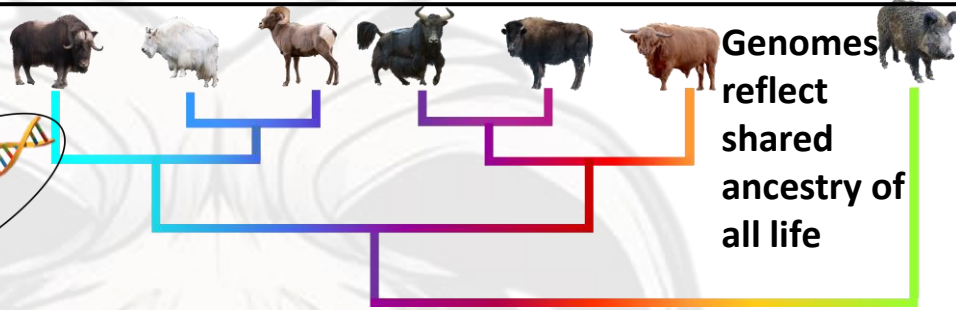
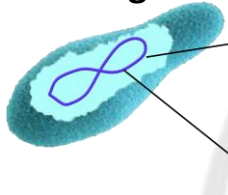




Genomics

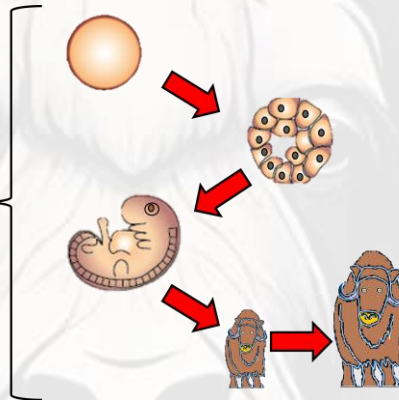


Genomes (DNA) found in all organisms



Genomes reflect shared ancestry of all life

Genomes instruct cells to make organisms from conception to maturity



In mammals, genomes represent two volume 'recipe books', with a volume coming from each parent

Specific instructions (genes) are written in a genomic language (a genetic or DNA 'code') made of a 4-letter alphabet (nucleotides)

FOUR LETTER ALPHABET (NUCLEOTIDES)

AGTCACAGTCA

INSTRUCTIONS (GENES)

ATG ACT AAT TGT CCG ATG ...

AGTCACAGTCTCTGAAGTCACAGTCTCTGA

MUTATION

ACTCACAGTCTCTGAAGTCACAGTCTCTIA

PARENT



OFFSPRING



VARIATION!

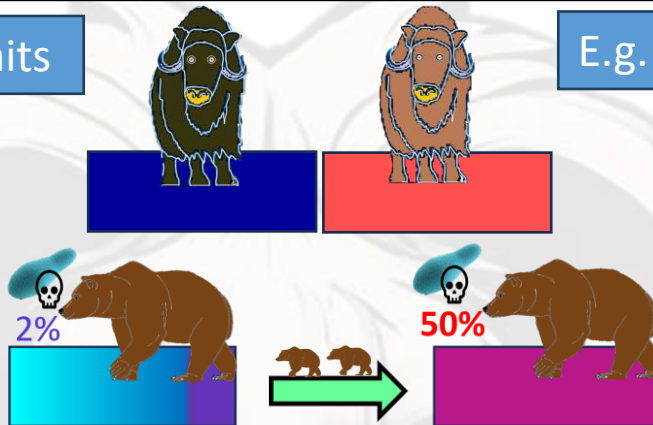
Variation exists in genes due to mutation producing nucleotide changes (SNPs). This may result in variable traits which we can see to preserve, harvest and manage.

Scanning species for large numbers of nucleotide variants (SNPs) from whole genome sequencing technology forms the basis for multiple genomics-based tool applications

Whole Genome Sequencing Process: 1) Sequence a high-quality reference genome for species ; 2) Sequence multiple genomes from different populations using reference genome as guide; 3) Identify varying genomic areas (e.g., SNPs) as markers for tools.

Genomic basis of traits

Populations may vary in genomic diversity underpinning desirable traits (e.g., pelt color/quality, immunity)

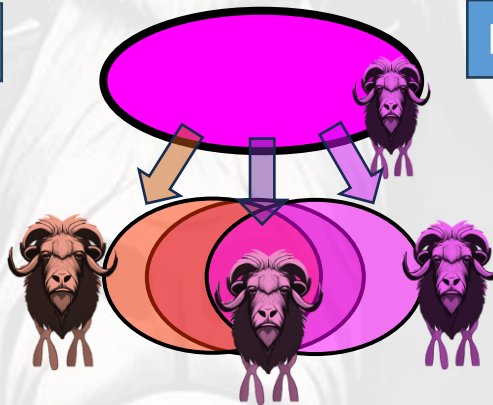


E.g.

Linking **SNPs** with traits may identify useful genes which could be introduced into vulnerable populations

Population structure

Outwardly indistinct populations with limited interbreeding may reflect multiple independent or semi-independent populations

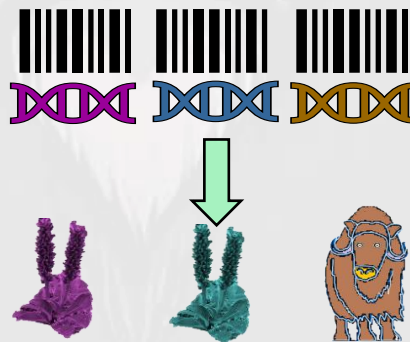


E.g.

Thousands to millions of **SNPs** can identify hidden populations and identify inbreeding

Metagenomics

Analysis of **DNA barcodes** (species-specific DNA tags) may identify multiple species at once and place them in a broader ecosystem context



E.g.

Change in food eaten by Muskoxen may be monitored in response to climate-induced shifts in vegetation

Environmental DNA

Non-invasive sampling may democratize, scale-up and empower community biodiversity surveys



E.g.

Informative predictions of future northerly movements by southern species (e.g., invasive species).

Funding



ARCTIC



Organizers

