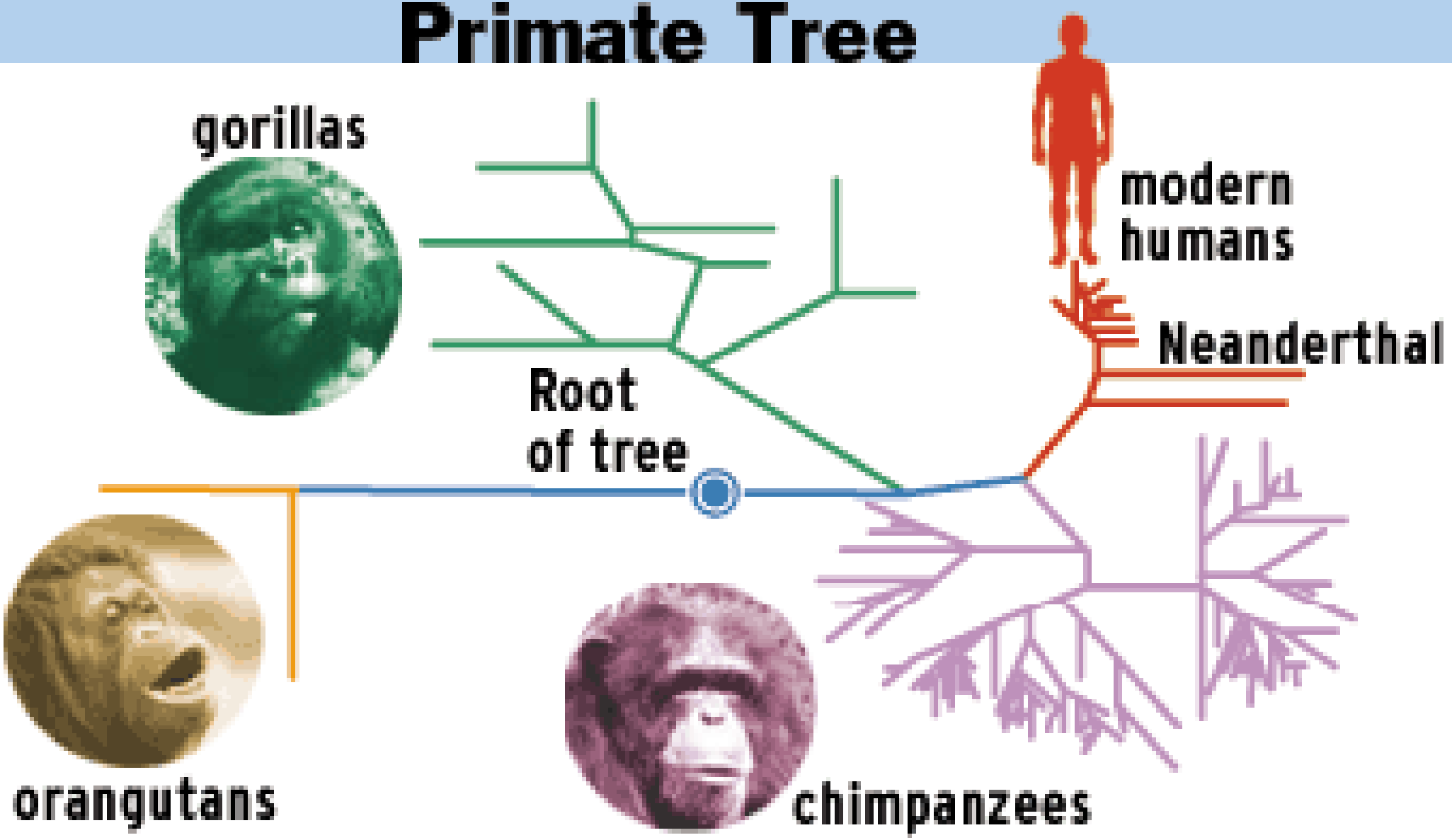
Primate Tree



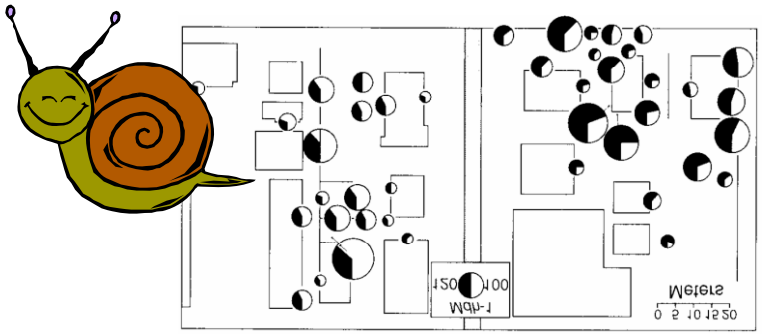
How does genetic structure **change?**

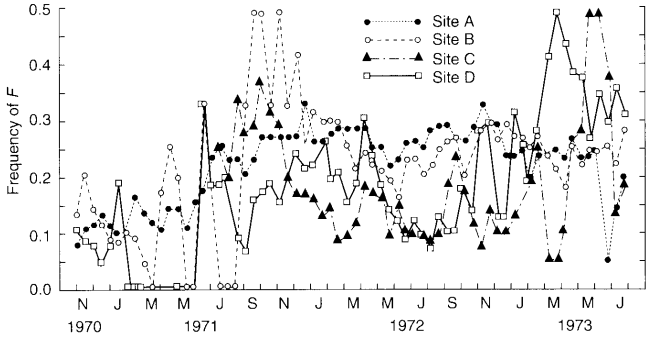
changes in allele frequencies and/or genotype frequencies through time

- mutation
- migration
- natural selection
- genetic drift
- non-random mating

POLIMORPHISM (VARIATION)

Genetic variation in space and time



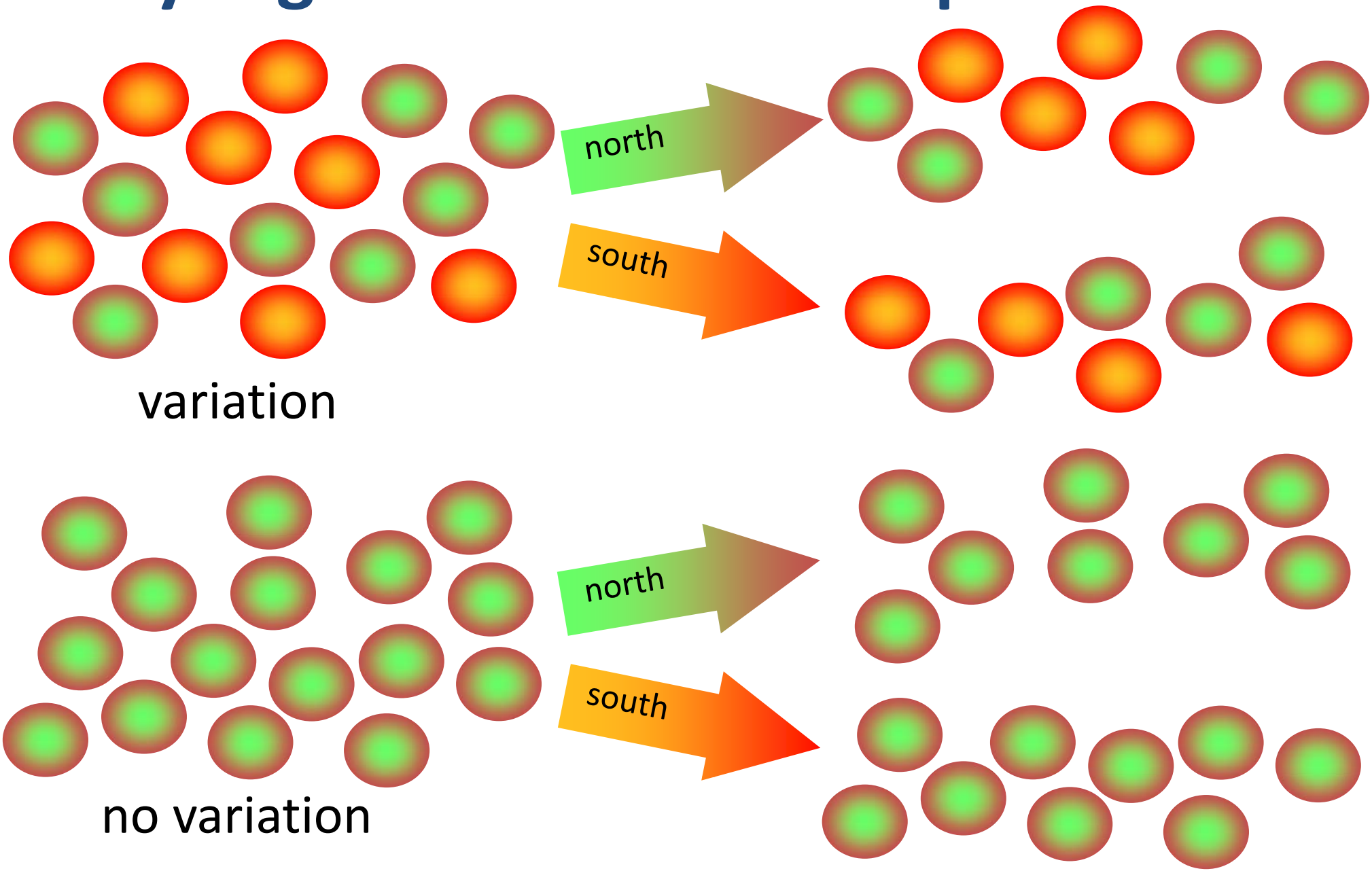


Why is genetic variation important?

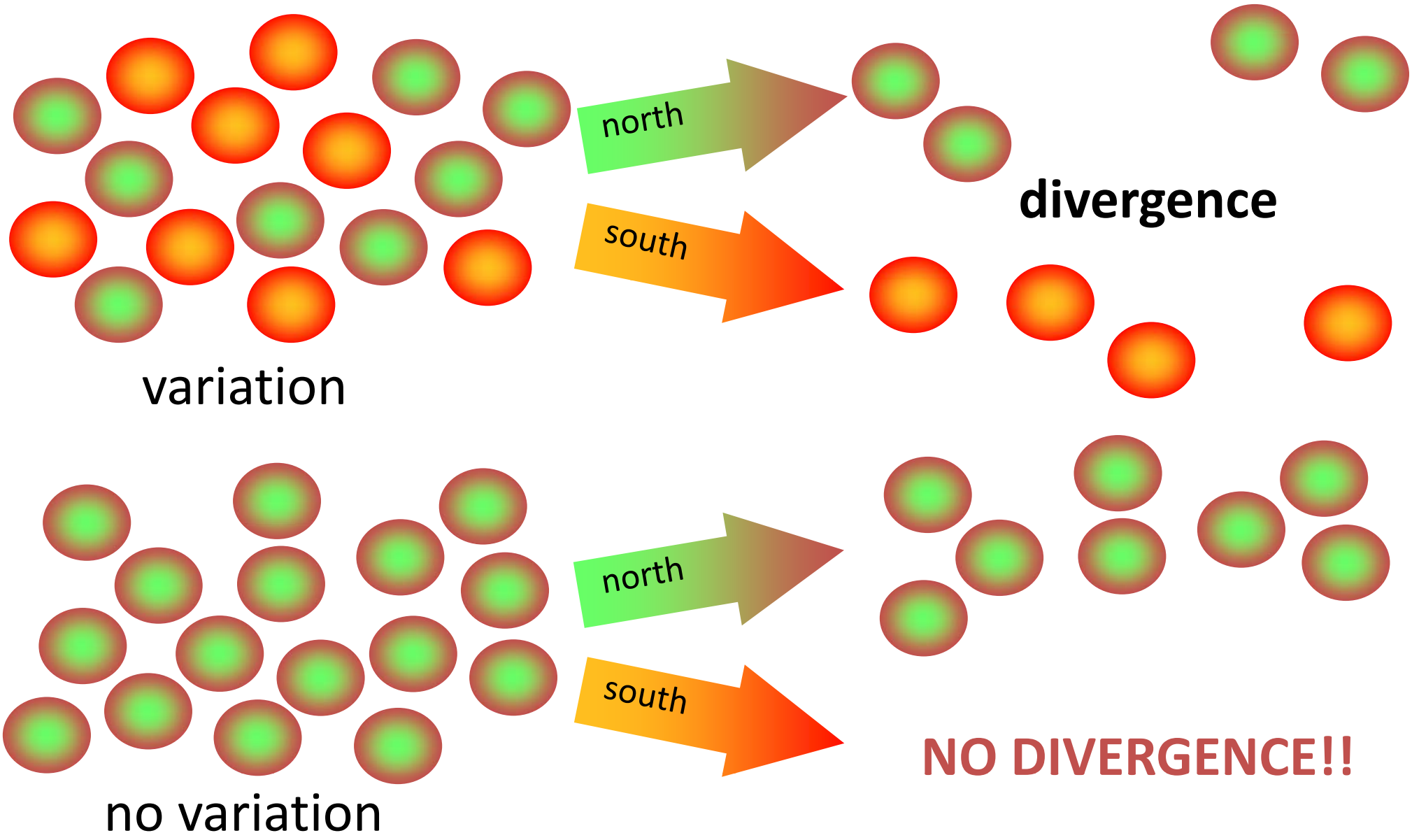
potential for change in genetic structure

- adaptation to environmental change
  - conservation
- divergence of populations
  - biodiversity

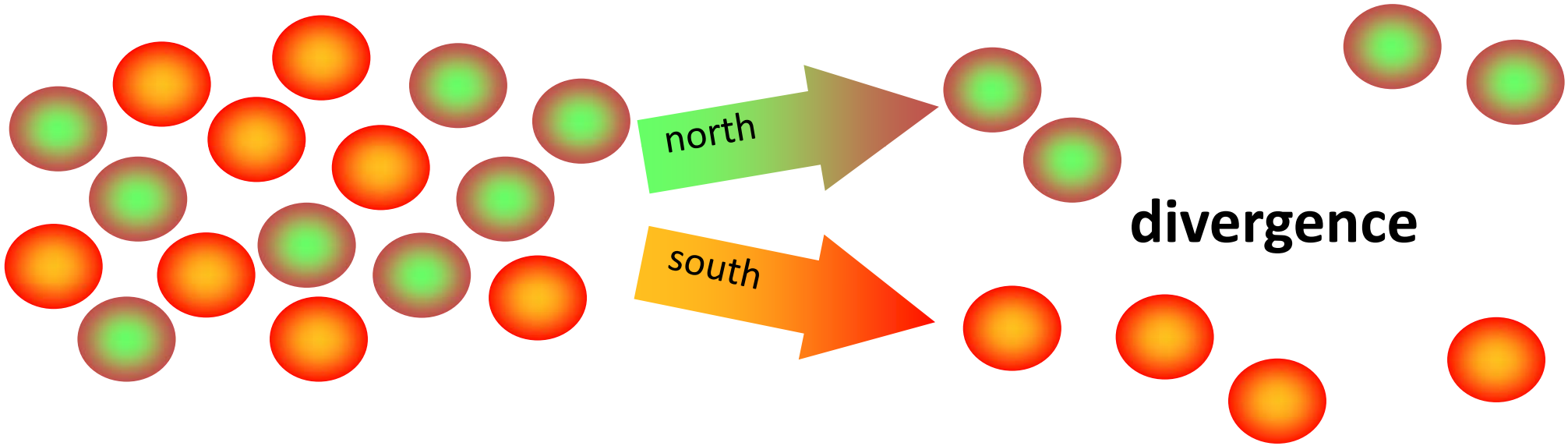
Why is genetic variation important?



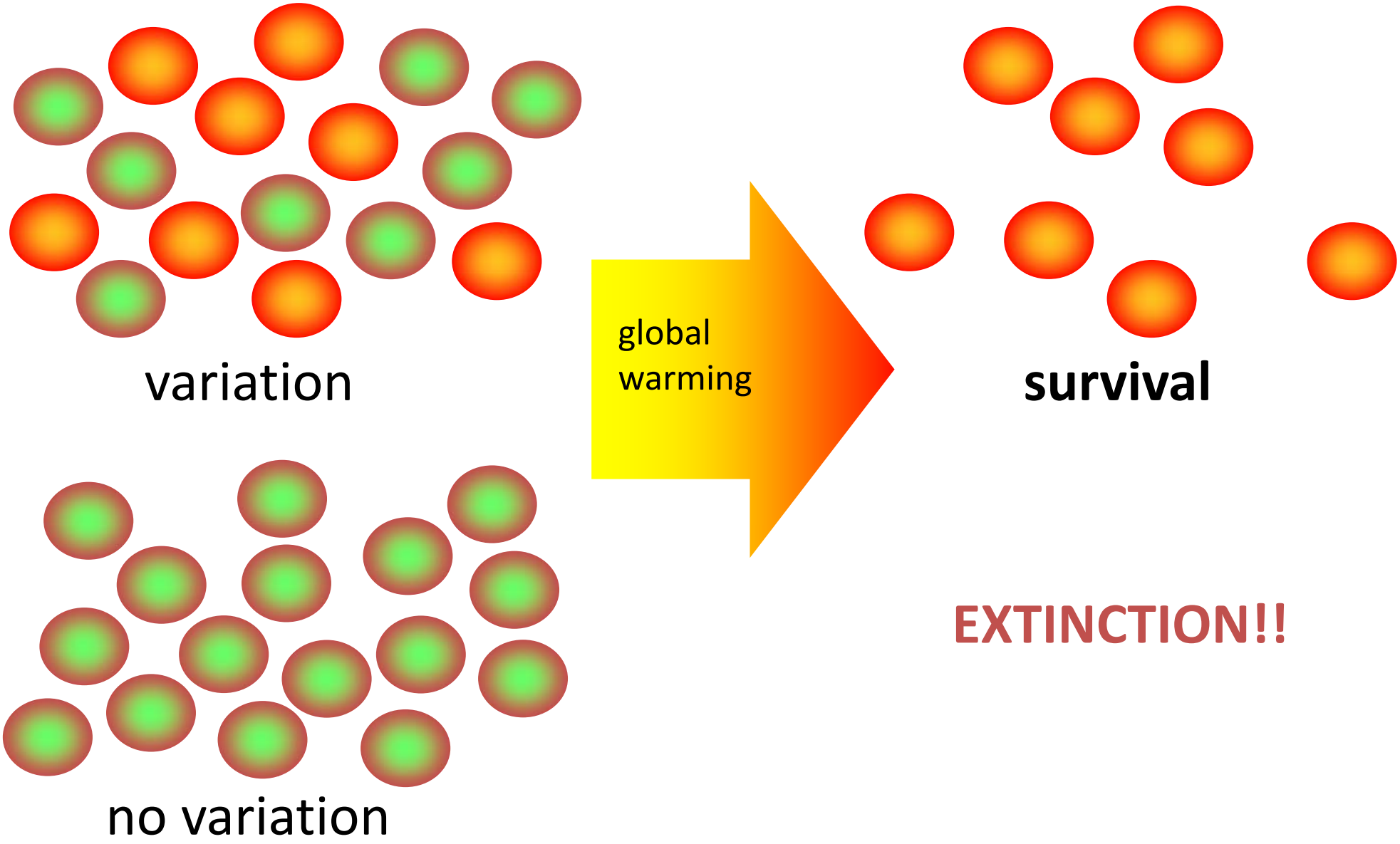
Why is genetic variation important?

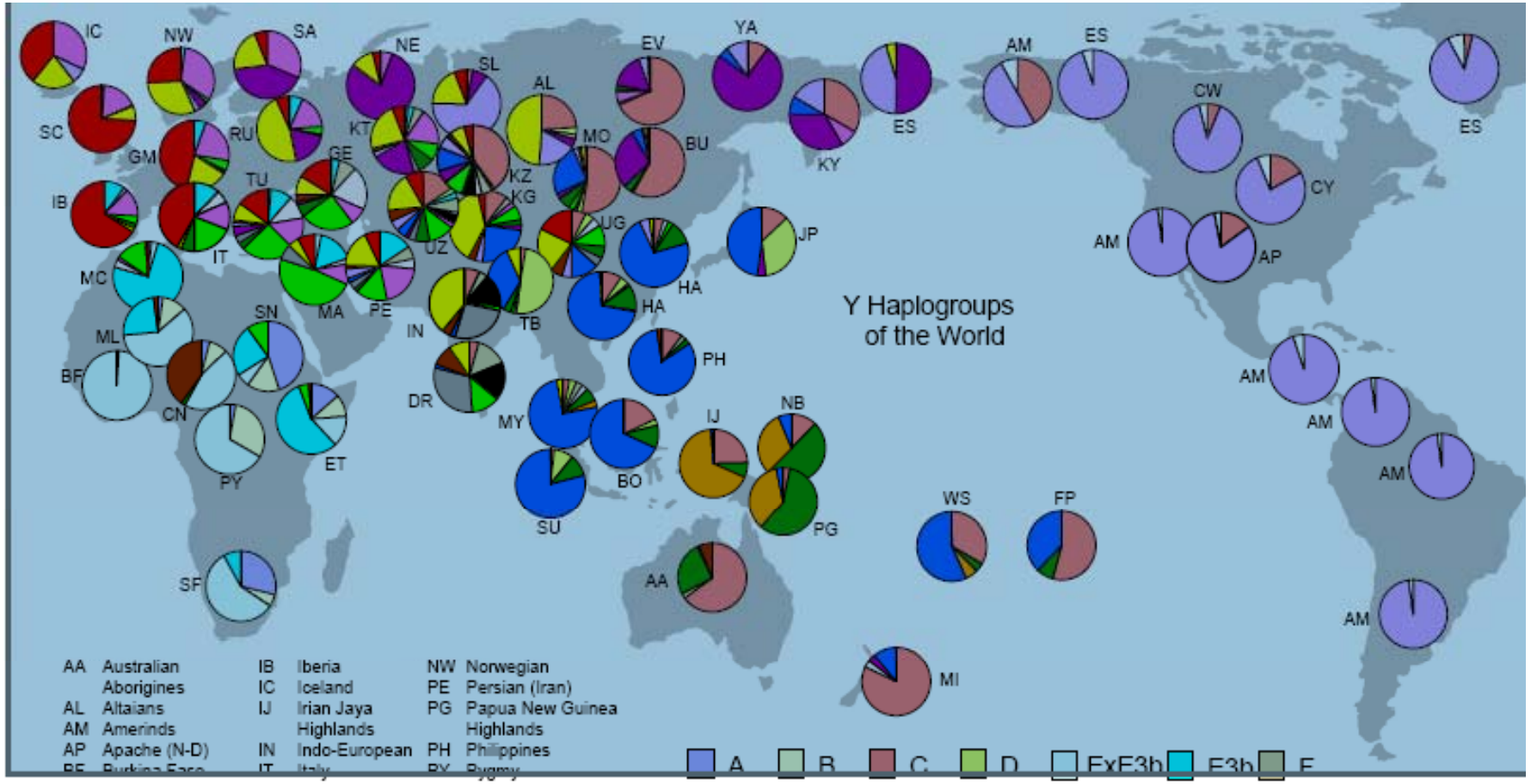


Natural selection can cause populations to diverge



Why is genetic variation important?

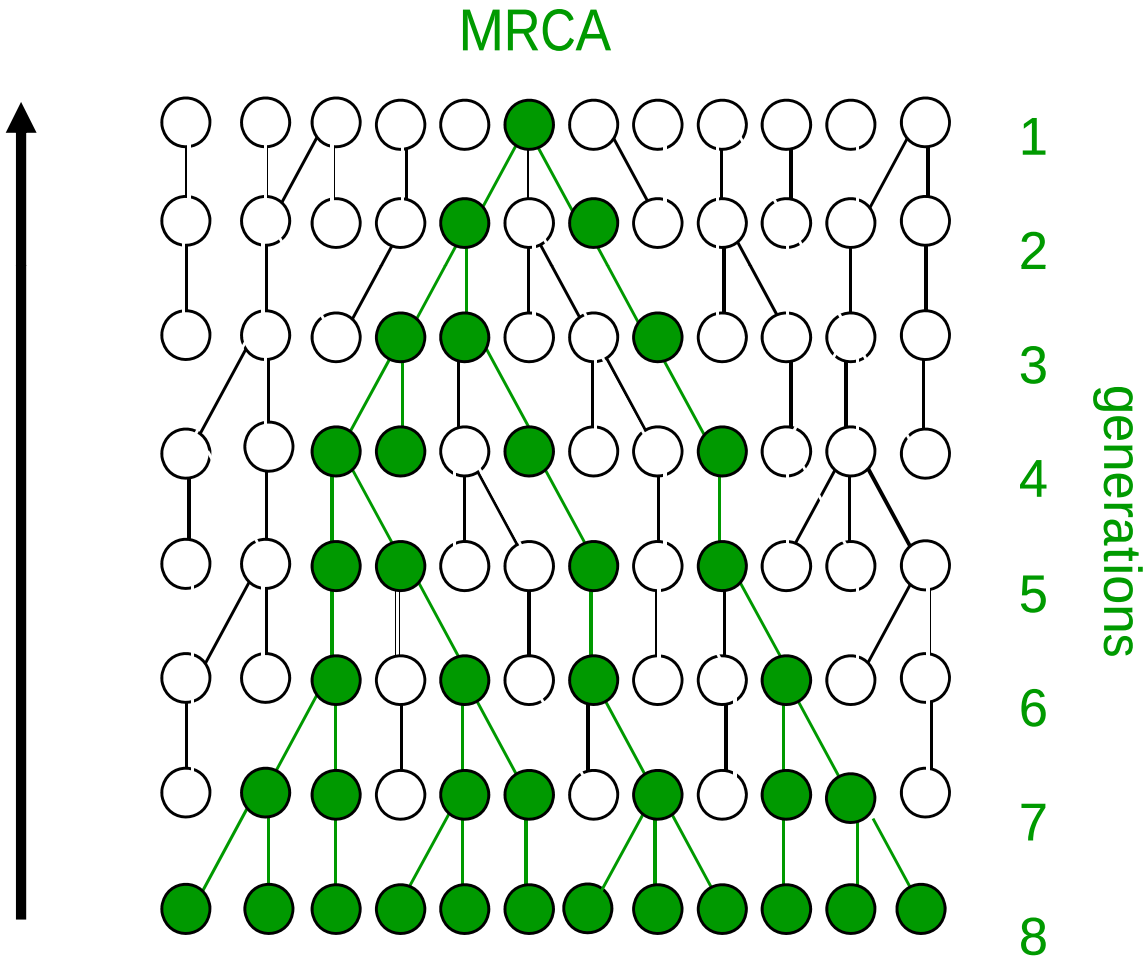


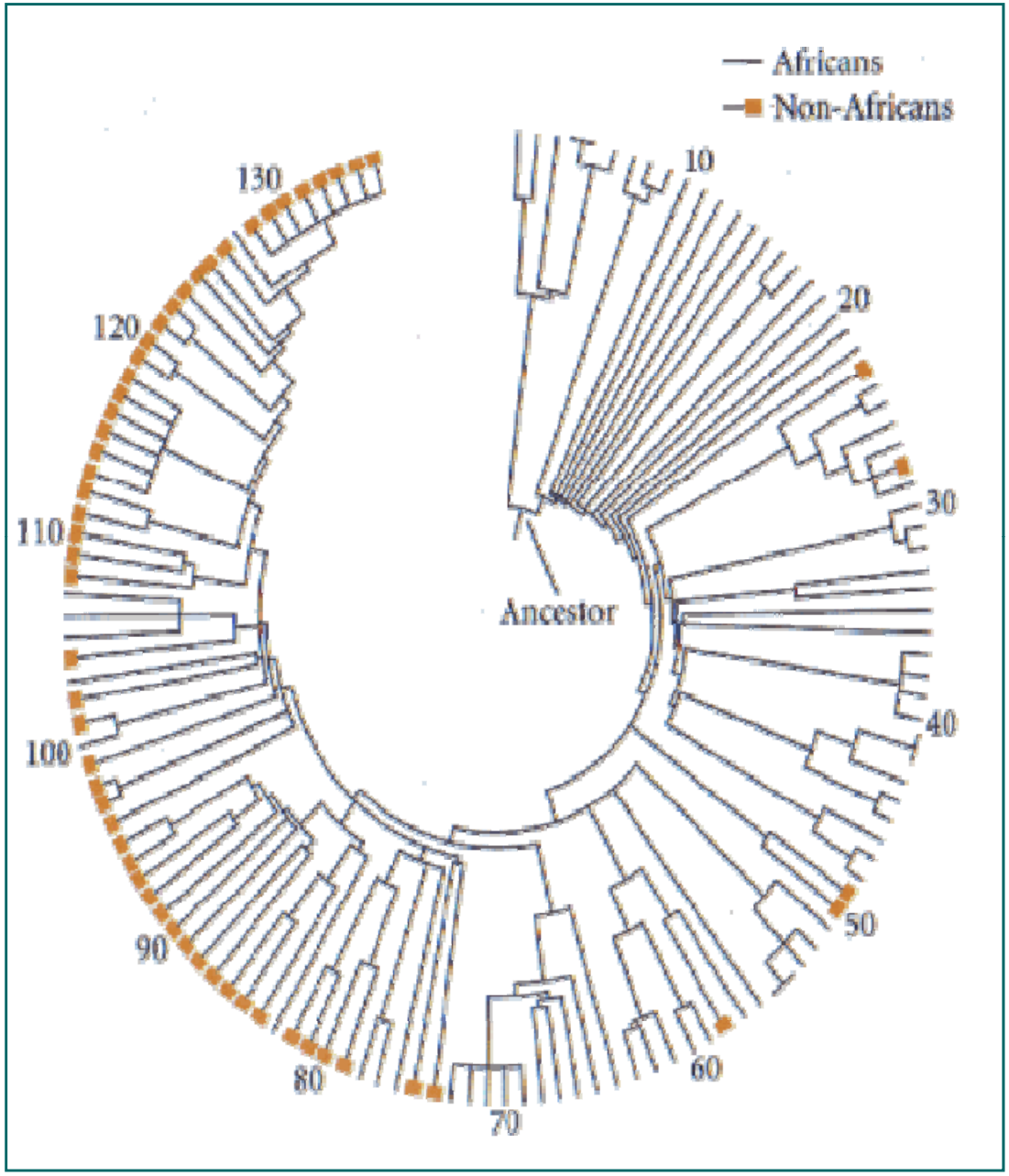


AA	Australian Aborigines	IB	Iberia	NW	Norwegian
AL	Altaians	IC	Iceland	PE	Persian (Iran)
AM	Amerinds	IJ	Irian Jaya Highlands	PG	Papua New Guinea Highlands
AP	Apache (N-D)	IN	Indo-European	PH	Philippines
BF	Burkina Faso	IT	Italy	PY	Pygmy
BO	Borneo	JP	Japan	RU	Russia
BU	Buryats	KG	Kyrgyzstan	SA	Saami
CN	Cameroon	KT	Kazan Tatar	SC	Scotland
CW	Chippeway (N-D)	KY	Koryaks	SL	Selkups
CY	Cheyenne	KZ	Kazakhstan	SF	South Africa
DR	Dravidian	MA	Mideast Arabs	SN	Sudan
ES	Eskimos	MC	Morocco	SU	Sumatra
ET	Ethiopia	MI	Maori	TB	Tibet
EV	Evenks	ML	Mali	TU	Turkish
FP	French Polynesia	MO	Mongols	UG	Uygurs
GE	Georgia-Armenia	MY	Malaysia	UZ	Uzbek
GM	Germany	NB	New Britain	WS	Western Samoa
HA	Han Chinese	NE	Nenets	YA	Yakuts

The data in this map is supposed to represent the situation before the recent European expansion beginning about 1500 AD. In some cases such as some Native American tribes and the Maori this can be done reliably because STR typing was done. In other cases, especially in America, it is guesswork. The "Other" sectors in America indicate this. Native American groups are labeled by language group as Amerind, Na-Dene (N-D), and Eskimo. F, K, L, and P are in some cases "catchall" groups because some researchers did not use enough markers for a full haplotype determination.

Y Adam and mtDNA Eve

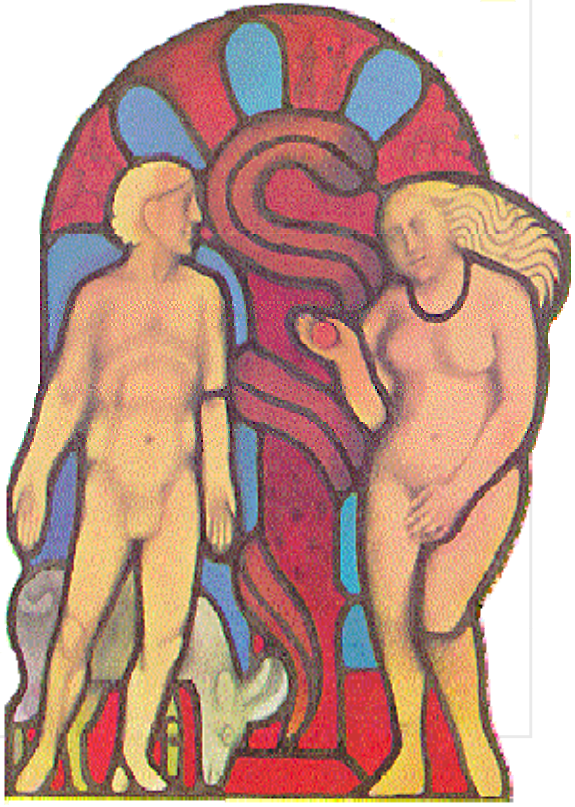




Allan Wilson, Mark Stoneking y Rebecca Cann de la Universidad de California (Can *y cols.*, 1.987) publican en *Nature* la hipótesis popularizada posteriormente como la "*Eva mitocondrial*".

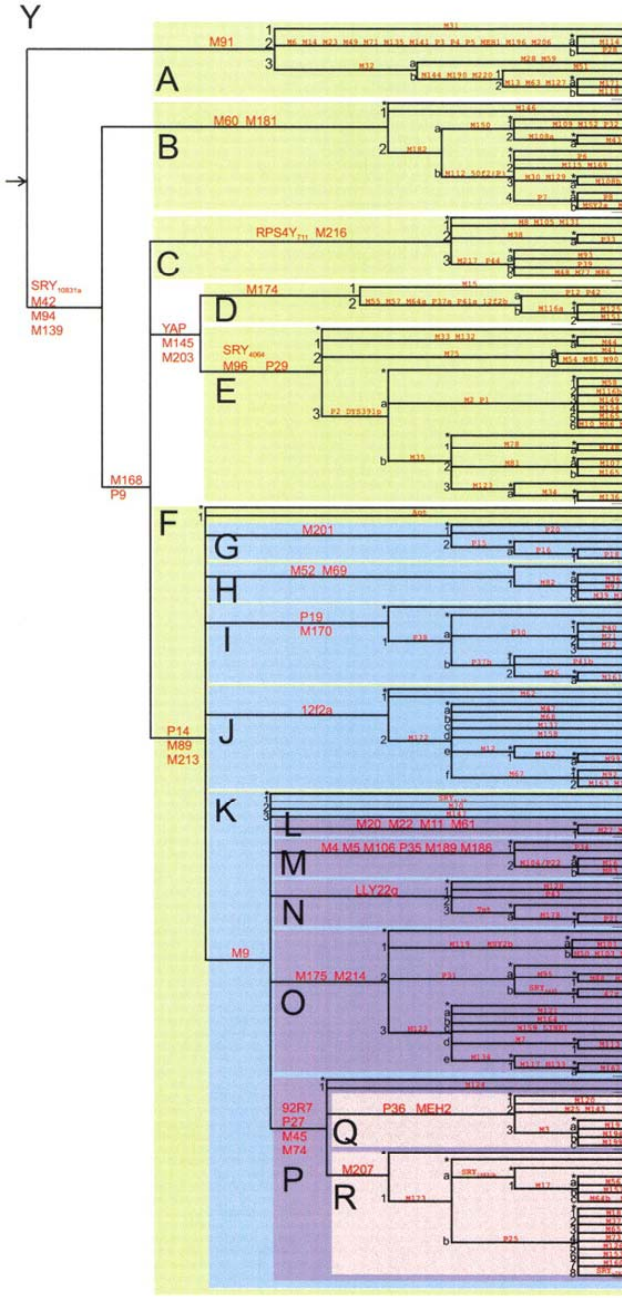
GRADO DE DIVERSIDAD GÉNICA

RECONSTRUCCIÓN GENEALÓGICA: RAÍZ EN EL CONTINENTE AFRICANO

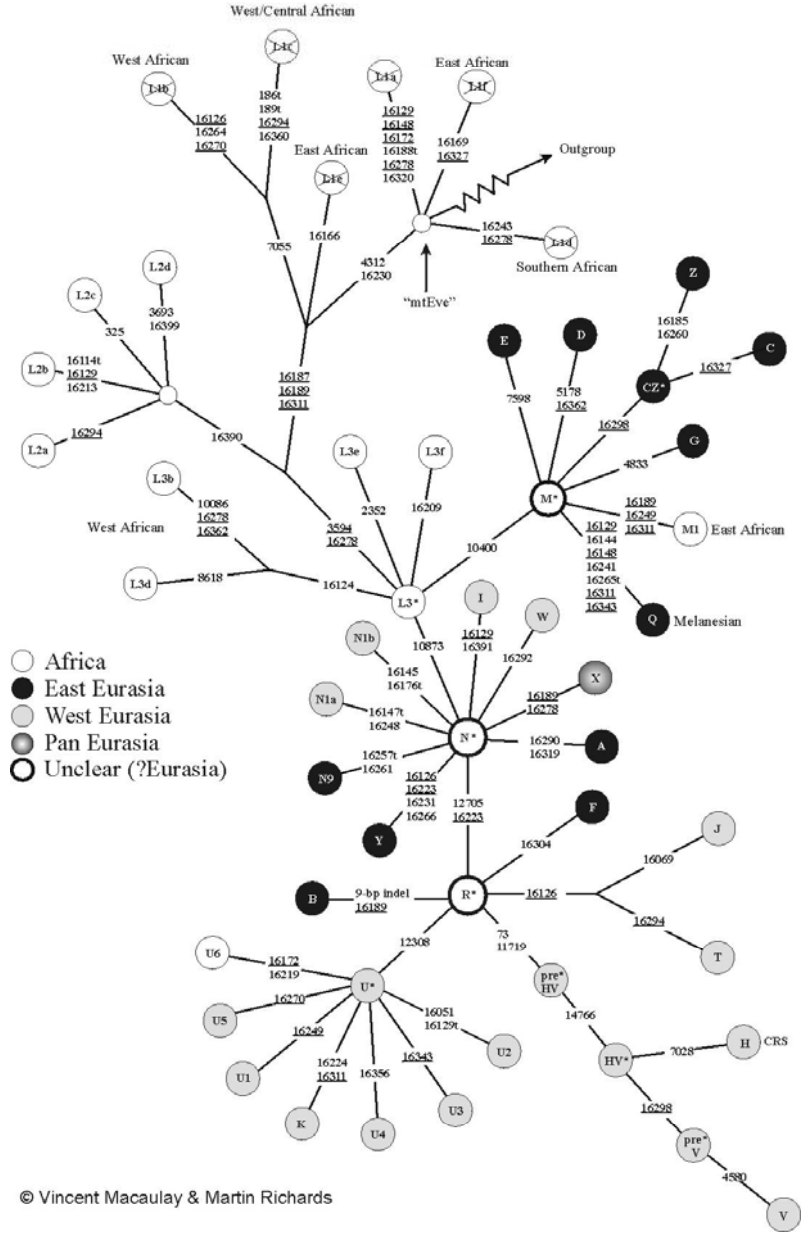


Uniparental markers: Y-chromosome and mtDNA

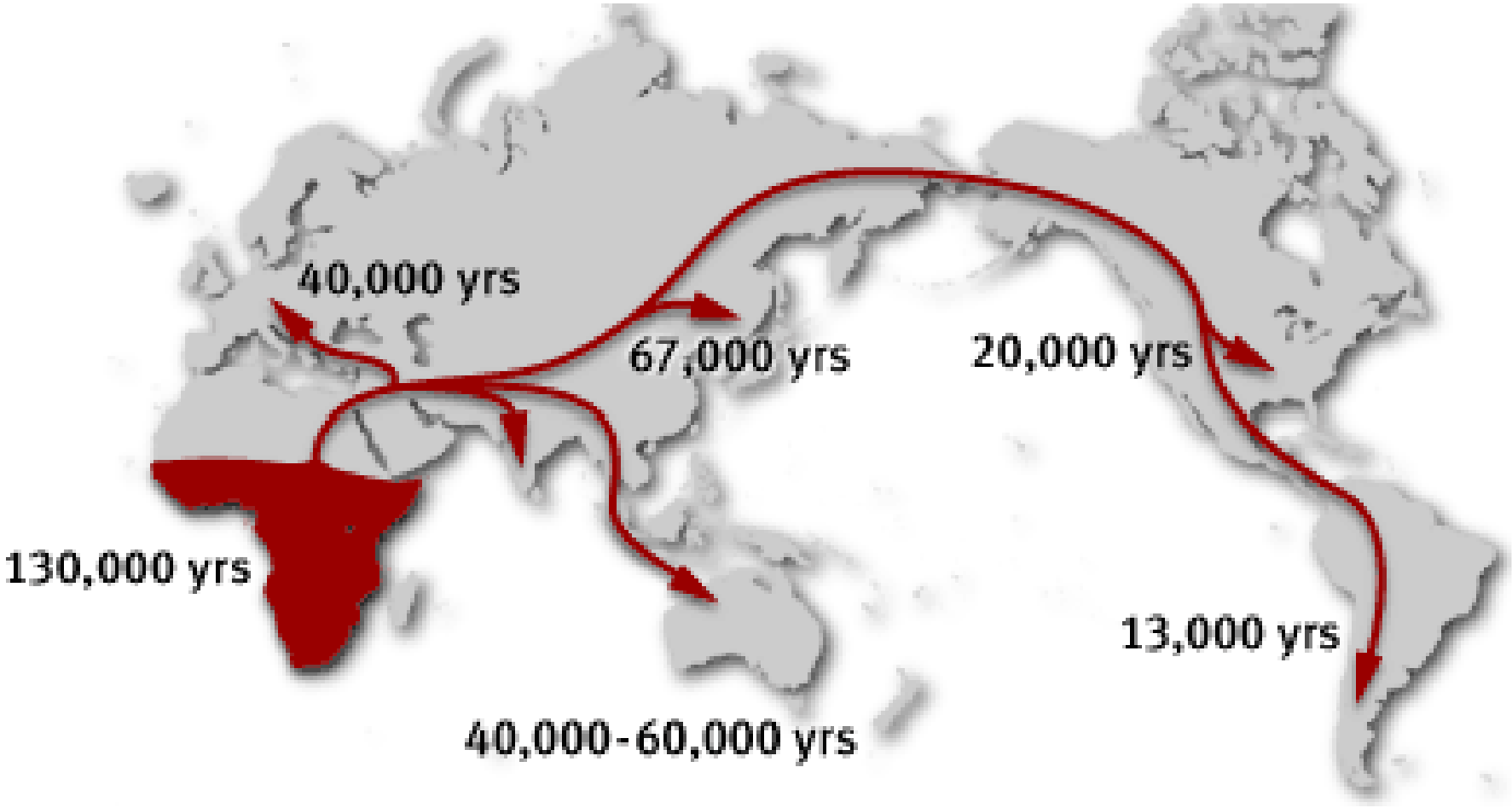
Y-chromosome phylogeny



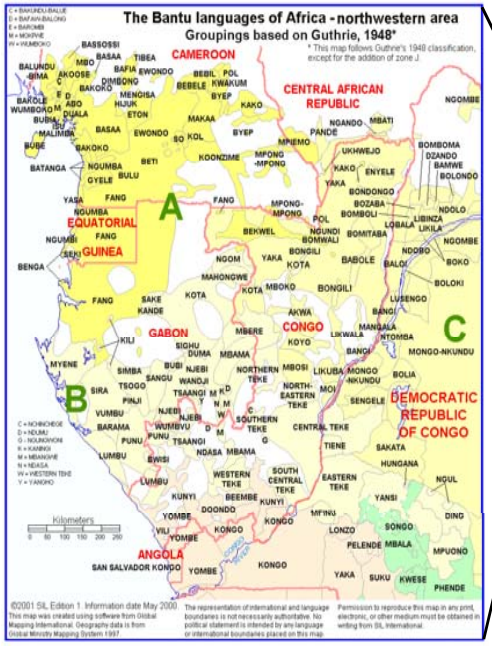
mtDNA phylogeny

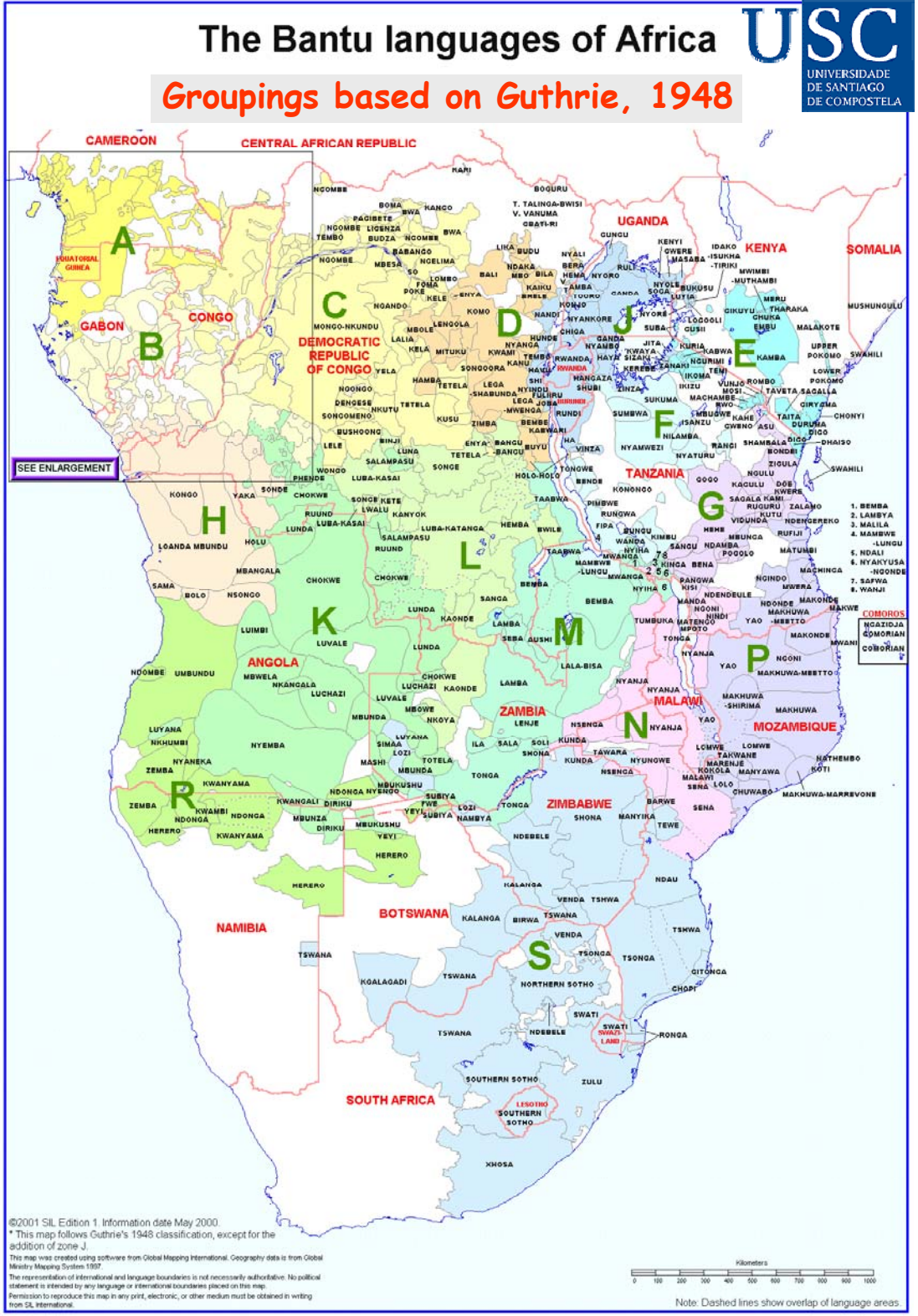


“Out of Africa”




Niger-Kordofanian
Nilo-Saharan
Afro-Asiatic
Khoisan
Malayo-Polynesian





Africa is home to the world's largest language phylum, Niger-Congo, with 1,489 languages (the next largest being Austronesian)

750 million in Africa-400 million Africans speak Niger-Congo, 240 million have a Bantu language

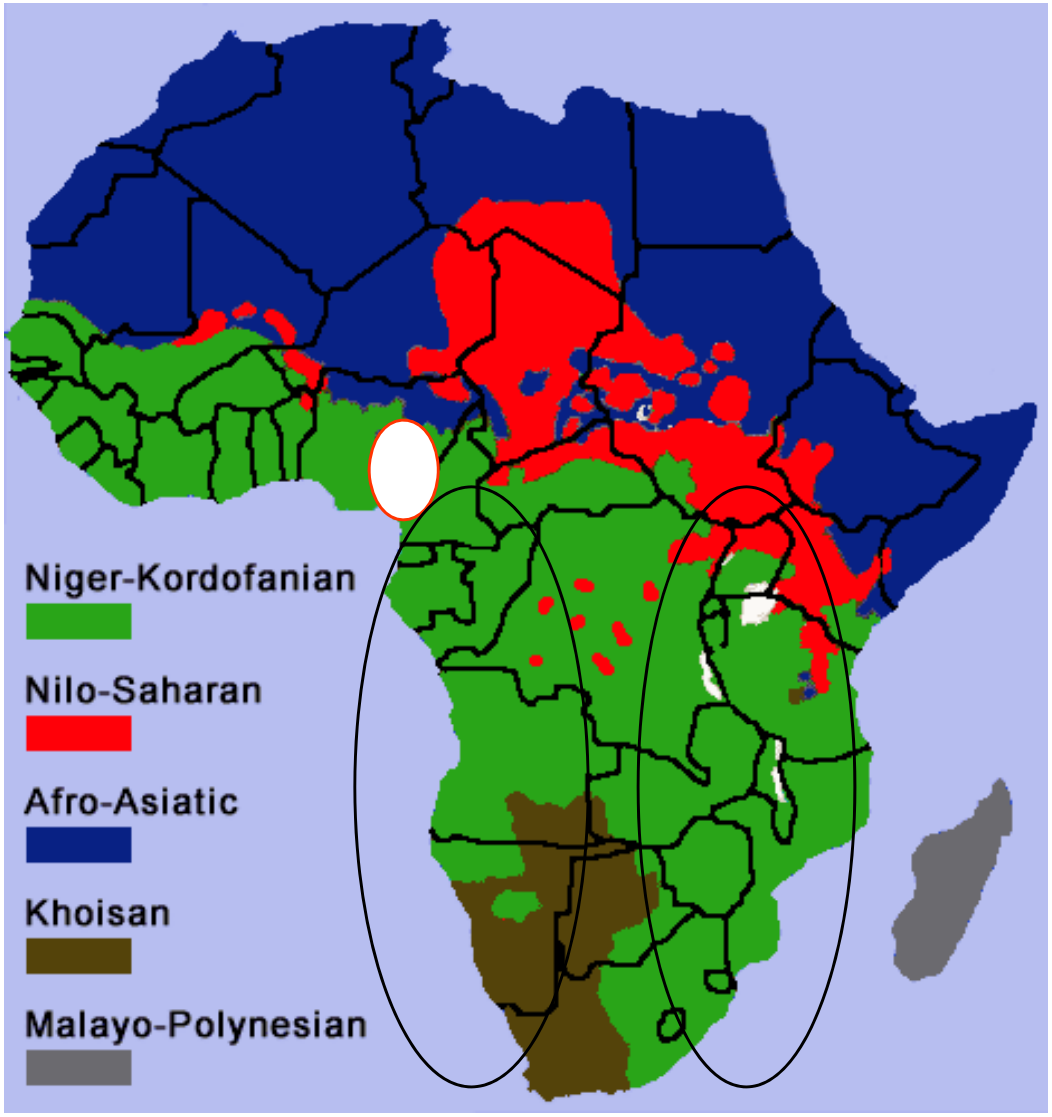
1/3 africans speak a bantu language as their native language

.- nearest neighbours of Bantu languages within Niger-Congo

.- the highest diversity within the Bantu family itself

are found in east Nigeria and west Cameroon

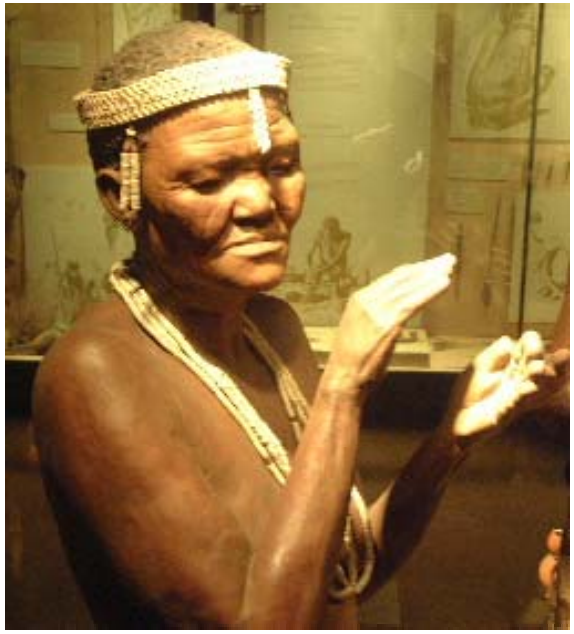
both suggest that this may have been the **'core' area of the Bantu dispersal**



Hypothesis supported by linguistic evidence Khoisan (languages isolates in E Africa)

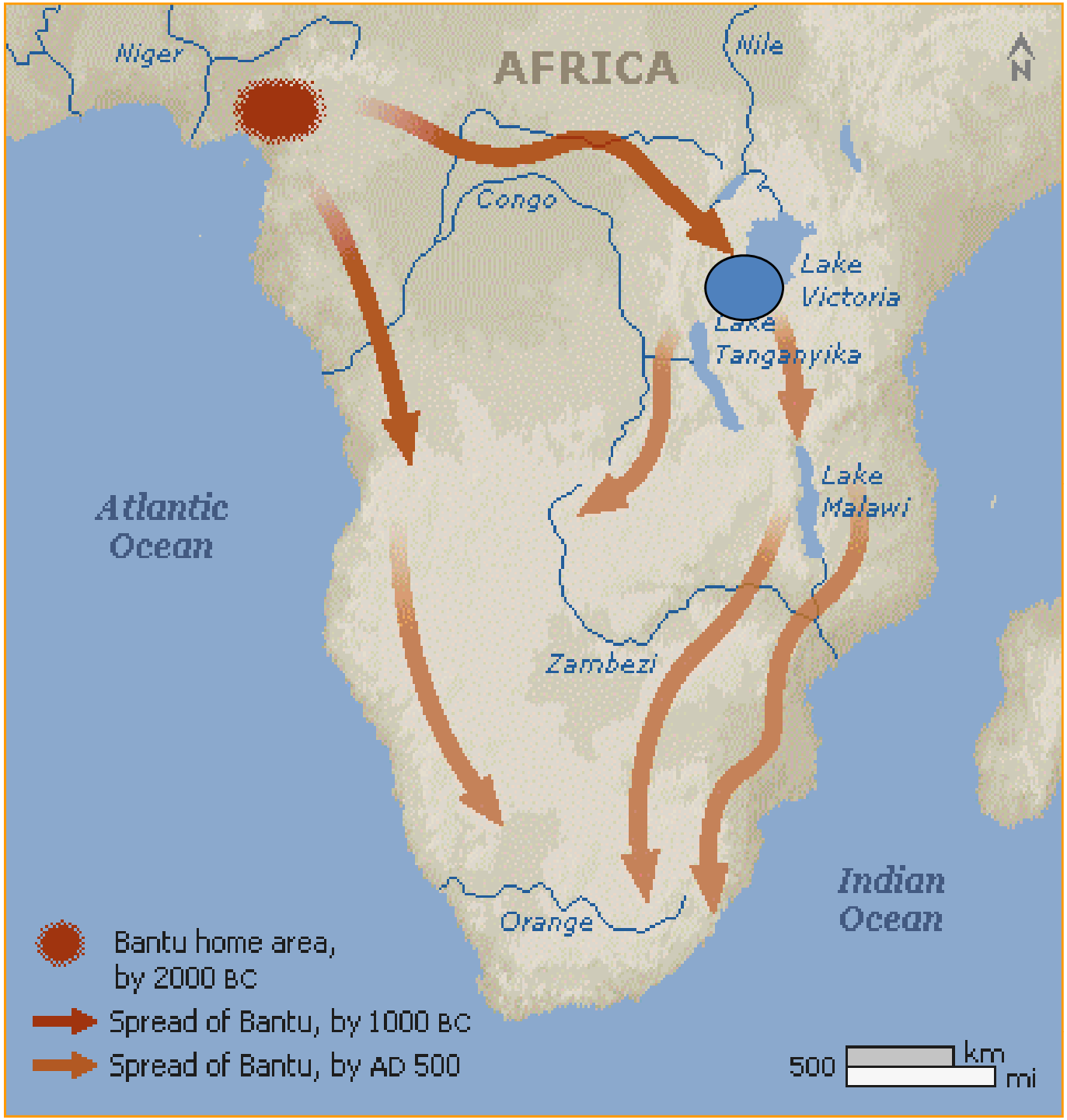
Bantu migration into South Africa began in the 3rd century AD with the occupation of the fertile eastern and coastal stretches of the country, where they came into contact with the Khoikhoi

The name Khokhoi means 'men of men'. They spread out across Southern Africa, and migrating south 2,000 years ago brought pastoralism (animal herding)



The San lived by hunting and gathering in small nomadic 'bands' (pushed to the desert areas by Khoikhoi pushed down by bantu expansion)

Clicks in Bantu Ls ⇐ *Khoisan Ls*



Bantu farmers adopted invented a type of grain that grows in winter as opposite to the Mediterrenean type of agriculture.

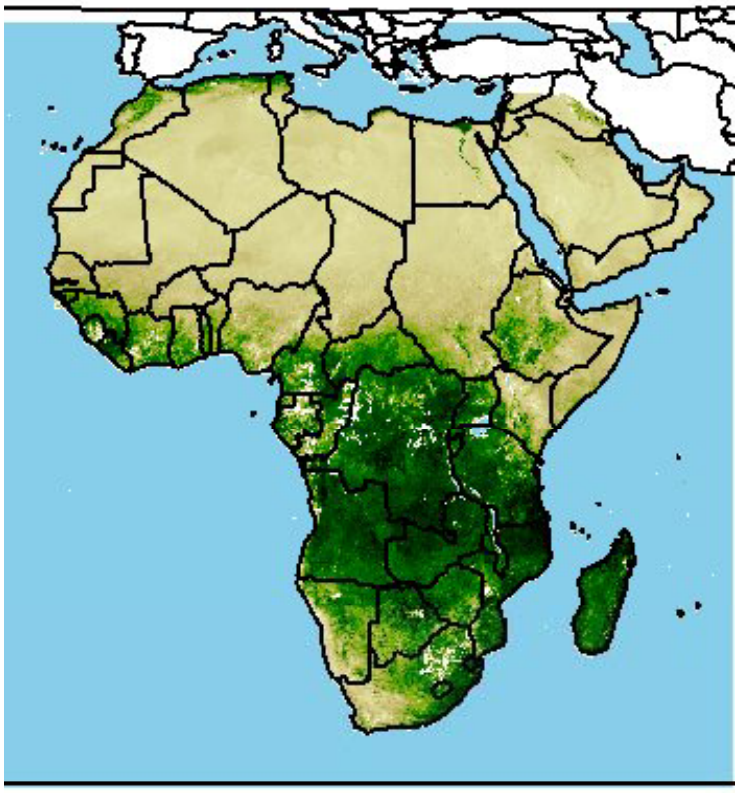
Later on they developped new technologies which would give them clear advantages during the expansion:

.- iron making

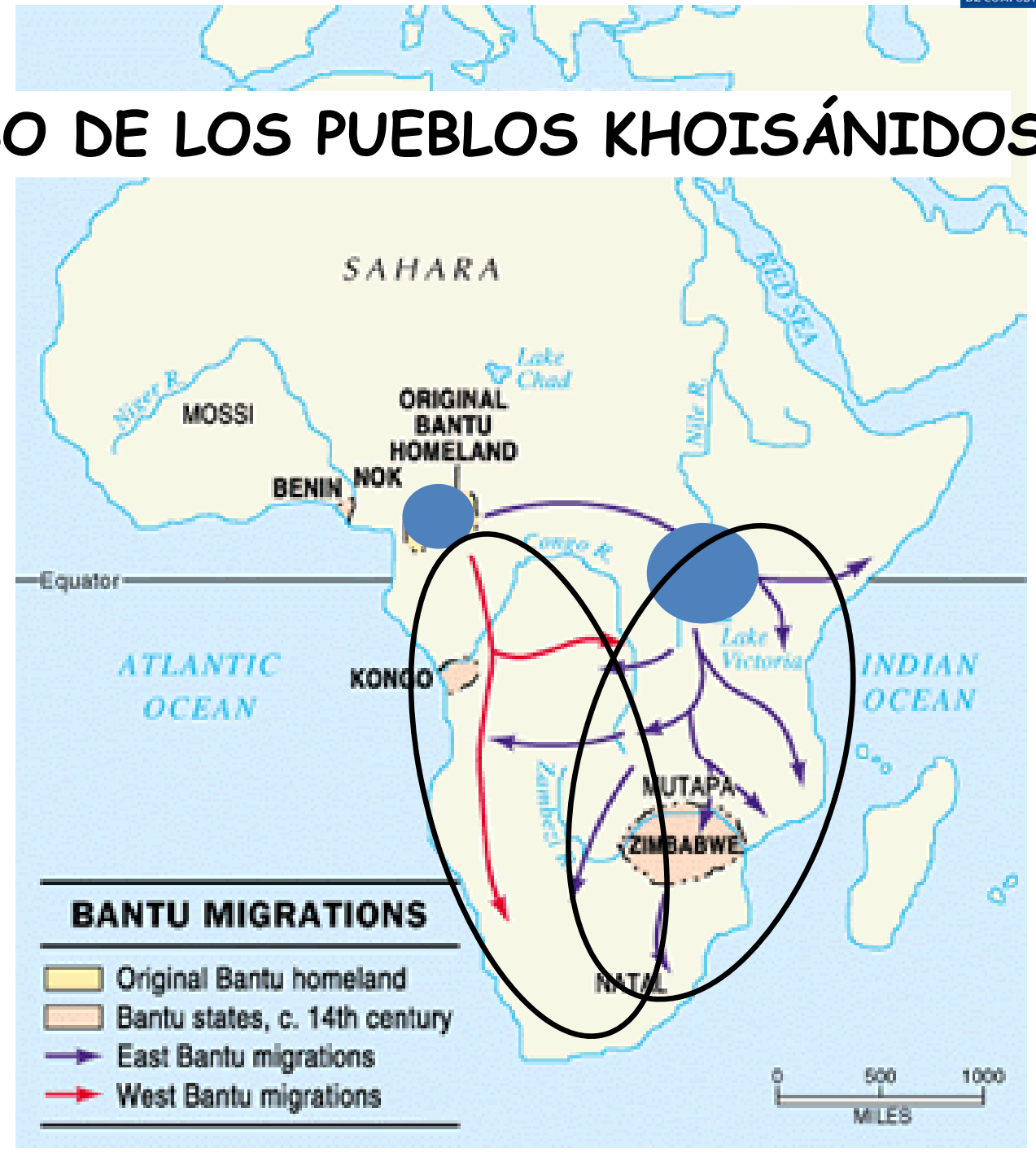
.- growing of domesticated bananas and plantains (north-eastern corner of equatorial rain forest)

BANTU EXPANSION

RETROCESO DE LOS PUEBLOS KHOISÁNIDOS



Bantu migrations are believed to be one of the largest in the history



BANTU DISPERSAL-S
Can genetics help?

Is this a true story?

Proto-Bantu origins

Dispersals themselves

Numbers of people involved in the process

What happen to the populations leaving in the area?

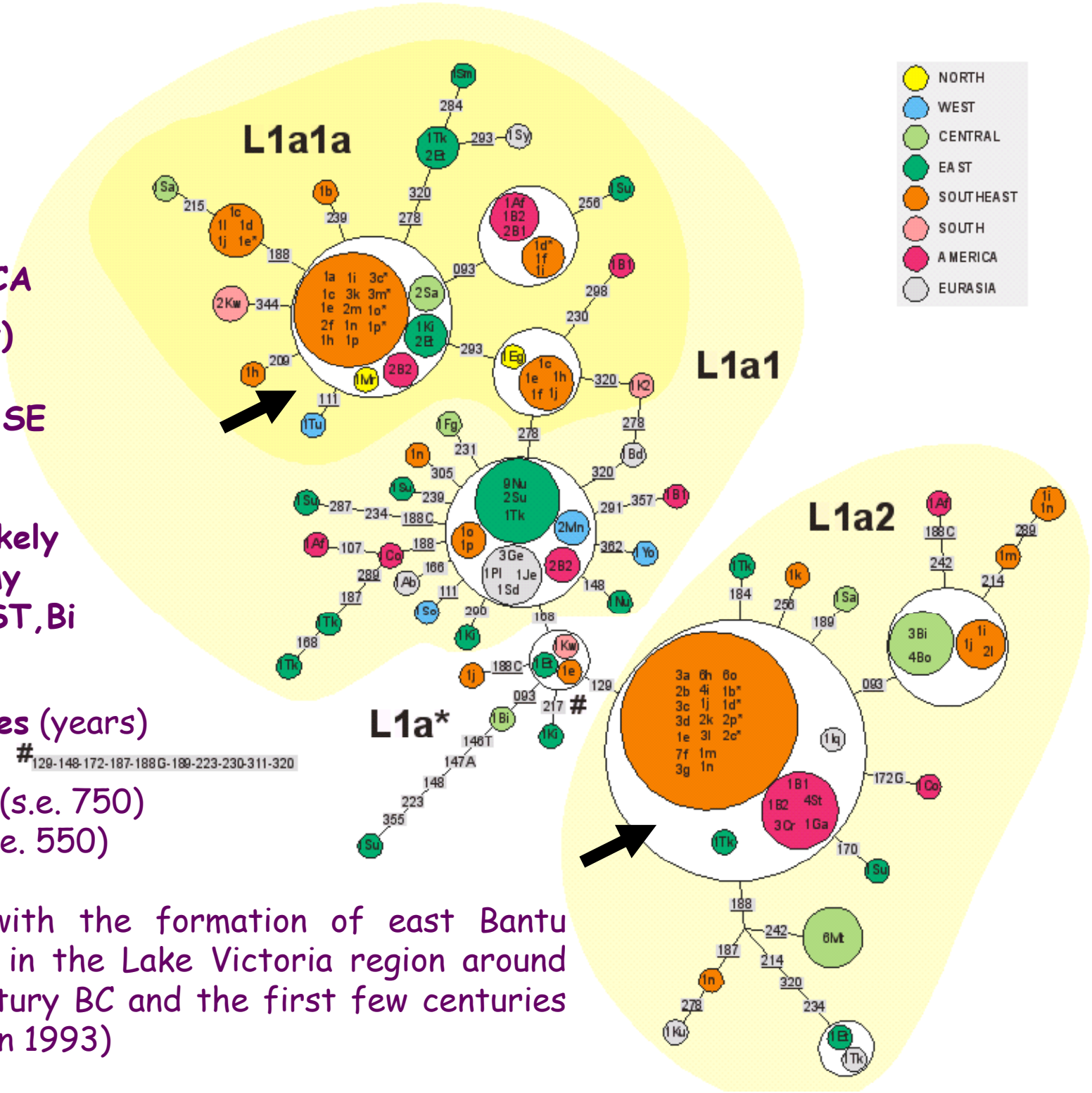
L1
Includes MRCA
(~ 150,000y)
L1a
20-25% E,C,SE
2% W
<1% N, S
East origin likely
Freq. in pigmy
Presence in ST,Bi
E-CE-SE

Founder types (years)

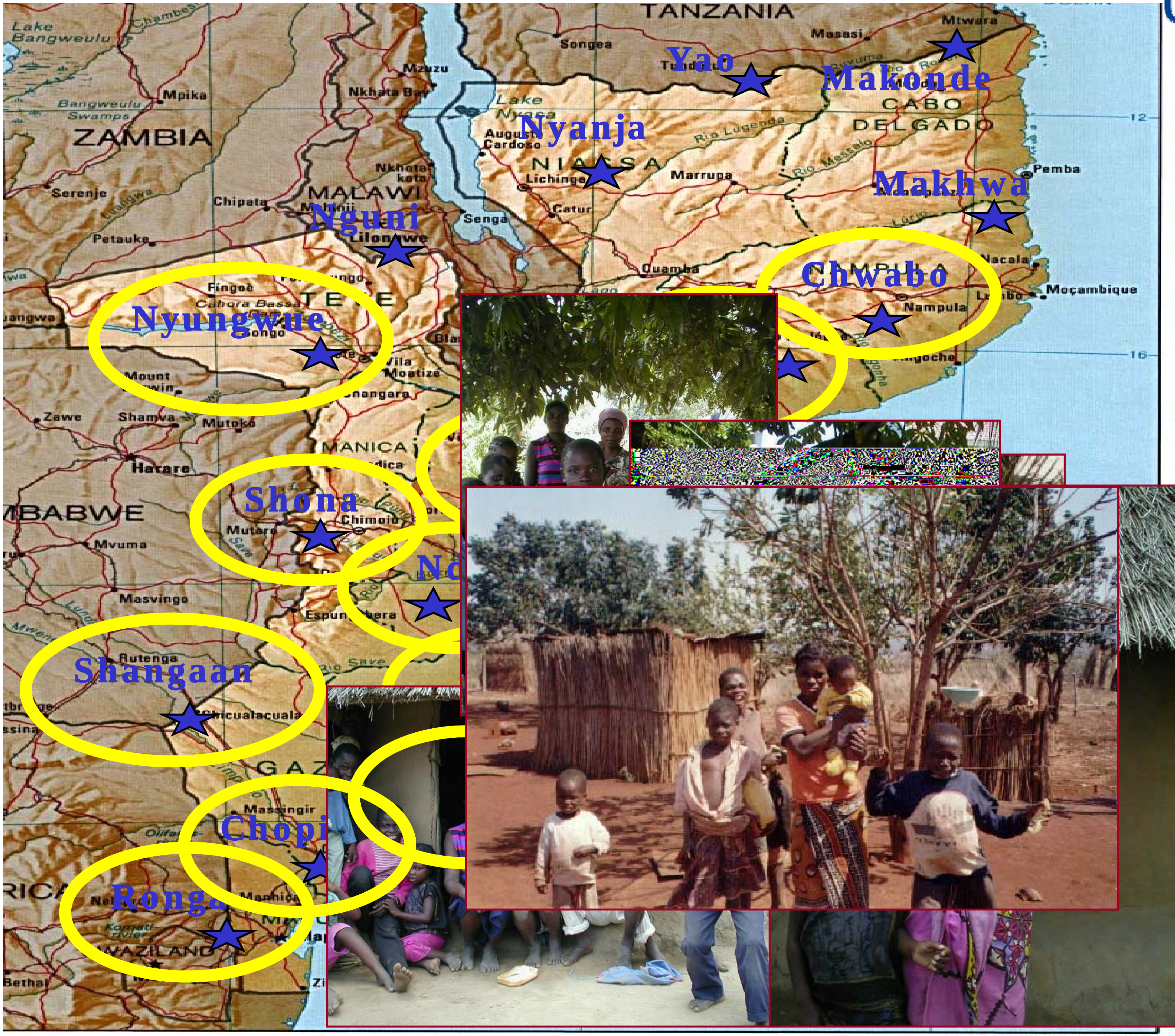
#129-148-172-187-188G-189-223-230-311-320

L1a1a: 1,900 (s.e. 750)
L1a2: 800 (s.e. 550)

Consistent with the formation of east Bantu communities in the Lake Victoria region around the last century BC and the first few centuries AD (Phillipson 1993)



USC
UNIVERSIDADE
DE SANTIAGO
DE COMPOSTELA



Base 802419 (A05253) 12-95

mtDNA and Bantu dispersals

Two different components

Ancestral types carried by the people living in the region before the arrival of Bantu speakers

(Khoisan lineages, L1d) 6% of the total lineages in the Bantu speakers:

.- assimilation on arrival

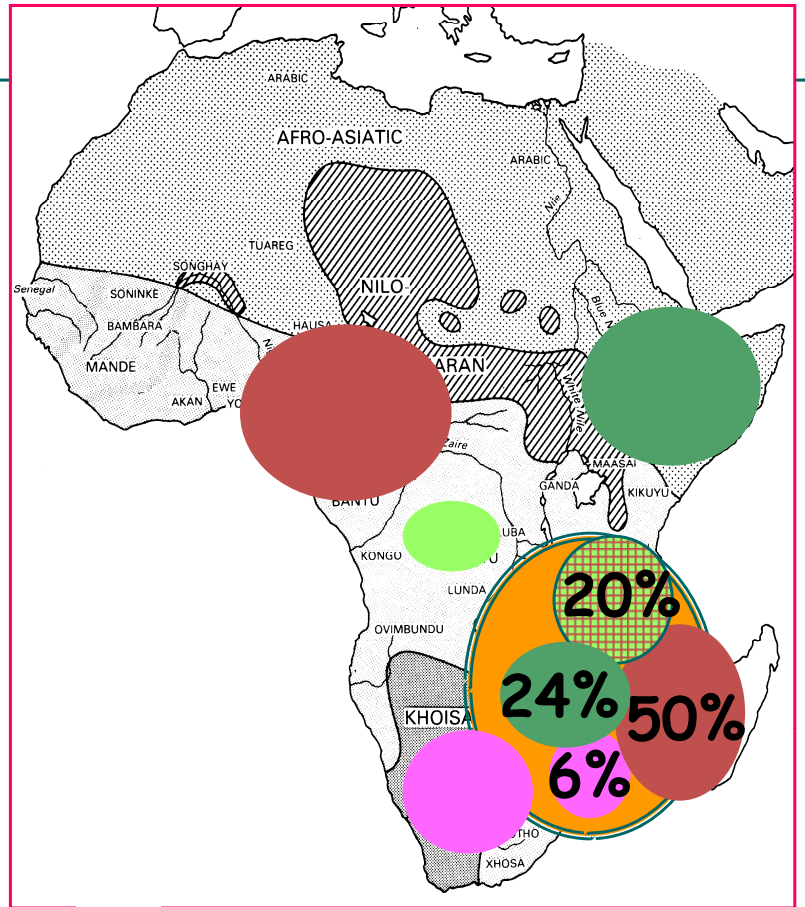
.- subsequent gene flow (there are not strong founder effects)

Types brought with the Bantu speakers themselves

.- 2/4 west Africa (4.000 y.a.)

.- 1/4 east Africa (2.000 y.a.)

.- 1/5 central or west central Africa



Bantu expansion

Khoisan contribution is higher in female component

6% mtDNA lineages

0,3% Y chr lineages

Higher drift on the male than on the female line during the Bantu dispersals

Higher levels of assimilation on the female side

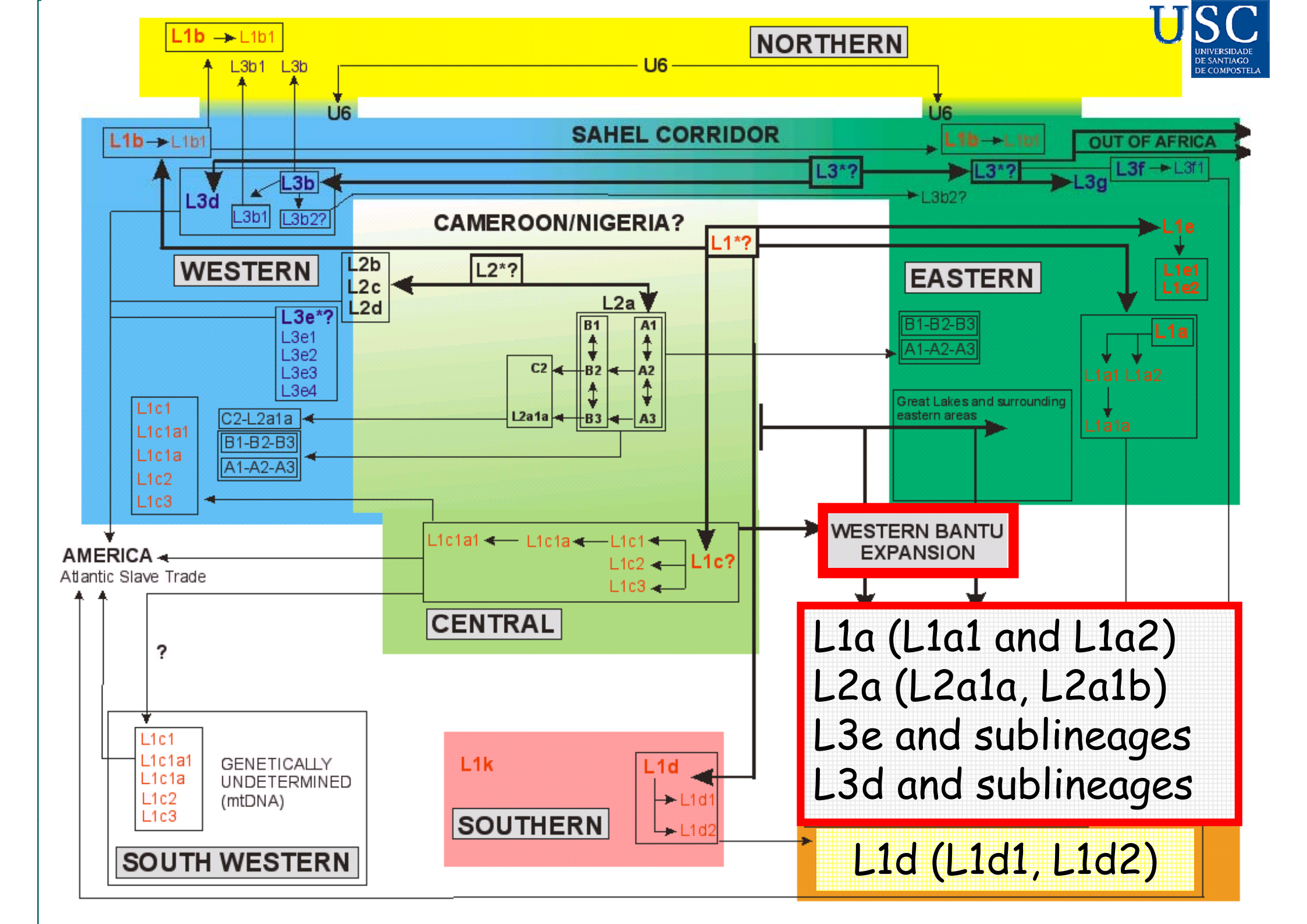
Larger female efective population size in the dispersing groups

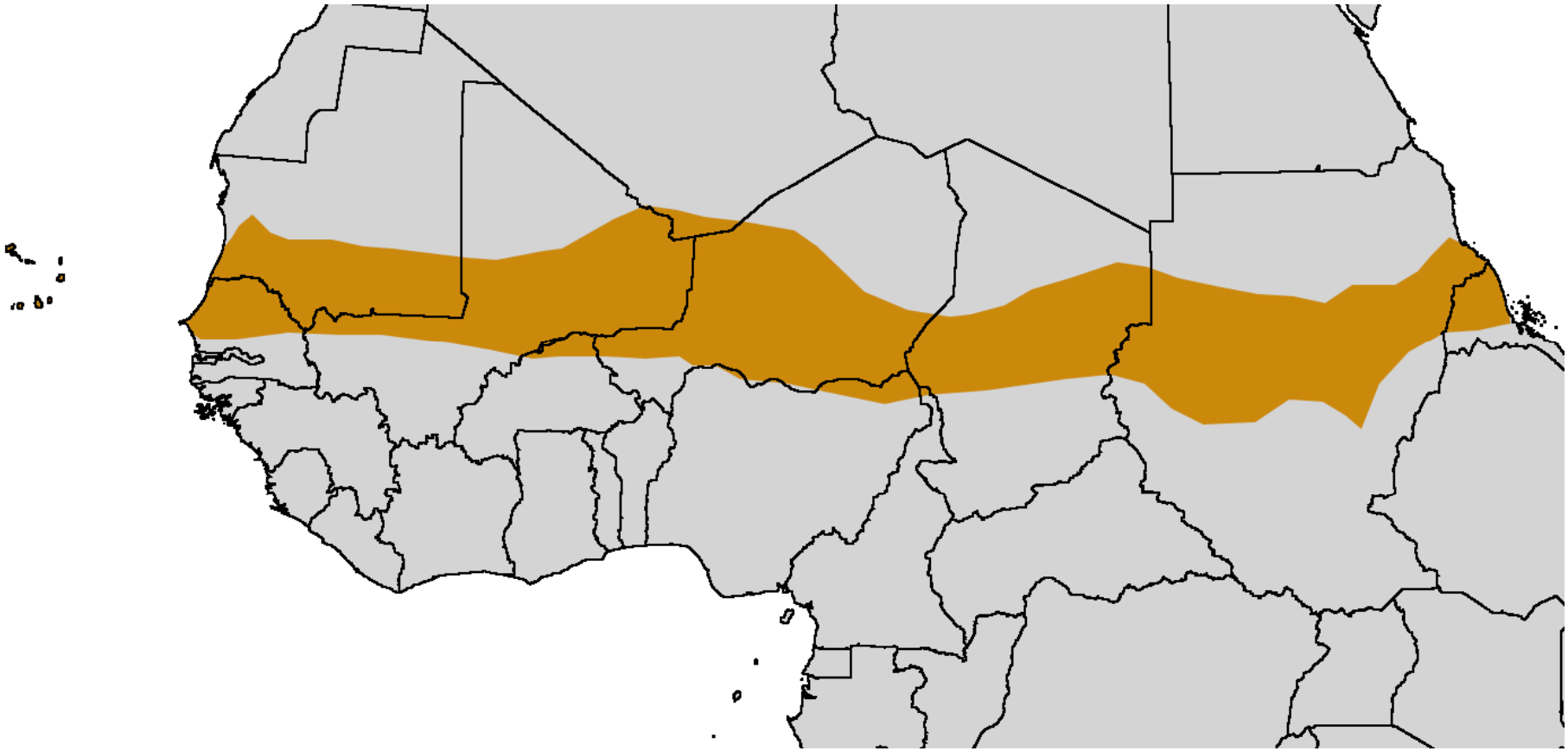
Lack of Khoisan lineages in Angola, point to a basically Bantu substrate of the extant Angolan gene pool.

Thus, the Bantu expansion was clearly more demic (in the sense of population replacement) in the southwest than in the southeast, where remanents of ancient settlers (related to extant Khoisan) are evident

Insights into the western Bantu dispersal: mtDNA lineage analysis in Angola.

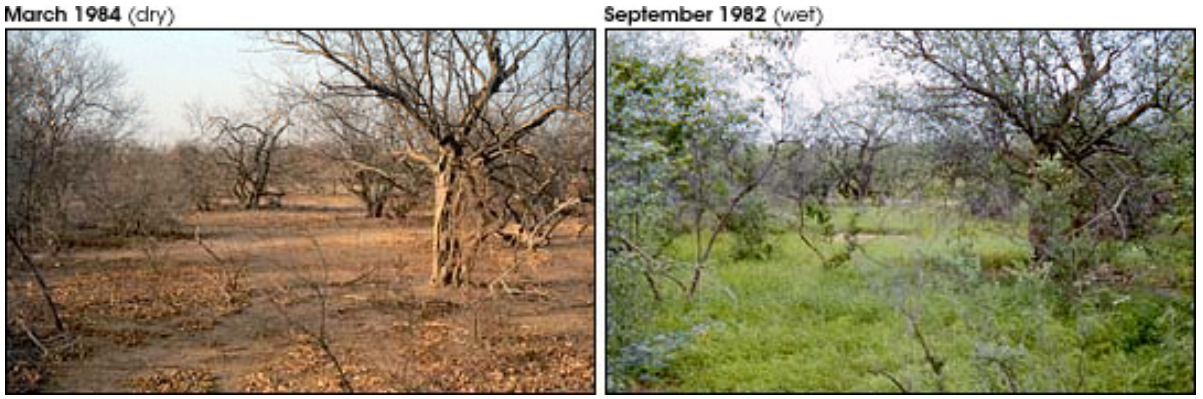
Plaza S, Salas A et al.. Hum Genet. 2004 Oct;115(5):439-47


L1b → L1b1
NORTHERN
L3b1
L3b
U6
U6
U6
SAHEL CORRIDOR
L1b → L1b1
L1b → L1b1
OUT OF AFRICA
L3d
L3b
L3b1
L3b2?
L3*?
L3*?
L3g
L3f → L3f1
L3b2?
CAMEROON/NIGERIA?
L1*?
L1e
WESTERN
L2b
L2c
L2d
L2*?
L2a
EASTERN
L1e1
L1e2
L3e*?
L3e1
L3e2
L3e3
L3e4
B1
A1
B1-B2-B3
A1-A2-A3
L1a
C2
B2
A2
L1a1 L1a2
L1a1a
L2a1a
B3
A3
Great Lakes and surrounding eastern areas
L1c1
L1c1a1
L1c1a
L1c2
L1c3
C2-L2a1a
B1-B2-B3
A1-A2-A3
WESTERN BANTU EXPANSION
AMERICA
Atlantic Slave Trade
L1c1a1
L1c1a
L1c1
L1c2
L1c3
L1c?
CENTRAL
?
L1a (L1a1 and L1a2)
L2a (L2a1a, L2a1b)
L3e and sublineages
L3d and sublineages
L1c1
L1c1a1
L1c1a
L1c2
L1c3
GENETICALLY UNDETERMINED (mtDNA)
SOUTH WESTERN
L1k
L1d
L1d1
L1d2
SOUTHERN
L1d (L1d1, L1d2)

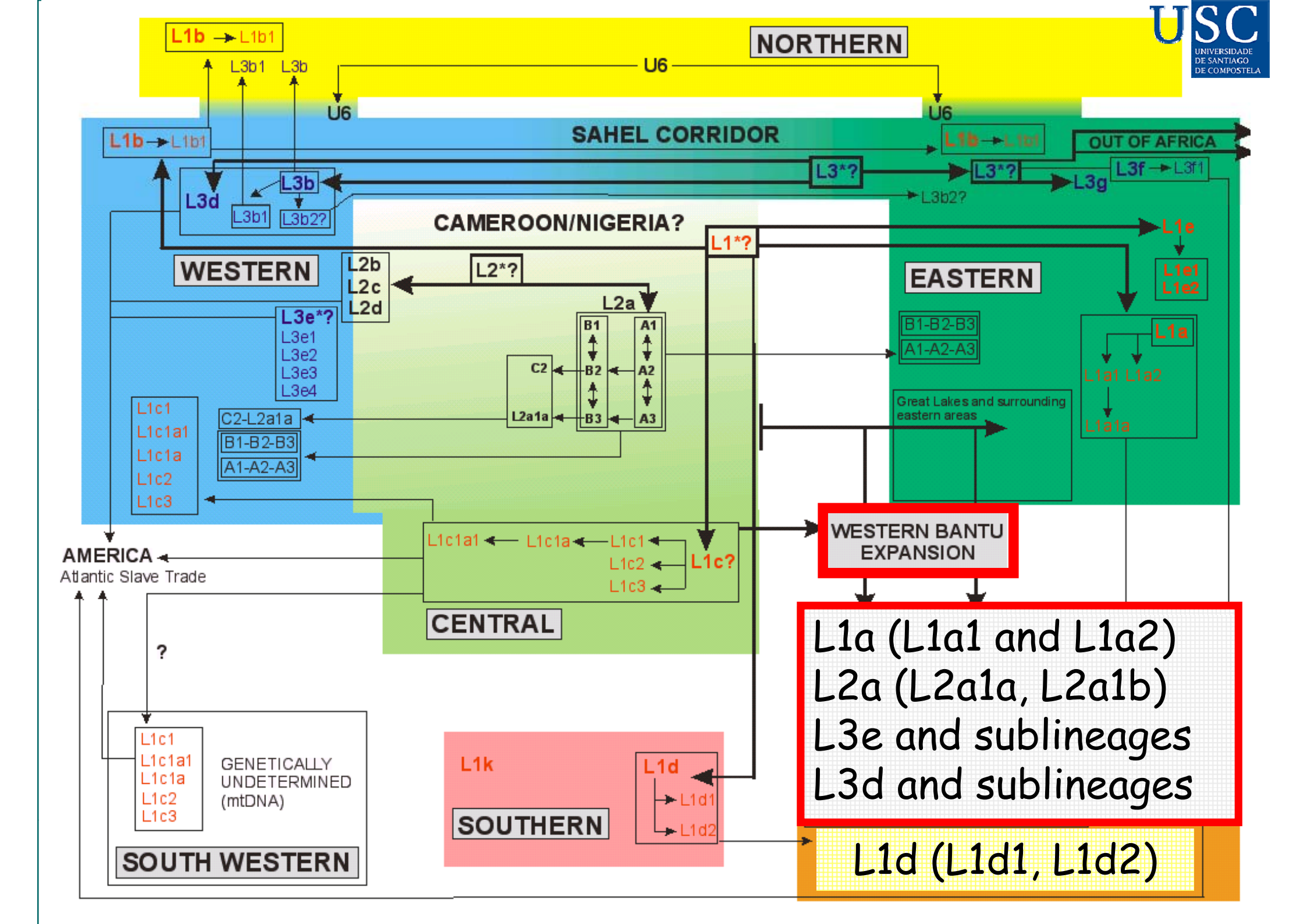


The Sahel runs 2,400 miles (3862 km) from the Atlantic Ocean in the west to the Red Sea in the east, in a belt that varies from several hundred to a thousand kilometers (620 miles) in width, covering an area of 3,053,200 square kilometers (1,178,800 square miles). It is a transitional ecoregion of semi-arid grasslands, savannas, and thorn shrublands lying between the wooded Sudanian savanna to the south and the Sahara to the north.[1] The countries of the Sahel today include Senegal, Mauritania, Mali, Burkina Faso, Niger, Nigeria, Chad, Sudan, and Eritrea.

Históricamente es la cuna de algunos los Grandes Imperios medievales africanos como el Imperio de Ghana y el Imperio de Malí, que se beneficiaron de la privilegiada posición de intermediarios en el comercio entre el área de Guinea y el norte de África. Cultivos de gramíneas y fibras, así como la ganadería y el comercio del oro y la sal son las economías tradicionales.
El límite norte del Sahel, siguiendo la isoyeta media de 150 mm de lluvia, en el período 1931 - 1960, que cruza el continente africano de este a oeste, se encuentra entre 50 y 100 km más al norte que la misma isoyeta en el período 1968 - 1997. Ciudades importantes en esta franja que ha quedado más seca: Nuakchott, en Mauritania; Agadez, en Níger; Jartum, en Sudán.



The first instances of domestication of plants for agricultural purposes in Africa occurred in the Sahel region circa 5000 BCE, when sorghum and African Rice *(Oryza glaberrima)* began to be cultivated. Around this time, and in the same region, the small Guineafowl were domesticated. Around 4000 BCE the climate of the Sahara and the Sahel started to become drier at an exceedingly fast pace. This climate change caused lakes and rivers to shrink rather significantly and caused increasing desertification. This, in turn, decreased the amount of land conducive to settlements and helped to cause migrations of farming communities to the more humid climate of West Africa.[4]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NORTHERN
L3b1
L3b
U6
U6
U6
SAHEL CORRIDOR
L1b → L1b1
L1b → L1b1
OUT OF AFRICA
L3d
L3b
L3b1
L3b2?
L3*?
L3*?
L3g
L3f → L3f1
L3b2?
CAMEROON/NIGERIA?
L1*?
L1e
WESTERN
L2b
L2c
L2d
L2*?
L2a
EASTERN
L1e1
L1e2
L3e*?
L3e1
L3e2
L3e3
L3e4
B1
A1
B1-B2-B3
A1-A2-A3
L1a
C2
B2
A2
L1a1 L1a2
L1a1a
L2a1a
B3
A3
Great Lakes and surrounding eastern areas
L1c1
L1c1a1
L1c1a
L1c2
L1c3
C2-L2a1a
B1-B2-B3
A1-A2-A3
WESTERN BANTU EXPANSION
AMERICA
Atlantic Slave Trade
L1c1a1
L1c1a
L1c1
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L3e and sublineages
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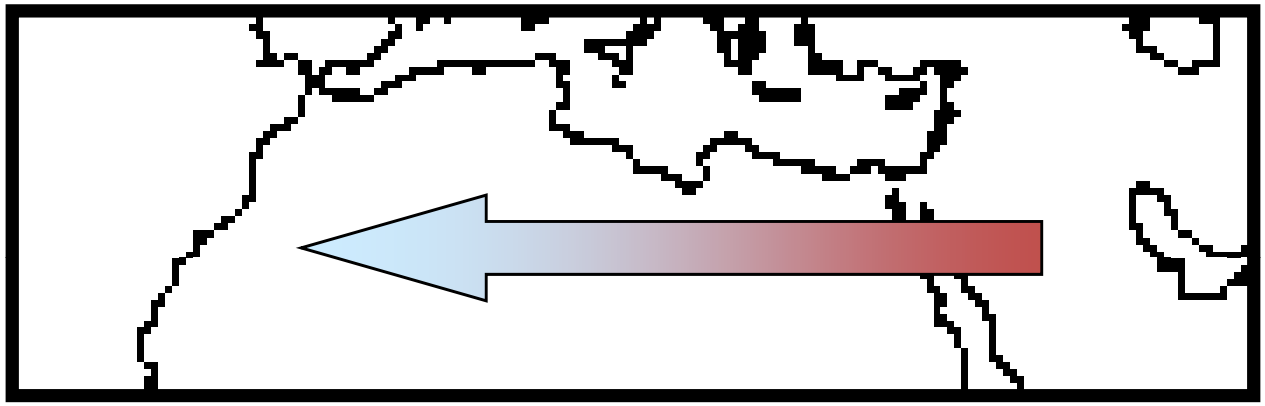
SOUTH WESTERN
L1k
L1d
L1d1
L1d2
SOUTHERN
L1d (L1d1, L1d2)

Western Mediterranean populations: Conclusions

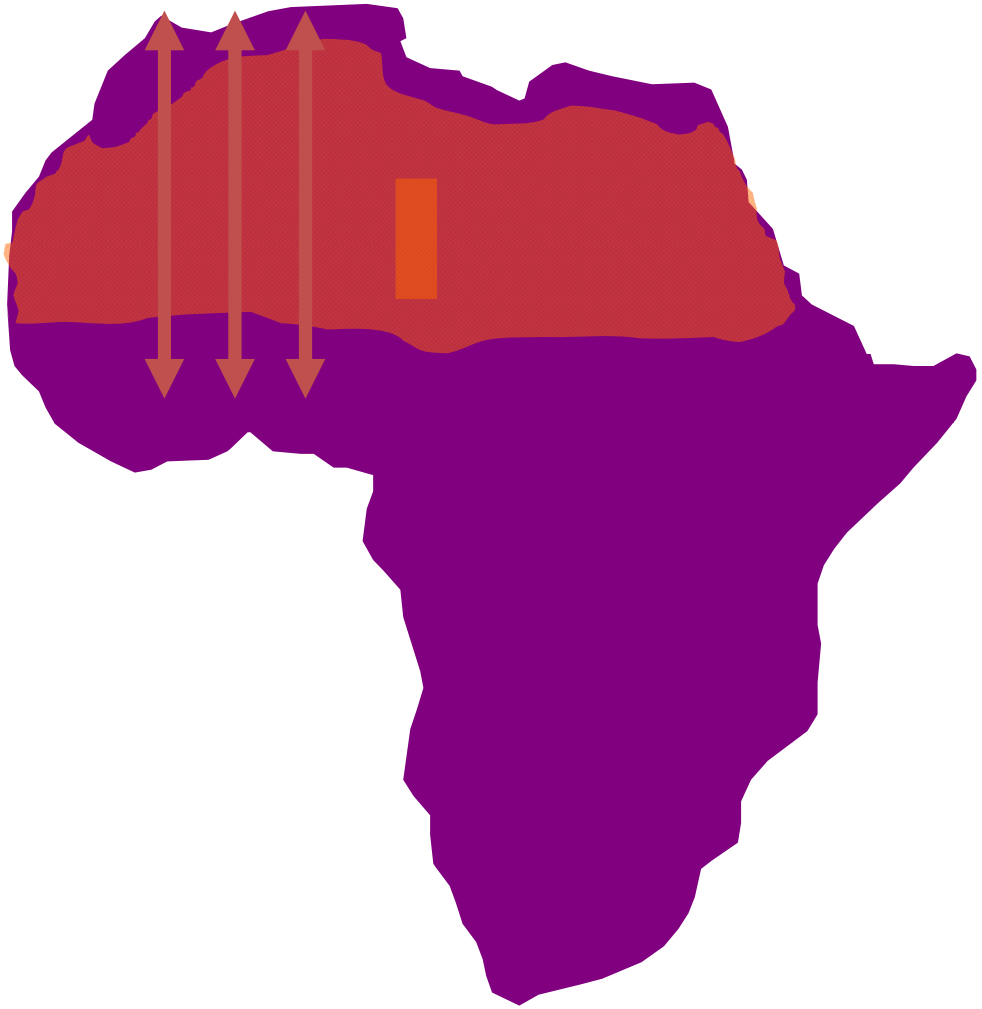
3) No differences between Berber and Arab samples



Arabisation in the Maghreb (7th and 11th C A.D.):

Cultural replacement with little demographic impact

2) Sub-Saharan flow detected in some NW African samples

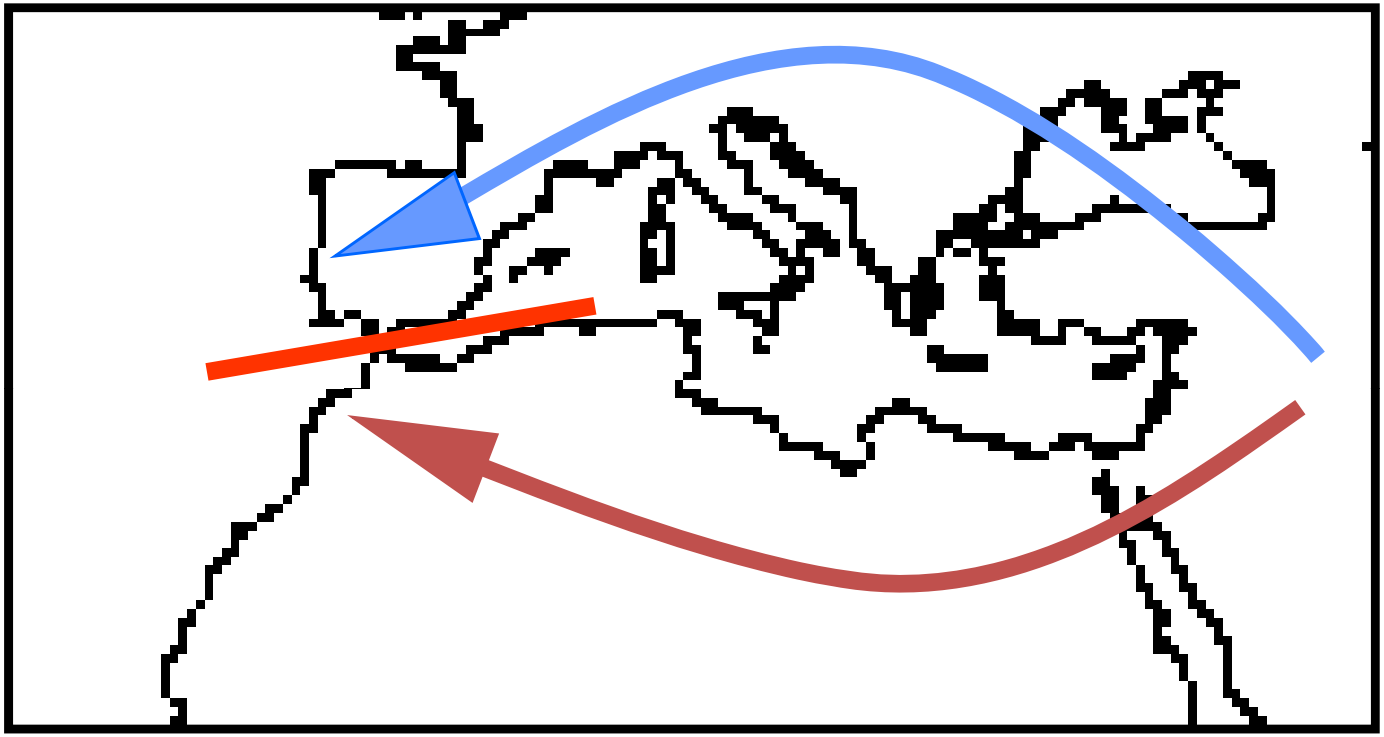


Continuous gene flow through the Sahara desert

South-north gradient of sub-Saharan admixture

Western Mediterranean populations: Conclusions

1) Clear genetic difference between NW Africa and SW Europe



The Palaeolithic and Neolithic may have run in parallel along the two shores

Gibraltar Straits may have acted as a geographical barrier

Impact in Iberia of Arab occupation??

Northern Europe was gradually recolonized from refugia after the Last Glacial Maximum (LGM), ~20,000 years ago (Housley et al. 1997). The two major refugia were in southwestern France/Cantabria (Atlantic and western Mediterranean zone) and Ukraine/Central Russian Plain (Periglacial zone), but other minor refugia could have existed in between (Dolukhanov 2000).