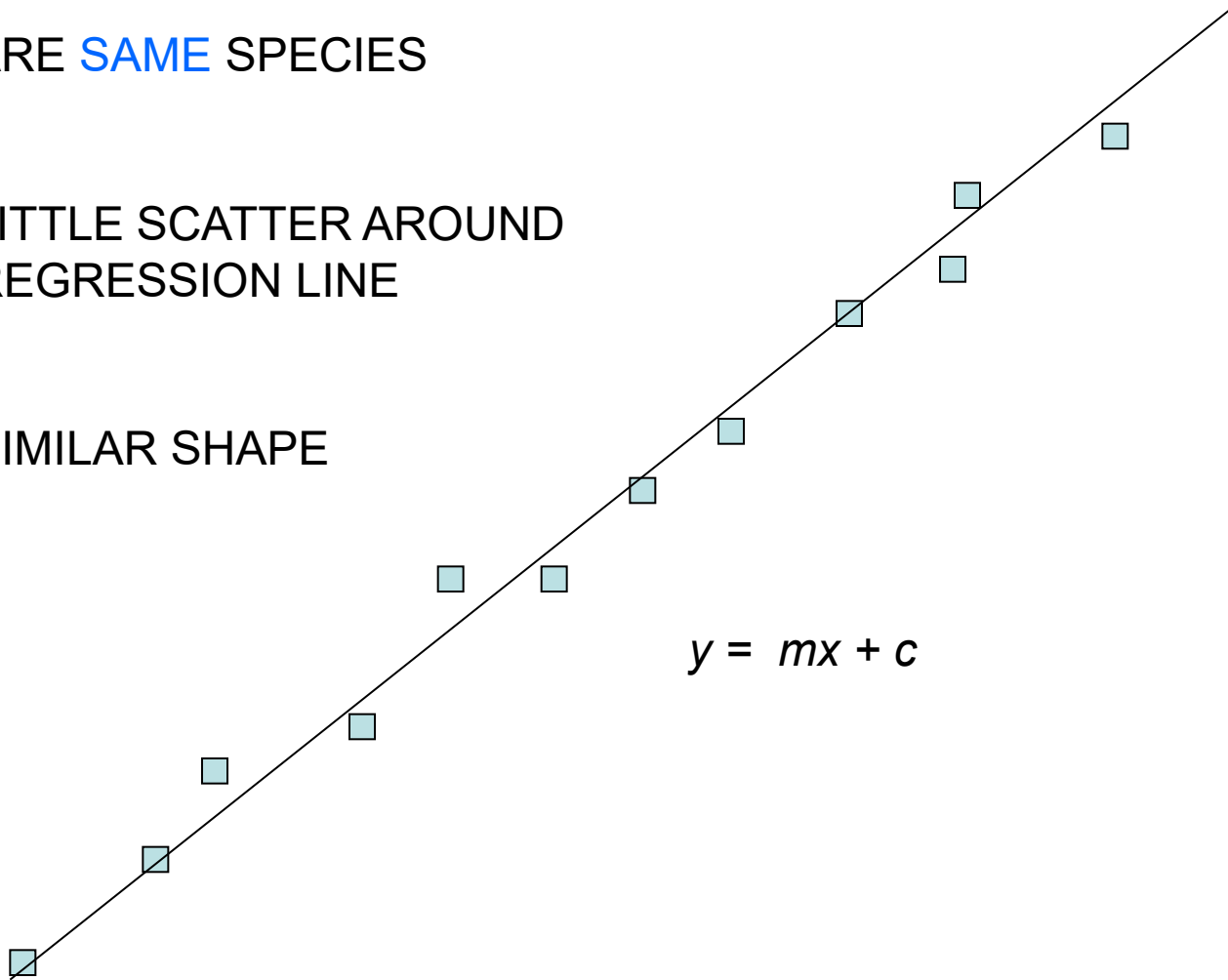
LITTLE SCATTER AROUND
REGRESSION LINE

SIMILAR SHAPE

$$y = mx + c$$

B

MEASUREMENTS OF SPECIMEN A



SPECIMENS A AND B
ARE **SAME** SPECIES

LITTLE SCATTER AROUND
REGRESSION LINE

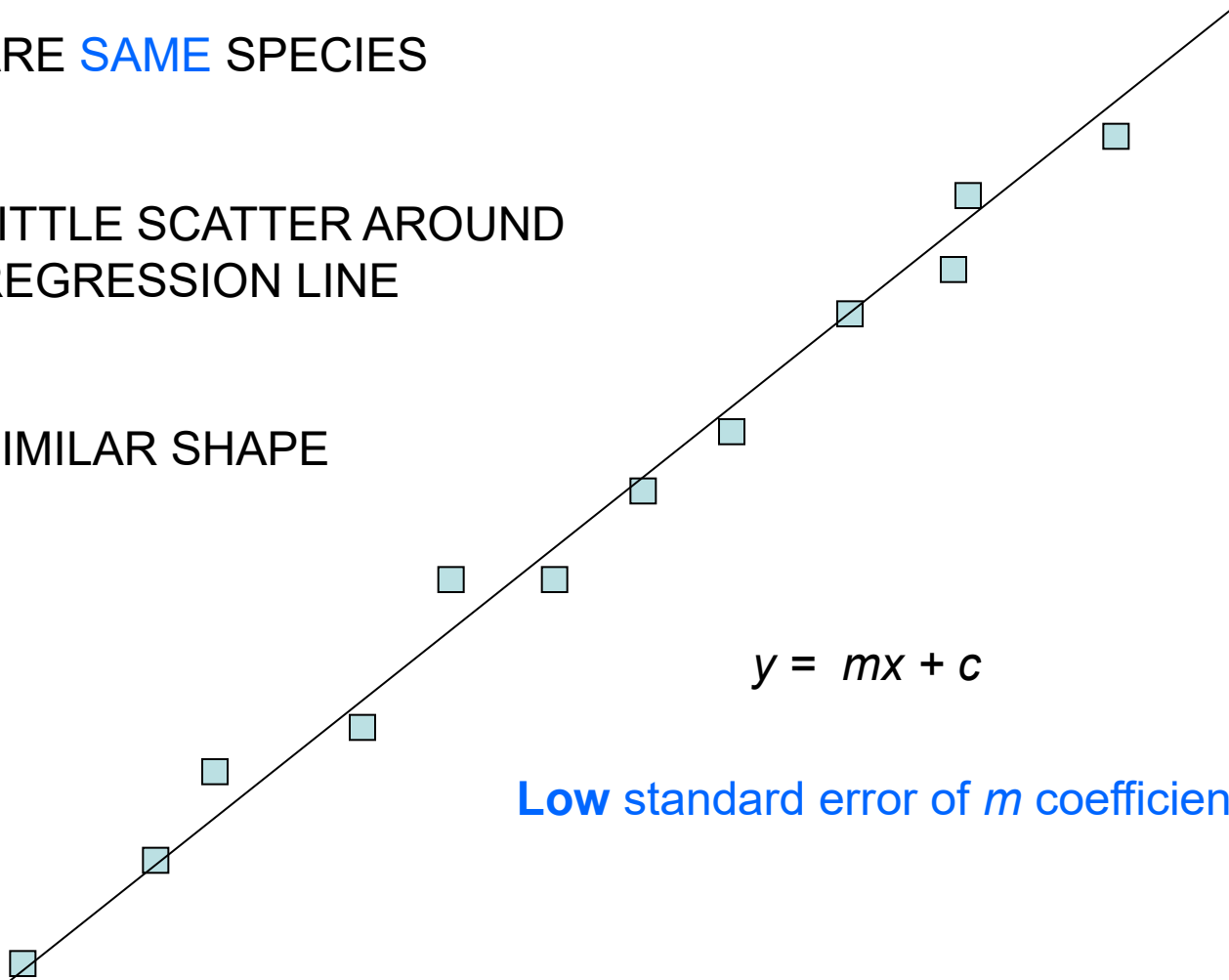
SIMILAR SHAPE

B

$$y = mx + c$$

Low standard error of *m* coefficient: (*sem*)

MEASUREMENTS OF SPECIMEN A



FOSSILS A AND B

HAVE A HIGH PROBABILITY OF
CONSPECIFICITY

LITTLE SCATTER AROUND
REGRESSION LINE

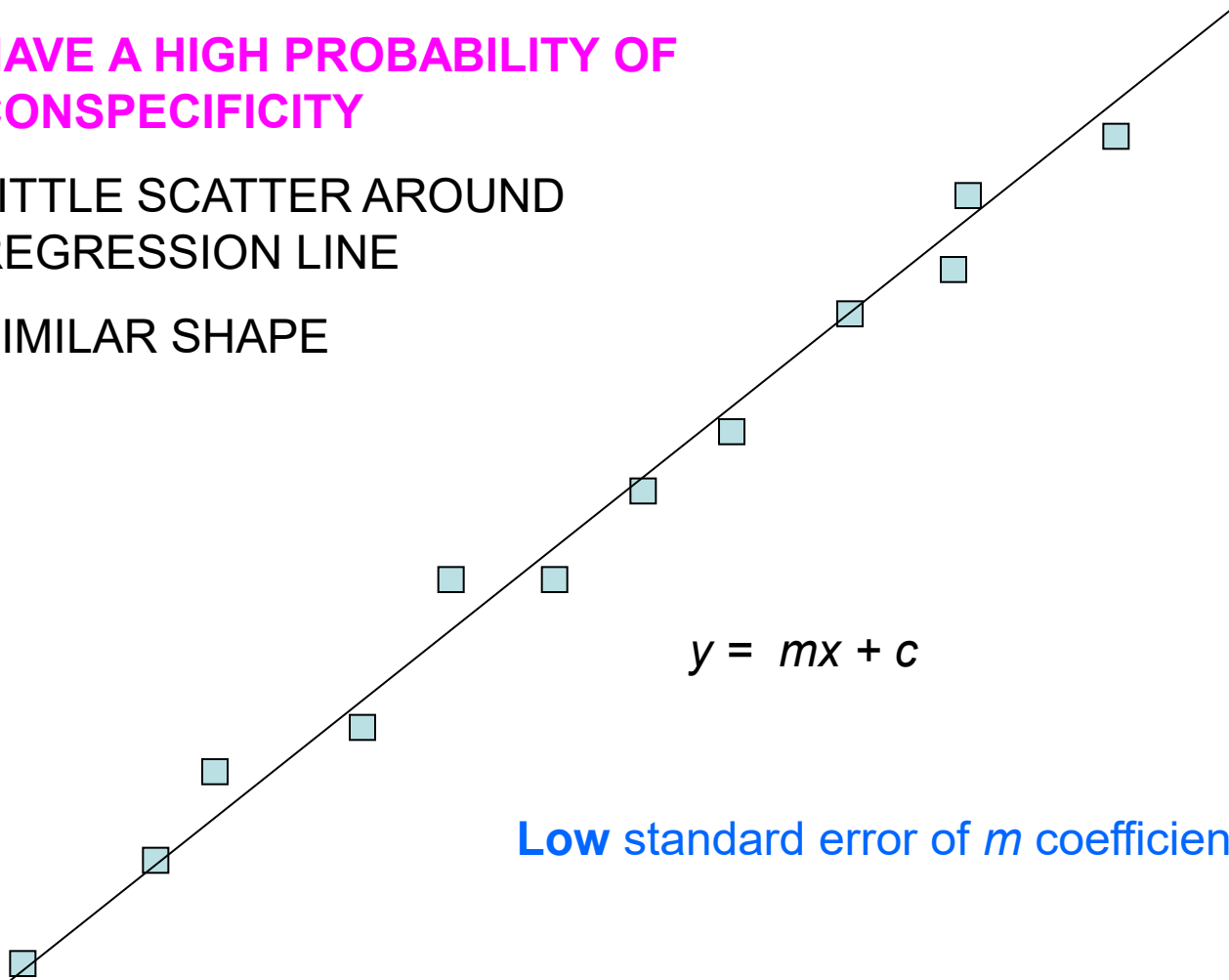
SIMILAR SHAPE

B

$$y = mx + c$$

Low standard error of m coefficient: (sem)

MEASUREMENTS OF SPECIMEN A



CHALLENGE

- WHAT IS THE FRAME OF REFERENCE FOR ASSESSING “PROBABILITIES OF CONSPECIFICITY” ?

EXPLORATORY STUDY:

PAIRWISE COMPARISONS OF SPECIMENS
OF EXTANT ANIMALS THAT CERTAINLY
BELONG TO THE SAME SPECIES

EXPLORATORY STUDY:

PAIRWISE COMPARISONS OF SPECIMENS OF
EXTANT ANIMALS THAT CERTAINLY BELONG TO
THE SAME SPECIES

FOR EXAMPLE:

SKULL MEASUREMENTS OF WILDEBEEST A

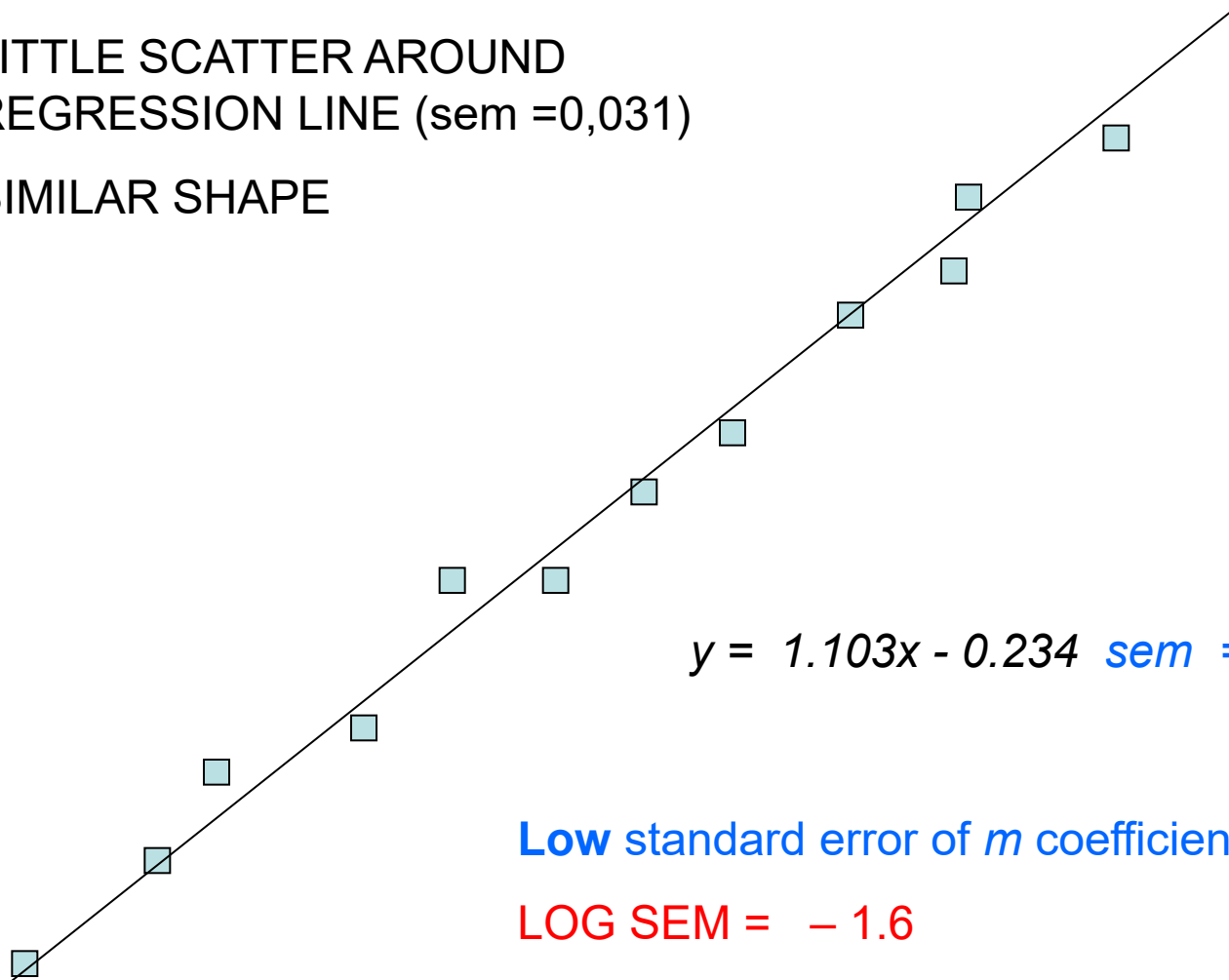
SKULL MEASUREMENTS OF WILDEBEEST B

SPECIMENS A AND B

LITTLE SCATTER AROUND
REGRESSION LINE (sem = 0,031)

SIMILAR SHAPE

B



Low standard error of m coefficient: (sem)

LOG SEM = - 1.6

MEASUREMENTS OF WILDEBEEST SPECIMEN A

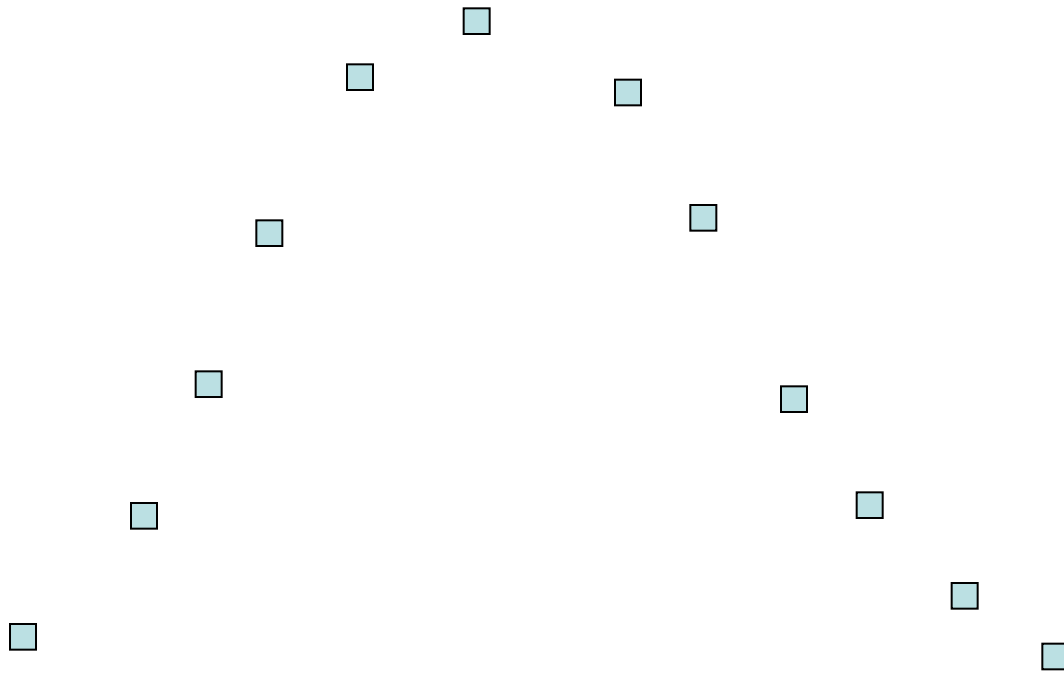
LOG NORMAL DISTRIBUTION OF SEM VALUES OBTAINED FROM CONSPECIFIC PAIRS

LOG MEAN SEM = -1.61 +/- 0.23

BASED ON 76 MODERN TAXA

n = 1424 SPECIMENS

N



LOG STANDARD ERROR OF m (LOG sem) BASED ON PAIRWISE COMPARISONS

MEAN LOG SEM FOR VERTEBRATES

-1.61 +/- 0.23 (n = 1252)

MEAN LOG SEM FOR INVERTEBRATES

-1.61 +/- 0.20 (n = 172)

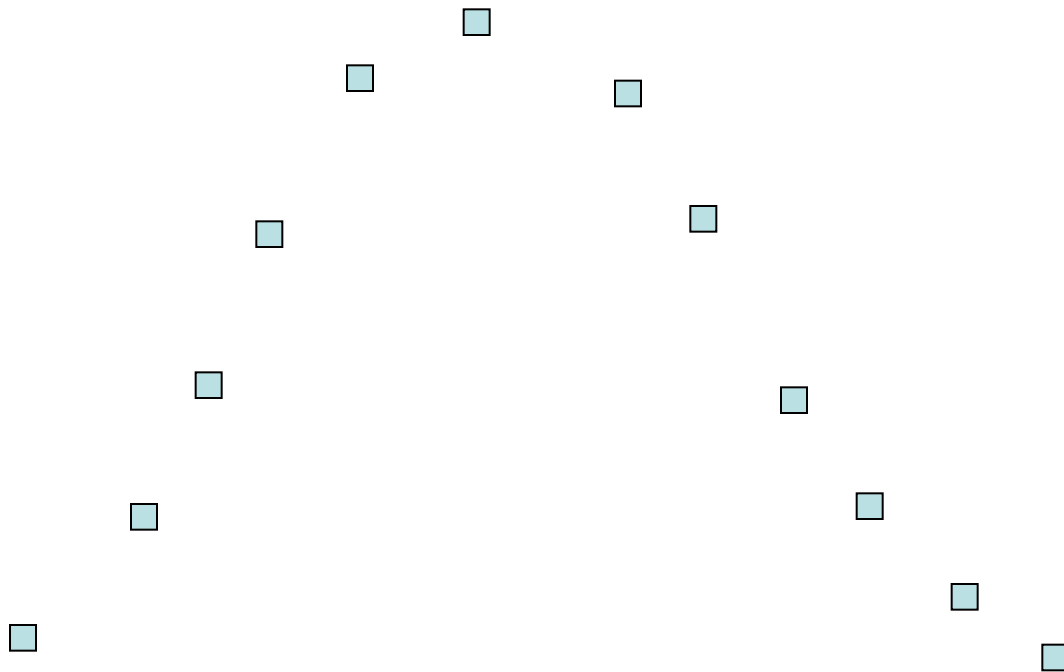
A STATISTICAL DEFINITION OF A SPECIES

LOG MEAN SEM = -1.61 +/- 0.23

BASED ON 76 MODERN TAXA

VERTEBRATES AND INVERTEBRATES

N

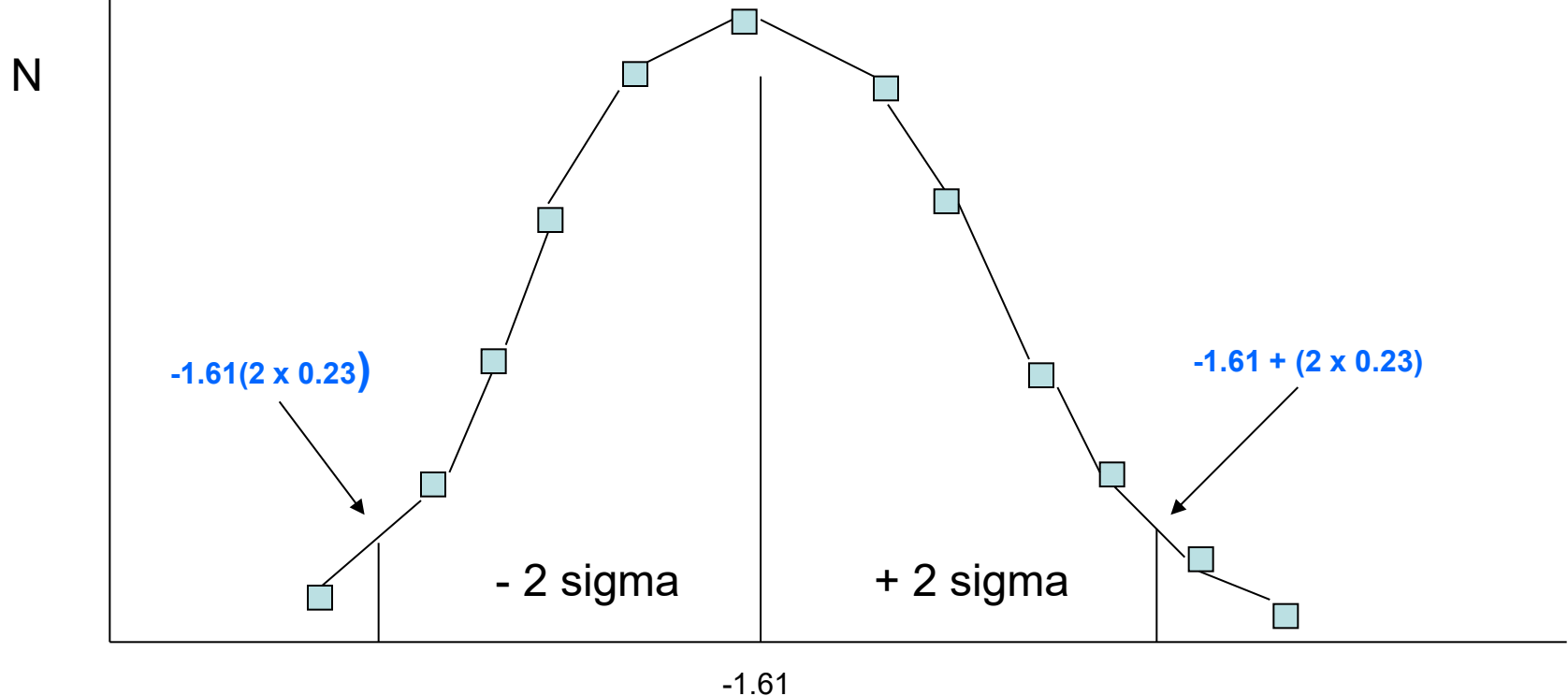


LOG STANDARD ERROR OF *m* (LOG sem) BASED ON PAIRWISE COMPARISONS

A STATISTICAL DEFINITION OF A SPECIES

LOG MEAN SEM = -1.61 ± 0.23

**95 % CONFIDENCE LIMITS OF THE
DISTRIBUTION OF LOG sem VALUES**

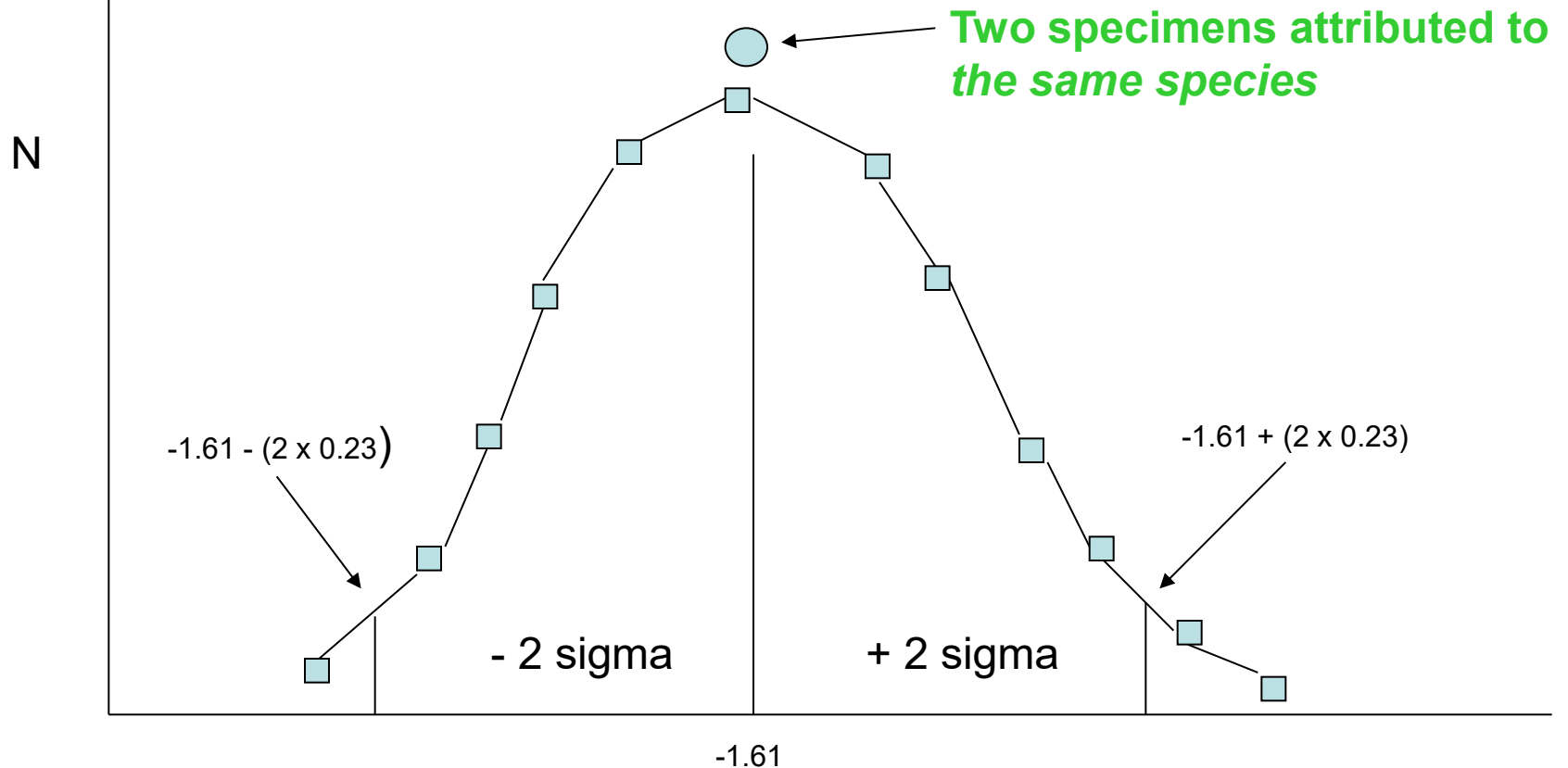


LOG STANDARD ERROR OF m (LOG sem) BASED ON PAIRWISE COMPARISONS

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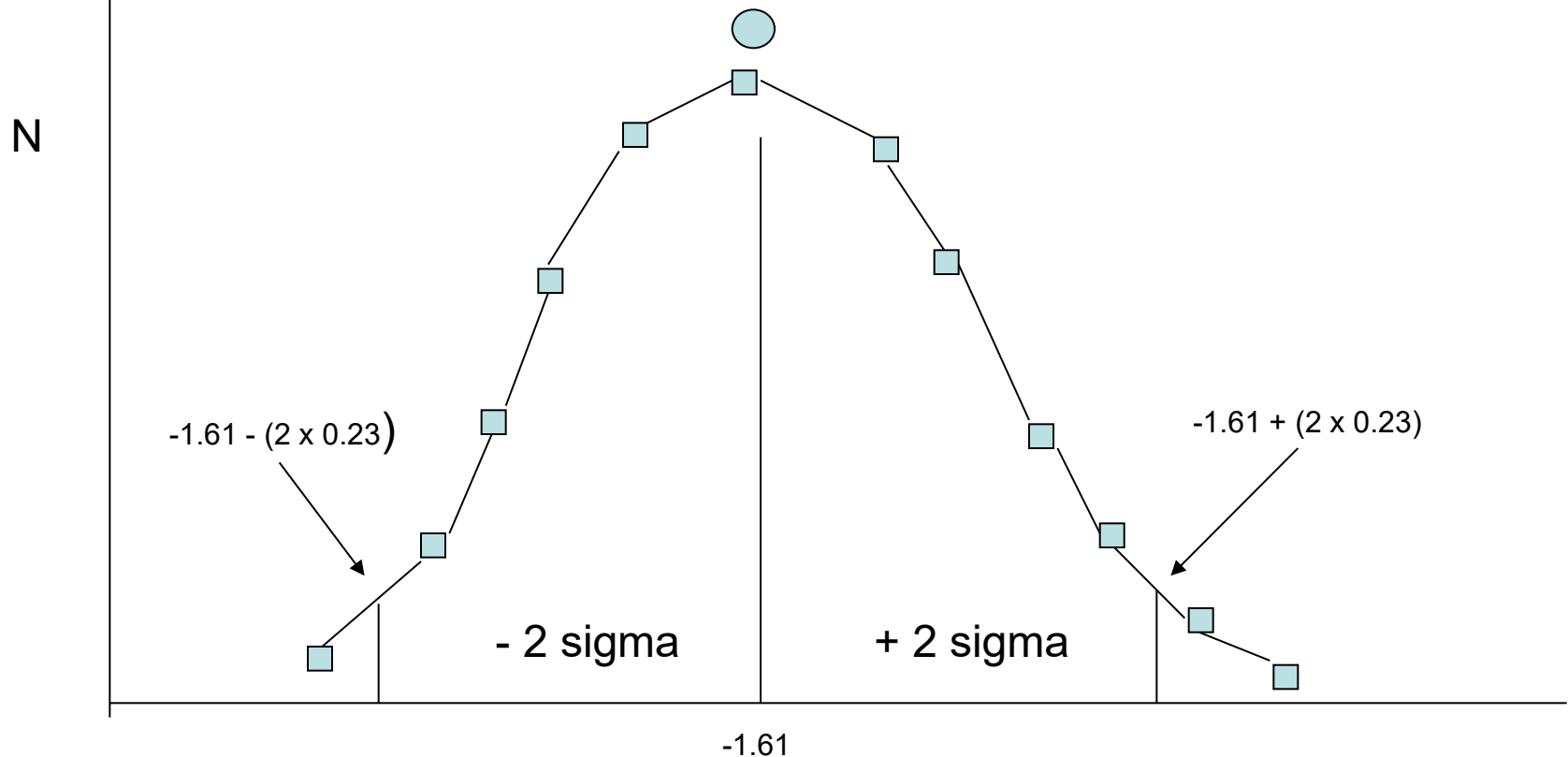


LOG STANDARD ERROR OF m (LOG sem) BASED ON PAIRWISE COMPARISONS

A STATISTICAL DEFINITION OF A SPECIES

$$\text{LOG MEAN SEM} = -1.61 \pm 0.23$$

APPROXIMATION OF A
BIOLOGICAL SPECIES CONSTANT ? $T = -1.61$



**APPLICATION OF THIS
MORPHOMETRIC TECHNIQUE
TO A COMPARISON BETWEEN
AUSTRALOPITHECUS SEDIBA (MH1)
AND OTHER TAXA**

Y AXIS

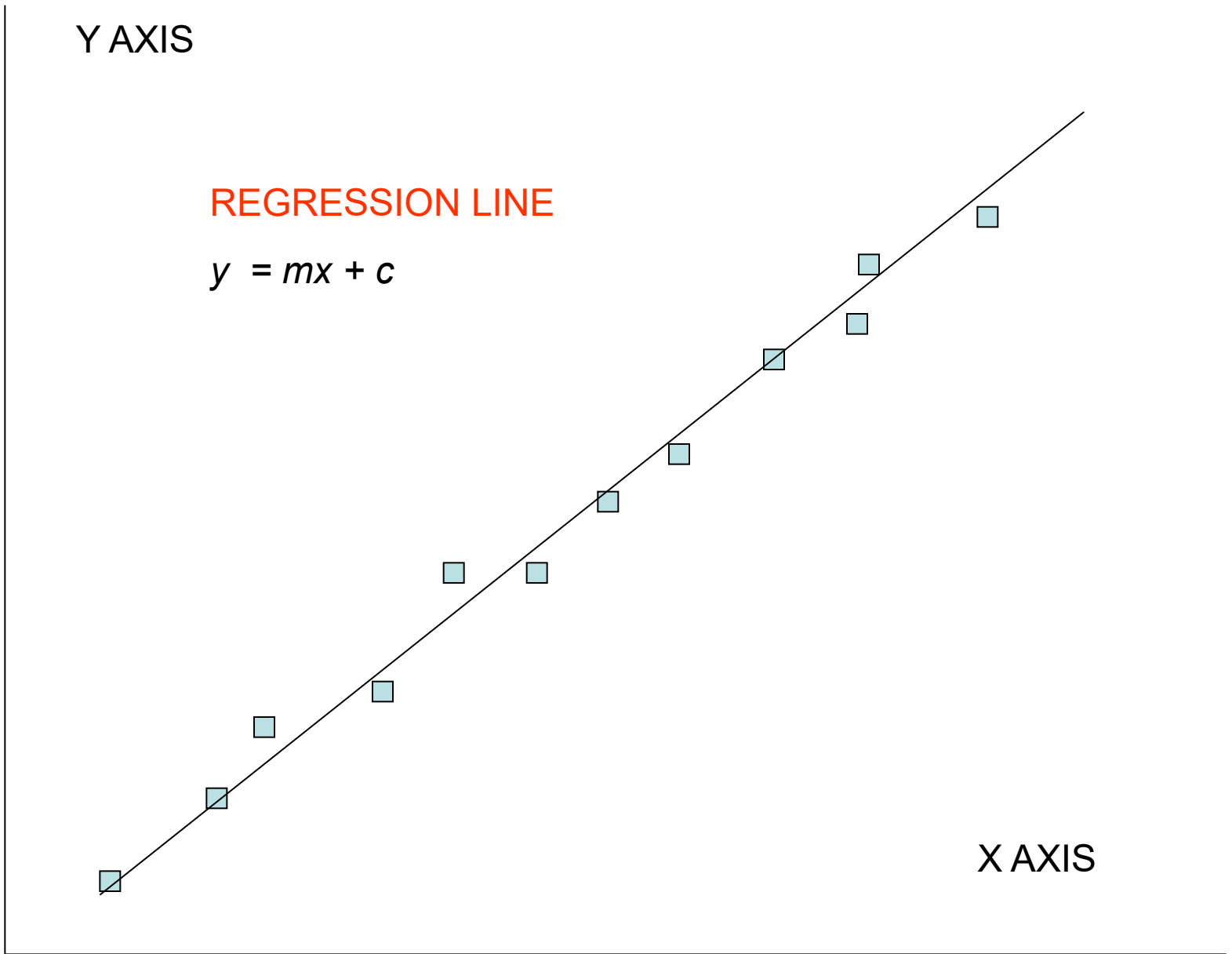
REGRESSION LINE

$$y = mx + c$$

B

X AXIS

MEASUREMENTS OF MH 1 (*A. sediba*)



Cranial measurements of
MH 1 (*Australopithecus sediba* holotype)

compared to cranial measurements of other
Plio-Pleistocene hominin taxa:

Australopithecus africanus

Australopithecus afarensis

Homo habilis

Homo rudolfensis

Homo erectus/ergaster

Using means for each cranial variable
for each taxon, based on data published by
Berger *et al* (2010)



STS 5



KNM-ER 1813



MH 1



KNM-ER 3733

Mya

1

2

3

-0.8

-1.0

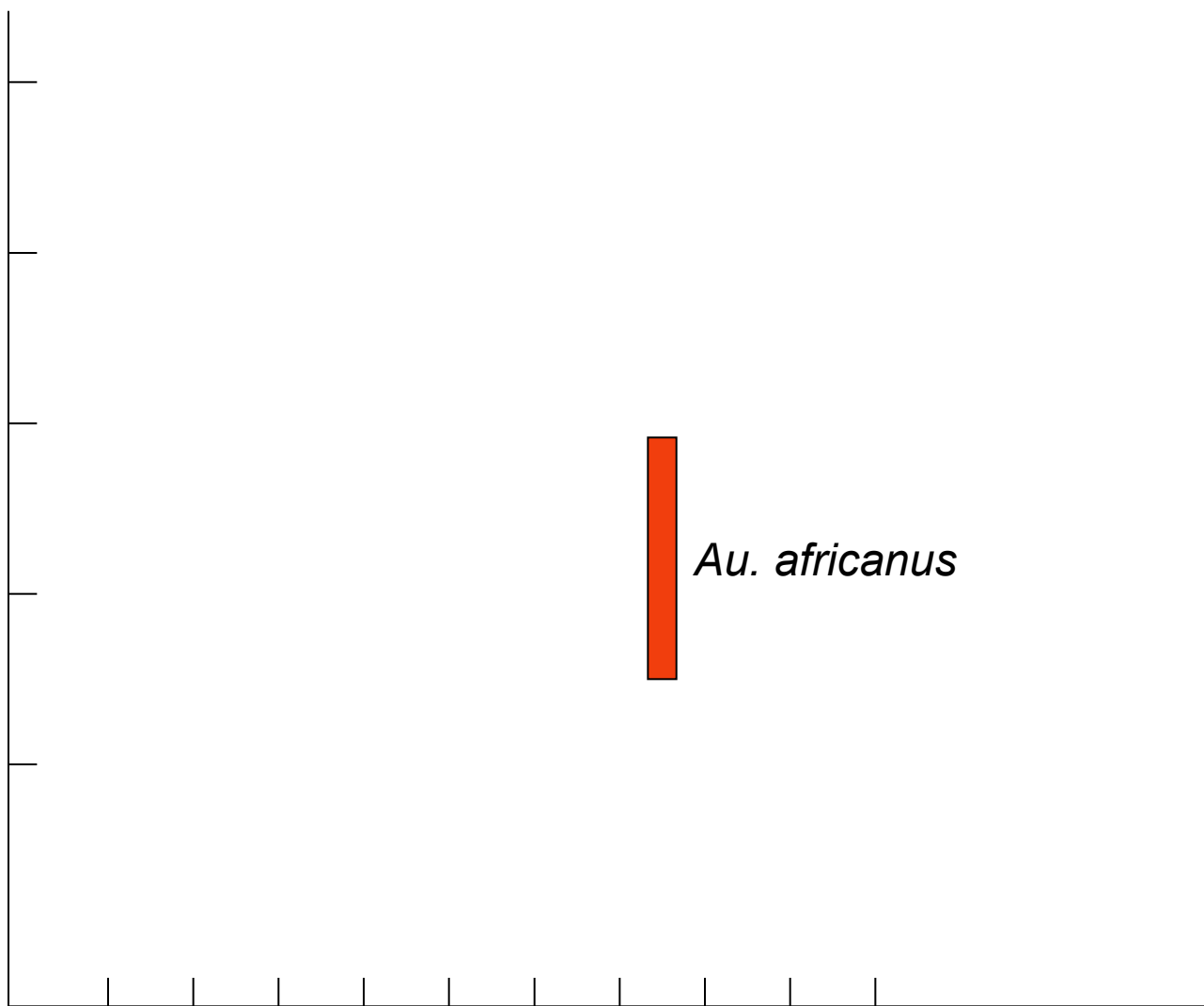
-1.2

-1.4

-1.6

LOG sem relative to MH1

Au. africanus



Mya

1

2

3

H. habilis

Au. africanus

-0.8

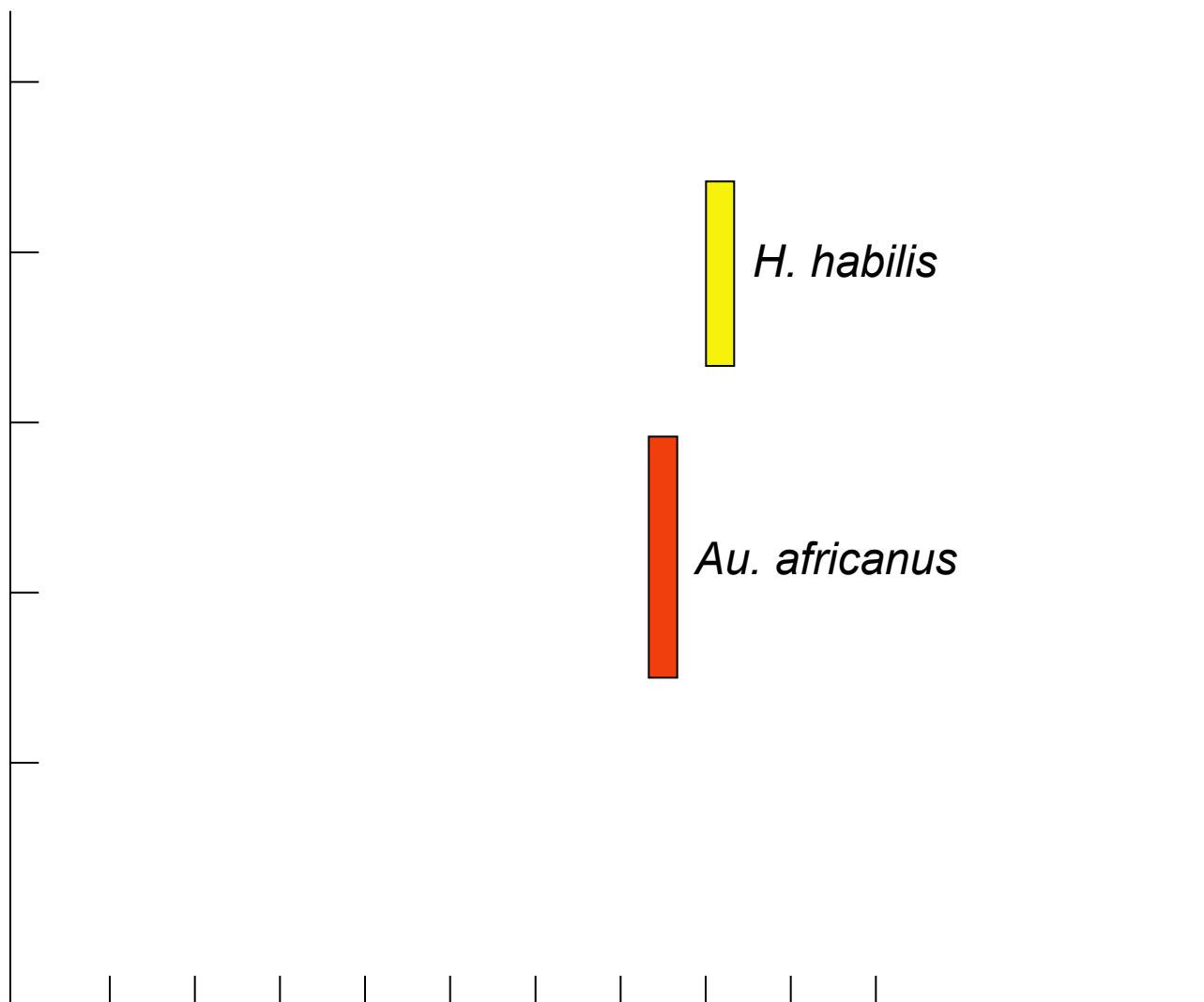
-1.0

-1.2

-1.4

-1.6

LOG sem relative to MH1



Mya

1

2

3

H. habilis

Au. sediba

Au. africanus

-0.8

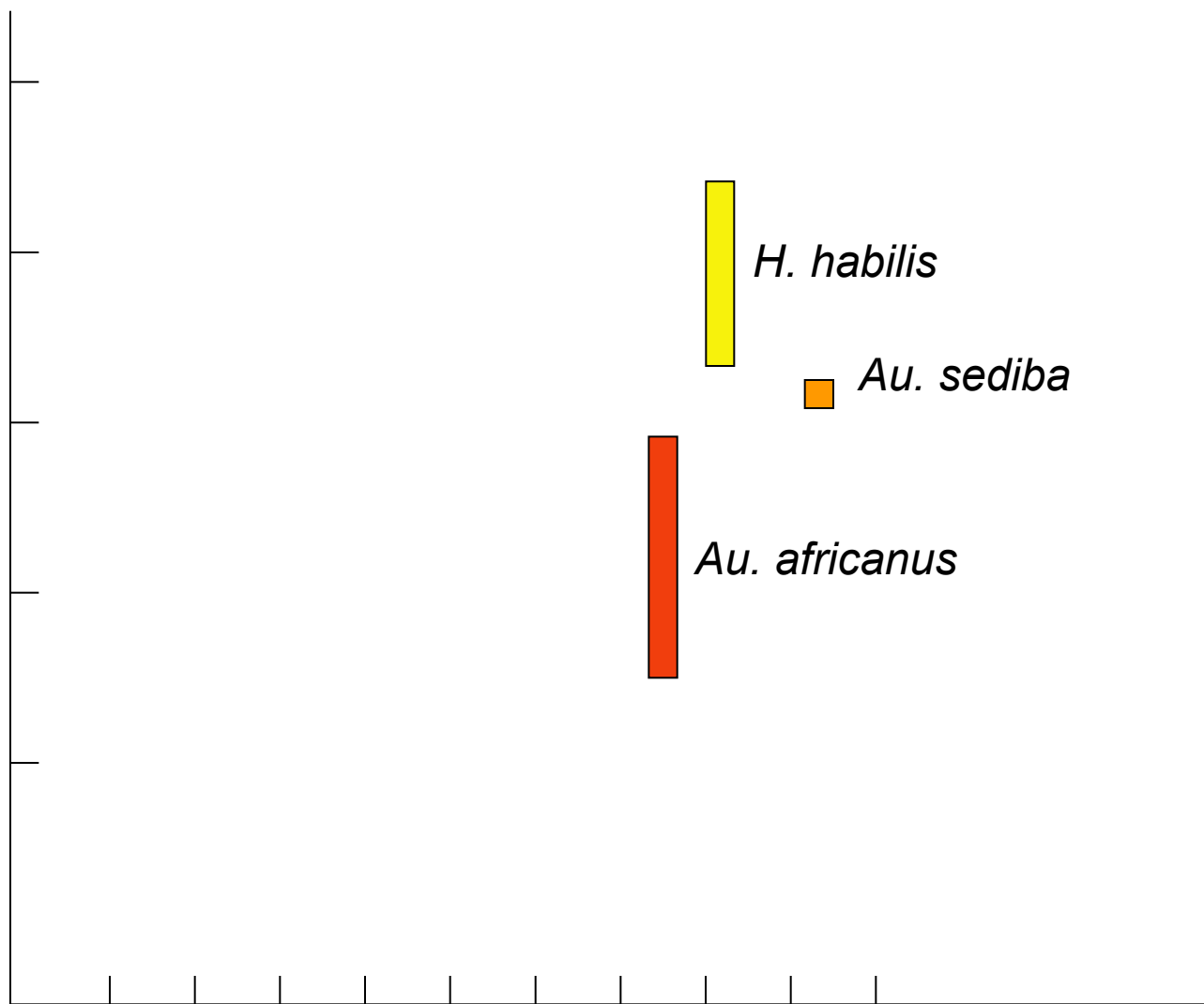
-1.0

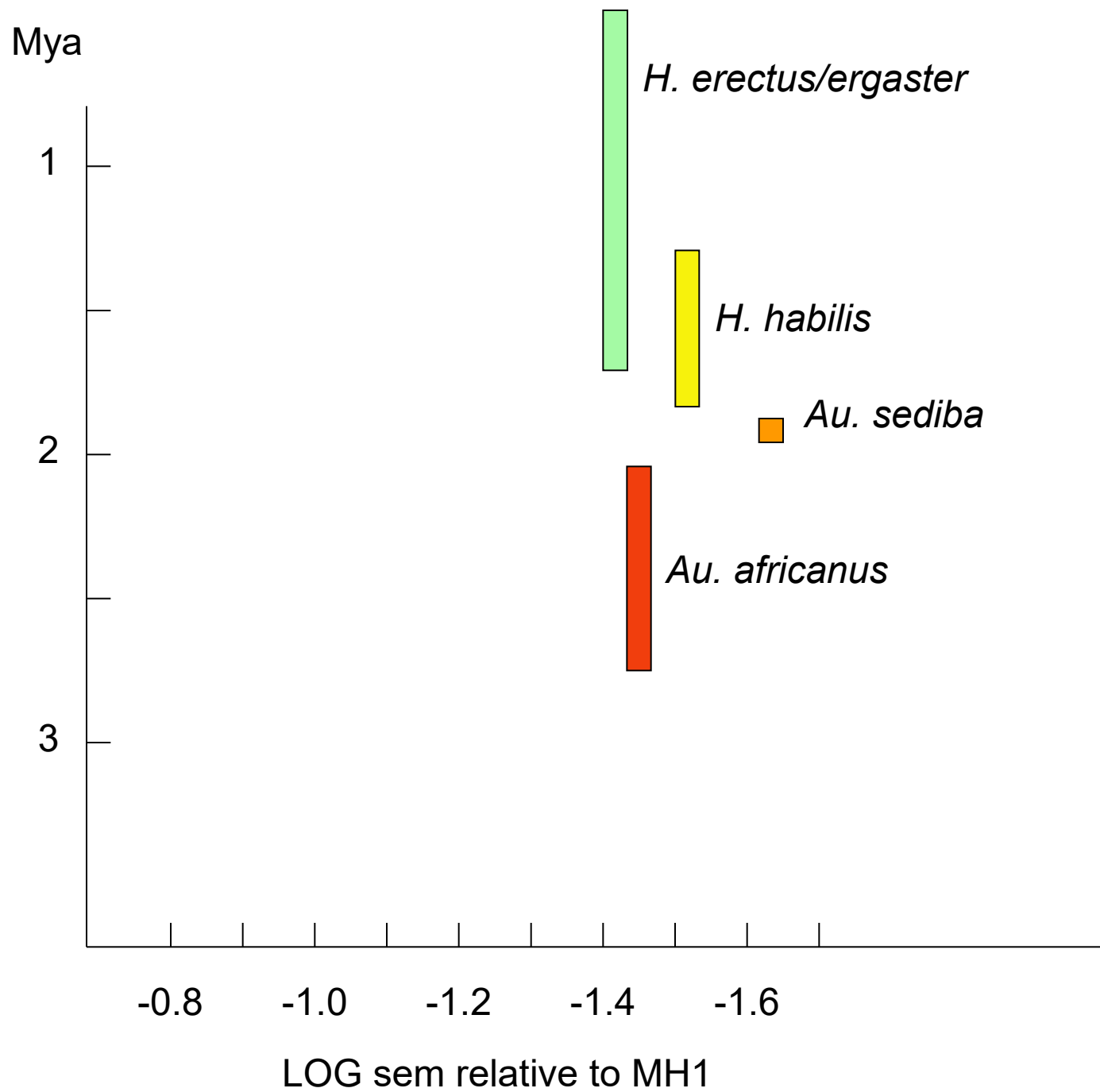
-1.2

-1.4

-1.6

LOG sem relative to MH1







STS 5



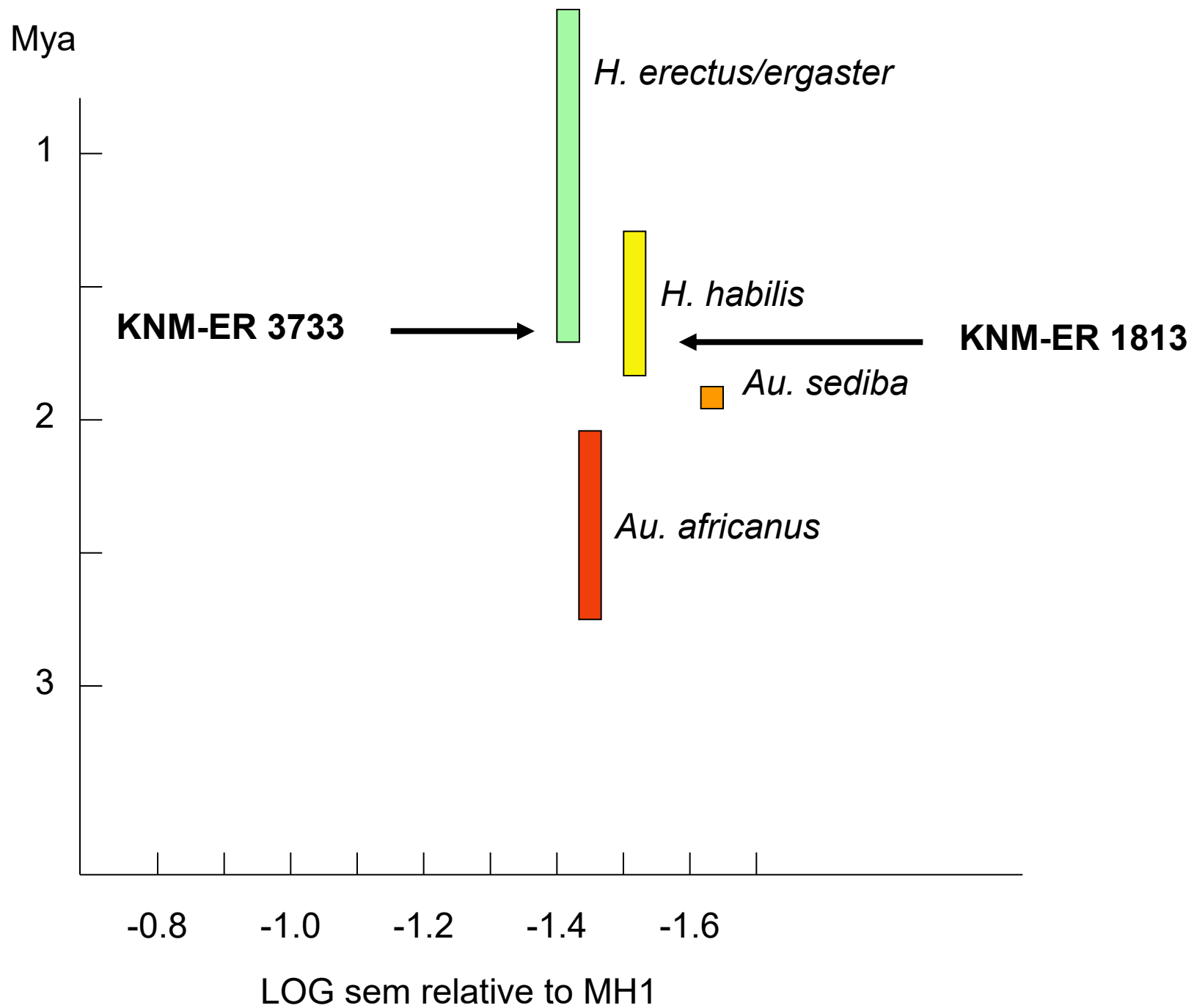
KNM-ER 1813

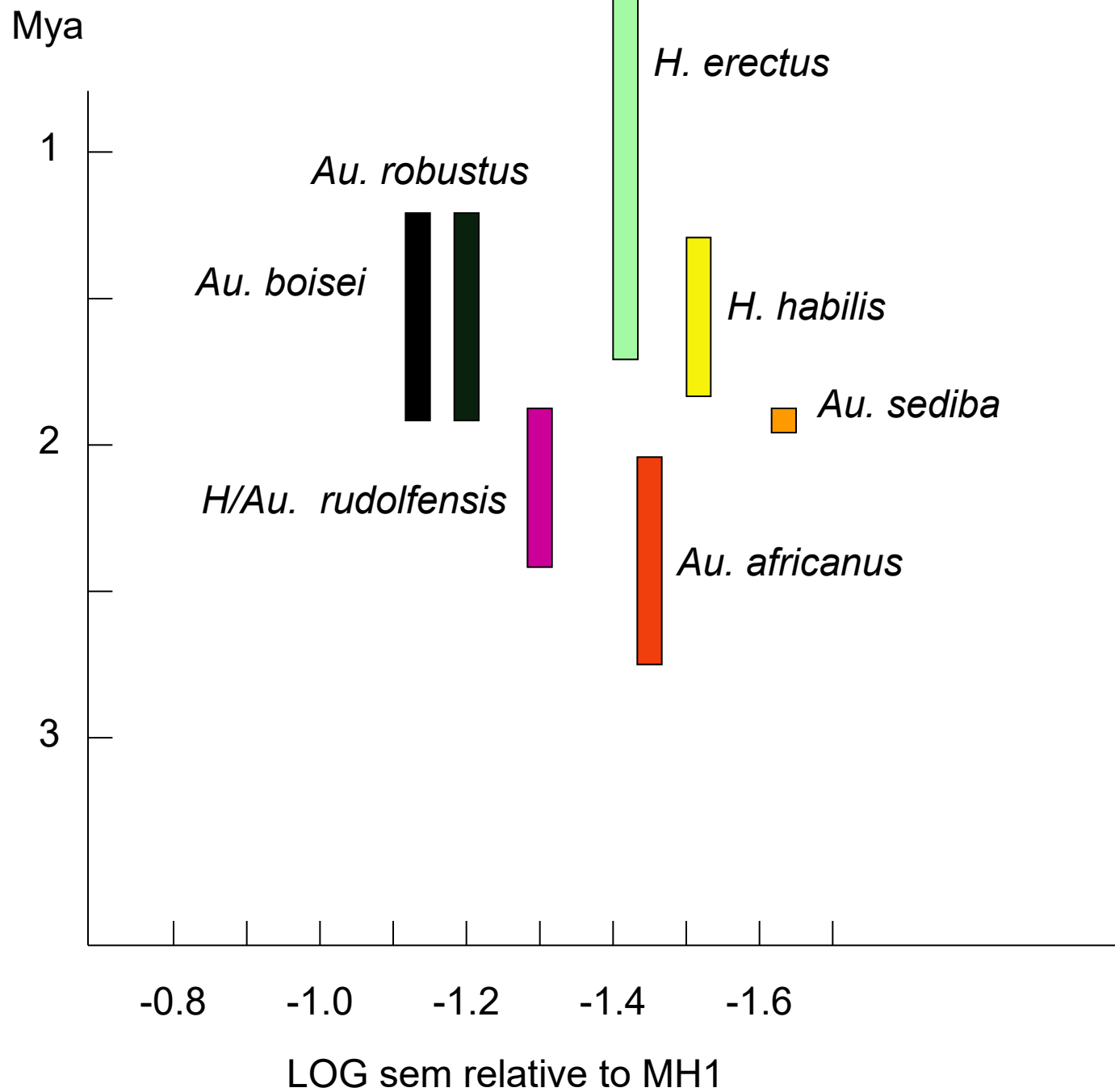


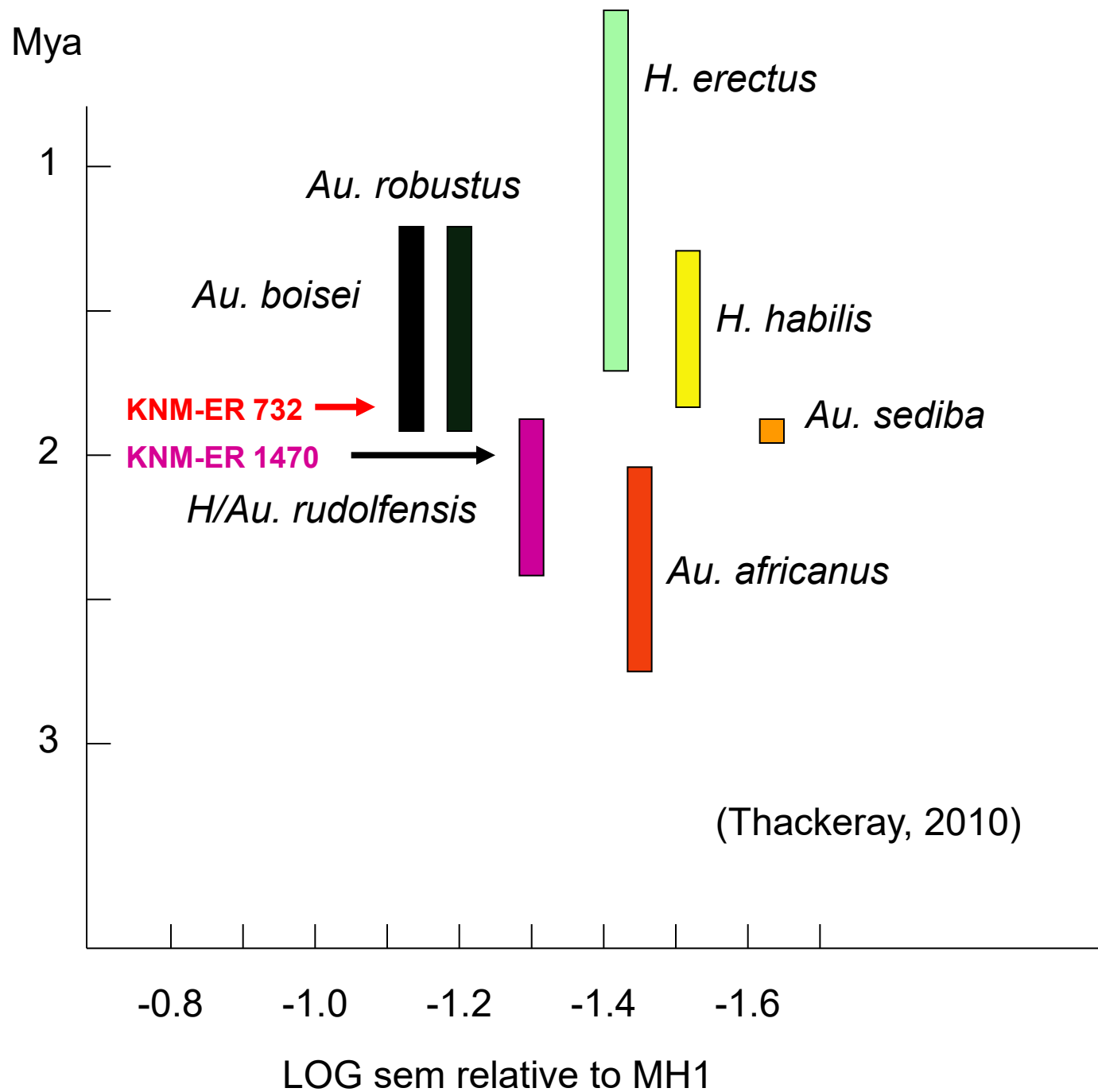
MH 1



KNM-ER 3733





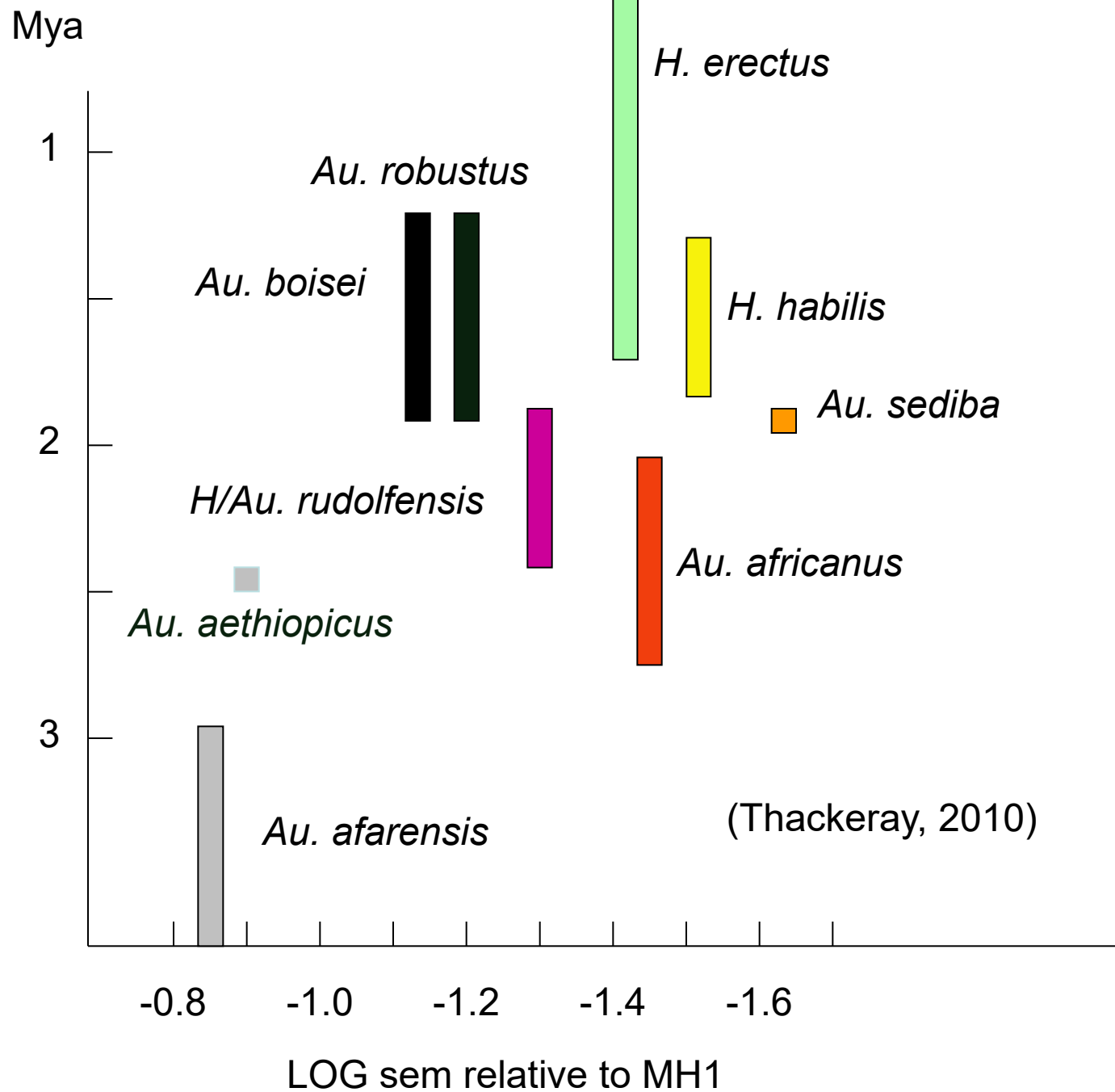




KNM ER-732

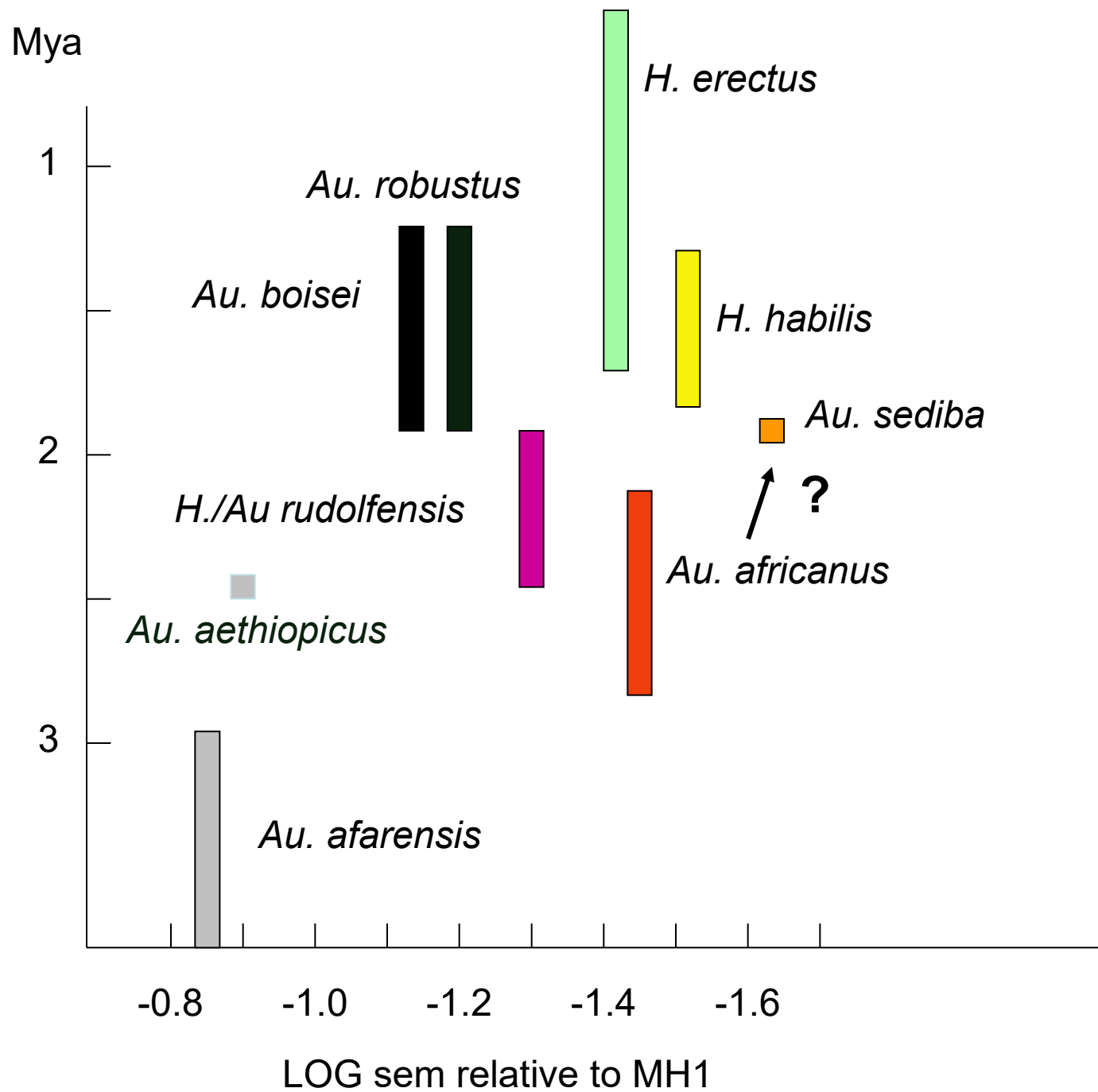


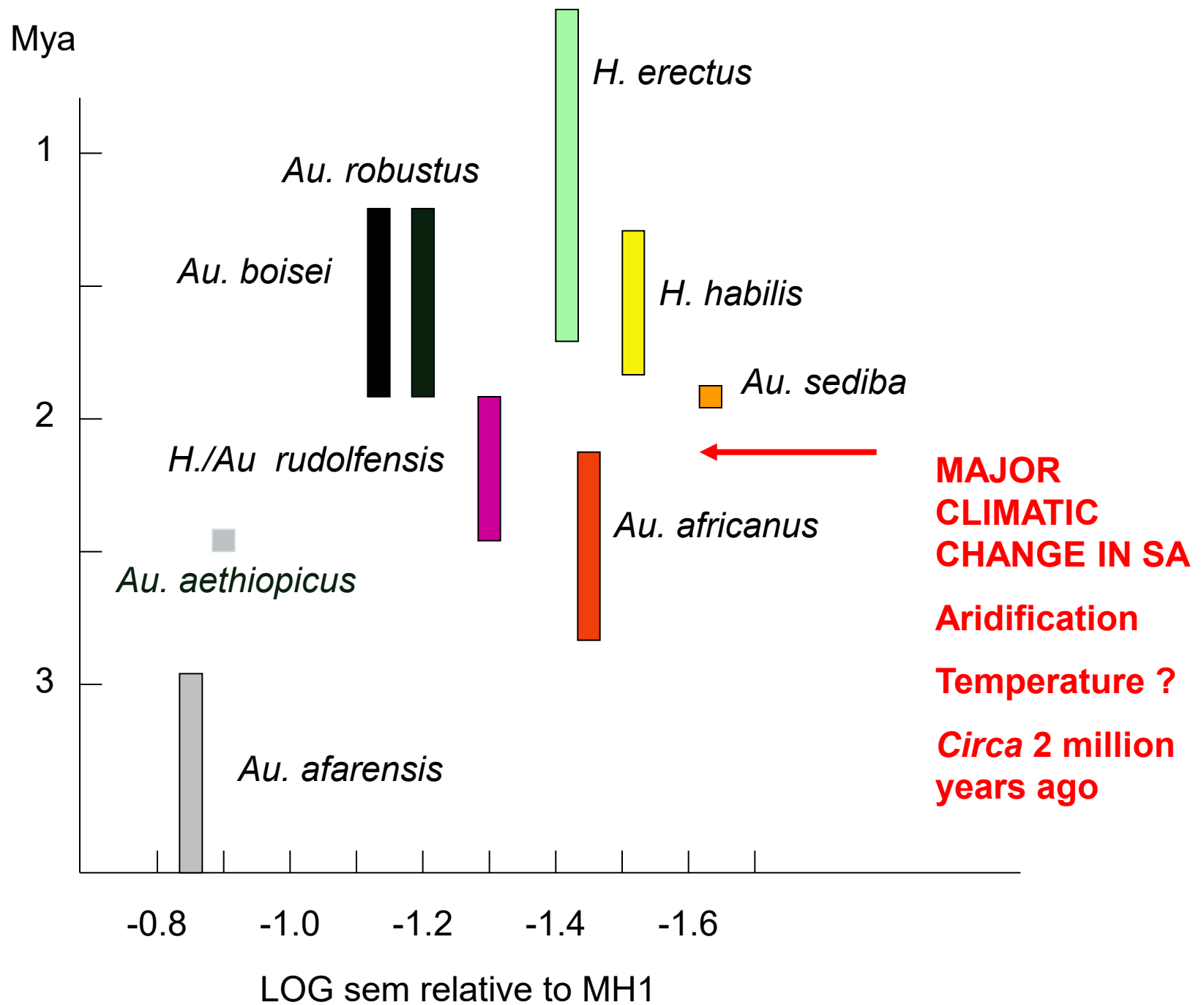
KNM ER-1470



**CAN WE BE TEMPTED TO DRAW LINES BETWEEN TAXA,
TO OBTAIN A PHYLOGENY ?**

**IS IT POSSIBLE TO USE LOG_{sem} STATISTICS TO
GENERATE AN OBJECTIVE PHYLOGENY ?**





THERE IS A NEED NOT ONLY TO

IDENTIFY CLIMATIC CHANGE,

BUT ALSO

TO QUANTIFY CHANGES IN PALAEO-CLIMATE

**THERE IS A NEED TO NOT ONLY TO
IDENTIFY CLIMATIC CHANGE,**

BUT ALSO

TO QUANTIFY CHANGES IN PALAEO-CLIMATE

HOW TO DO THIS ?

QUANTIFICATION OF TEMPERATURE OR OTHER ENVIRONMENTAL VARIABLES FROM MULTIVARIATE ANALYSIS OF RELATIVE ABUNDANCES OF FAUNA (RODENTS, INSECTIVORES, FORAMINIFERA) OR POLLEN IN SEQUENCES OF ASSEMBLAGES THROUGH TIME

Eg. Factor Analysis

$$FS = \sum (PCN\ i \times FL\ i)$$

Where FS = a Factor Score for any faunal assemblage A

PCN i is the percentage occurrence of species i

FL 1 is the Factor Loading on Factor 1 for species i

$\sum$ is the sum of the products of (**PCN i** x **FL i**)

ASSEMBLAGE A

LEVEL1

SPECIES 1

SPECIES 2

SPECIES 3

▪

▪

▪

SPECIES 18

SPECIES 19

SPECIES 20

ASSEMBLAGE

A

LEVEL 1

SPECIES 1

SPECIES 2

SPECIES 3

.

.

.

SPECIES 18

SPECIES 19

SPECIES 20

B

LEVEL 2

SPECIES 1

SPECIES 2

SPECIES 3

SPECIES 4

SPECIES 19

SPECIES 20

ASSEMBLAGE

A	B	C
LEVEL 1	LEVEL 2	LEVEL 3
SPECIES 1	SPECIES 1	
SPECIES 2	SPECIES 2	
SPECIES 3	SPECIES 3	SPECIES 3
.	SPECIES 4	SPECIES 4
.		SPECIES 5
.		
SPECIES 18		
SPECIES 19	SPECIES 19	
SPECIES 20	SPECIES 20	SPECIES 20

FOR ANY **ASSEMBLAGE A**

CALCULATE PERCENTAGE OCCURRENCE (PCN) OF EACH SPECIES

PCN SPECIES 1

PCN SPECIES 2

PCN SPECIES 3

•

•

•

PCN SPECIES 18

PCN SPECIES 19

PCN SPECIES 20

USING A DATABASE IN WHICH ALL ASSEMBLAGES ARE TAKEN TOGETHER AND SUBJECTED TO FACTOR ANALYSIS:

IDENTIFY THOSE SPECIES WHICH HAVE THE HIGHEST AND LOWEST LOADINGS ON THE FIRST FACTOR (FACTOR 1)

FACTOR 1 LOADING (FL) FOR SPECIES 1

FACTOR 1 LOADING (FL) FOR SPECIES 2

FACTOR LOADING (FL) FOR SPECIES 3

.

.

.

FACTOR 1 LOADING (FL) FOR SPECIES 18

FACTOR 1 LOADING (FL) FOR SPECIES 19

FACTOR 1 LOADING (FL) FOR SPECIES 20

USING A DATABASE IN WHICH ALL ASSEMBLAGES ARE TAKEN TOGETHER AND SUBJECTED TO FACTOR ANALYSIS:

IDENTIFY THOSE SPECIES WHICH HAVE THE HIGHEST AND LOWEST LOADINGS ON THE FIRST FACTOR (FACTOR 1)

FACTOR 1 LOADING (FL) FOR SPECIES 1 FL = 0.9

FACTOR 1 LOADING (FL) FOR SPECIES 2 FL = 0.8

FACTOR LOADING (FL) FOR SPECIES 3 FL = 0.7

▪

▪

▪

FACTOR LOADING FOR SPECIES 18 FL = -0.7

FACTOR LOADING FOR SPECIES 19 FL = -0.8

FACTOR LOADING FOR SPECIES 20 FL = -0.9

USING A DATABASE IN WHICH ALL ASSEMBLAGES ARE TAKEN TOGETHER AND SUBJECTED TO FACTOR ANALYSIS:

IDENTIFY THOSE SPECIES WHICH HAVE THE HIGHEST AND LOWEST LOADINGS ON THE FIRST FACTOR (FACTOR 1)

FACTOR 1 LOADING (FL) FOR SPECIES 1	FL = 0.9	Today in
FACTOR 1 LOADING (FL) FOR SPECIES 2	FL = 0.8	warm
FACTOR LOADING (FL) FOR SPECIES 3	FL = 0.7	regions

▪

▪

▪

FACTOR LOADING FOR SPECIES 18	FL = -0.7
FACTOR LOADING FOR SPECIES 19	FL = -0.8
FACTOR LOADING FOR SPECIES 20	FL = -0.9

USING A DATABASE IN WHICH ALL ASSEMBLAGES ARE TAKEN TOGETHER AND SUBJECTED TO FACTOR ANALYSIS:

IDENTIFY THOSE SPECIES WHICH HAVE THE HIGHEST AND LOWEST LOADINGS ON THE FIRST FACTOR (FACTOR 1)

FACTOR 1 LOADING (FL) FOR SPECIES 1	FL = 0.9	Today in
FACTOR 1 LOADING (FL) FOR SPECIES 2	FL = 0.8	warm
FACTOR LOADING (FL) FOR SPECIES 3	FL = 0.7	regions

▪

▪

▪

FACTOR LOADING FOR SPECIES 18	FL = -0.7	Today
FACTOR LOADING FOR SPECIES 19	FL = -0.8	in cold
FACTOR LOADING FOR SPECIES 20	FL = -0.9	regions

$$FS = \sum (PCNi \times FLi)$$

Where FS = a Factor Score for any faunal assemblage A

PCNi is the percentage occurrence of species i

FLi is the Factor Loading on Factor 1 for species i

SUMMARY STATISTICS BASED ON FACTOR 1, **SSF1**

FOR A SEQUENCE OF ASSEMBLAGES THROUGH TIME

$$FS = \sum (PCN_i \times FL_i)$$

Where FS = a Factor Score for any faunal assemblage A

PCN_i is the percentage occurrence of species i

FL_i is the Factor Loading on Factor 1 for species i

SUMMARY STATISTICS BASED ON FACTOR 1

SSF1 STANDARDISED FROM LOWEST (0) TO HIGHEST (100)

$$FS = \sum (PCN_i \times FL_i)$$

Where FS = a Factor Score for any faunal assemblage A

PCN_i is the percentage occurrence of species i

FL_i is the Factor Loading on Factor 1 for species i

SUMMARY STATISTICS BASED ON FACTOR 1

SSF1 STANDARDISED FROM **LOWEST (0)** TO **HIGHEST (100)**

SSF1 STATISTICS CAN PROVIDE AN INDEX OF VARIABILITY IN TEMPERATURE THROUGH TIME

SSF1 = 0 COLDEST SSF1 = 100 WARMEST IN SEQUENCE

**THIS EXPLORATORY STATISTICAL APPROACH
HAS BEEN APPLIED TO QUATERNARY SEQUENCES OF:**

FORAMINIFERA FROM DEEP SEA CORES (Thackeray 1987)

**RODENTS AND INSECTIVORES FROM SOUTH AFRICAN CAVE SEQUENCES
(Thackeray 1987)**

POLLEN SPECTRA FROM WONDERKRATER (Scott and Thackeray, 1987)

USING A DATABASE IN WHICH MICROFAUNAL ASSEMBLAGES ARE
TAKEN TOGETHER AND SUBJECTED TO FACTOR ANALYSIS:

IDENTIFY THOSE SPECIES WHICH HAVE THE HIGHEST AND LOWEST
LOADINGS ON THE FIRST FACTOR (FACTOR 1)

Saccostumus campestris

Crocidura hirta

Today occurs in

warm regions

▪

▪

▪

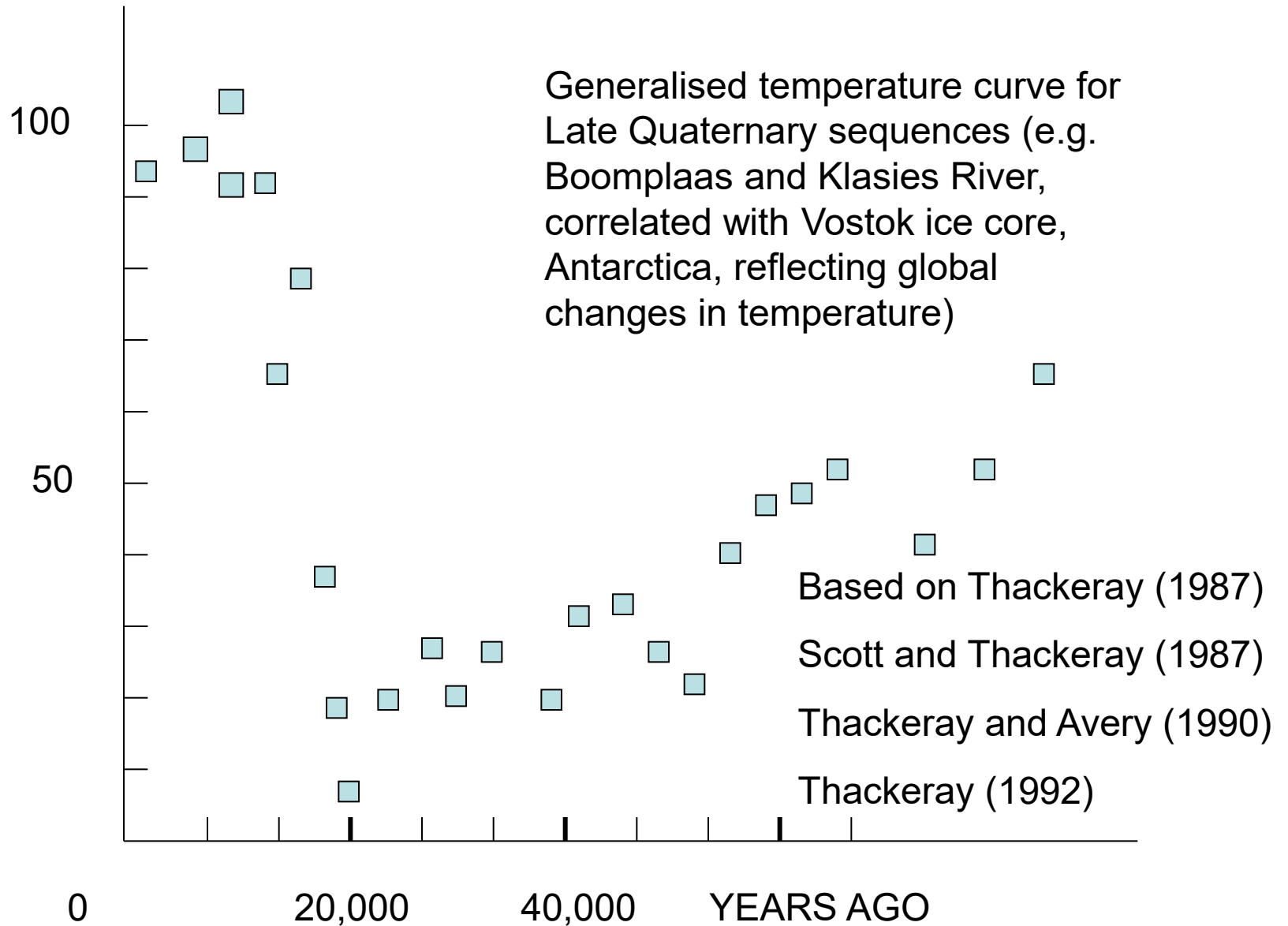
Otomys saundersae

Myosorex varius

Today occurs in

cold regions

TEMPERATURE INDEX



**COMPARISON BETWEEN
DEUTERIUM ISOTOPE RATIOS
(VOSTOK ICE CORE)
AND RADIO-CARBON DATED
FAUNAL ASSEMBLAGES
FROM BOOMPLAAS FOR WHICH
SSF1 TEMPERATURE INDICES
HAVE BEEN CALCULATED:**

$$r = 0.95$$

**THE SAME APPROACH CAN BE APPLIED TO AN ANALYSIS
OF FACTOR 2**

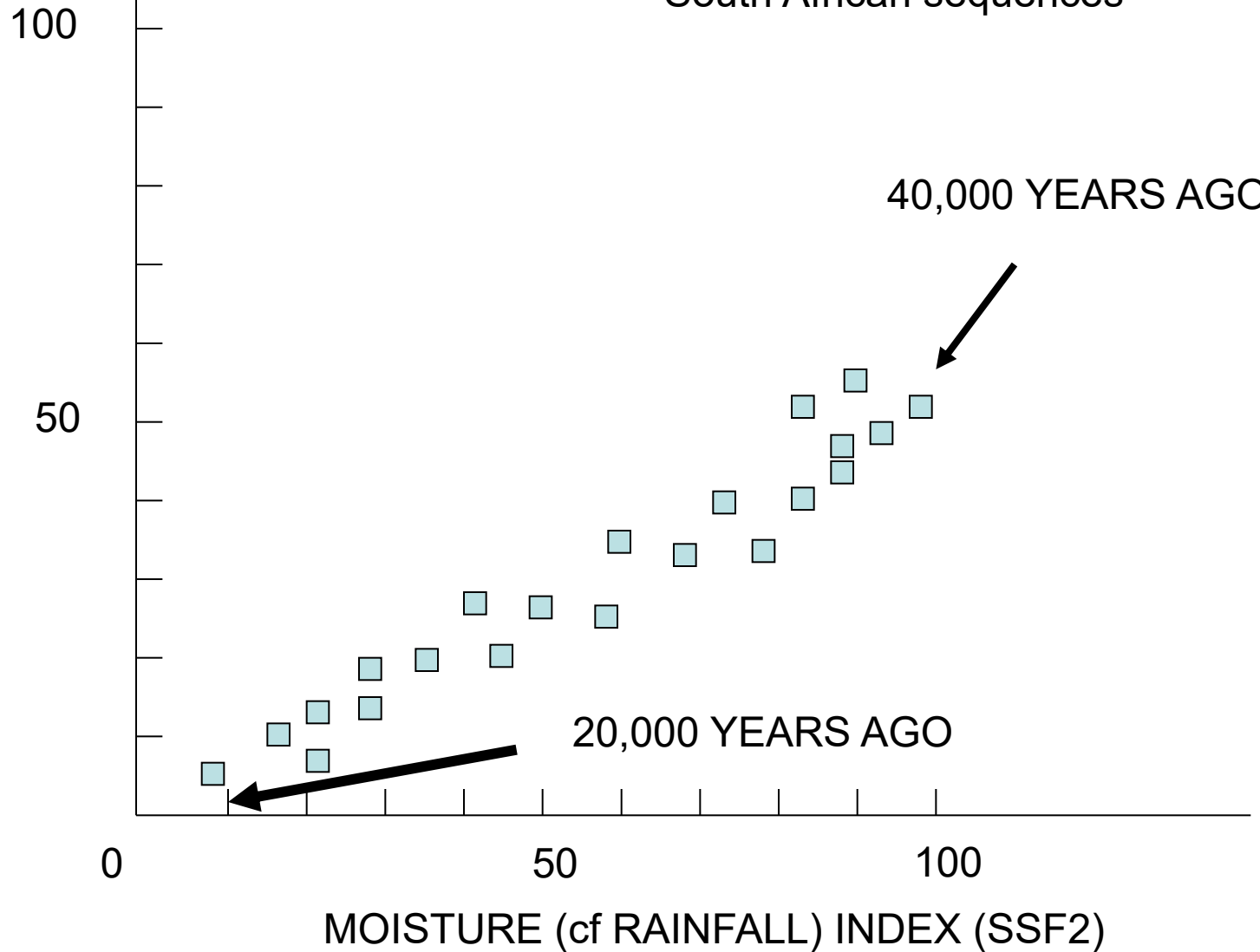
**SPECIES WITH HIGH LOADING ON FACTOR 2:
TODAY FOUND IN MOIST ENVIRONMENTS**

**SPECIES WITH LOW LOADING ON FACTOR 2:
TODAY FOUND IN DRY ENVIRONMENTS**

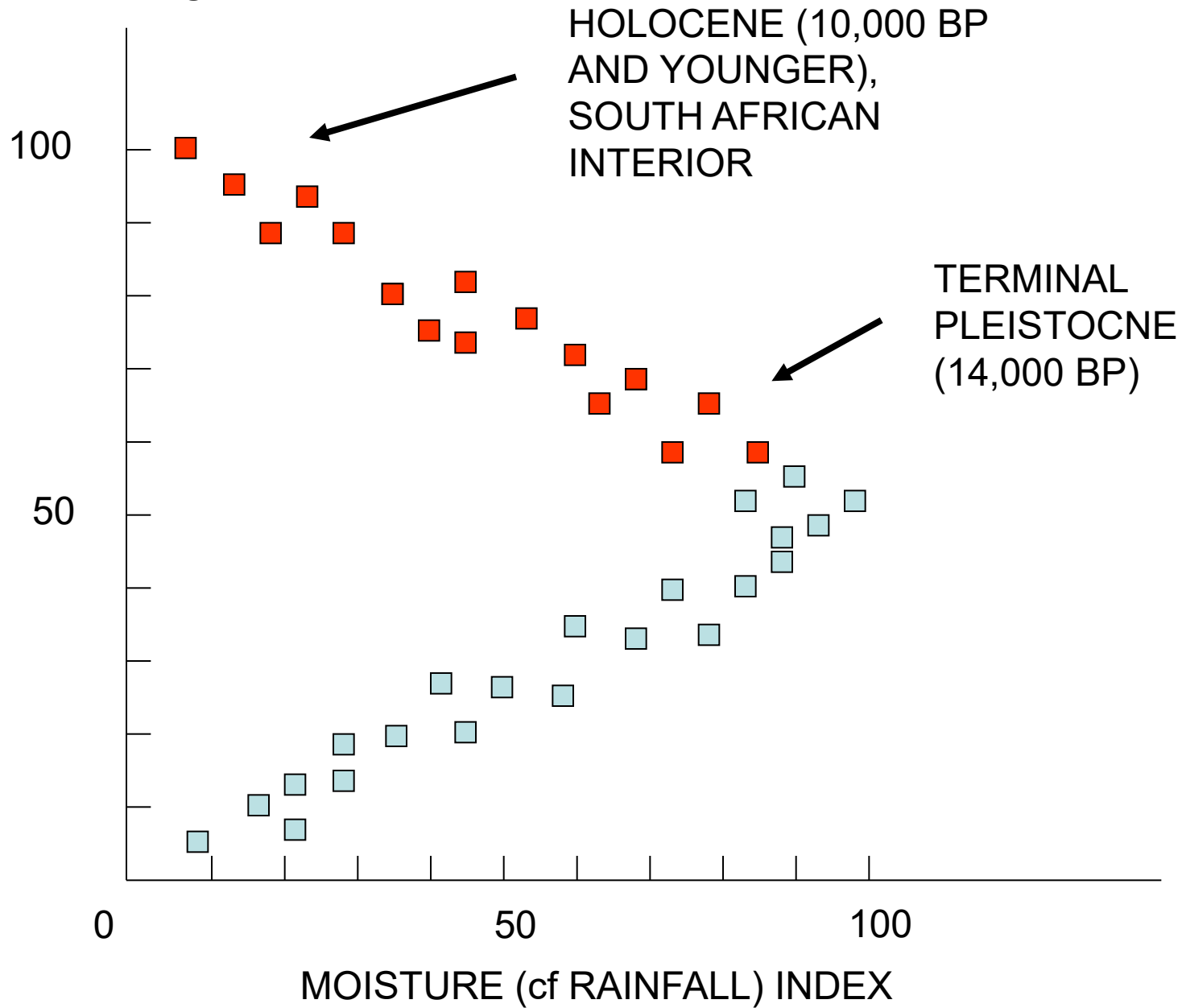
**SSF2: SUMMARY STATISTIC BASED ON FACTOR 2 FOR A
SEQUENCE OF ASSEMBLAGES THROUGH TIME:
MOISTURE INDEX**

TEMPERATURE INDEX

Generalised results for sequences from
Boomplaas and other Late Quaternary
South African sequences

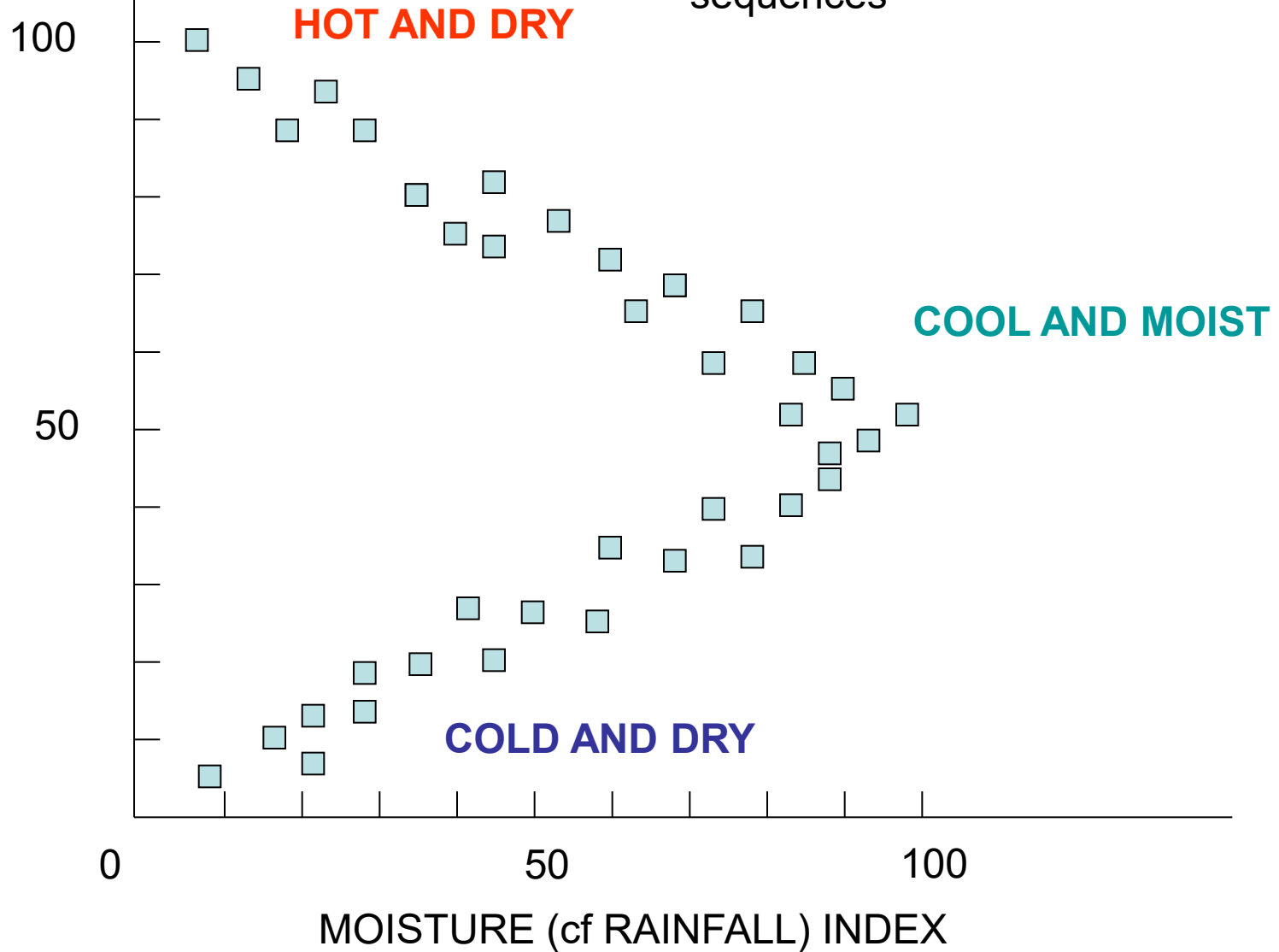


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Generalised results obtained from
rodents, insectivores and pollen
spectra, South African Late Quaternary
sequences



**THESE RESULTS HAVE BEEN OBTAINED
FOR PERIODS WITHIN THE QUATERNARY
ASSOCIATED WITH NATURAL CHANGES IN CLIMATE**

**CHANGES IN TEMPERATURE ARE RELATED TO
CHANGES IN THE EARTH'S ORBIT AROUND THE SUN
("MILANKOVICH CYCLES"):**

**OBLIQUITY (40,000 YEAR PERIODICITY)
ECCENTRICITY (100,000 YEAR PERIODICITY)
PRECESSION (20,000 YEAR PERIODICITY)**

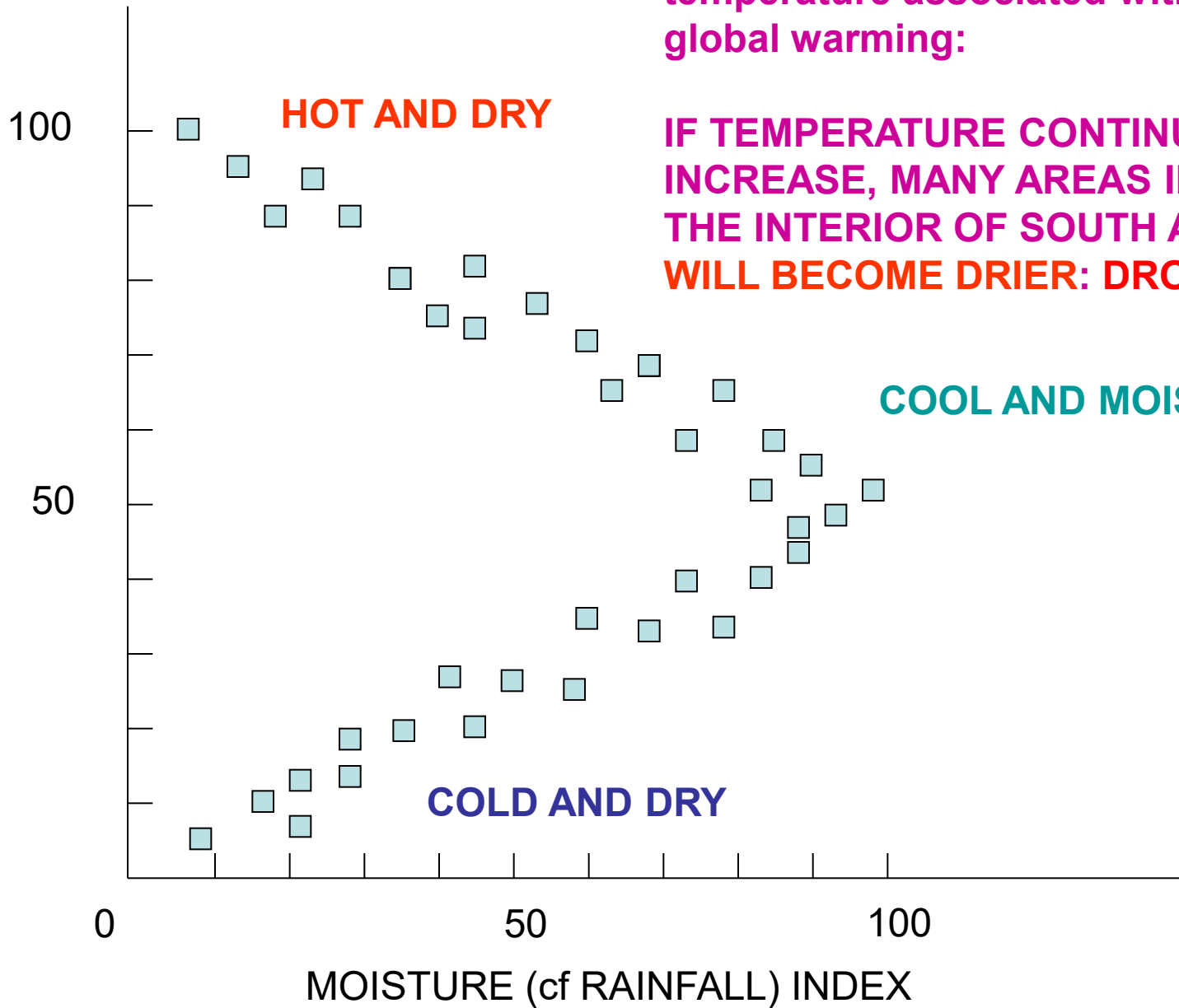
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**CHANGES IN MOISTURE ARE PARTLY RELATED TO
CHANGES IN THE AVAILABILITY OF WATER TO FALL
AS RAIN, RELATED TO EVAPORATION OF WATER OFF THE
OCEANS**

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Implications for future changes in temperature associated with global warming:

IF TEMPERATURE CONTINUES TO INCREASE, MANY AREAS IN THE INTERIOR OF SOUTH AFRICA WILL BECOME DRIER: DROUGHT

**FASTEST RATE OF INCREASE IN
TEMPERATURE FOR SOUTH AFRICAN LATE
QUATERNARY SEQUENCES:**

1 DEGREE CELSIUS PER 1000 YEARS

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**PREDICTED RATE OF INCREASE IN
TEMPERATURE IN THE
IMMEDIATE FUTURE:**

1 DEGREE CELSIUS PER DECADE ?

**FASTEST RATE OF INCREASE IN
TEMPERATURE FOR SOUTH AFRICAN LATE
QUATERNARY SEQUENCES:**

1 DEGREE CELSIUS PER 1000 YEARS

**CURRENT RATE OF INCREASE IN
TEMPERATURE:**

1 DEGREE CELSIUS PER DECADE ?

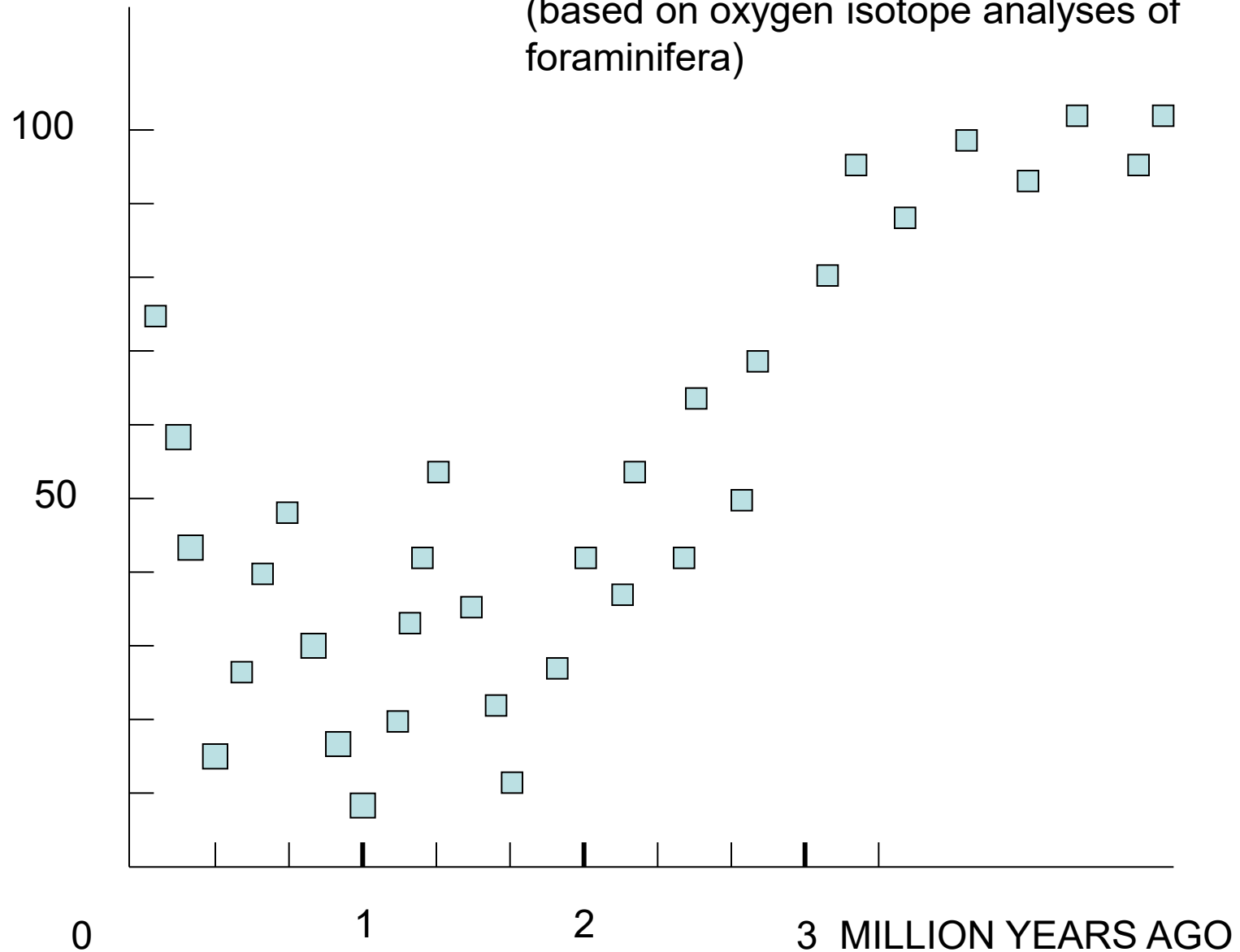
IMPLICATION:

**THE PREDICTED RATE OF TEMPERATURE
CHANGE WITHIN THE NEXT CENTURY IS
ABNORMALLY HIGH**

(ANTHROPOGENIC CAUSES ?)

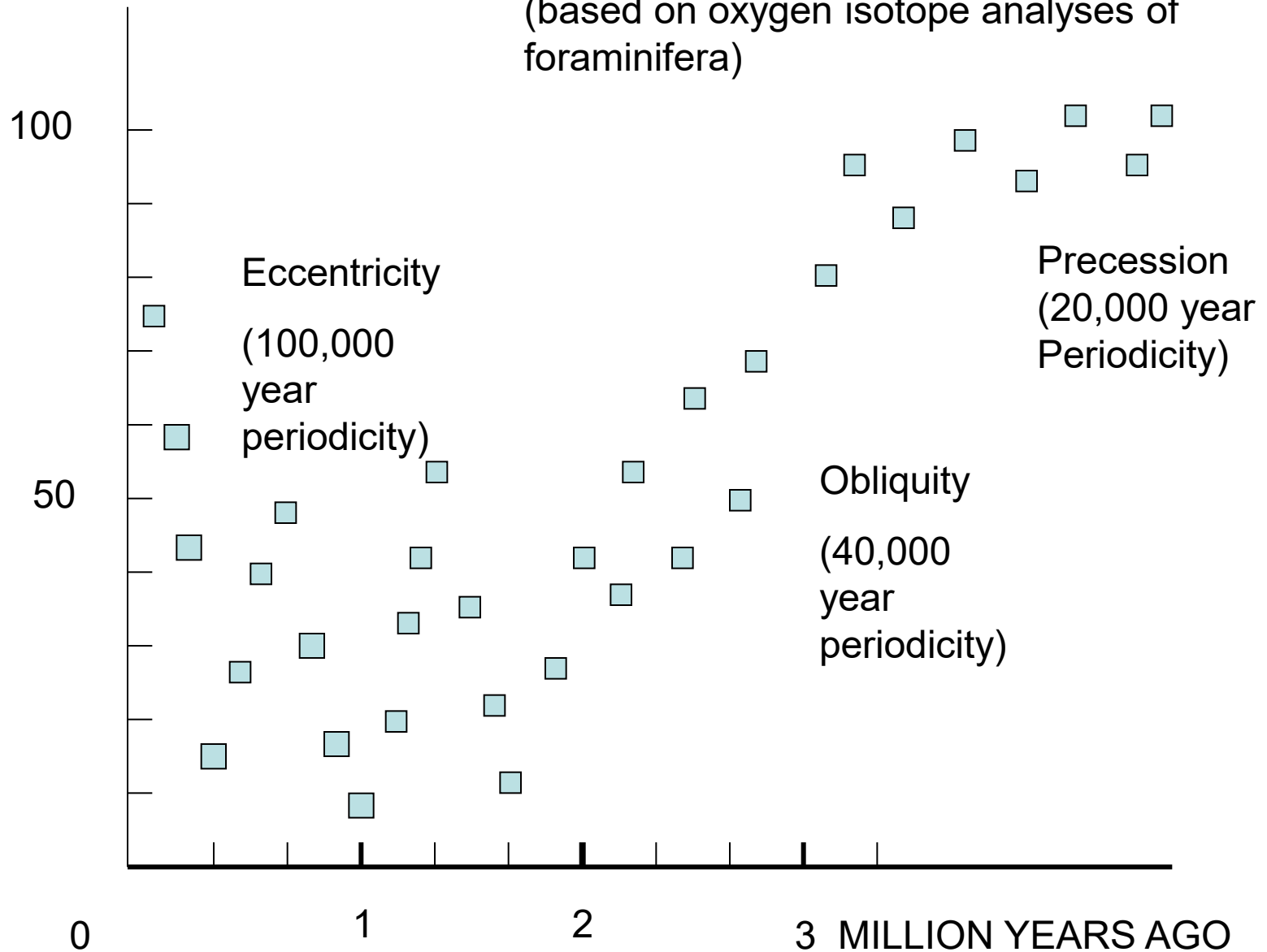
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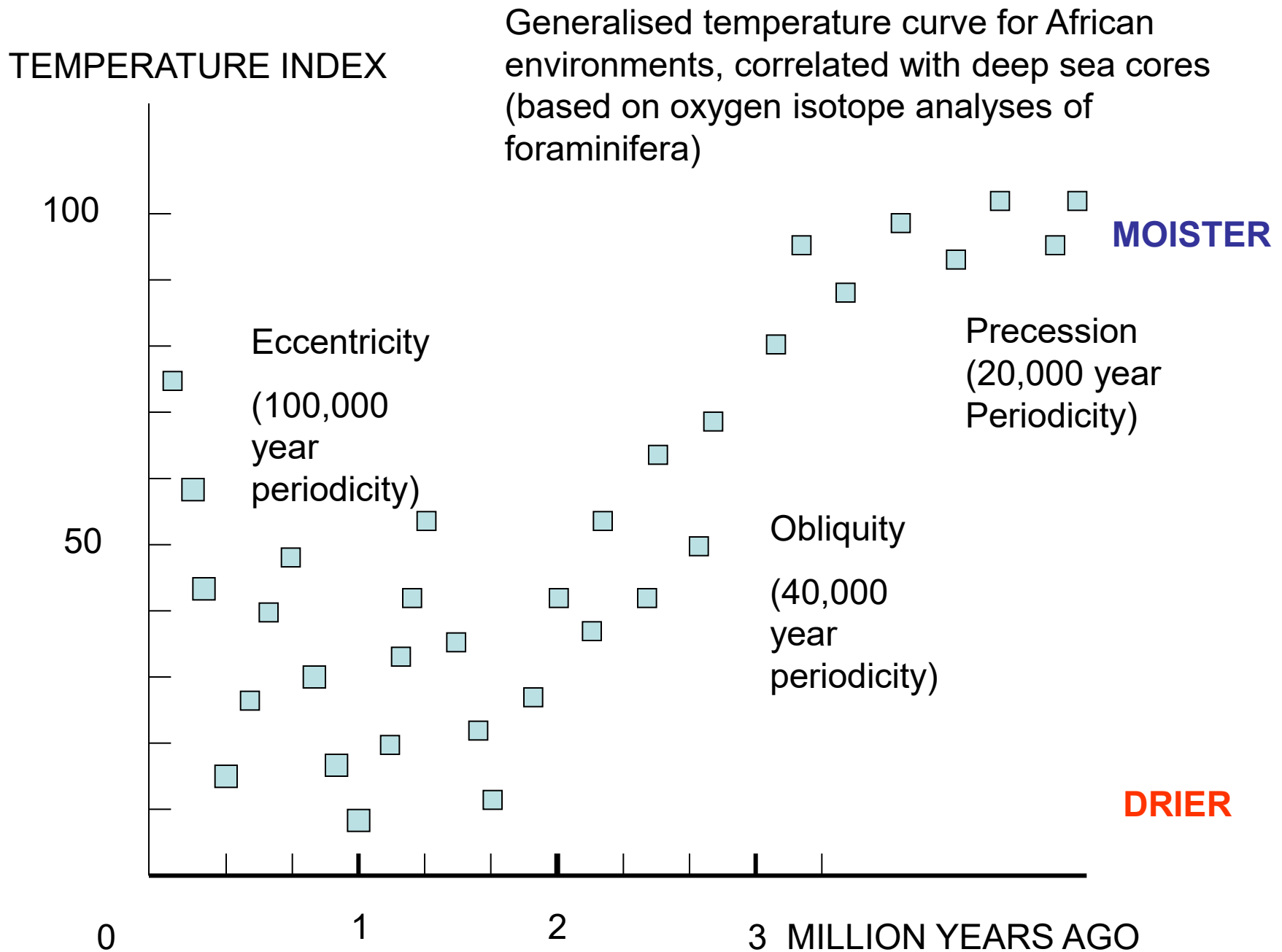
Generalised temperature curve for African environments, correlated with deep sea cores (based on oxygen isotope analyses of foraminifera)

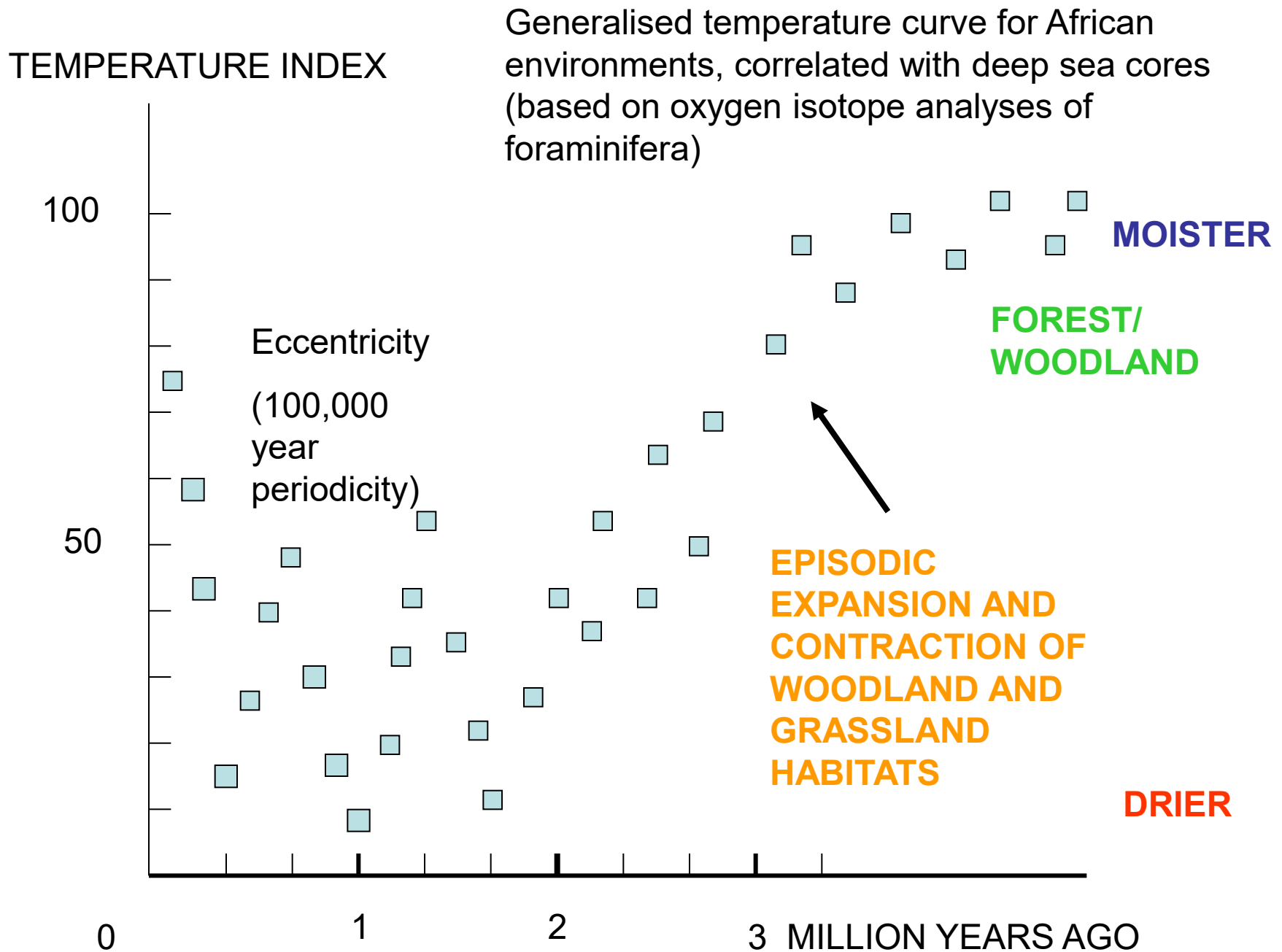


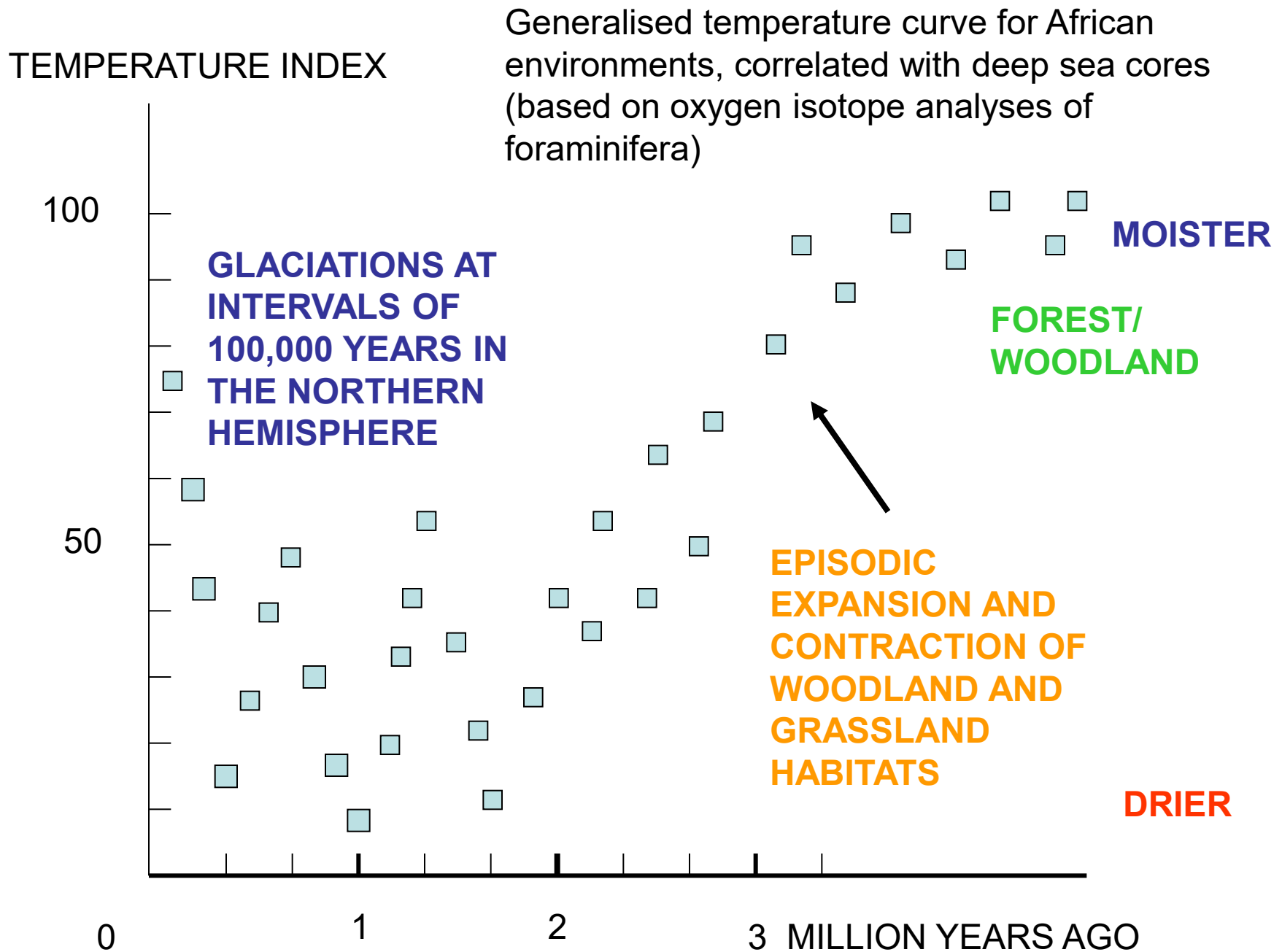
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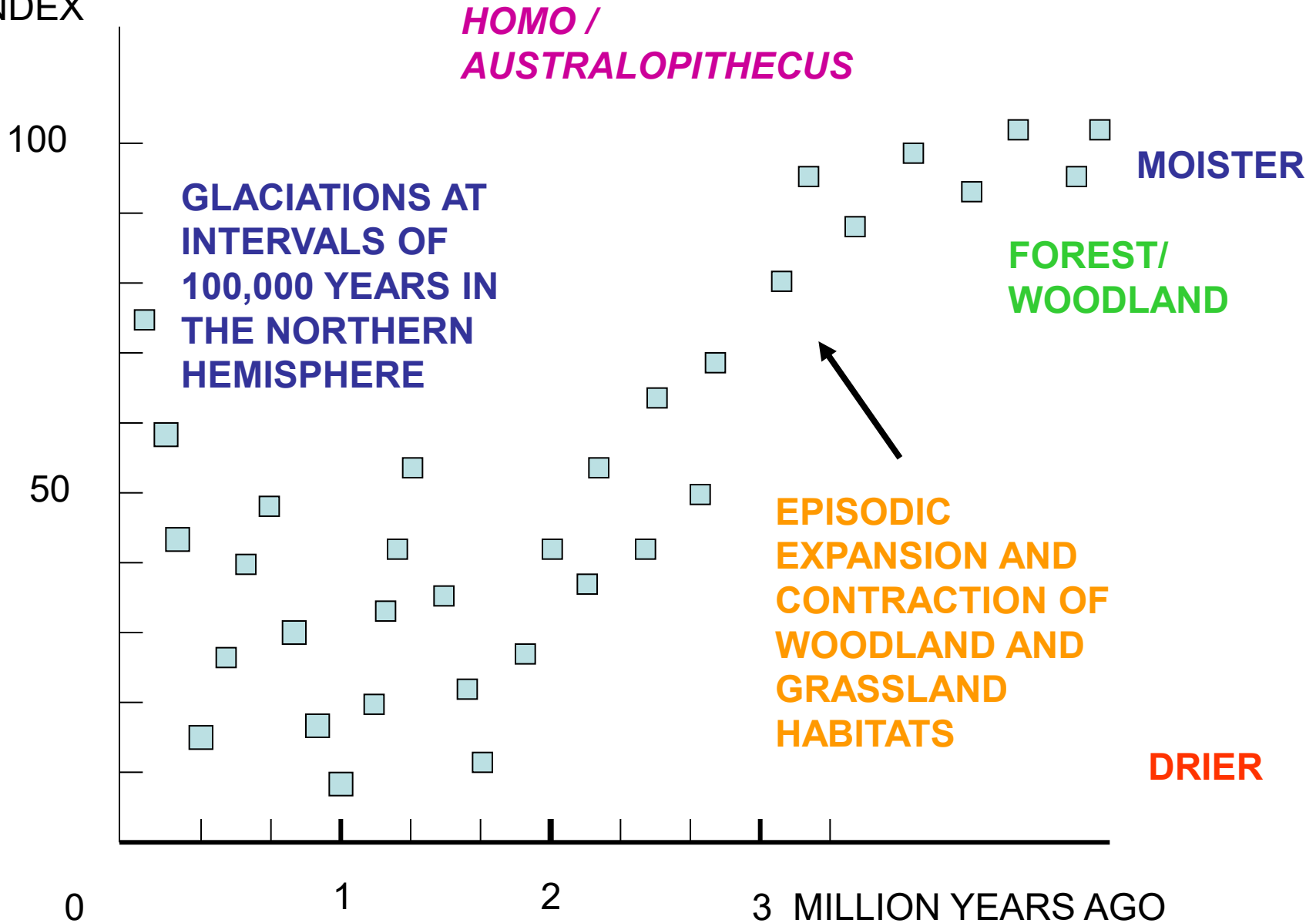






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**THE ORIGIN OF THE GENUS *HOMO*
IS ASSOCIATED WITH
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**C.K. BRAIN
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RAINFALL

HABITAT

DISTRIBUTION AND ABUNDANCE OF POPULATIONS

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**THE TRANSITION
BETWEEN *AUSTRALOPITHECUS* AND HOMO
IS WITHOUT A CLEAR BOUNDARY**

**MALAPA HOMINIDS (MH 1 AND MH2), *AUSTRALOPITHECUS SEDIBA*
HAVE A MOSAIC OF CHARACTERS,
AND MAY WELL BE TRANSITIONAL BETWEEN
AUSTRALOPITHECUS AND HOMO**

CHALLENGES FOR THE FUTURE

**RECOGNISING THAT PALAEO-ANTHROPOLOGY IS INTERDISCIPLINARY,
A FUNDAMENTAL CHALLENGE IS TO INTEGRATE PALAEOCLIMATIC DATA
WITH EVIDENCE FOR
CHANGES IN AFRICAN HABITATS ON A CONTINENTAL SCALE,
AFFECTING THE DISTRIBUTIONS AND RELATIVE ABUNDANCES
OF POPULATIONS THROUGH TIME-
IN TURN INFLUENCING GENE POOLS,
AND ULTIMATELY INFLUENCING MORPHOLOGY (ANATOMY)**

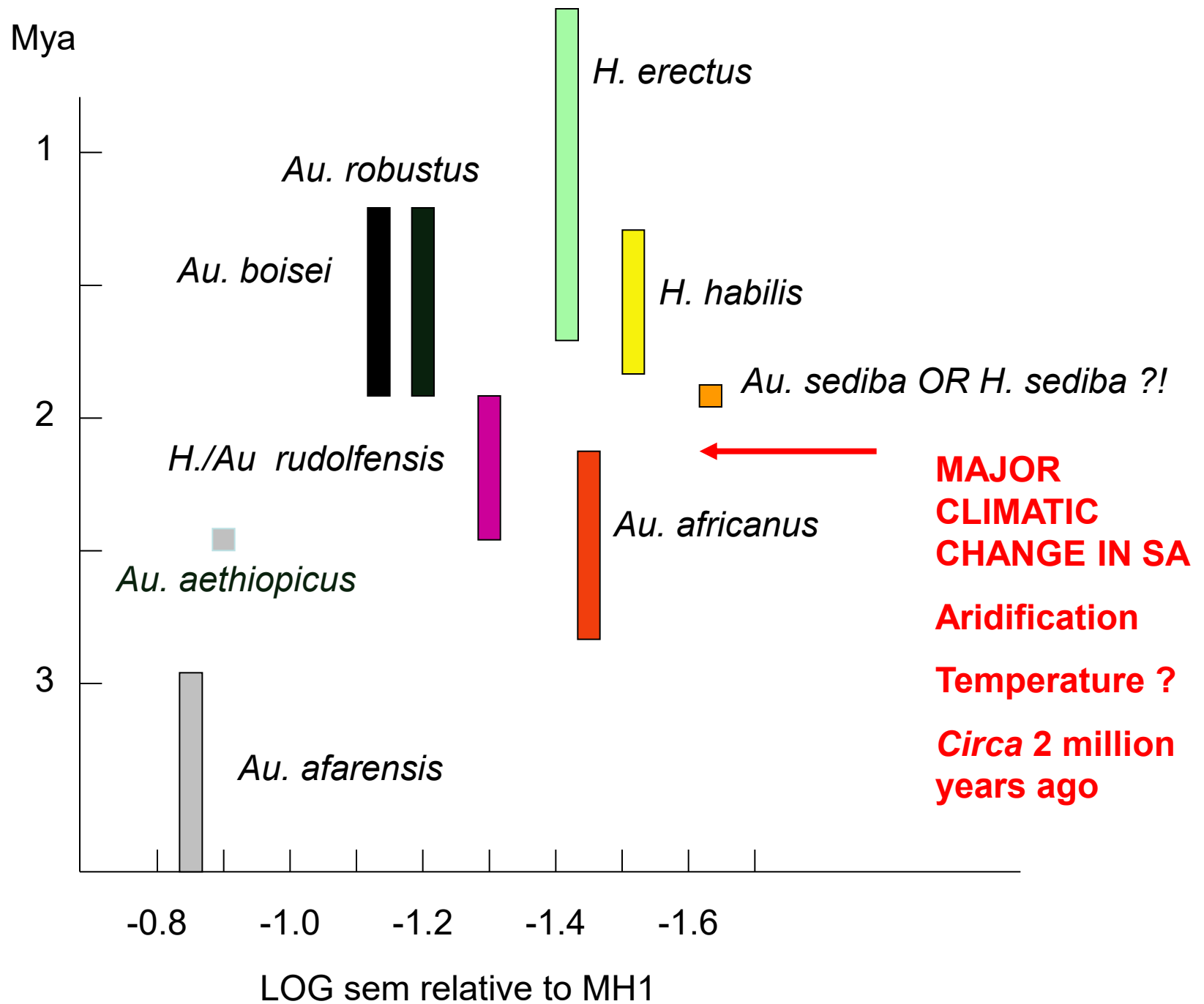
CHALLENGES FOR THE FUTURE

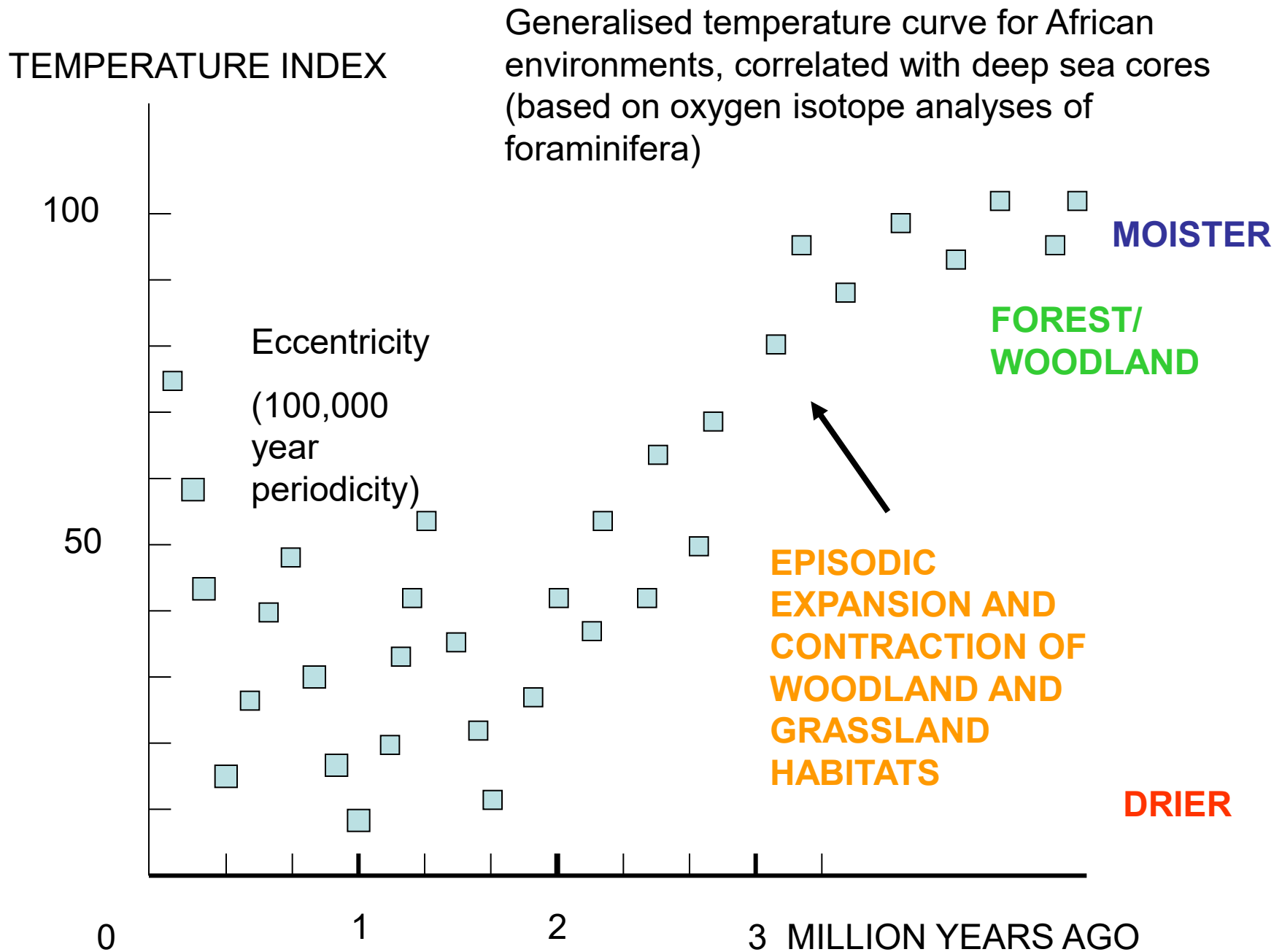
**MODELLING CHANGES IN AFRICAN HABITATS,
BASED ON OXYGEN ISOTOPE RATIOS FROM DEEP SEA CORES.**

**RELATING HABITATS TO FAUNAL (NON-HOMINID)
DISTRIBUTIONS AND RELATIVE ABUNDANCE**

**HOW DID THE DISTRIBUTIONS AND RELATIVE ABUNDANCES
OF HOMINIDS CHANGE THROUGH TIME
IN RESPONSE TO CHANGES IN PALAEOENVIRONMENTS ?**

**HOMINID SPECIES DIVERSITY :
*AUSTRALOPITHECUS – HOMO***





CONCLUSION

**THE INSTITUTE FOR HUMAN EVOLUTION
AT THE UNIVERSITY OF THE WITWATERSRAND
IS AT THE CUTTING EDGE
OF PALAEOANTHROPOLOGY**

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