Biological aspects of human variation

1

Phenotypic variation: the hallmark of our species

Display at the Maropeng Museum in South Africa

2

Remember:

Phenotype = genotype + environment

- Most complex phenotypic traits (e.g., height, body proportions, etc.) are:
  - Polygenic (influenced by many genes)
  - Influenced by the environment (climate, culture, etc.): epigenetics, developmental plasticity, and so on

3

Adaptation

Functional modification of a structure, physiology or behavior of an organism that promotes survival in a particular ecological niche

4

Human variation & adaptations

- Our species evolved in/across Africa, with contributions to the *H. sapiens* genotype and phenotype from various local populations across the entire continent
- Therefore, our early ancestors were adapted to and thrived in different environments across Africa, including:
  - Relatively high to very high UV regimes
  - Relatively high to very high temperatures
  - Low to moderate altitude

5

Human variation and adaptations

- As *H. sapiens* populations spread out of Africa around 100 Ka, they were strongly affected by genetic drift (serial bottlenecks and founder effects) and natural selection due to new environmental stressors
- Humans are EXCEPTIONALLY ADAPTABLE biologically, behaviorally & culturally
- Took less than 100,000 years to adapt to many different environments on Earth!

6

Types of adaptation

- Genetic
  - change in allele frequencies over time, 'hard wired'
  - skeletal or soft-tissue or physiological

- Non-genetic: adjustment or accommodation
  - Cultural (material culture - clothes, shelter)
  - Behavioral (lessen stress through behavior)
  - Acclimatization - temporary & reversible (body copes temporarily with local environmental stress)
  - Developmental - permanent, but not inherited (how the body grows to cope with stress)

7

Major environmental stressors

- Thermal stress: temperature extremes, (humans are more heat than cold-tolerant, having evolved in Africa)
- Solar radiation: UV rays (damage skin)
- Altitudinal stress: low oxygen (hypoxia), cold temperature, solar radiation

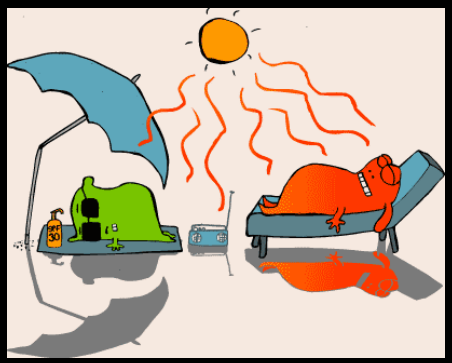
8

Heat & UV stress

- Heat cramps (lack of salt) - muscle spasms
- Heat exhaustion (dehydration) - dizziness, nausea, loss of coordination, headache etc.
- Heat stroke (lack of water & salt) - high core body temp. 103F/39.4 C, no sweating, vomiting, rapid pulse etc.; convulsions & unconsciousness @ 108F/42 C
- UV stress - skin cancer

9

Adaptations to heat & UV



- Cultural – clothes, air conditioning, shelters, sunscreen
- Behavioral - stay in shade (reduce solar radiation)
- Acclimatization – sweating, vasodilation, reduce core temperature, tanning
- Developmental
  - increased perspiration

10

Cold stress

- 79F/26C: blood vessels of skin start contracting
- 68F/20C: shivering
- 41F/5C: unconscious after few hours

11

Adaptations to cold

- Cultural - clothes, heating, hot water bottles, shelter
- Behavioral - huddle with people or other animals (reduces surface area to mass)
- Acclimatization – shivering, vasoconstriction, increase basal metabolic rate
- Developmental - high extremity temperature, increased number of red blood cells & vascularization

12

Altitude stress

Multiple stressors:

1. more intense UV radiation
2. extreme cold
3. hypoxia (reduced oxygen intake)
   - Less concentrated oxygen at higher altitudes
   - Hypoxia exerts greatest stress on humans out of all of these!
   - Increased rates of infant mortality, miscarriage, low birth weights

13

High altitude adaptations

- Cultural - oxygen masks, pressurized airplanes
- Behavioral - reduce activity to reduce oxygen consumption
- Acclimatization - hyperventilation, increased blood flow, increased Hb
- Developmental - barrel chests, brain centers insensitive to hypoxia, larger hearts, 20-30% larger lungs

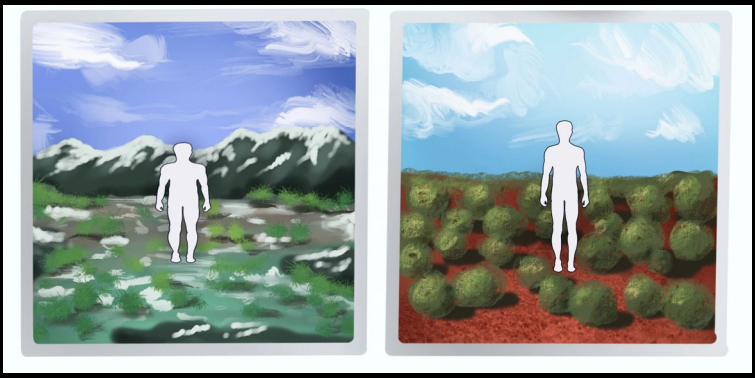
14

Geographically patterned variation

- OFTEN DISTRIBUTED IN A CLINE
- A cline is a gradual change in the frequency of genotypes & phenotypes from one geographic region to another

15

Genetic adaptations: body proportions

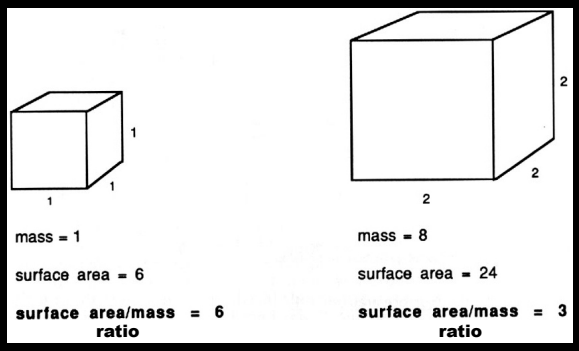


Cold environments: human populations tend to be stockier, w/ longer torsos, shorter limbs

Warm environments: more slender, w/ longer limbs, shorter torsos

16

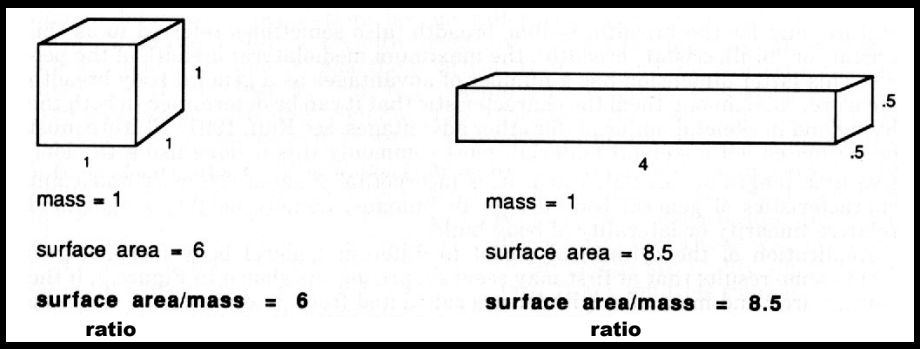
Bergmann's rule (1847)



- Body mass greater in populations living in colder climates
- As mass increases, relative surface area decreases → reduced heat loss
- Lost heat = lost energy, so being big is advantageous in cold environments

17

Allen's rule (1877)



- Colder climates = shorter appendages
- Warmer climates = longer appendages
- In warm climates surface area can be increased while keeping mass constant by assuming a more linear form → increased heat loss

18

Body proportions in non-human mammals

Fennec fox lives in the desert, where their long ears and legs keep them cool

Arctic fox lives in the Arctic, where their short ears and legs keep them warm

19

19

The biology of skin color

20

Genetic adaptations: skin color

- All humans have same number of melanocytes for producing melanin (pigment that results in skin color)
- Different amounts of melanin produced (darker skin = higher level of melanin production)
- Melanin functions to filter out harmful ultraviolet light
- How and why is the range of skin color adaptive in different environments?

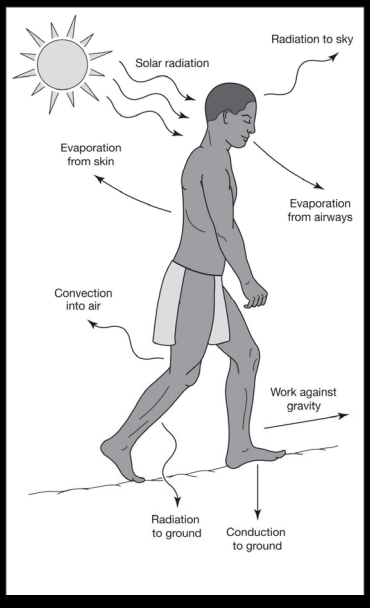
21

Early hominins likely needed protection from UV rays

- Lighter skin covered with dark hair
- Darker skin of exposed areas

22

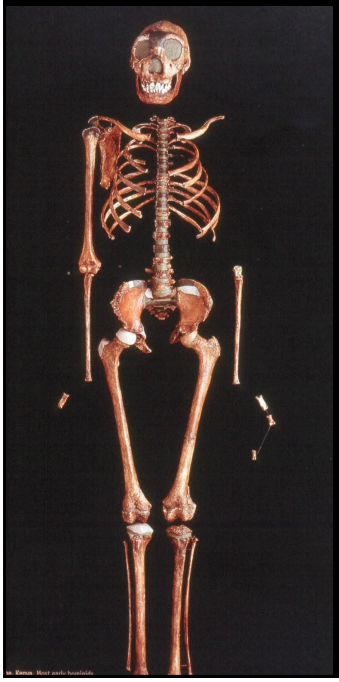
May mean dark skin is a shared derived trait in *Homo*



Reconstruction of the Nariokotome Boy (KNM-WT 15000, *Homo erectus*)

23

Genus *Homo*

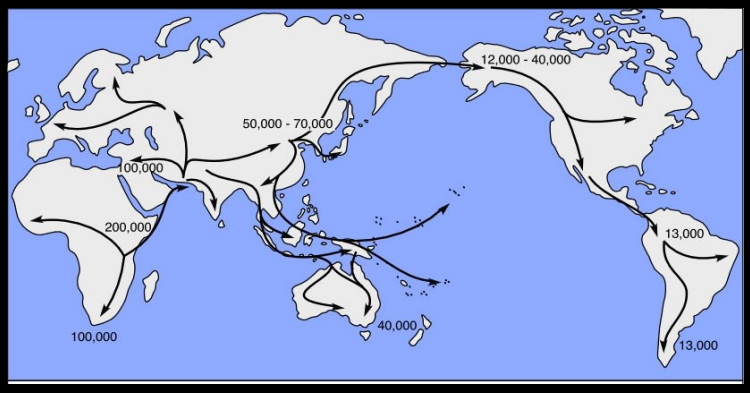


- Expansion into hot, more open environments within Africa
- Selective pressure to keep cool
  - body proportions adapted for dissipating heat
  - ↑ sweat glands
  - ↓ body hair
  - selective pressure for protection from UV radiation → darker skin color

24

Plasticity of human skin color

- Multiple changes in skin color as *H. sapiens* expanded across different latitudes



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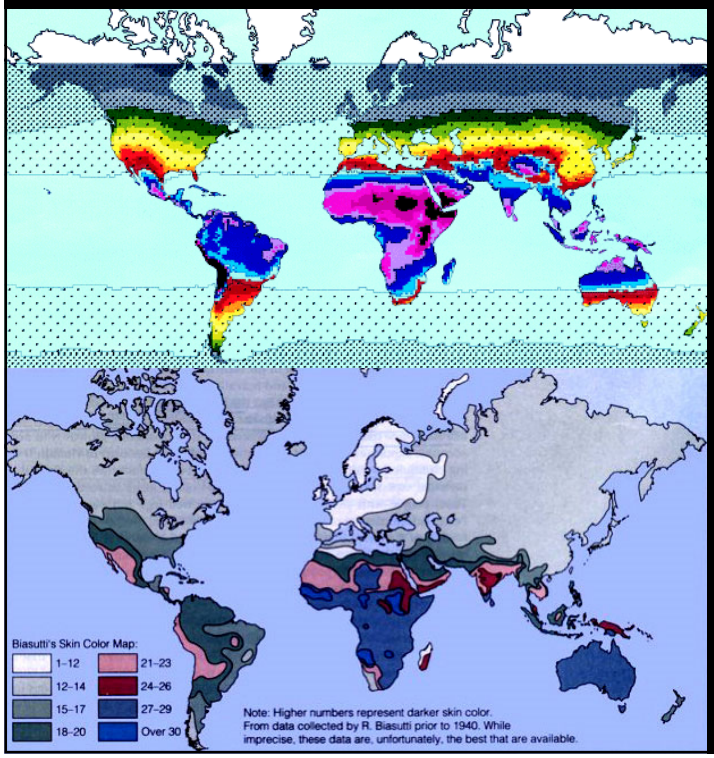
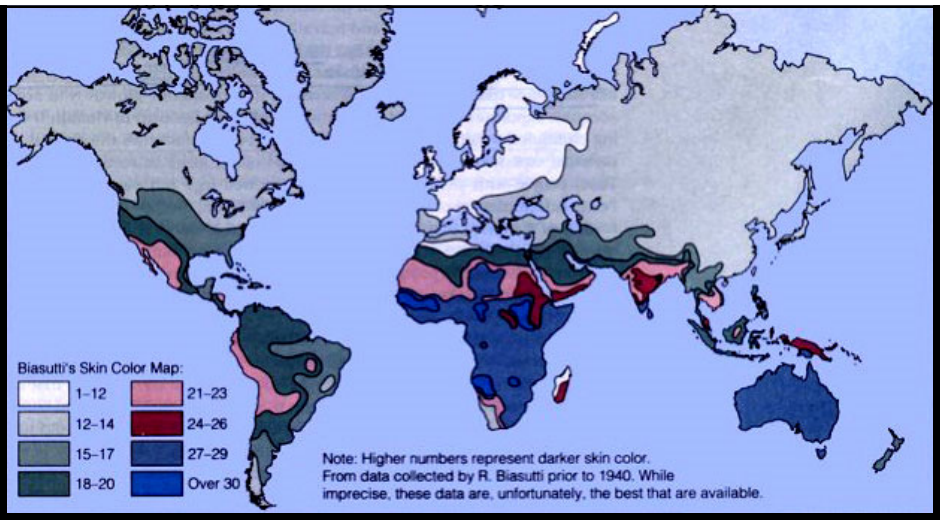


UV radiation distribution

violet = higher, stippled = very low

Skin color distribution

26

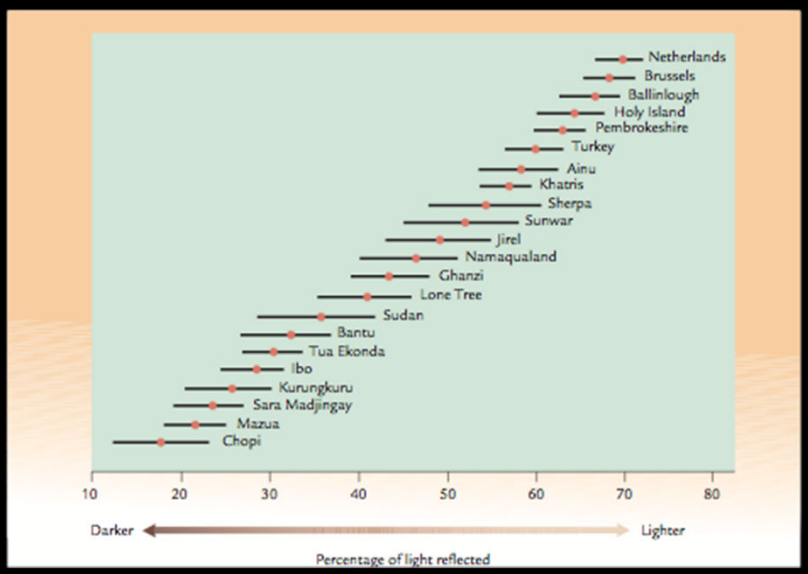


Skin color is a genetic adaptation:

- Populations with darker skin colors closer to the equator
- Lighter skin color further away from the equator
- Skin color shows a continuous variation from very light to very dark – CLINAL VARIATION!

27

Remember: variation within populations!



28

Skin color

- Ultraviolet (UV) radiation causes:
  - skin cancer
    - People with darker skin color are at less risk for skin cancer due to protection from UV light
    - Skin cancer rarely affects pre-reproductive individuals!
  - breakdown of **folate**
    - Folate is involved in DNA synthesis, sperm production, red blood cell formation, & aspects of neural development
    - Low levels of folate during pregnancy linked to various developmental problems, particularly neural tube defects (e.g., spina bifida)

29

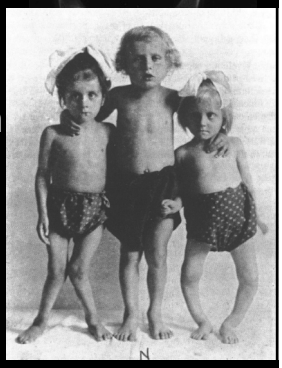
Then why evolve light skin color?

- Cloudy & cold regions away from the equator get less sun – particularly as skin is covered most of the time by clothing
- Melanin levels decrease away from equator
  - To allow UV radiation to enter deep layer of skin
  - This allows production of vitamin D_3 - essential for normal bone growth, maintenance, and absorption of calcium

30

Rickets

- lack of vitamin D in children can lead to rickets
- causes bow legged bones that become soft & can no longer support body weight
- pelvic deformation → obstetric problems for women
- Major problem in early 20th century: urban children not getting enough sunlight
- People with dark skin still at risk for low vitamin D levels in areas of less intense UV radiation



31

Geographic variation exists, but…

There are not now,

nor have there ever been, any

'PURE'

(i.e., genetically homogenous) races

32

What do we mean when we say race is not biological?

- Doesn't mean that race doesn't exist, or that everyone is the same!
- Human variation is complex and does not lend itself to rigid typological categories, which are social constructs
- BUT – just because race isn't biological, it doesn't mean it's not a real, lived experience with measurable effects on our biology and health!

33

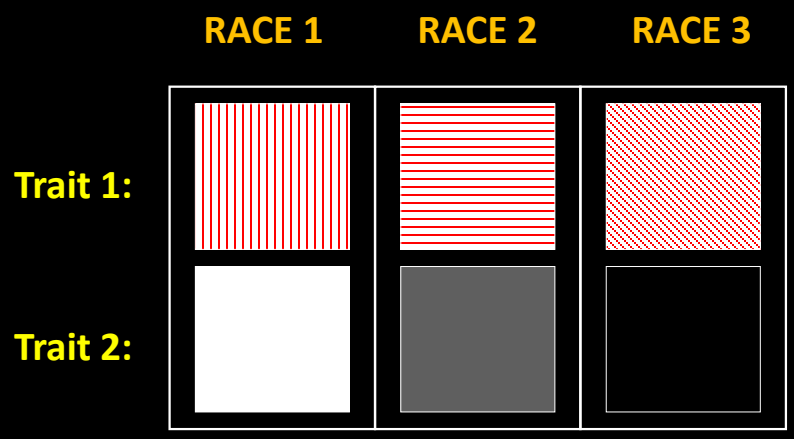
Testing biological race

- *If* race is biological, we would expect to see:
  - All of the traits associated with a single race would be concordant (seen only with each other, in that race)
  - Race definitions would be discrete, meaning there is no gradual changes in traits between races

34

Testing biological race

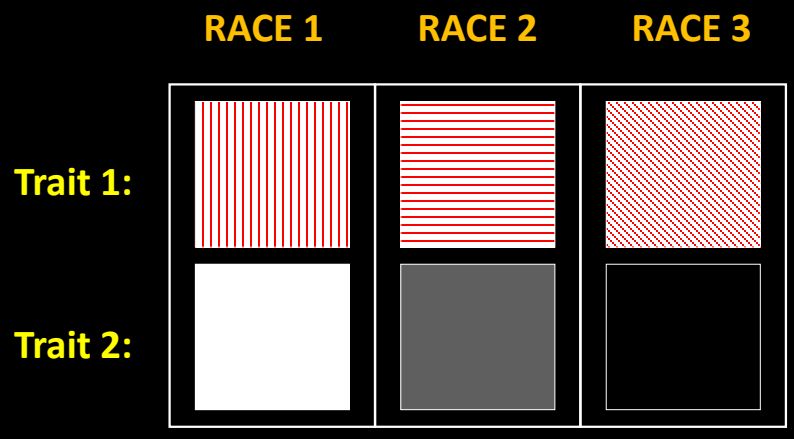
Imagine 2 traits hypothesized as racial markers:



35

Testing biological race

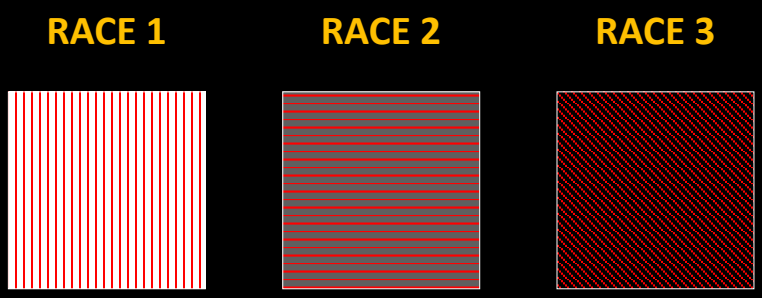
Under the typological view of race, we predict **concordance of traits** (see both traits in one race)



36

Testing biological race

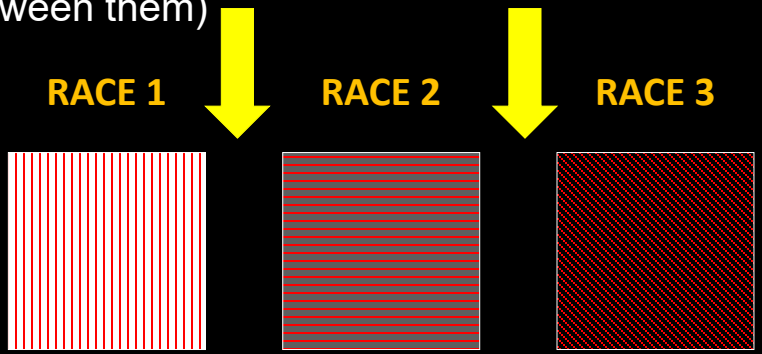
Under the typological view of race, we predict **concordance of traits** (see both traits in one race)



37

Testing biological race

Under the typological view of race, we predict **discrete racial groups** (no gradual change between them)

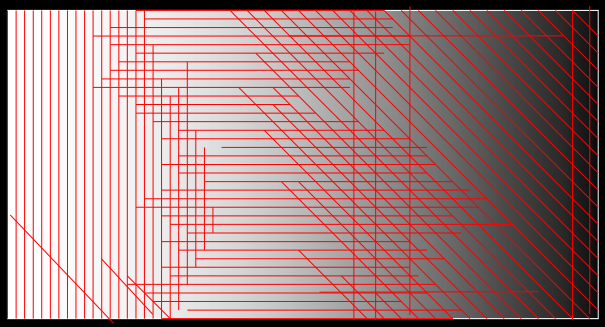


38

Distribution of biological variation

Traits are not concordant

Range of variation is continuous, not discrete

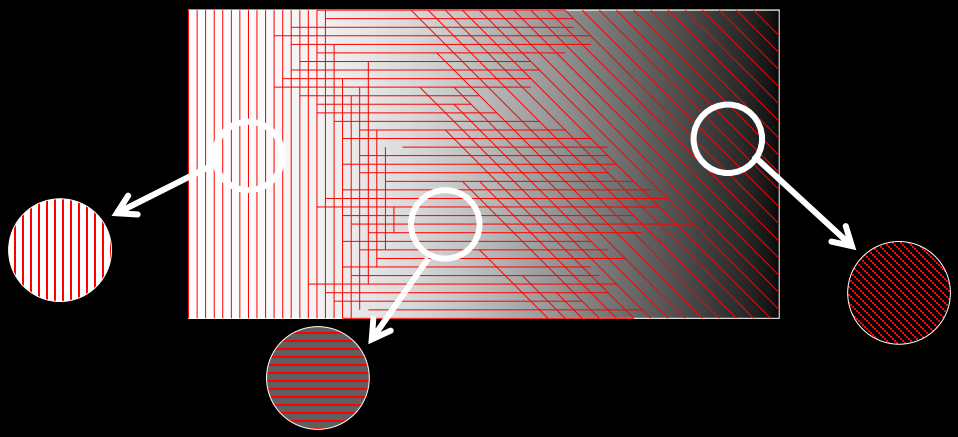


- **Cline:** a gradual change in some phenotypic characteristic from one population to the next

39

Distribution of biological variation

What we tend to focus on when we talk about distinct racial categories:



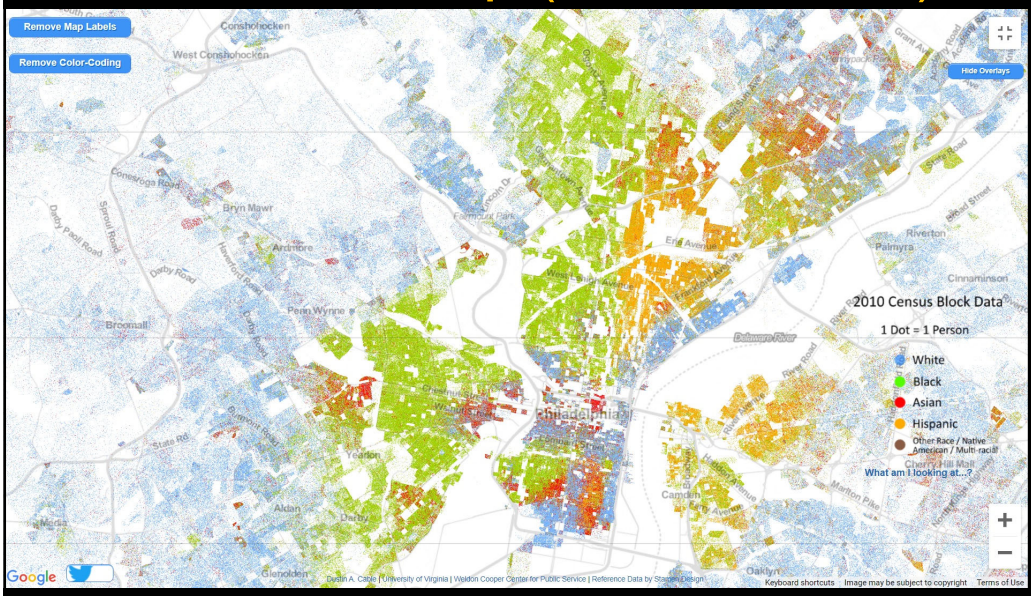
40

Distribution of genetic variation

- Result of evolutionary, historic, and ongoing social, political, economic, and other cultural processes (e.g., migration, segregation, cultural mate preferences) that influence population structure
  - e.g. lingering effects of residential segregation affect racial composition of different neighborhood across major cities in the US
  - Can contribute to the perception of discrete races as opposed to clines

41

Racial dot map (2010 census)

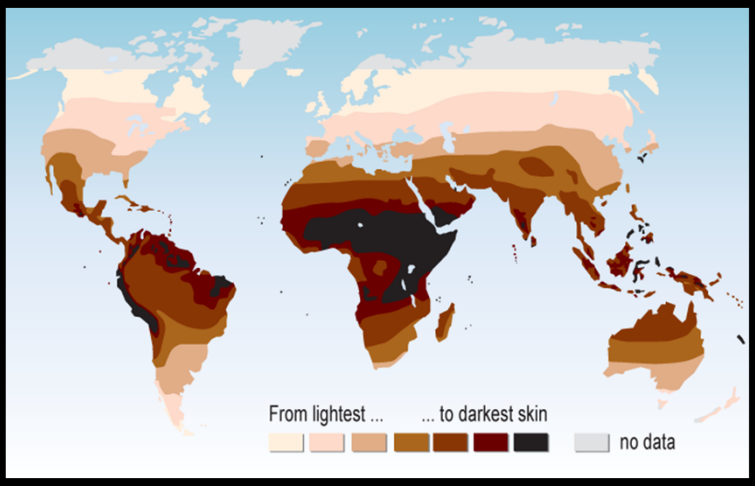


http://racialdotmap.demographics.coopercenter.org/

42

Clines example: Skin color

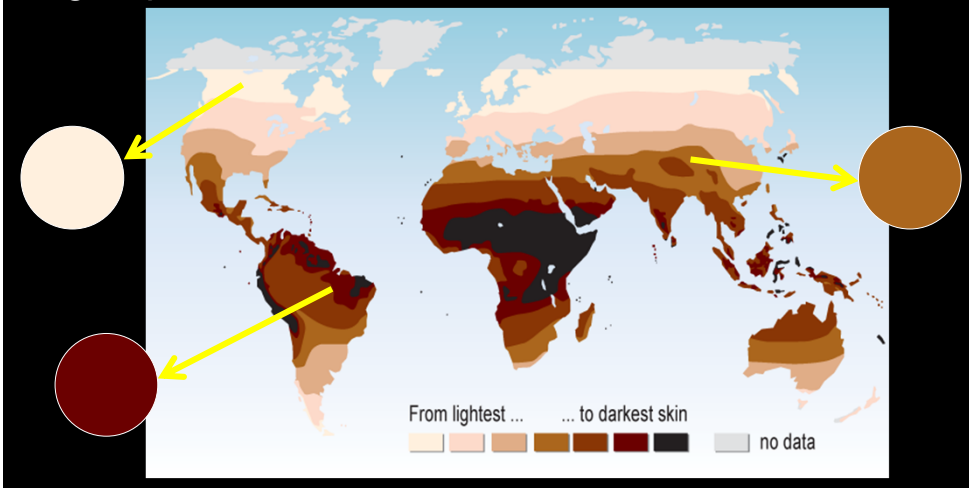
Frequency of each skin color changes with geography



43

Clines example: Skin color

But we commonly focus on skin color as discrete groups



44

The reality of "racial" classification

Humans DO show phenotypic variation that is geographically structured, BUT…

there is NO SINGLE natural classification scheme for the human species!

Most of the genetic variation within humans is present WITHIN rather than BETWEEN so-called "races"

45

Lewontin *et al.* 1972

- Examined what proportion of the total amount of variation present in a sample of many worldwide populations was present within each local population
- Found that 85% of total variation in the world was present WITHIN local groups!
- Even if all of humankind were wiped out except for any local population - say Inuit or BMC students - this population would still contain on average 85% of the genetic variation present in the human species!

46

Variation

- Much greater within groups than between groups!

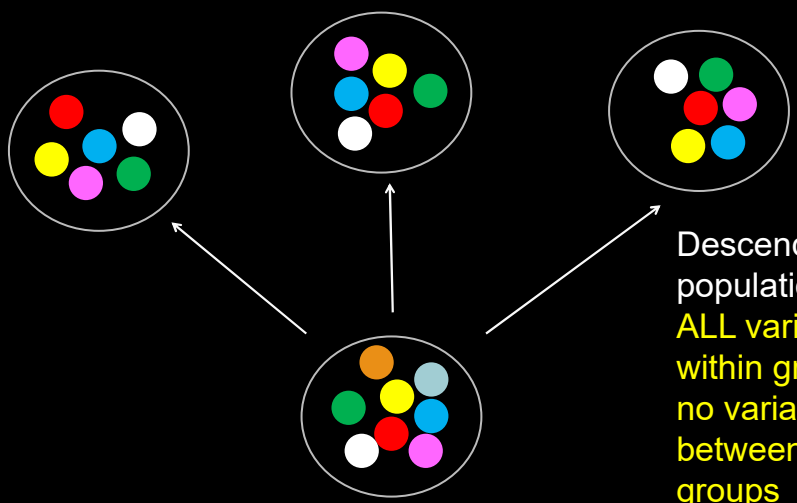
Table 2. A summary of the results of this study and of previous comparable studies

Polymorphism	Loci, *n*	Groups, *n*	Average variance components, %		
			Within samples	Among samples within groups	Among groups
Protein (Lewontin 1972; ref. 1)	17	7	85.4	8.3	6.3
Protein (Latter 1980; ref. 3)*	18	6	83.8–87.0	5.5–6.6	7.5–10.4
Protein (Ryman *et al.* 1983; ref. 5)†	25	3	86.0	2.8	11.2
DNA (this study)‡	109	4–5	84.4	4.7	10.8

*Latter used three different statistical techniques.
†The study by Ryman *et al.* incorporates the data of ref. 4.
‡Average of three data sets weighted for the number of loci.

47

More variation within than between groups

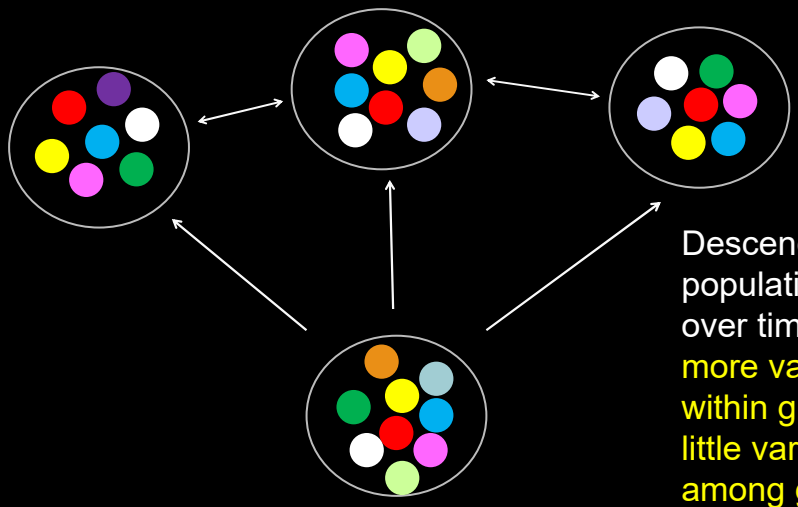


Descendent populations: ALL variation within groups, no variation between groups

Parent population

48

More variation within than between groups



Descendent populations over time: more variation within groups, little variation among groups

Parent population

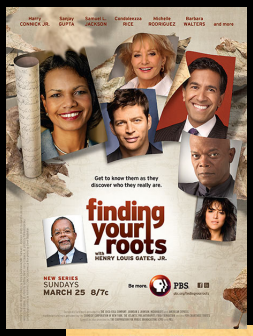
49

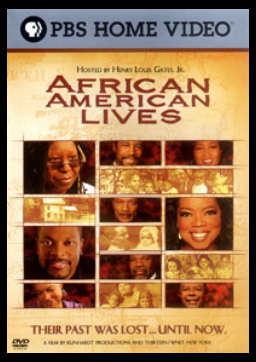
Types of DNA markers

- Sequences consist of various combinations of 4 bases: A, T, C, G
- Single nucleotide polymorphisms (SNP)
  - e.g. ATTCG vs. ATTTG
- Tandem repeats – repeating pattern of multiple nucleotides adjacent to each other (e.g., ATTCG ATTCG ATTCG)
  - <10 repeats: microsatellites or short tandem repeats (STR)
  - 10-60 repeats: minisatellite
  - Unknown #: variable number tandem repeat (VNTR)

50

Genetic ancestry





51

Population histories

- Y-chromosome: inherited from sperm
- mtDNA: inherited from the ovum

Do not recombine

- Haplogroups:
  - defined by unique event polymorphisms (e.g., SNP)
  - reflect more ancient population history
  - Branches on the human family tree – people within haplogroups more closely related
- Haplotypes:
  - lineages within a haplogroup (all share the founder SNP mutation)
  - defined by tandem repeats (e.g., STR)
  - reflect more recent ancestry

52

Y-chromosome haplogroups

Y-chromosome "Adam"

- Deepest lineages in sub-Saharan Africa
- non-African lineages contain only a subset of diversity found within Africa

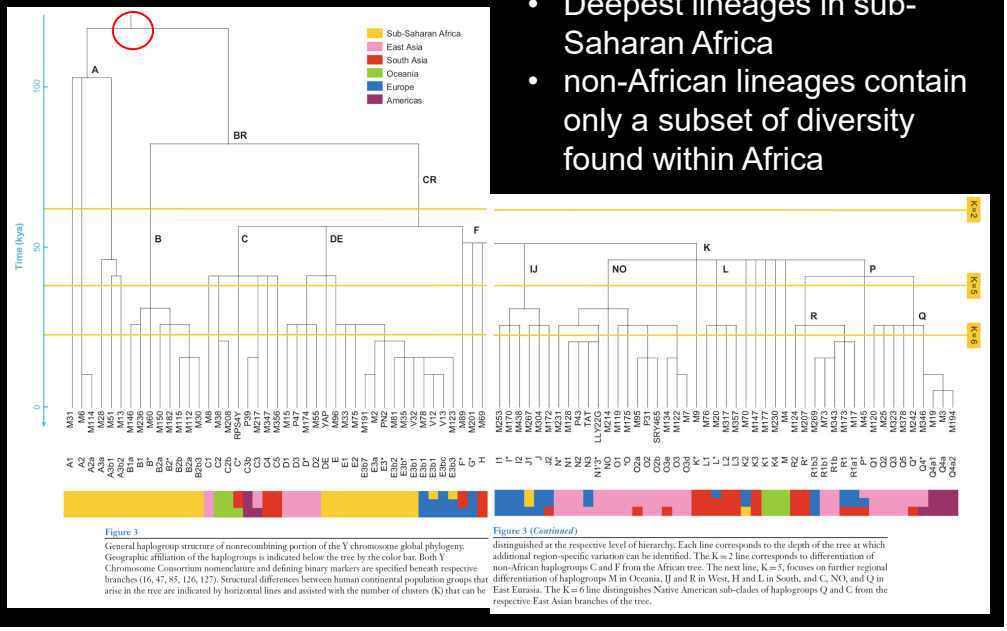
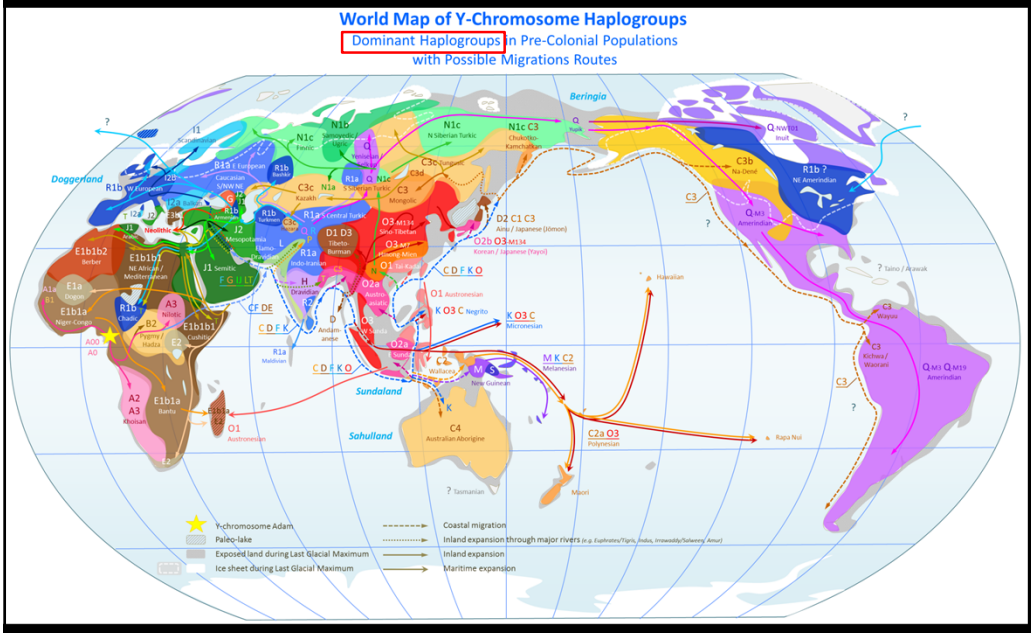


Figure 3
General haplogroup structure of nonrecombining portion of the Y chromosome global phylogeny. Geographic affiliation of the haplogroups is indicated below the tree by the color bar. Both Y Chromosome Consortium nomenclature and defining binary markers are specified beneath respective branches (16, 47, 85, 126, 127). Structural differences between human continental population groups that arise in the tree are indicated by horizontal lines and assisted with the number of clusters (K) that can be distinguished at the respective level of hierarchy. Each line corresponds to the depth of the tree at which additional region-specific variation can be identified. The K = 2 line corresponds to differentiation of non-African haplogroups C and F from the African tree. The next line, K = 5, focuses on further regional differentiation of haplogroups M in Oceania, IJ and R in West, H and L in South, and C, NO, and Q in East Eurasia. The K = 6 line distinguishes Native American sub-clades of haplogroups Q and C from the respective East Asian branches of the tree.

Figure 3 (*Continued*)

53

Y-chromosome haplogroups



54

mtDNA haplogroups

mitochondrial "Eve"

- Similar to Y-chromosome
- Deepest lineages in sub-Saharan Africa
- non-African lineages contain only a subset of diversity found within Africa

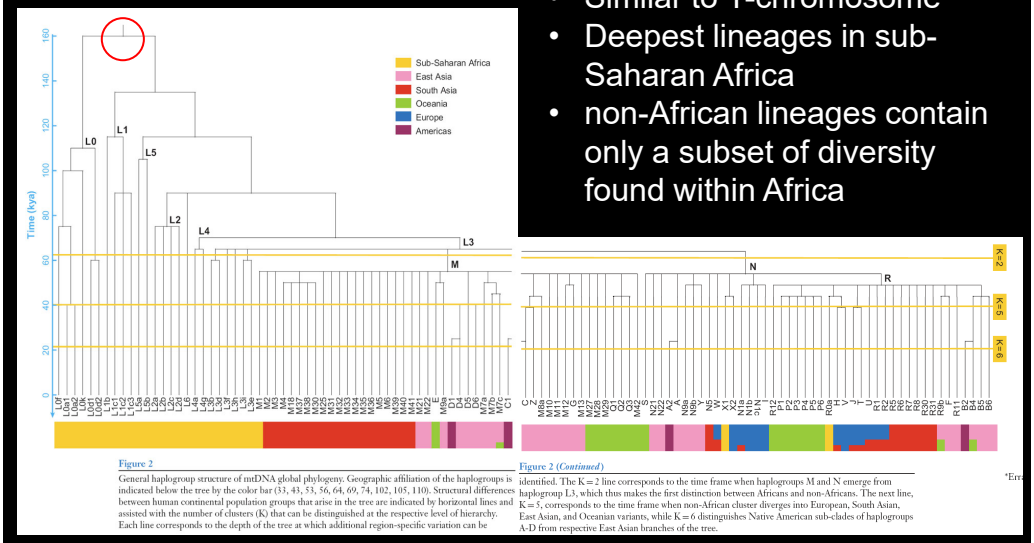
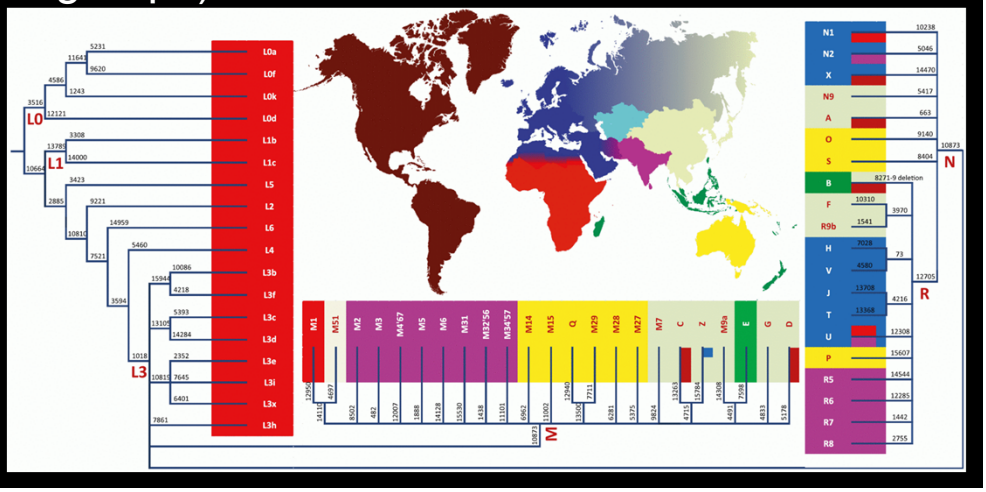


Figure 2
General haplogroup structure of mtDNA global phylogeny. Geographic affiliation of the haplogroups is indicated below the tree by the color bar (33, 43, 53, 56, 64, 69, 74, 102, 105, 110). Structural differences between human continental population groups that arise in the tree are indicated by horizontal lines and assisted with the number of clusters (K) that can be distinguished at the respective level of hierarchy. Each line corresponds to the depth of the tree at which additional region-specific variation can be identified. The K = 2 line corresponds to the time frame when haplogroups M and N emerge from haplogroup L3, which thus makes the first distinction between Africans and non-Africans. The next line, K = 5, corresponds to the time frame when non-African cluster diverges into European, South Asian, East Asian, and Oceanian variants, while K = 6 distinguishes Native American sub-clades of haplogroups A–D from respective East Asian branches of the tree.

55

mtDNA haplogroups

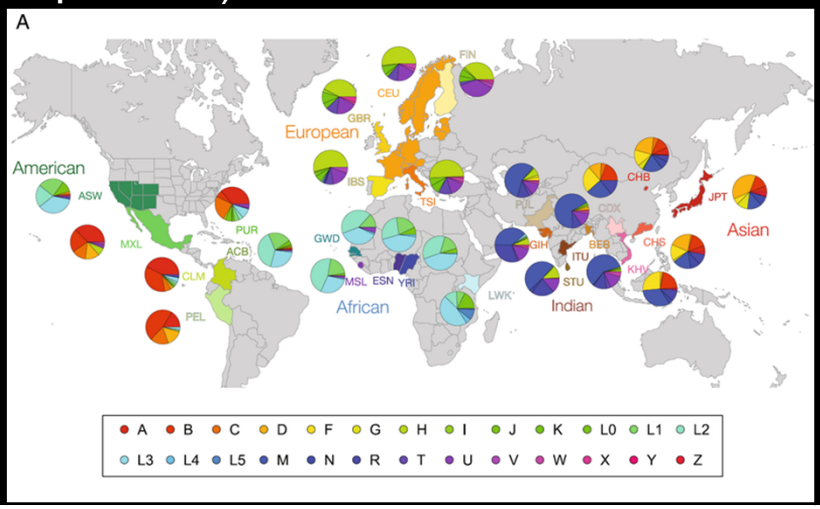
- This is one way to portray this (as discrete groups)



56

mtDNA haplogroups

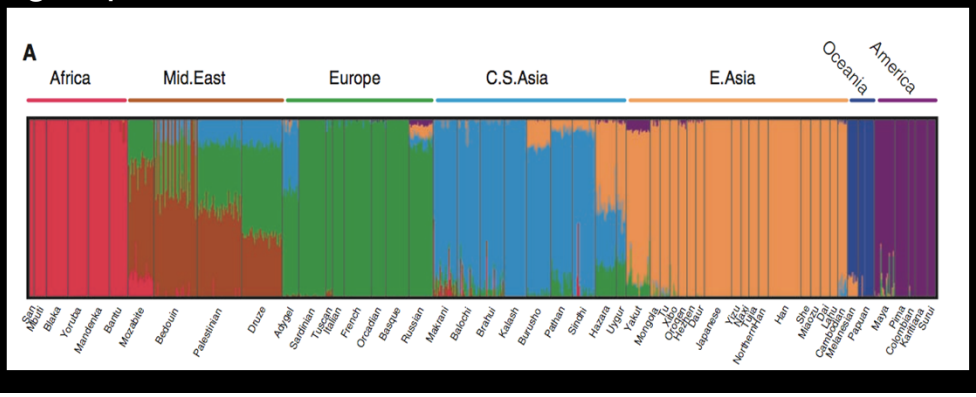
- This is a better way of showing this (as proportions)



57

Genome-wide global population structure

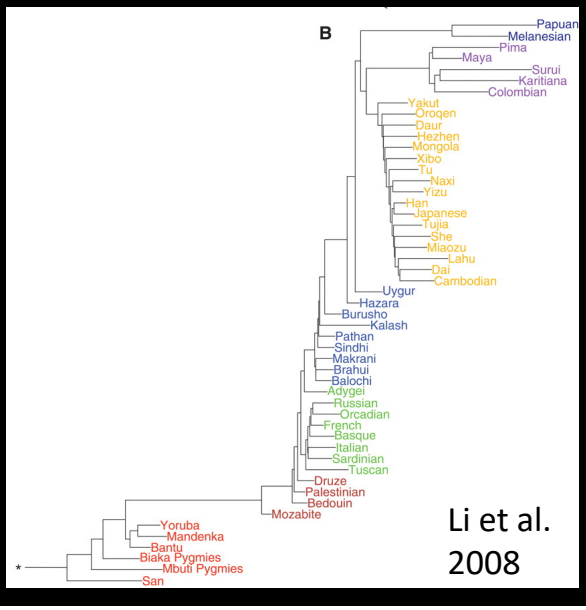
- Inferred from 650,000 SNPs (out of 4-5 million) from 938 individuals from 51 populations (Li et al. 2008)
- Program instructed to produce between 2 and 7 groups



58

Genome-wide global population structure

- Sequence of branching events reflects pattern of dispersals of *H. sapiens* around the world:
  - single origin in Africa
  - serial founder effects
  - Additional branching within regions



Li et al. 2008

59

Genome-wide global population structure

- Analysis of molecular variance for autosomal loci (22 non-sex chromosomes)
  - within-population variation: 88.9 ± 0.3 %
  - among-population-within-group (i.e., geographical region): 2.1 ± 0.05%
  - among geographical regions: 9.0 ± 0.3%

Li et al. 2008

60

Importance of sampling approaches

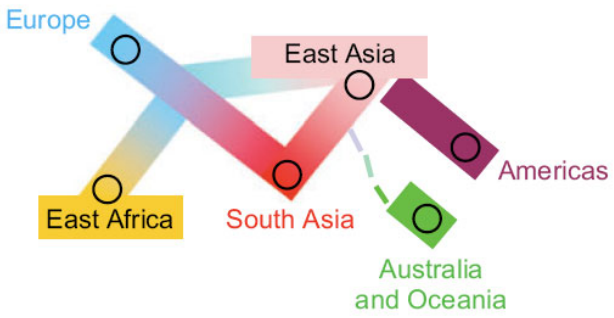
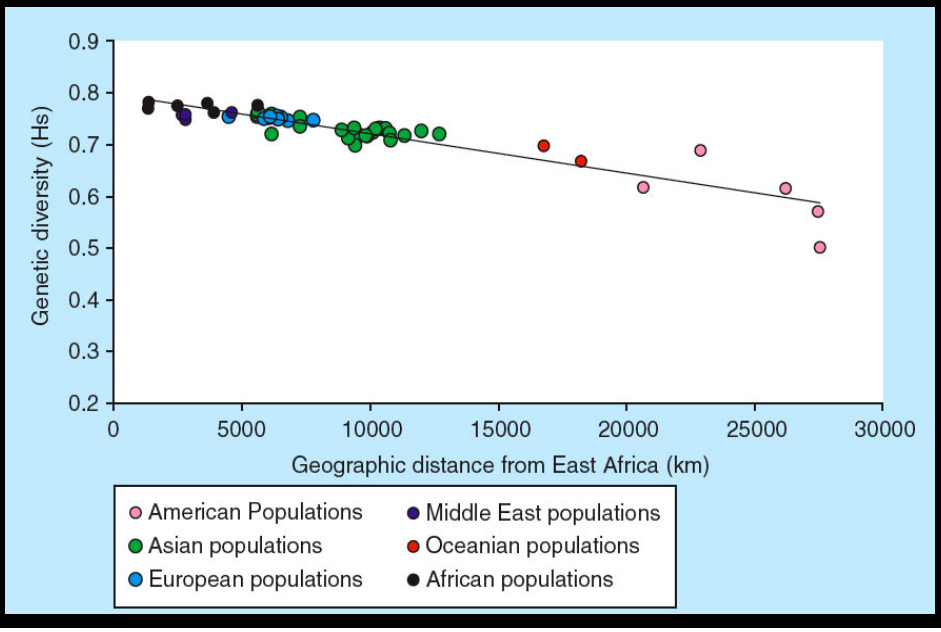


Figure 1

Clusters or clines of genetic diversity? Genetic structure of human populations could well be compatible with both concepts as clines would not be detected if there was no genetic patterning. Circles indicate theoretical sampling points, each with particular allelic frequency pattern. Blended colors between the circles denote the clines.

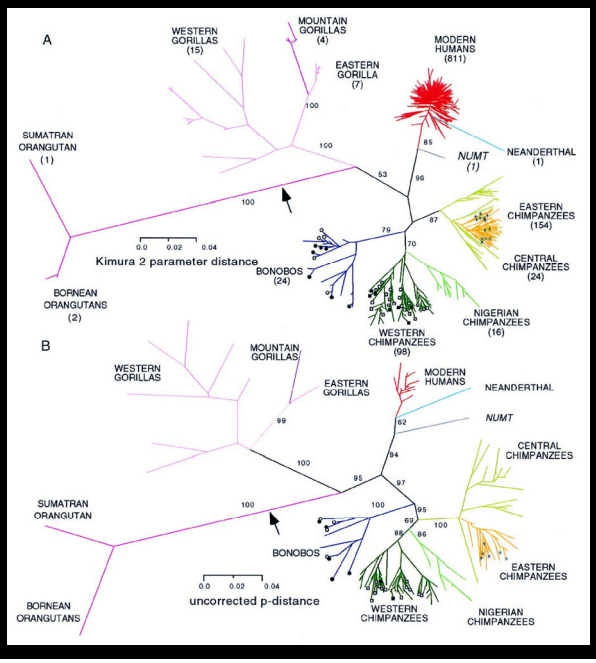
61

Genetic diversity ~ geographic distance from Africa



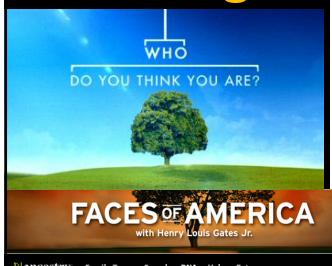
62

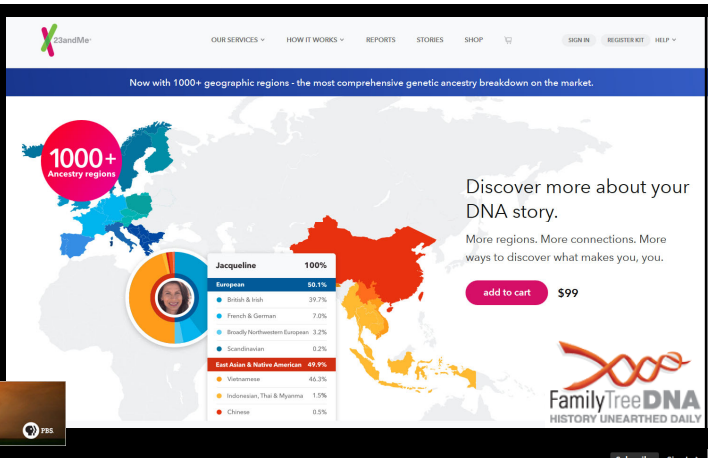
Primate genetic diversity

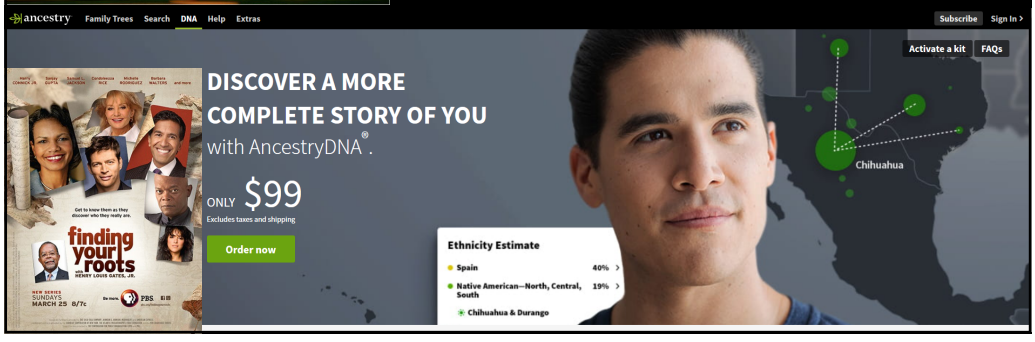


63

Genetic ancestry testing







64

Misconceptions about genetic ancestry

- Mitochondrial “Eve” and Y-chromosome “Adam” were the only people around
- Nope! Just happened to be the last common ancestor of the lineages that survived until today – there were many other people and lineages around at the time!

65

Some issues with genetic ancestry testing

- The farther you go back in time, you actually have MORE ancestors!
  - e.g. 10 generations ago (~300 years), we each have 4095 cumulative ancestors, each of whom contributed (on average) 0.097% to our DNA
  - 20 generations (~600 y): > 2 million
  - 30 generations: (~1000 y) > 2 billion
- NOT unique: repetition of ancestors
  - Everyone who lived in Western Eurasia 1000 years ago who has descendants today is an ancestor of every person of European ancestry living today
  - Everyone in the world shares an ancestor in the last 2000-4000 years!

66

Issues with genetic ancestry testing

- Reinforces ideas that humans can be subdivided into discrete groups
  - Calling it "ethnicity" – there are no genetic markers for different ethnic groups anywhere!
- Identifying geographic regions as places of origin with great precision
  - It's a matter of probabilities! Misleading! (Also, those categories are nonsensical & inconsistent.)
  - Genetic databases primarily reflect people living in different regions TODAY, not in the past
  - Being from a place ≠ being typical/representative of that place!

67

Issues with genetic ancestry testing

- Different concerns for minoritized and historically excluded groups around the world
  - History of exploitation for Western science (including using DNA samples or cells for undisclosed purposes)
  - There is a need & initiatives for better representation AND more control over DNA samples (data sovereignty)

68

Issues with genetic ancestry testing

- Native Americans:
  - Indigenous, sovereign nations – own criteria for belonging to those groups (Tribal Nations)
  - DNA and aDNA used to re-colonize indigenous identity and belonging by imposing a framework of genetic kinship as (the only) valid criterion (e.g., the Ancient One; Elizabeth Warren)
- African-Americans:
  - Mostly descended from people forcibly brought to the Americas through the slave trade
  - When genealogical records are missing, or end, DNA could be the only way to recover some aspect of one's family history

69