Genetic diversity

**Population and Evolutionary Genetics**

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Basics of genetics

- The genetic information of each organism is located in the sequence of the nucleotides of its DNA

  - The total genetic information for an organism is called **genome**

- The genome contains many elements, among which genes

  - A **gene** carries the information about the expression of a characteristic (trait) in an organism

    - Obviously, reality is more complex!
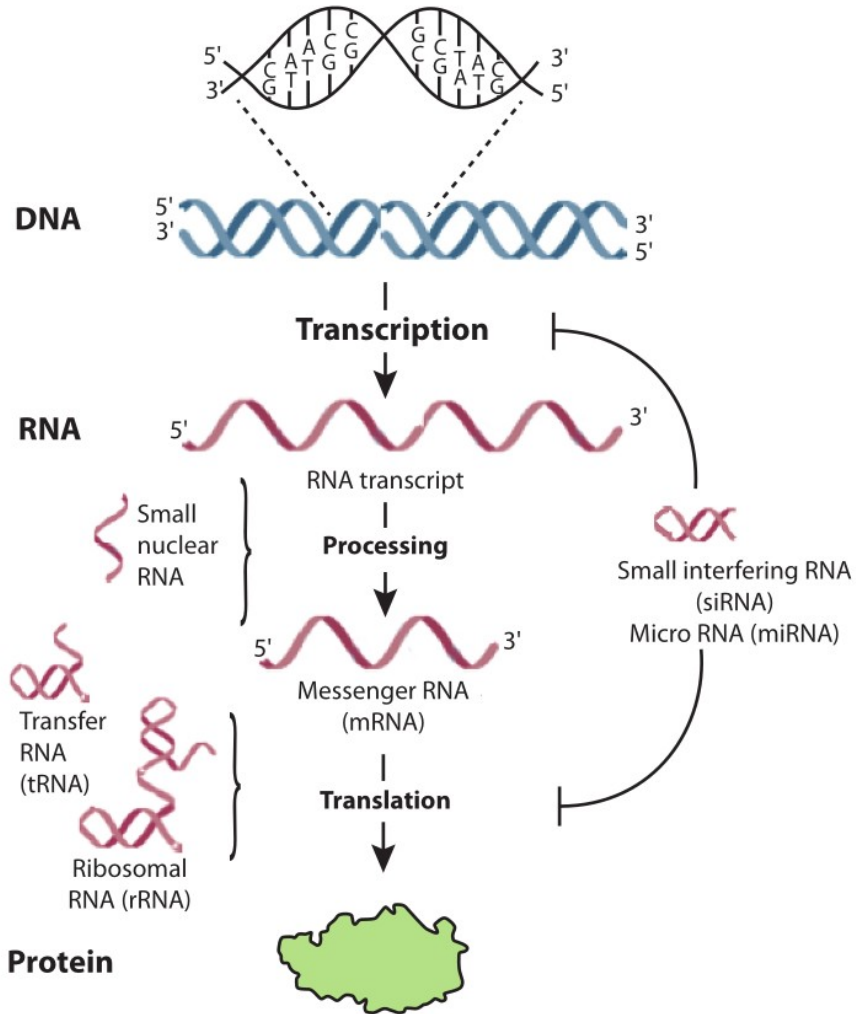
In the expression of a protein-coding gene, the sequence of bases in the DNA is transcribed into an RNA molecule that undergoes chemical modifications (processing) to produce the messenger RNA that is translated into a polypeptide chain.

Transcription and translation require specialized RNA molecules, many of which contain self-complementary sequences that can fold and pair, forming hairpins or trefoil structures.

Other small RNA molecules may inhibit transcription or translation. Specialized proteins are also essential at each stage of transcription, processing and translation.
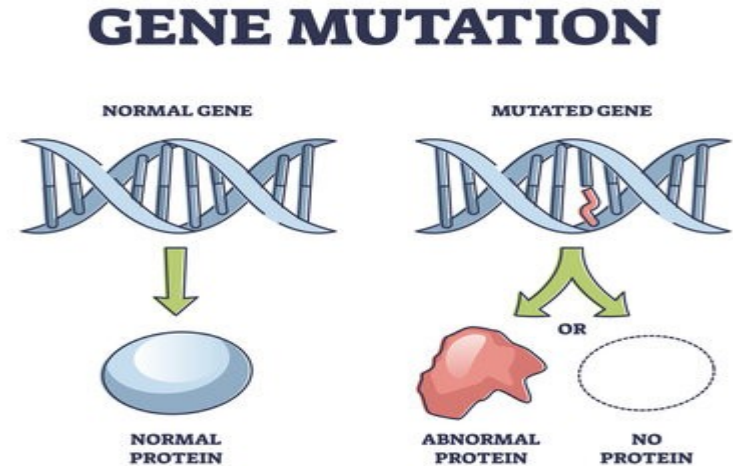
Table 1.1 The standard genetic code

First nucleotide in codon (5′ end)	Second nucleotide in codon				Third nucleotide in codon (3′ end)
	U	C	A	G	
U	UUU Phe/F	UCU Ser/S	UAU Tyr/Y	UGU Cys/C	U
	UUC Phe/F	UCC Ser/S	UAC Tyr/Y	UGC Cys/C	C
	UUA Leu/L	UCA Ser/S	UAA Stop	UGA Stop	A
	UUG Leu/L	UCG Ser/S	UAG Stop	UGG Trp/W	G
C	CUU Leu/L	CCU Fro/P	CAU His/H	CGU Arg/R	U
	CUC Leu/L	CCC Pro/P	CAC His/H	CGC Arg/R	C
	CUA Leu/L	CCA Pro/P	CAA Gln/Q	CGA Arg/R	A
	CUG Leu/L	CCG Pro/P	CAG Gln/Q	CGG Arg/R	G
A	AUU Ile/I	ACU Thr/T	AAU Asn/N	AGU Ser/S	U
	AUC Ile/I	ACC Thr/T	AAC Asn/N	AGC Ser/S	C
	AUA Ile/I	ACA Thr/T	AAA Lys/K	AGA Arg/R	A
	AUG Met/M	ACG Thr/T	AAG Lys/K	AGG Arg/R	G
G	GUU Val/V	GCU Ala/A	GAU Asp/D	GGU Gly/G	U
	GUC Val/V	GCC Ala/A	GAC Asp/D	GGC Gly/G	C
	GUA Val/V	GCA Ala/A	GAA Glu/E	GGA Gly/G	A
	GUG Val/V	GCG Ala/A	GAG Glu/E	GGG Gly/G	G

Basics of genetics

- Genetic changes are inherited to the next generation and this procedure involves two stages:

    - A **mutation** changes the DNA and creates a new alternative version of the genome

    - **Natural selection** and other evolutionary forces change the proportions (frequencies) of these alternative versions of genomes in a population

Mutation

- **Random** changes in DNA from errors during copying
    - Changes are caused in the genome
- May create an alternative form of a gene
    - **Allele**

GENE MUTATION

NORMAL GENE

MUTATED GENE

NORMAL PROTEIN

ABNORMAL PROTEIN

OR

NO PROTEIN

Gene locus and genotype
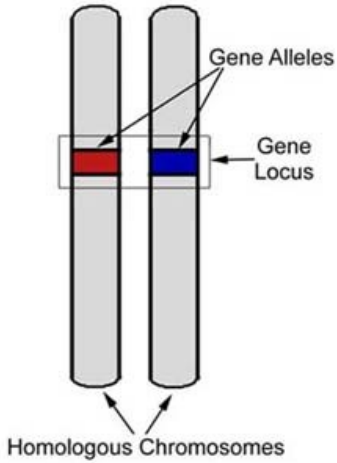
- A **gene locus** is a position in the genome where we can observe one or more alleles in different individuals for the same gene

- A genotype is the combination of alleles carried by one given individual in a given set of loci

- In a diploid species, one **genotype** at one locus carries two alleles

  ◦ **Homozygous** or **heterozygous** genotype

- Phenotype: The result of the combined action of environment and genes

- **Polymorphism**: the occurrence of more than one gene type (allele) in a gene locus

  ◦ Or, the existence of genetic diversity

Types of polymorphisms
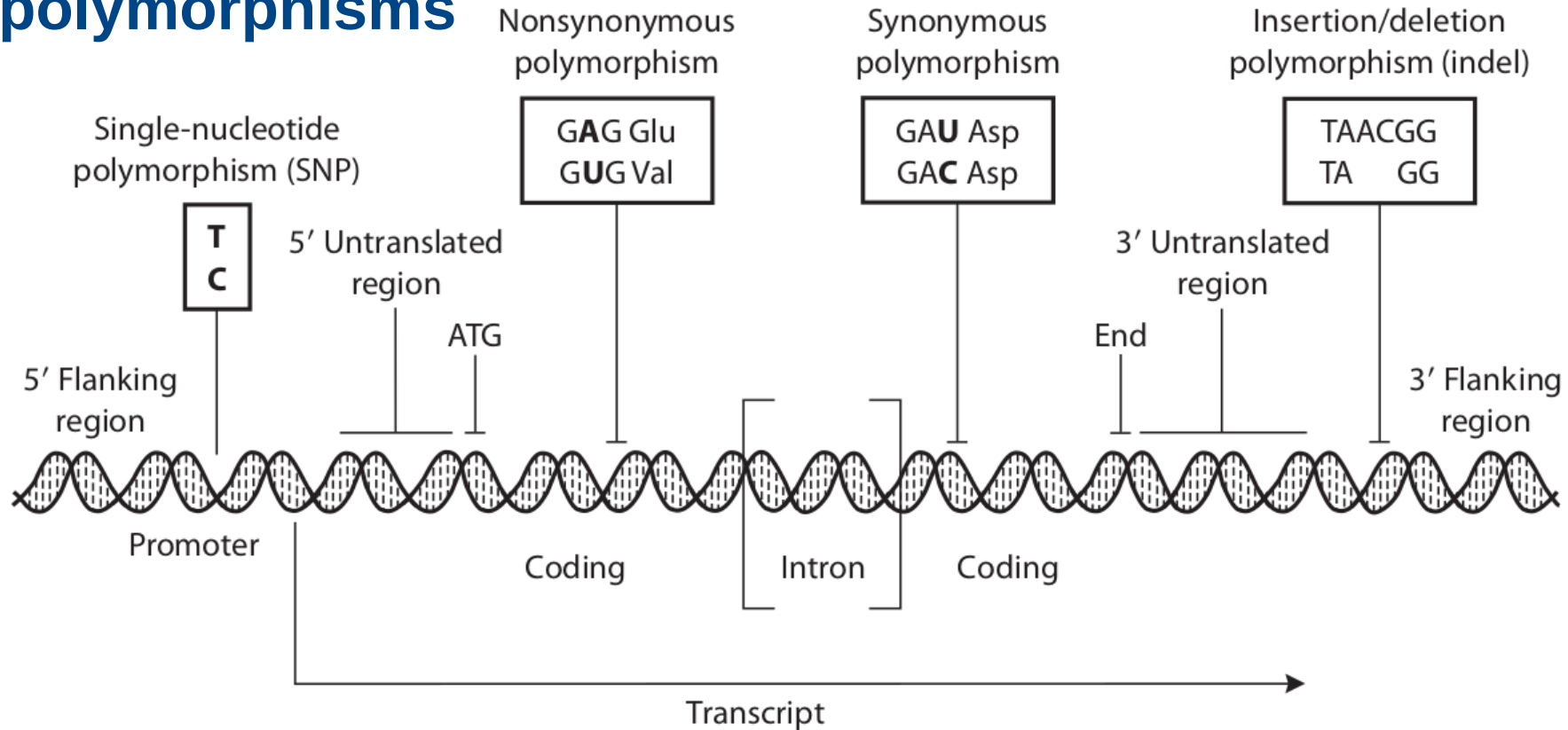
Figure 1.2 The organization of a protein-coding gene showing the major types of DNA polymorphisms that can occur with regard to individual base pairs.

Single Nucleotide Polymorphism - SNP

Single-nucleotide polymorphism (SNP)

5' Unt
re

5' Flanking region

Promoter
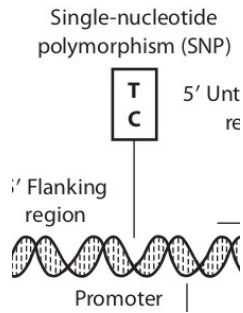
- The acronym SNP stands for a single nucleotide polymorphism, where individuals in the population may differ in terms of the nucleotide pair present in a **specific position** in DNA

- The SNP defines two "alleles" (T and C in the picture) and three genotypes: TA homozygous, homozygous CG or heterozygous (TA in one molecule and CG in the corresponding position in DNA of the homologous chromosome)

  - The word "allele" is in quotation marks because the SNP concept applies on all sequences, not only coding regions

SNPs

- Available data on the human genome show that any two randomly selected genomes are likely to differ at about three million nucleotide positions

  ◦ We are 99.5-99.8% the same

- About one million SNPs are found in protein-coding genes

  ◦ About two-thirds of SNPs in protein-coding genes are located in introns
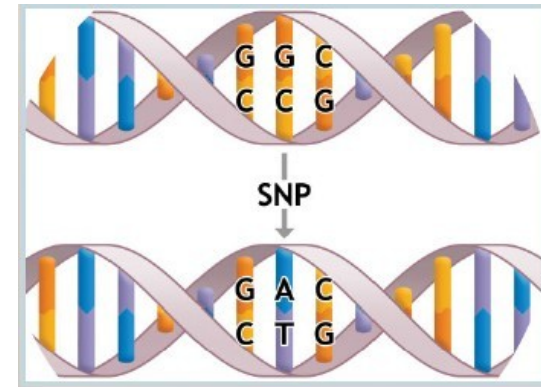
Nonsynonymous polymorphism

GAG Glu
GUG Val

- Nonsynonymous (missense) polymorphism

  ◦ A SNP present in the coding region that changes a codon, which leads to an **amino acid replacement** in the polypeptide chain

- E.g. in the image example, replacing the polymorphic nucleotide in RNA (A vs. U) results to a polymorphism for the codons GAG vs. GUG

  ◦ GAG specifies Glu (glutamic acid), while GUG specifies Val (valine)

  ◦ In the human genome, a Glu/Val polymorphism at amino acid position 6 in beta-globin gene is responsible for sickle cell disease

  ◦ On average, each human is heterozygous for approx. **6000** polymorphisms in amino acids

11

Synonymous polymorphism

- A synonymous polymorphism is a SNP present in the coding region which produces a synonymous codon and does not result in a substitution of amino acids in the polypeptide chain

  - In the example, a GAU is changed to a GAC, both of which code for Asp (aspartic acid)

  - Synonymous polymorphisms are sometimes called **silent** polymorphisms

  - Any two random human genomes differ by about 7000 synonymous nucleotide positions

- The existence of silent polymorphisms is not indifferent to organisms

  - In many organisms certain codons are preferred, especially in mRNAs that encode high-abundance proteins, as speed and accuracy are affected by translation, protein folding and its stability

Add / remove (indel)

- An indel is an addition/subtraction polymorphism

  ◦ Indels in protein-coding exons are rare and are usually found in flanking regions

  ◦ Most indels are less than 10 base pairs, but some are much larger

  ◦ Very large indels (1-5 kb) are caused by intervening transposable elements

Insertion/deletion
polymorphism (indel)

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TAACGG
TA    GG
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Simple Tandem Repeat - STR

- Polymorphism known as simple tandem repeat- STR, where the "alleles" differ according to the number of copies of a single nucleotide sequence that are repeated along the DNA

- Each STR has the potential to display multiple alleles in the population
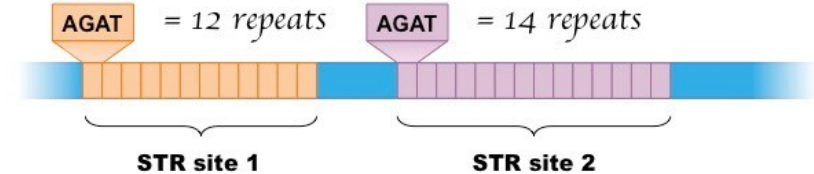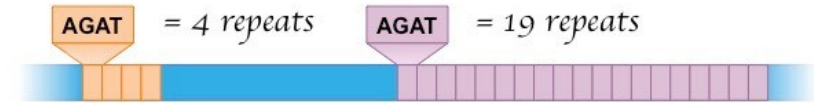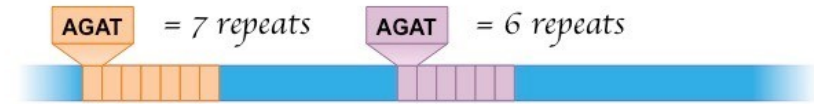
Simple Sequential Repeat - STR

- STRs in which the repeat unit is 2-9 bp are called **microsatellites** (SSR) and those with a recurrent unit of 10-60 bp are called **mini-satellites** (VNTR)

- STRs are useful because they exist in thousands of scattered regions throughout the genome and each has a potentially large number of alleles

- Each genome can be uniquely identified according to the particular allele present in a relatively small number of polyallelic STR sites on different chromosomes
  - **DNA fingerprinting**

Why do we care about genetic polymorphisms?

- To estimate the levels of genetic diversity in populations with different history, structure, demographic situation, etc.

- To link polymorphisms with risk factors to specific diseases

- To identify individuals among others in a population (e.g. criminology, origin, determination of kinship, etc.)

- To link polymorphisms with production characters in agricultural plants and animals

- To monitor risks to key species regarding their exposure to environmental hazards

- For the study of the evolution of human populations or other species

- For phylogenetic investigations on groups of species

- To protect biodiversity

Genetic diversity

- For each gene there may be more alleles in a population

    - **Genetic diversity**

- Each allele can exist in different ratios (*frequencies*)
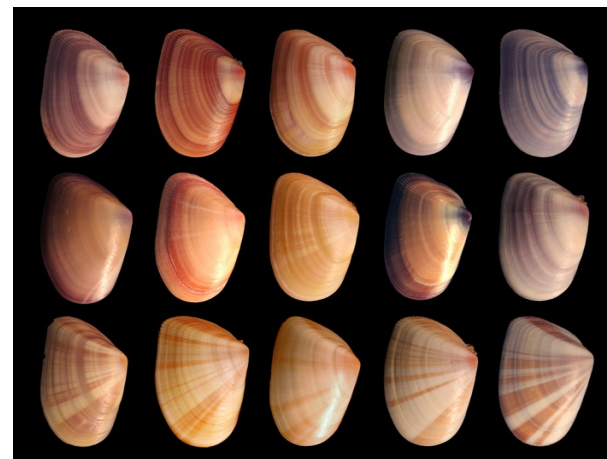
Genetic diversity

- Genetic differences between organisms have the form of different alleles for the same genes
  - Alleles are in pairs for each gene and form a **genotype**

The human races have no genetic basis

Richard Lewontin

Comparison of genetic variation between two native populations from different continents

Population one

Population two

Genetic variation shared by both groups

Genetic variation unique to each group

85 percent of genetic variation is shared by both groups

15 pecent of genetic variation is unique to each group

- Human populations vary little
- The diversity within populations is much greater than differentiation between them
- *RC Lewontin 1972: The Apportionment of Human Diversity. Evolutionary Biology*

19

Genetic diversity varies in space

Differences between two populations of snails in two adjacent city blocks, in the enzyme zone MDH-1, where the road is likely to be a point of change in genetic diversity in the area
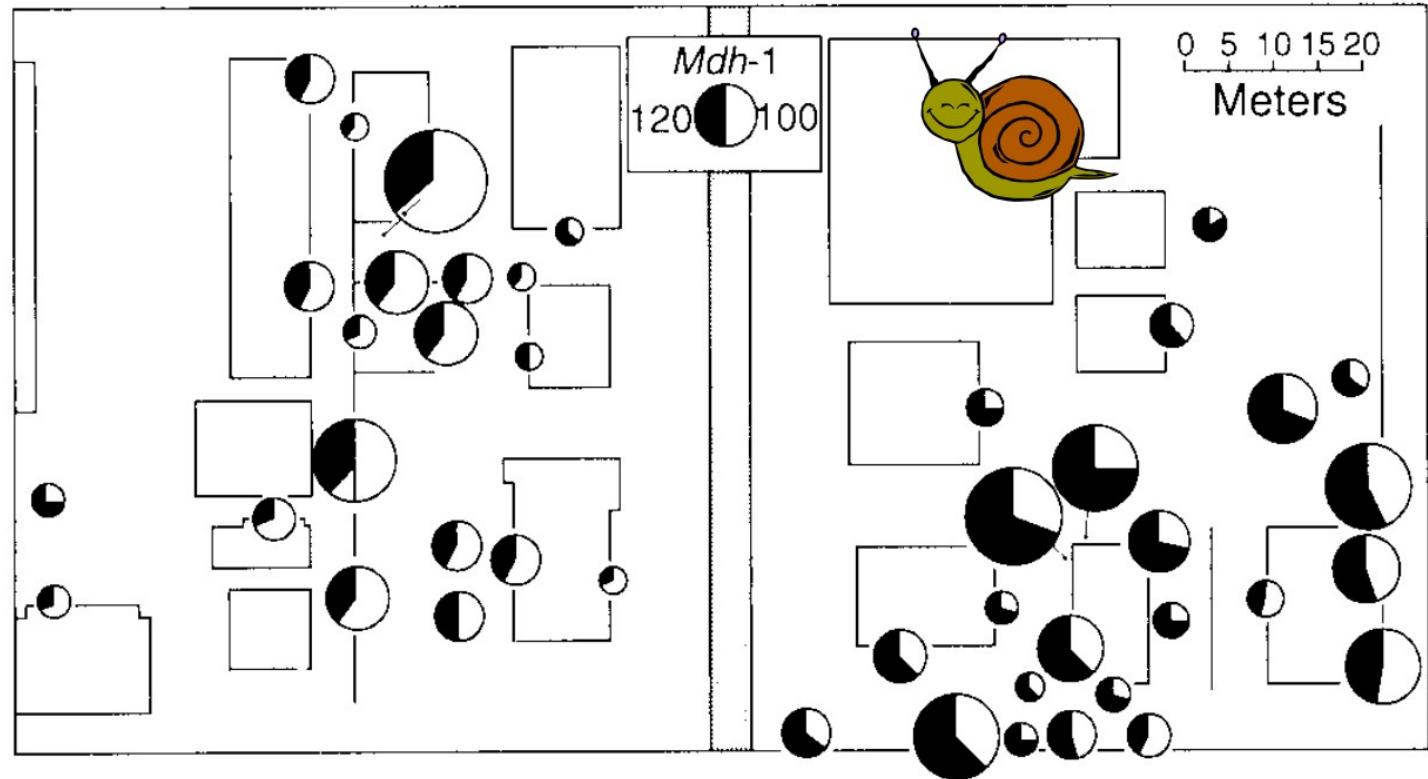
Genetic diversity changes over time

Genetic diversity in populations almost never remains constant, but changes over time

Changes in genetic diversity over time lead to **evolution**

The evolution of species is the process that led to the current diversity of life
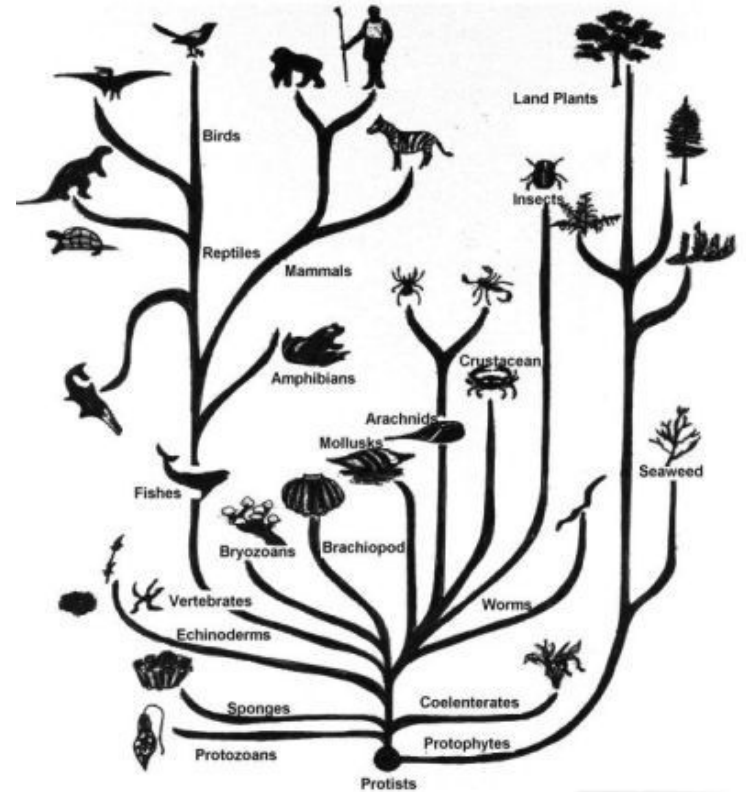
Population

- A set of similar inter-reproducing organisms

  ◦ A species
      − Not always
  ◦ A geographical area
      − Not always
  ◦ Reproducibility

- The population as a whole has one **gene pool** with specific genetic structure

- A population may also consist of subpopulations

DNA polymorphism research techniques: molecular markers

RC Lewontin

- Protein polymorphisms
  - Electrophoresis of alloenzymes (isoenzymes)
- Nucleotide polymorphisms (DNA & RNA)
  - By using restriction enzymes
    - Restriction Fragment Length Polymorphisms (RFLPs)
  - By using PCR
    - Random molecular dominant markers (iSSR, RAPD)
    - STR
    - With simultaneous use of PCR & restriction enzymes (AFLPs, PCR-RFLPs)
- With sequencing technologies

Plant	Sample	Population	Latitude	Longitude	SNP1	SNP2	SNP3	SNP4	SNP5	SNP6	SNP7	SNP8	SNP9	SNP10	SNP11	SNP12	SNP13	SNP14	SNP15	SNP16	SNP17	SNP18	SNP19	SNP20	SNP21	SNP22	SNP23	SNP24
900	1	Laista1	39.96868386	20.99789507	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
901	2	Laista1	39.97243543	20.99980303	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
902	3	Laista1	39.97902573	20.99238403	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
903	4	Laista1	39.98135938	20.99241043	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/G
904	5	Laista1	39.98305714	20.99223054	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
909	6	Laista1	39.97902943	20.98282963	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
913	8	Laista2	39.99659551	20.9515825	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
915	9	Laista2	40.00702338	20.95387095	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/G
917	10	Laista2	40.00497438	20.95473515	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
918	11	Laista2	40.00441432	20.95364733	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
919	12	Laista2	40.00696321	20.95912121	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1002	13	Vermio1	40.61530233	21.95176588	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
1003	14	Vermio1	40.61636471	21.95325831	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1004	15	Vermio1	40.61729914	21.9536317	C/T	G/G	C/G	A/A	A/A	C/C	A/G	G/G	C/C	A/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	G/G	C/G	A/G	C/T	C/G	A/A	A/C
1005	16	Vermio1	40.61853276	21.95513081	C/C	G/G	C/C	C/C	G/G	T/T	A/A	G/G	A/A	G/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	A/G	A/G	A/G	C/T	C/C	A/G	A/C
1008	17	Vermio1	40.62140865	21.95069267	C/C	G/G	C/C	C/C	A/A	C/T	A/A	G/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1009	18	Vermio1	40.61919817	21.94745027	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1011	19	Vermio2	40.61692858	21.94747247	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1012	20	Vermio2	40.61602284	21.94770116	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1013	21	Vermio2	40.61517572	21.9476798	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1014	22	Vermio2	40.61520667	21.94688687	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1015	23	Vermio2	40.61563394	21.94609362	C/C	C/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1016	24	Vermio2	40.61550366	21.94535291	C/T	G/G	C/C	A/C	A/G	C/T	A/A	G/G	A/C	G/G	C/T	A/T	C/C	C/C	A/G	A/G	A/G	A/G	C/G	A/G	C/T	C/C	A/A	A/C
3701	25	Tymfi1	39.99978444	20.81702219	C/C	G/G	C/C	C/C	A/A	C/T	A/A	G/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	G/C	A/A	T/T	C/C	G/G	G/A
3702	26	Tymfi1	40.00008019	20.82615545	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/C	A/A	T/T	C/C	G/G	A/A
3703	27	Tymfi1	40.00240321	20.81791944	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3704	28	Tymfi1	40.00058735	20.81870654	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/G
3707	30	Tymfi1	39.9925894	20.82069406	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	T/T	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	G/G
3708	31	Tymfi1	39.99260547	20.82029515	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/G
3709	32	Tymfi2	39.99237061	20.82059882	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/G
3711	33	Tymfi2	39.99188837	20.82042212	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/C	A/A	T/T	C/C	G/G	G/A
3712	34	Tymfi2	39.99211359	20.8191118	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	G/A
3714	35	Tymfi2	39.99198699	20.82138952	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3715	36	Tymfi2	40.00122054	20.81618245	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3802	37	Metsovo1	39.80913423	21.16995889	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/C	A/A	T/T	C/C	G/G	G/A
3803	38	Metsovo1	39.79671429	21.17854949	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
	7				C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	C/C	G/G	C/G	A/A	T/T	C/C	G/G	A/G
	6				C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A
	1				C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A
	3				C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/G
	6				C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/G
	4				C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/G
	2				C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
	2				C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	T/T	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A
	2				C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A
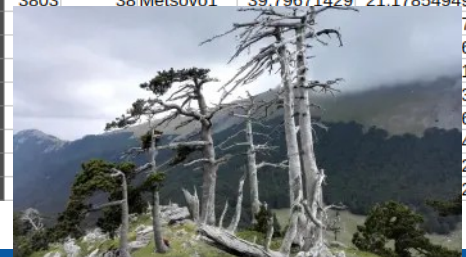
Pinus heldreichii

Inventory of genetic diversity

- A gene locus with two alleles, A and a

  - p: the frequency of the A allele

  - q: the frequency of allele a

- The three possible genotypes are AA, Aa and aa

  - P: the frequency of AA genotype

  - H: the frequency of genotype Aa

  - Q: the frequency of genotype aa

- *What is "frequency"?*

Frequency of an observation in a sample

- In a sample of size N, we make the observation of the phenomenon **x** for **Nx** times:

  - The absolute frequency of x in the sample is N_x

  - The relative frequency of x in the sample is N_x/N

- For example, in a sample of 100 people we observe that 32 are children under 10 years of age. Which is the absolute and which is the relative frequency of children under 10 years of age?

  - The absolute frequency of x in the sample is $N_x = 32$

  - The relative frequency of x in the sample is $N_x/N = 32/100 = 0.32$

- When referring to genotype or allele frequencies, we usually mean the relative frequencies

Allele and genotype frequencies

Genotype frequencies

$$P = \frac{N_{AA}}{N}$$

$$H = \frac{N_{Aa}}{N}$$

$$Q = \frac{N_{aa}}{N}$$

Allele frequencies

$$p = \frac{2N_{AA} + N_{Aa}}{2N}$$

$$q = \frac{2N_{aa} + N_{Aa}}{2N}$$

Example

In a population with 200 people, in a gene with two alleles (A & a), we observe the genotypes in the table: Calculate the frequencies of alleles A and a.

Genotype	Number	A	a
AA	83		
Aa	62		
aa	55		

Example

In a population with 200 people, in a gene with two alleles (A & a), we observe the genotypes in the table: calculate the frequencies of alleles A and a.

Genotype	Number	A	a
AA	83	166	0
Aa	62	62	62
aa	55	0	110

Example

In a population with 200 people, in a gene with two alleles (A & a), we observe the genotypes in the table: calculate the frequencies of alleles A and a.

Genotype	Number	A	a			
AA	83	166	0	228/400	=	0.57 A
Aa	62	62	62	172/400	=	0.43 a
aa	55	0	110			

Example

In a population with 200 people, in a gene with two alleles (A & a), we observe the genotypes in the table: calculate the frequencies of alleles A and a.

Can we find the frequencies of alleles from those of genotypes?

Genotype	Number	Frequency genotype
AA	83	0.415
Aa	62	0.31
aa	55	0.275

Example

In a population with 200 people, in a gene with two alleles (A & a), we observe the genotypes in the table: calculate the frequencies of alleles A and a.

Can we find the frequencies of alleles from those of genotypes?

Genotype	Number	Frequency genotype	
AA	83	0.415	0.57 A
Aa	62	0.31	1/2
aa	55	0.275	1/2 → 0.43 a

Genes with more alleles

In a population, for the ABO blood group gene, the following absolute genotype frequencies are observed.

Genotype	Absolute frequency
AA	24
AO	12
AB	22
BB	14
BO	16
OO	12
	100

What are the allele frequencies?
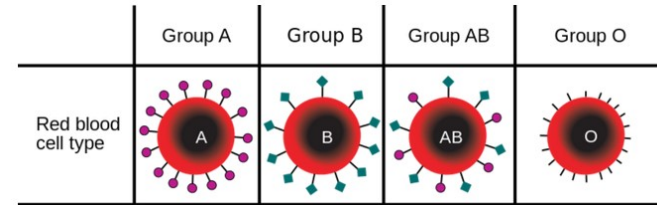
heterozygosity

- Heterozygosity of an organism
  - The ratio of heterozygous gene loci to the total number of gene loci in the genome
- Heterozygosity of a population
  - At a gene locus, it is the ratio of heterozygous genotypes to the total number of individuals in a population
  - It is also called **observed heterozygosity**
- What is the heterozygosity of the population in the previous example?

Plant	Sample	Population	Latitude	Longitude	SNP1	SNP2	SNP3	SNP4	SNP5	SNP6	SNP7	SNP8	SNP9	SNP10	SNP11	SNP12	SNP13	SNP14	SNP15	SNP16	SNP17	SNP18	SNP19	SNP20	SNP21	SNP22	SNP23	SNP24
900	1	Laista1	39.96868386	20.99789507	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
901	2	Laista1	39.97243543	20.99980303	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
902	3	Laista1	39.97902573	20.99238403	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	C/C	A/A
903	4	Laista1	39.98135938	20.99241043	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	C/C	A/G
904	5	Laista1	39.98305714	20.99223054	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	C/C	A/A
909	6	Laista1	39.97902943	20.98282963	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
913	8	Laista2	39.99659551	20.9515825	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	C/C	A/A
915	9	Laista2	40.00702338	20.95387095	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	C/C	A/G
917	10	Laista2	40.00497438	20.95473515	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/G
918	11	Laista2	40.00441432	20.95364733	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	C/C	A/A
919	12	Laista2	40.00696321	20.95912121	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	C/C	A/A
1002	13	Vermio1	40.61530233	21.95176588	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	C/C	A/G
1003	14	Vermio1	40.61636471	21.95325831	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/G
1004	15	Vermio1	40.61729914	21.9536317	C/T	G/G	C/G	A/A	A/A	C/C	A/G	G/G	C/C	A/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	G/G	C/G	A/G	C/T	C/G	A/G	A/C
1005	16	Vermio1	40.61853276	21.95513081	C/C	G/G	C/C	C/C	G/G	T/T	A/A	G/G	A/A	G/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	A/G	A/G	A/G	C/T	C/C	A/G	A/C
1008	17	Vermio1	40.62140865	21.95069267	C/C	G/G	C/C	C/C	A/A	C/T	A/A	G/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
1009	18	Vermio1	40.61919817	21.94745027	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
1011	19	Vermio2	40.61692858	21.94747247	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
1012	20	Vermio2	40.61602284	21.94770116	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
1013	21	Vermio2	40.61517572	21.9476798	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
1014	22	Vermio2	40.61520667	21.94688687	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
1015	23	Vermio2	40.61563394	21.94609362	C/C	C/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
1016	24	Vermio2	40.61550366	21.94535291	C/T	G/G	C/C	A/C	A/G	C/T	A/A	G/G	A/C	G/G	C/T	A/T	C/C	C/C	A/G	A/G	A/G	A/T	C/G	A/G	C/T	C/C	A/G	A/C
3701	25	Tymfi1	39.99978444	20.8170	C/G	C/G	G/C						G/A	A/A			G/G			G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3702	26	Tymfi1	40.00008019	20.8261	C/G	C/G							A/A	A/A			G/G			G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	G/A
3703	27	Tymfi1	40.00240321	20.8179	C/C	G/G	C/C		A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C			G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
3704	28	Tymfi1	40.00058735	20.8187	C/C	G/G	C/C						A/A	G/G			G/G			G/G	G/G	G/G	C/G	A/A	T/T	C/C	C/C	A/G
3707	30	Tymfi1	39.9925894	20.8206	C/C	G/G	C/C	C/C	A/A	T/T	A/A		A/A	A/A			G/G	T/T	C/C	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	G/G
3708	31	Tymfi1	39.99260547	20.8202												T/T	G/G	C/T	C/C	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/G
3709	32	Tymfi1	39.99237061	20.8205												T/T	G/G	C/T	C/C	G/G	G/G	G/G	C/G	A/A	T/T	C/C	C/C	A/G
3711	33	Tymfi2	39.99188837	20.8204	C/G	C/G		C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	C/C	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3712	34	Tymfi2	39.99211359	20.8191	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/T	C/C	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
3714	35	Tymfi2	39.99198699	20.8213	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
3715	36	Tymfi2	40.00122054	20.8161	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
3802	37	Metsovo1	39.80913423	21.1699	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/C	A/A	T/T	C/C	C/C	G/A
3803	38	Metsovo1	39.79671429	21.17854949	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
3804	39	Metsovo1	39.79694374	21.18242887	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/G
3805	40	Metsovo1	39.79701374	21.18382736	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
3808	41	Metsovo1	39.80735672	21.19169771	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
3810	42	Metsovo1	39.79940768	21.19265193	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
3813	43	Metsovo2	39.74956505	21.22406256	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/G
3814	44	Metsovo2	39.75156841	21.23628264	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
3816	45	Metsovo2	39.75295623	21.23139552	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	T/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	C/C	A/A
3818	47	Metsovo2	39.76337286	21.22775652	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/G

In the Laista population, at SNP19, calculate the genotype and allele frequencies and find the observed heterozygosity

Plant	Sample	Population	Latitude	Longitude	SNP1	SNP2	SNP3	SNP4	SNP5	SNP6	SNP7	SNP8	SNP9	SNP10	SNP11	SNP12	SNP13	SNP14	SNP15	SNP16	SNP17	SNP18	SNP19	SNP20	SNP21	SNP22	SNP23	SNP24
900	1	Laista1	39.96868386	20.99789507	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
901	2	Laista1	39.97243543	20.99980303	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
902	3	Laista1	39.97902573	20.99238403	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
903	4	Laista1	39.98135938	20.99241043	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
904	5	Laista1	39.98305714	20.99223054	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
909	6	Laista1	39.97902943	20.98282963	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
913	8	Laista2	39.99659551	20.9515825	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A
915	9	Laista2	40.00702338	20.95387095	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
917	10	Laista2	40.00497438	20.95473515	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
918	11	Laista2	40.00441432	20.95364733	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A
919	12	Laista2	40.00696321	20.95912121	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1002	13	Vermio1	40.61530233	21.95176588	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1003	14	Vermio1	40.61636471	21.95325831	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1004	15	Vermio1	40.61729914	21.9536317	C/T	G/G	C/G	A/A	A/A	C/C	A/G	G/G	C/C	A/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	G/G	C/G	A/G	C/T	C/G	A/G	A/C
1005	16	Vermio1	40.61853276	21.95513081	C/C	G/G	C/C	C/C	G/G	T/T	A/A	G/G	A/A	G/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	A/G	A/G	A/G	C/T	C/C	A/G	A/C
1008	17	Vermio1	40.62140865	21.95069267	C/C	G/G	C/C	C/C	A/A	C/T	A/A	G/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1009	18	Vermio1	40.61919817	21.94745027	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1011	19	Vermio2	40.61692858	21.94747247	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1012	20	Vermio2	40.61602284	21.94770116	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1013	21	Vermio2	40.61517572	21.9476798	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1014	22	Vermio2	40.61520667	21.94688687	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1015	23	Vermio2	40.61563394	21.94609362	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1016	24	Vermio2	40.61550366	21.94535291	C/T	G/G	C/C	A/C	A/G	C/T	A/A	G/G	A/C	G/G	C/T	A/T	C/C	C/C	A/G	A/G	A/G	A/G	C/C	A/G	C/T	C/C	A/G	A/C
3701	25	Tymfi1	39.99978444	20.8170	C/C	G/G	C/G	C/C	A/A	T/T	A/A	A/A	G/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3702	26	Tymfi1	40.00008019	20.826	C/C	G/G	C/G	C/C	A/A	T/T	A/A	A/A	G/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3703	27	Tymfi1	40.00240321	20.81791	C/C	G/G	C/C	C/C	A/A	A/G	A/G	A/A	G/G	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3704	28	Tymfi1	40.00058735	20.8187	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	G/G	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3707	30	Tymfi1	39.9925894	20.82069	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	G/G	A/A	T/T	G/G	T/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/G
3708	31	Tymfi1	39.99260547	20.82029	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	G/G	A/A	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3709	32	Tymfi2	39.99237061	20.82059	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	G/G	A/A	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3711	33	Tymfi2	39.99188837	20.82042	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3712	34	Tymfi2	39.99211359	20.8191	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3714	35	Tymfi2	39.99198699	20.82138	C/C	G/G	C/C	C/C	A/A	A/G	A/A	A/A	G/G	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3715	36	Tymfi2	40.00122054	20.8161	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	G/G	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3802	37	Metsovo1	39.80913423	21.16995	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3803	38	Metsovo1	39.79671429	21.17854	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	G/G	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3804	39	Metsovo1	39.79694374	21.18242	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	A/A	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3805	40	Metsovo1	39.79701374	21.18382	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3808	41	Metsovo1	39.80735672	21.19169	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	G/G	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3810	42	Metsovo1	39.79940768	21.19265	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	G/G	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3813	43	Metsovo2	39.74956505	21.22406	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3814	44	Metsovo2	39.75156841	21.23628	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3816	45	Metsovo2	39.75295623	21.23139552	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	T/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3818	47	Metsovo2	39.76337286	21.22775652	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A

In the Laista population, at SNP18, calculate the genotype and allele frequencies and find the observed heterozygosity

In which of the two SNPs is there more variation for this population?

Metrics of genetic diversity

- Observed heterozygosity is often used to express the magnitude of genetic diversity

  ◦ But it is not always the appropriate indicator

- The number of alleles observed in a gene in a population is the simplest measure of diversity

  ◦ Also called abundance of alleles *n*

Plant	Sample	Population	Latitude	Longitude	SNP1	SNP2	SNP3	SNP4	SNP5	SNP6	SNP7	SNP8	SNP9	SNP10	SNP11	SNP12	SNP13	SNP14	SNP15	SNP16	SNP17	SNP18	SNP19	SNP20	SNP21	SNP22	SNP23	SNP24
900	1	Laista1	39.96868386	20.99789507	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
901	2	Laista1	39.97243543	20.99980303	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
902	3	Laista1	39.97902573	20.99238403	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
903	4	Laista1	39.98135938	20.99241043	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
904	5	Laista1	39.98305714	20.99223054	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
909	6	Laista1	39.97902943	20.98282963	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
913	8	Laista2	39.99659551	20.9515825	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A
915	9	Laista2	40.00702338	20.95387095	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
917	10	Laista2	40.00497438	20.95473515	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
918	11	Laista2	40.00441432	20.95364733	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A
919	12	Laista2	40.00696321	20.95912121	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1002	13	Vermio1	40.61530233	21.95176588	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1003	14	Vermio1	40.61636471	21.95325831	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1004	15	Vermio1	40.61729914	21.9536317	C/T	G/G	C/G	A/A	A/A	C/C	A/G	G/G	C/C	A/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	G/G	C/G	A/G	C/T	C/G	A/G	A/C
1005	16	Vermio1	40.61853276	21.95513081	C/C	G/G	C/C	C/C	G/G	T/T	A/A	G/G	A/A	G/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	A/G	A/G	A/G	C/T	C/C	A/G	A/C
1008	17	Vermio1	40.62140865	21.95069267	C/C	G/G	C/C	C/C	A/A	C/T	A/A	G/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1009	18	Vermio1	40.61919817	21.94745027	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A
1011	19	Vermio2	40.61692858	21.94747247	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1012	20	Vermio2	40.61602284	21.94770116	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1013	21	Vermio2	40.61517572	21.9476798	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1014	22	Vermio2	40.61520667	21.94688687	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1015	23	Vermio2	40.61563394	21.94609362	C/C	C/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1016	24	Vermio2	40.61550366	21.94535291	C/T	G/G	C/C	A/C	A/G	C/T	A/A	G/G	A/C	G/G	C/T	A/T	C/C	C/C	A/G	A/G	A/G	A/G	C/C	A/G	C/T	C/C	A/G	A/C
3701	25	Tymfi1	39.99978444	20.81702219	C/C	G/G	C/C	C/C	A/A	C/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3702	26	Tymfi1	40.00008019	20.82615545	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
3703	27	Tymfi1	40.00240321	20.81791944	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
3704	28	Tymfi1	40.00058735	20.81870654	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3707	30	Tymfi1	39.9925894	20.82069406	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	T/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/G
3708	31	Tymfi1	39.99260547	20.82029515	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3709	32	Tymfi2	39.99237061	20.82050982	C/C	G/G	C/C	C/C	A/A	A/A	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G						
3711	33	Tymfi2	39.99188837	20.82042212	C/C	G/G	C/C	C/C																				
3712	34	Tymfi2	39.99211359	20.8191118	C/C	G/G																						
3714	35	Tymfi2	39.99198699	20.82138952	C/C																		C/C					
3715	36	Tymfi2	40.00122054	20.81618245																			C/C					
3802	37	Metsovo1	39.80913423	21.16995889	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	G/A
3803	38	Metsovo1	39.79671429	21.17854949	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3804	39	Metsovo1	39.79694374	21.18242887	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3805	40	Metsovo1	39.79701374	21.18382736	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A
3808	41	Metsovo1	39.80735672	21.19169771	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3810	42	Metsovo1	39.79940768	21.19265193	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3813	43	Metsovo2	39.74956505	21.22406256	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3814	44	Metsovo2	39.75156841	21.23628264	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3816	45	Metsovo2	39.75295623	21.23139552	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	T/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3818	47	Metsovo2	39.76337286	21.22775652	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A

At SNP18, which population has greater allele abundance, Laista or Vermio?

38

Plant	Sample	Population	Latitude	Longitude	SNP1	SNP2	SNP3	SNP4	SNP5	SNP6	SNP7	SNP8	SNP9	SNP10	SNP11	SNP12	SNP13	SNP14	SNP15	SNP16	SNP17	SNP18	SNP19	SNP20	SNP21	SNP22	SNP23	SNP24
900	1	Laista1	39.96868386	20.99789507	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
901	2	Laista1	39.97243543	20.99980303	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
902	3	Laista1	39.97902573	20.99238403	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
903	4	Laista1	39.98135938	20.99241043	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/G
904	5	Laista1	39.98305714	20.99223054	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
909	6	Laista1	39.97902943	20.98282963	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
913	8	Laista2	39.99659551	20.9515825	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
915	9	Laista2	40.00702338	20.95387095	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/G
917	10	Laista2	40.00497438	20.95473515	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/G
918	11	Laista2	40.00441432	20.95364733	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
919	12	Laista2	40.00696321	20.95912121	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1002	13	Vermio1	40.61530233	21.95176588	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
1003	14	Vermio1	40.61636471	21.95325831	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1004	15	Vermio1	40.61729914	21.9536317	C/T	G/G	C/G	A/A	A/A	C/C	A/G	G/G	C/C	A/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	G/G	C/G	A/G	C/T	C/G	A/G	A/C
1005	16	Vermio1	40.61853276	21.95513081	C/C	G/G	C/C	C/C	G/G	T/T	A/A	G/G	A/A	G/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	A/G	A/G	A/G	C/T	C/C	A/G	A/C
1008	17	Vermio1	40.62140865	21.95069267	C/C	G/G	C/C	C/C	A/A	C/T	A/A	G/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1009	18	Vermio1	40.61919817	21.94745027	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1011	19	Vermio2	40.61692858	21.94747247	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1012	20	Vermio2	40.61602284	21.94770116	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1013	21	Vermio2	40.61517572	21.9476798	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1014	22	Vermio2	40.61520667	21.94688687	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1015	23	Vermio2	40.61563394	21.94609362	C/C	C/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1016	24	Vermio2	40.61550366	21.94535291	C/T	G/G	C/C	A/C	A/G	C/T	A/A	G/G	A/C	G/G	C/T	A/T	C/C	C/C	A/G	A/G	A/G	A/G	C/G	A/G	C/T	C/C	A/G	A/C
3701	25	Tymfi1	39.99978444	20.81702219	C/C	G/G	C/C	C/C	A/A	C/C	A/A	G/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	G/A
3702	26	Tymfi1	40.00008019	20.82615545	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3703	27	Tymfi1	40.00240321	20.81791944	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3704	28	Tymfi1	40.00058735	20.81870654	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3707	30	Tymfi1	39.9925894	20.82069406	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	T/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/G
3708	31	Tymfi1	39.99260547	20.82029515	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3709	32	Tymfi2	39.99237061	20.82050882	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3711	33	Tymfi2	39.99188837	20.82042212	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3712	34	Tymfi2	39.99211359	20.8191118	C/G	G/G	C/C	C/C	A/A	C/C	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3714	35	Tymfi2	39.99198699	20.82138952	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3715	36	Tymfi2	40.00122054	20.81618245	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3802	37	Metsovo1	39.80913423	21.16995889	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	G/A
3803	38	Metsovo1	39.79671429	21.17854949	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3804	39	Metsovo1	39.79694374	21.18242887	C/C	G/G	C/C	C/C	A/A	A/A	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
3805	40	Metsovo1	39.79701374	21.18382736	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3808	41	Metsovo1	39.80735672	21.19169771	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3810	42	Metsovo1	39.79940768	21.19265193	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3813	43	Metsovo2	39.74956505	21.22406256	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3814	44	Metsovo2	39.75156841	21.23628264	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3816	45	Metsovo2	39.75295623	21.23139552	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	T/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3818	47	Metsovo2	39.76337286	21.22775652	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/G

At SNP24, which population has greater allele abundance, Laista or Vermio?

Indicators of equal distribution

- The number of alleles does not take their frequency into account

  ○ Rare and common alleles are weighted equally

- But allele frequencies affect genetics diversity, so we use indices of equal distribution of allele frequencies

  ○ Which of the two populations has the greater genetic diversity?

		Population A	Population B
A	p	0.1	0.55
a	q	0.9	0.45

Functional number of alleles

- To find the number of alleles that are relatively frequent in the population we use the functional number of alleles (n_e):

$$n_e = \left(\sum p_i^2 \right)^{-1}$$

- It is 1 / the sum of the squares of the frequencies of all alleles in a population

Expected heterozygosity

- Derivative of functional number of alleles is a metric, most often used in genetic research

  - It is called gene dispersion or **expected heterozygosity** and is denoted by H_e

  - It is the probability that two random alleles out of a sample will be different

$$H_e = 1 - \sum p_i^2$$

  - It is 1 - the sum of the squares of the frequencies of all the alleles of a population

Indicators of equal distribution

- Calculate the functional number of alleles and the expected heterozygosity for these two populations

		Population A	Population B
A	p	0.1	0.55
a	q	0.9	0.45

Plant	Sample	Population	Latitude	Longitude	SNP1	SNP2	SNP3	SNP4	SNP5	SNP6	SNP7	SNP8	SNP9	SNP10	SNP11	SNP12	SNP13	SNP14	SNP15	SNP16	SNP17	SNP18	SNP19	SNP20	SNP21	SNP22	SNP23	SNP24
900	1	Laista1	39.96868386	20.99789507	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
901	2	Laista1	39.97243543	20.99980303	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
902	3	Laista1	39.97902573	20.99238403	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
903	4	Laista1	39.98135938	20.99241043	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/G
904	5	Laista1	39.98305714	20.99223054	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
909	6	Laista1	39.97902943	20.98282963	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
913	8	Laista2	39.99659551	20.9515825	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
915	9	Laista2	40.00702338	20.95387095	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/G
917	10	Laista2	40.00497438	20.95473515	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
918	11	Laista2	40.00441432	20.95364733	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
919	12	Laista2	40.00696321	20.95912121	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1002	13	Vermio1	40.61530233	21.95176588	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
1003	14	Vermio1	40.61636471	21.95325831	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1004	15	Vermio1	40.61729914	21.9536317	C/T	G/G	C/G	A/A	A/A	C/C	A/G	G/G	C/C	A/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	G/G	C/G	A/G	C/T	C/G	A/G	A/C
1005	16	Vermio1	40.61853276	21.95513081	C/C	G/G	C/C	C/C	G/G	T/T	A/A	G/G	A/A	G/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	A/G	A/G	A/G	C/T	C/C	A/G	A/C
1008	17	Vermio1	40.62140865	21.95069267	C/C	G/G	C/C	C/C	A/A	C/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1009	18	Vermio1	40.61919817	21.94745027	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1011	19	Vermio2	40.61692858	21.94747247	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1012	20	Vermio2	40.61602284	21.94770116	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1013	21	Vermio2	40.61517572	21.9476798	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1014	22	Vermio2	40.61520667	21.94688687	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1015	23	Vermio2	40.61563394	21.94609362	C/C	C/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1016	24	Vermio2	40.61550366	21.94535291	C/T	G/G	C/C	A/C	A/G	C/T	A/A	G/G	A/C	G/G	C/T	A/T	C/C	C/C	A/G	A/G	A/G	A/G	C/G	A/G	C/T	C/C	A/G	A/G
3701	25	Tymfi1	39.99978444	20.81702219	C/C	G/G	C/C	C/C	A/A	C/T	A/A	G/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3702	26	Tymfi1	40.00008019	20.82615545	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
3703	27	Tymfi1	40.00240321	20.81791944	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3704	28	Tymfi1	40.00058735	20.81870654	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3707	30	Tymfi1	39.9925894	20.82069406	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	T/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/G
3708	31	Tymfi2	39.99260547	20.82029515	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3709	32	Tymfi2	39.99237061	20.82059882	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3711	33	Tymfi2	39.99188837	20.82042212	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3712	34	Tymfi2	39.99211359	20.8191118	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3714	35	Tymfi2	39.99198699	20.82138952	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3715	36	Tymfi2	40.00122054	20.81618245	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3802	37	Metsovo1	39.80913423	21.16995889	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/C	A/A	A/A	T/T	C/C	G/G	G/A
3803	38	Metsovo1	39.79671429	21.17854949	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3804	39	Metsovo1	39.79694374	21.18242887	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	C/G	C/G	A/A	A/A	T/T	C/C	G/G	A/A
3805	40	Metsovo1	39.79701374	21.18382736	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3808	41	Metsovo1	39.80735672	21.19169771	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3810	42	Metsovo1	39.79940768	21.19265193	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	C/C	G/G	G/G	G/G	G/G	A/A	G/G	T/T	C/C	G/G	A/G
3813	43	Metsovo2	39.74956505	21.22406256	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3814	44	Metsovo2	39.75156841	21.23628264	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3816	45	Metsovo2	39.75295623	21.23139552	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3818	47	Metsovo2	39.76337286	21.22775652	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A	

At SNP24, calculate the expected heterozygosity for the Laista, Vermio and Tymfi populations.

Expected heterozygosity in humans from the Human Genome Diversity Project
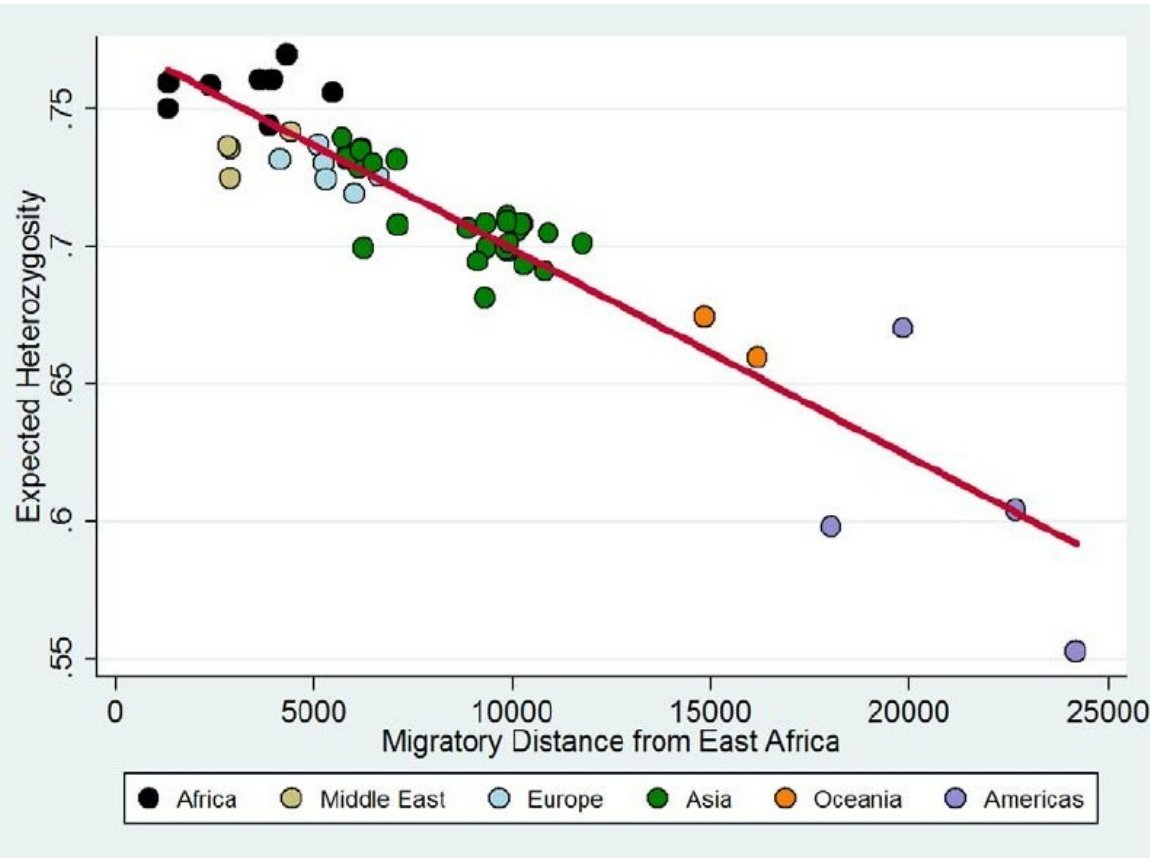
Variation in expected heterozygosity in specific human populations and at 783 SSR gene loci, in relation to distance from eastern Africa.

The high correlation (R^2) confirms the "out of Africa" scenario (Ramachandran et al. 2005)

45

Minor Allele Frequency - MAF

- The frequency of the **second** most frequent allele for a given SNP

    ◦ If the MAF is low, it means that the major (most frequent) allele for the SNP is more or less conserved and remains in the population

    ◦ When the SNP has two alleles, the MAF is the frequency of the rarer allele

- MAF helps differentiate common and rare SNP variants in a population

Plant	Sample	Population	Latitude	Longitude	SNP1	SNP2	SNP3	SNP4	SNP5	SNP6	SNP7	SNP8	SNP9	SNP10	SNP11	SNP12	SNP13	SNP14	SNP15	SNP16	SNP17	SNP18	SNP19	SNP20	SNP21	SNP22	SNP23	SNP24
900	1	Laista1	39.96868386	20.99789507	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
901	2	Laista1	39.97243543	20.99980303	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
902	3	Laista1	39.97902573	20.99238403	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
903	4	Laista1	39.98135938	20.99241043	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	C/C	A/G
904	5	Laista1	39.98305714	20.99223054	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
909	6	Laista1	39.97902943	20.98282963	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
913	8	Laista2	39.99659551	20.9515825	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
915	9	Laista2	40.00702338	20.95387095	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
917	10	Laista2	40.00497438	20.95473515	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/G
918	11	Laista2	40.00441432	20.95364733	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
919	12	Laista2	40.00696321	20.95912121	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1002	13	Vermio1	40.61530233	21.95176588	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
1003	14	Vermio1	40.61636471	21.95325831	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1004	15	Vermio1	40.61729914	21.9536317	C/T	G/G	C/G	A/A	A/A	C/C	A/G	G/G	C/C	A/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	G/G	C/G	A/G	C/T	C/G	A/G	A/C
1005	16	Vermio1	40.61853276	21.95513081	C/C	G/G	C/C	C/C	G/G	T/T	A/A	G/G	A/A	G/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	A/G	A/G	A/G	C/T	C/C	A/G	A/C
1008	17	Vermio1	40.62140865	21.95069267	C/C	G/G	C/C	C/C	A/A	C/T	A/A	G/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1009	18	Vermio1	40.61919817	21.94745027	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1011	19	Vermio2	40.61692858	21.94747247	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1012	20	Vermio2	40.61602284	21.94770116	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1013	21	Vermio2	40.61517572	21.9476798	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1014	22	Vermio2	40.61520667	21.94688687	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1015	23	Vermio2	40.61563394	21.94609362	C/C	C/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1016	24	Vermio2	40.61550366	21.94535291	C/T	G/G	C/C	A/C	A/G	C/T	A/A	G/G	A/C	G/G	C/T	A/T	C/C	C/C	A/G	A/G	A/G	A/G	C/G	A/G	C/T	C/C	A/G	A/G
3701	25	Tymfi1	39.99978444	20.81702219	C/C	G/G	C/C	C/C	A/A	C/C	G/A	A/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	G/C	A/A	T/T	C/C	G/G	G/A
3702	26	Tymfi1	40.00008019	20.82615545	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3703	27	Tymfi1	40.00240321	20.81791944	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3704	28	Tymfi1	40.00058735	20.81870654	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3707	30	Tymfi1	39.9925894	20.82069406	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	T/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/G
3708	31	Tymfi2	39.99260547	20.82029515	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3709	32	Tymfi2	39.99237061	20.82059882	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3711	33	Tymfi2	39.99188837	20.82042212	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3712	34	Tymfi2	39.99211359	20.8191118	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3714	35	Tymfi2	39.99198699	20.82138952	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3715	36	Tymfi2	40.00122054	20.81618245	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3802	37	Metsovo1	39.80913423	21.16995889	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/C	A/A	T/T	C/C	G/G	G/A
3803	38	Metsovo1	39.79671429	21.17854949	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3804	39	Metsovo1	39.79694374	21.18242887	C/C	G/G	C/C	C/C	A/A	A/A	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
3805	40	Metsovo1	39.79701374	21.18382736	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A
3808	41	Metsovo1	39.80735672	21.19169771	C/C	G/G	C/C	C/C	A/A	A/A	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A
3810	42	Metsovo1	39.79940768	21.19265193	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/G
3813	43	Metsovo2	39.74956505	21.22406256	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3814	44	Metsovo2	39.75156841	21.23628264	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3816	45	Metsovo2	39.75295623	21.23139552	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3818	47	Metsovo2	39.76337286	21.22775652	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A

At SNP24, calculate the MAF index for the Laista, Vermio and Tymfi populations. Which allele is most common in each population?

genetic distance

- The difference in genetic makeup (allele frequencies) between two populations is measured by genetic distance

  ○ There are many different methods of measuring genetic distance

- A simple genetic distance (Gregorius 1984):

  ○ half of the total absolute values of the differences between the allele frequencies of two populations

$$d_0 = \frac{1}{2} \sum \left| p_i - p_i' \right|$$

Genetic distance

Population A		Population B		
A	a	A	a	
p	q	p'	Q'	d0
1	0	1	0	0
0.9	0.1	1	0	0.1
0.5	0.5	1	0	0.5
0.4	0.6	0.6	0.4	0.2
0	1	1	0	1

Plant	Sample	Population	Latitude	Longitude	SNP1	SNP2	SNP3	SNP4	SNP5	SNP6	SNP7	SNP8	SNP9	SNP10	SNP11	SNP12	SNP13	SNP14	SNP15	SNP16	SNP17	SNP18	SNP19	SNP20	SNP21	SNP22	SNP23	SNP24
900	1	Laista1	39.96868386	20.99789507	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
901	2	Laista1	39.97243543	20.99980303	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
902	3	Laista1	39.97902573	20.99238403	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
903	4	Laista1	39.98135938	20.99241043	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/G
904	5	Laista1	39.98305714	20.99223054	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
909	6	Laista1	39.97902943	20.98282963	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
913	8	Laista2	39.99659551	20.9515825	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
915	9	Laista2	40.00702338	20.95387095	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
917	10	Laista2	40.00497438	20.95473515	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
918	11	Laista2	40.00441432	20.95364733	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
919	12	Laista2	40.00696321	20.95912121	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1002	13	Vermio1	40.61530233	21.95176588	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
1003	14	Vermio1	40.61636471	21.95325831	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1004	15	Vermio1	40.61729914	21.9536317	C/T	G/G	C/G	A/A	A/A	C/C	A/G	G/G	C/C	A/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	G/G	C/G	A/G	C/T	C/G	A/G	A/C
1005	16	Vermio1	40.61853276	21.95513081	C/C	G/G	C/C	C/C	G/G	T/T	A/A	G/G	A/A	G/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	A/G	A/G	A/G	C/T	C/C	A/G	A/C
1008	17	Vermio1	40.62140865	21.95069267	C/C	G/G	C/C	C/C	A/A	C/T	A/A	G/A	A/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1009	18	Vermio1	40.61919817	21.94745027	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1011	19	Vermio2	40.61692858	21.94747247	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1012	20	Vermio2	40.61602284	21.94770116	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1013	21	Vermio2	40.61517572	21.9476798	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1014	22	Vermio2	40.61520667	21.94688687	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1015	23	Vermio2	40.61563394	21.94609362	C/C	C/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1016	24	Vermio2	40.61550366	21.94535291	C/T	G/G	C/C	A/C	A/G	C/T	A/A	G/G	A/C	G/G	C/T	A/T	C/C	C/C	A/G	A/G	A/G	A/G	C/G	A/G	C/T	C/C	A/G	A/G
3701	25	Tymfi1	39.99978444	20.81702219	C/C	G/G	C/C	C/C	A/A	C/T	A/A	G/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3702	26	Tymfi1	40.00008019	20.82615545	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3703	27	Tymfi1	40.00240321	20.81791944	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3704	28	Tymfi1	40.00058735	20.81870654	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3707	30	Tymfi1	39.9925894	20.82069406	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	T/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/G
3708	31	Tymfi1	39.99260547	20.82029515	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3709	32	Tymfi2	39.99237061	20.82059882	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	A/A	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3711	33	Tymfi2	39.99188837	20.82042212	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/C	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3712	34	Tymfi2	39.99211359	20.8191118	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3714	35	Tymfi2	39.99198699	20.82138952	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3715	36	Tymfi2	40.00122054	20.81618245	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	A/A	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3802	37	Metsovo1	39.80913423	21.16995889	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3803	38	Metsovo1	39.79671429	21.17854949	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3804	39	Metsovo1	39.79694374	21.18242887	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3805	40	Metsovo1	39.79701374	21.18382736	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
3808	41	Metsovo1	39.80735672	21.19169771	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3810	42	Metsovo1	39.79940768	21.19265193	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3813	43	Metsovo2	39.74956505	21.22406256	C/C																						C/C	G/G	A/G
3814	44	Metsovo2	39.75156841	21.23628264		G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G
3816	45	Metsovo2	39.75295623	21.23139552	C/C											T/T	C/C	C/C	G/G	G/C	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G
3818	47	Metsovo2	39.76337286	21.22775652	C/C											T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/G

At SNP24, calculate the pairwise distances for the Laista, Vermio and Tymfi populations.

Table of genetic distances

	Askifus	Aradena	Zografou	Alepochori
Askifus	0,000			
Aradena	0.142	0,000		
Zografou	0.257	0.259	0,000	
Alepochori	0.267	0.270	0.161	0,000

Cupressus sempervirens
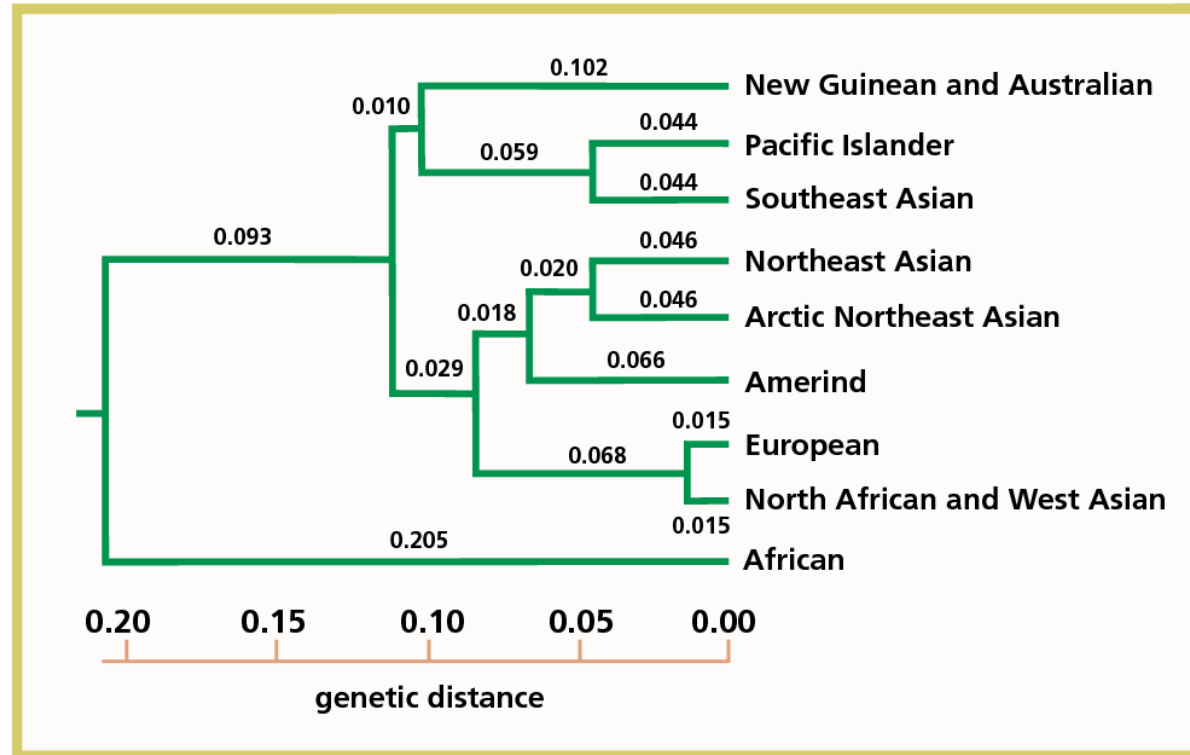
Dendrogram

- We can visualize genetic
  distances with a dendrogram
  - e.g. UPGMA
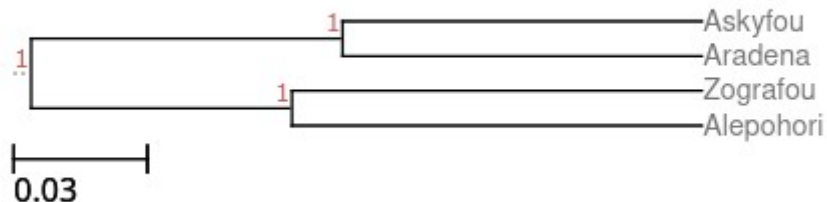
Phylogenetic tree

- This is an illustration of a phylogenetic hypothesis

- It can be formed by genetic distances

- The phylogenetic tree of the human races

  - The application of molecular genetic approaches to the study of human evolution L.Cavalli-Sforza, M. Feldman 2003, Nature Genetics

BOB CRIMI

Plant	Sample	Population	Latitude	Longitude	SNP1	SNP2	SNP3	SNP4	SNP5	SNP6	SNP7	SNP8	SNP9	SNP10	SNP11	SNP12	SNP13	SNP14	SNP15	SNP16	SNP17	SNP18	SNP19	SNP20	SNP21	SNP22	SNP23	SNP24
900	1	Laista1	39.96868386	20.99789507	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
901	2	Laista1	39.97243543	20.99980303	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
902	3	Laista1	39.97902573	20.99238403	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
903	4	Laista1	39.98135938	20.99241043	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	C/C	A/G
904	5	Laista1	39.98305714	20.99223054	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
909	6	Laista1	39.97902943	20.98282963	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
913	8	Laista2	39.99659551	20.9515825	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
915	9	Laista2	40.00702338	20.95387095	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
917	10	Laista2	40.00497438	20.95473515	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/G
918	11	Laista2	40.00441432	20.95364733	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
919	12	Laista2	40.00696321	20.95912121	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1002	13	Vermio1	40.61530233	21.95176588	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
1003	14	Vermio1	40.61636471	21.95325831	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1004	15	Vermio1	40.61729914	21.9536317	C/T	G/G	C/G	A/A	A/A	C/C	A/G	G/G	C/C	A/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	G/G	C/G	A/G	C/T	C/G	A/G	A/C
1005	16	Vermio1	40.61853276	21.95513081	C/C	G/G	C/C	C/C	G/G	T/T	A/A	G/G	A/A	G/G	C/T	A/G	C/C	C/T	A/G	A/G	A/G	A/G	A/G	A/G	C/T	C/C	A/G	A/C
1008	17	Vermio1	40.62140865	21.95069267	C/C	G/G	C/C	C/C	A/A	C/T	A/A	G/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1009	18	Vermio1	40.61919817	21.94745027	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1011	19	Vermio2	40.61692858	21.94747247	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1012	20	Vermio2	40.61602284	21.94770116	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1013	21	Vermio2	40.61517572	21.9476798	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1014	22	Vermio2	40.61520667	21.94688687	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1015	23	Vermio2	40.61563394	21.94609362	C/C	C/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
1016	24	Vermio2	40.61550366	21.94535291	C/T	G/G	C/C	A/C	A/G	C/T	A/A	G/G	A/C	G/G	C/T	A/T	C/C	C/C	A/G	A/G	A/G	A/G	C/G	A/G	C/T	C/C	A/G	A/G
3701	25	Tymfi1	39.99978444	20.81702219	C/C	G/G	C/C	C/C	A/A	C/C	A/A	G/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3702	26	Tymfi1	40.00008019	20.82615545	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3703	27	Tymfi1	40.00240321	20.81791944	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3704	28	Tymfi1	40.00058735	20.81870654	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3707	30	Tymfi1	39.9925894	20.82069406	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	T/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/G
3708	31	Tymfi1	39.99260547	20.82029515	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/G
3709	32	Tymfi2	39.99237061	20.82059882	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3711	33	Tymfi2	39.99188837	20.82042212	C/C	G/G	C/C	C/C	A/A	T/T	A/A	A/A	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3712	34	Tymfi2	39.99211359	20.8191118	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3714	35	Tymfi2	39.99198699	20.82138952	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3715	36	Tymfi2	40.00122054	20.81618245	C/C	G/G	C/C	C/C	A/A	C/C	A/A	A/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3802	37	Metsovo1	39.80913423	21.16995889	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/A	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	G/A
3803	38	Metsovo1	39.79671429	21.17854949	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3804	39	Metsovo1	39.79694374	21.18242887	C/C	G/G	C/C	C/C	A/A	A/A	A/A	G/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	C/G	A/A	T/T	C/C	G/G	A/A
3805	40	Metsovo1	39.79701374	21.18382736	C/C																						G/G	A/A
3808	41	Metsovo1	39.80735672	21.19169771																							G/G	A/A
3810	42	Metsovo1	39.79940768	21.19265193	C/C																						G/G	A/A
3813	43	Metsovo2	39.74956505	21.22406256	C/C																						G/G	A/A
3814	44	Metsovo2	39.75156841	21.23628264	C/C	G/G	C/C	C/C	A/A	A/A	A/A	G/G	A/A	G/G	T/T	G/G	C/T	C/C	G/G	G/G	G/G	G/G	C/C	A/A	T/T	C/C	G/G	A/A
3816	45	Metsovo2	39.75295623	21.23139552	C/C	G/G	C/C	C/C	A/A	T/T	A/A	G/G	A/A	G/G	T/T	G/G	T/T	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A
3818	47	Metsovo2	39.76337286	21.22775652	C/C	G/G	C/C	C/C	A/A	C/T	A/A	A/G	A/A	G/G	T/T	G/G	C/C	C/C	G/G	G/G	G/G	G/G	G/G	A/A	T/T	C/C	G/G	A/A

AtSNP24, from the genetic distances for the Laista, Vermio and Tymfi populations make a table and a UPGMA tree

54

Exercise

In the table you see the frequencies of the two alleles of the Hb gene responsible for the occurrence of sickle cell anemia, in Muslim populations of India.

Which population has the greatest expected heterozygosity?

Calculate pairwise genetic distances for all populations, construct a distance matrix and a UPGMA dendrogram.

Populations	Hb(p)	Hbs(q)
Sheikhs	0.8398	0.1602
Syed	0.8748	0.1252
Pathan	0.8756	0.1244
Mughal	0.8304	0.1696
Meitei	0.8469	0.1531
Naga	0.914	0.086

Shah et al. 2012

Why do we care about genetic diversity?

- It is about biodiversity within a species

  ◦ It makes it possible**adjustment**of organizations in changingenvironmental conditions

  ◦ It is the basis of human health and all human needs(e.g. nutrition, medicine, economy)

  ◦ It is the basis of evolution, and therefore of life on earth

ποικιλότητα

ομοιομορφία

Αλλαγή κλίματος

Επιβίωση

Εξαφάνιση!!