Populations

Population Dynamics at Play

Exploratory Game Orientation

This game aims to simulate the different mechanisms involved in the evolution of populations that change by the increase and decrease of genetic diversity through mechanisms such as: mutation, genetic recombination, migration, genetic drift, gene flow, natural and sexual selection, bottleneck effect, founder effect, panmixia, inbreeding, and outbreeding. To simplify the comprehension of these processes, we eliminated the chronological order, condensed their scale (thousands of years) to the game's duration, and focused only on the "colour" characteristic, not considering other multiple characteristics or the genetic diversity derived from genetic recombination during reproduction.

PLAYERS
3-5

AGES
14+

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BY NC ND

REPÚBLICA PORTUGUESA

fct Fundação para a Ciência e a Tecnologia

Ancestry Traveller

Populations

PROJECT "HUMAN DIVERSITY ALONG THE MAGALHÃES CIRCUMNAVIGATION SPACE: GENETICS, HISTORY AND CULTURE"

The Voyage

This game was developed in the scope of a project that came to rise within the celebrations of the 500th anniversary of the circumnavigation voyage. The Voyage carried through by Fernão Magalhães (1519 - 1522) may be considered the first-ever global voyage. In a way, this first circumnavigation replicated, by sea and in reverse, the great voyage of the *Homo sapiens* (modern man).

PROPOSTA DE EXPLORAÇÃO:

Fernão Magalhães and Juan Sebastián Elcano's Voyage is not directly broached in the **game "Populations".**

To further explore this topic, we suggest:

1. Explore Magalhães's full journey in the **magalhaes2020 app**, produced by the newspaper Expresso.
2. Read **"Series: Encounters, equivocations, and extensions of memory: legacies of the circumnavigation voyage"** written by researchers in our project, offering a critical perspective on the history of the voyage trailed by Magalhães and Elcano.
3. Use a didactic tool created in this project, **3D Globe**, and associated instructions. One of our suggestions is to use the globe together with the **Population Education's interactive tool**. This app allows you to explore the evolution of the population in correlation with historical events. Students can go over historical events that occurred during the period spanning the circumnavigation voyage, which took place between 1519 and 1522. By exploring events happening, say, between 1500 and 1550, students can then discuss geopolitical circumstances between the Iberian Peninsula and the place of destination, the Maluku Islands.

The Game: Populations

This game was developed in the scope of the project *"Human diversity along the Magalhães circumnavigation space: genetics, history and culture"*, within the celebrations of the Voyage carried through by Fernão Magalhães (1519 - 1522), often considered the first-ever global voyage.

To understand this great journey of humanity and how it influenced the variability of current populations, we will learn basic concepts of **population genetics**. This game explores the mechanisms involved in the genetic evolution of populations, such as mutation, genetic recombination, migration, genetic drift, gene flow, natural and sexual selection, bottleneck effect, founder effect, panmixia, inbreeding and exogamy.

The game aims to introduce knowledge about population genetics in a fun way, by simulating how diversity can evolve over time as a result of different phenomena, and also by exploring the risks of low diversity.

The diversity of today's populations, which have gone through countless natural phenomena and cultural changes, leads to the misperception that we are more different from each other than we really are. Actually, **humans only vary from each other in 0.1% of the genome** (which contains 3.1 billion base pairs), a direct result of being a very young species and, in a way, all belonging to the same family. Other mammals, such as wild boars or cats, show a diversity 4 times greater than that of humans. Even chimpanzees, whose population is very small and is the species closest to us, have a genetic diversity of almost 0.2%, twice that of ours.
Our long history of miscegenation and resulting increase in diversity is in stark contrast to the similarity we share due to our young age as a species. Despite social, historical and cultural conflicts, when we take an ancestry test, we are faced with the enormous contribution of migrations, prehistoric and historical, to our genetic heritage.

RESOURCES:

1. **Video "Are We All Related?"**
   This video uses mathematics and genetics to show us that we all come from the same family, and we all share ancestors.

2. **Video "The DNA Journey"**
   This video, produced by a travel company, went viral. They invited 67 people from all over the world to take an ancestry test. The result? They found that they had a lot more in common than they expected.

The game was produced on a small scale, with materials and three-dimensional features to improve gameability, but we also provide it in a format that can be printed with all the necessary elements. However, population pieces and paper pins are not very manageable, so we recommend that, if possible, you acquire/ produce sturdier pieces.

PRINT VERSION GAME | DOWNLOAD >>

RECOMMENDATION FOR EXPLORATION PRIOR TO THE GAME SESSION

Population genetics, related to evolution and natural selection, is a topic addressed in secondary education in most countries. However, the depth with which these topics are addressed varies greatly. To better understand some of the processes and events related to heredity and population genetics, students may be encouraged to watch videos available on YouTube relevant to the subject on their own.

EXPLORATION PROPOSAL:

1. **Video "Microevolution: What's an allele got to do with it?"**
   Concepts such as genes, alleles, natural selection, genetic drift, gene flow and Hardy-Weinberg equilibrium are addressed here. The video explains these concepts using animals as an example, not humans.

2. **Video "Why do we have different skin colors?"**
   This resource addresses the genetics of human populations (the main theme of the game). Issues such as genetic diversity, levels of genetic diversity, variations in skin color, gradations and ancestry are explained correctly and simply. The controversial notion of "race" is also explored, explaining how it is, in fact, a social construction, with no basis whatsoever in scientific facts.

3. **Video "Why Human Ancestry Matters: Crash Course Big History 205"**
   Watching this video will help wrap up the preparation for the game. It depicts a brief narrative of modern humans' expansion from their origin in Africa 300-200 thousand years ago. The contents herein narrated are similar to those portrayed in **our exhibition "A Journey Through Human Genetic Diversity"**, which served as the basis for the development of the game.

Before the game, be wary:

This information/rule set is included in the print material, but we once again emphasize the following recommendations:

a. Distributing the rules of the game prior to the session is advised, and participating students should do some independent reading before playing the game.

b. Disclaimer to students about the game: This game aims to simulate the different mechanisms involved in the evolution of populations, which are ever-changing with the increase or decrease of genetic diversity, through mechanisms such as mutation, genetic recombination, migration, genetic drift, gene flow, natural and sexual selection, bottleneck effect, founder effect, panmixia, inbreeding and exogamy. To simplify the understanding of these processes, we have eliminated the chronological order and condensed the scale (thousands of years) to the length of the game. We only use the characteristic "color" as a differentiator of populations, taking out of the equation other multiple characteristics or the genetic diversity derived from genetic recombination during reproduction. The events narrated in the game were inferred from research in the areas of population genetics, archaeology, anthropology, history, and climatology, all of which are important events in the evolution of *Homo sapiens*.

Suggestion for playing the game in the classroom:

The game *Populations* is set up to be played by 3 to 5 players. In a classroom setting (20-25 students), it will be necessary to prepare boards and other materials to divide the class into groups of up to 5 students.

We propose two possibilities to enact the game with a class:

a. *Populations* can be played by groups of 5 students, each group with its own board and playing independently, or

b. It can engage the whole class, divided into groups of 5, each group with its own board, and the game runs simultaneously, ending at the same time, as well.

In the latter case, rules governing the end of the game apply to the entire class and the member of the class whose population is the most diverse/ balanced among all the boards in play will win. In other words, when a player in the class, regardless of the group they are in, says STOP (see rules), the game ends for the whole class. All students in the class must calculate the SCORE (see rules) to determine the winner of each group and the overall class winner.

Details of the game can be found in the rule sheets.

Didactic exploration following the game session:

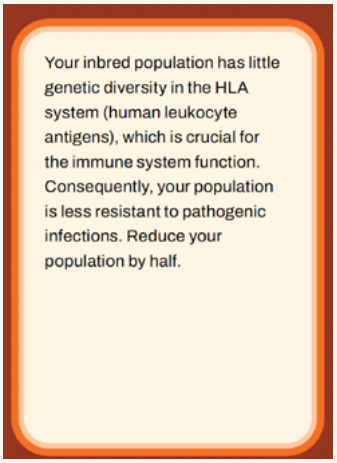
Teachers can explore the various concepts that emerged during the game (see list below) in the classroom using different models, depending on the characteristics of the class and time permitting.

Generally speaking, it should be possible to move forward with an open discussion of concepts, integrating different students' experiences during the game.

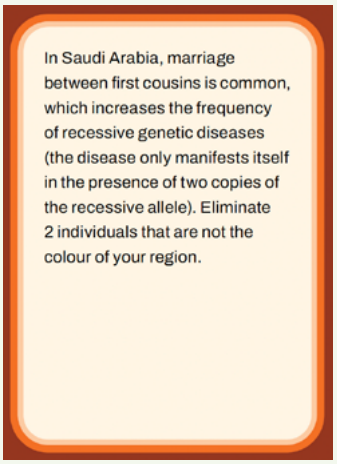
The game's dynamics allow students to experience the phenomena/processes contained in the included cards/consequences/actions, so learning occurs in a natural and spontaneous way.

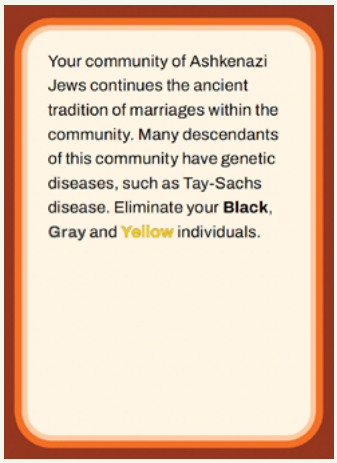
EXPLORATION PROPOSAL: Genetic Diversity

1. Discuss the concept of **genetic diversity**.
2. Analyze the example given in the following card and understand how **inbreeding** contributes to low diversity.

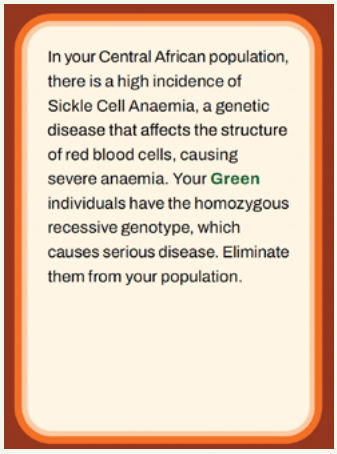


3. Based on these two cards, discuss how **inbreeding** can contribute to the loss of diversity and genetic risk accumulation.





4. The following card is an example of prevalence, in some populations, of homozygosity-derived deleterious **mutations**. Sickle Cell Anemia prevails in some regions of the globe because this mutation confers some resistance to infections such as Malaria, when in heterozygosity, albeit deleterious in homozygosity. Based on the card, discuss this phenomenon.

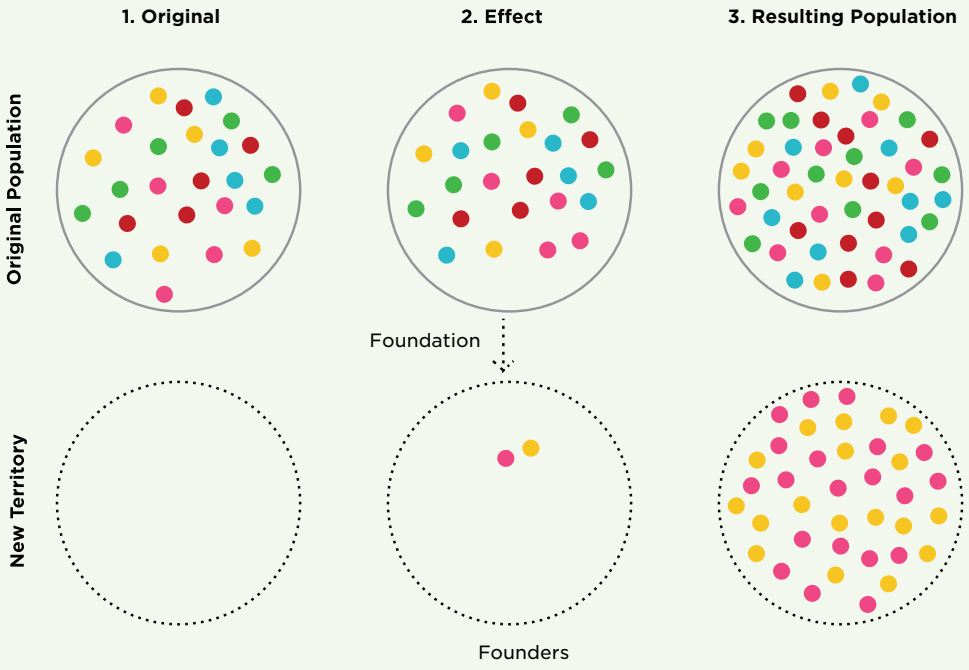


5. There is a certain proclivity to see selection as something that only acts negatively. But selection can be positive, as is the case with the following cards. Discuss the relationship between **positive and negative selection**, as well as how a given **mutation** may become more prevalent.

5. The **founder effect** and the **bottleneck** effect are phenomena that led to the reduction of diversity in some human populations at certain times in evolution, for example with the departure of *Homo sapiens* from Africa.

   Suggest to students that they draw diagrams using the game's simplified rules (such as using only the characteristic "color" and the principle that an individual of one color reproduces, giving rise to another individual of the same color), to explain the following cards and the loss of diversity. To do so, they can represent individuals in small circles, including the following steps: original population > effect> resulting population.

Example:



Your population arrived in Australia 50,000 years ago, originating from a small group of individuals. Go to the previous **Foundation Space**, fulfilling the space rule, **OR** choose 2 of your individuals to reset your population in the **Foundation Space** without fulfilling the space rule.

If there is no previous **Foundation Space**, return to the **Start Space**, but comply with the **Foundation Space** rule.

Your small group of individuals crossed the Bering Strait 25,000 - 20,000 years ago. Go to the previous **Foundation Space**, fulfilling the space rule, **OR** choose 1 of your individuals to reset your population in the **Foundation Space** without fulfilling the space rule.

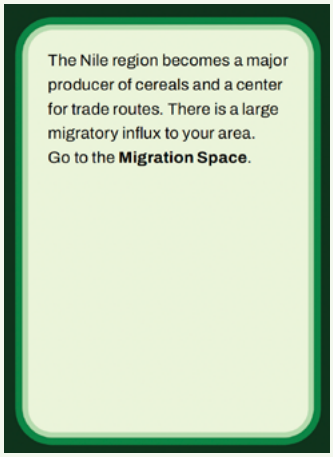
If there is no previous **Foundation Space**, return to the **Start Space**, but comply with the **Foundation Space** rule.

Disease

A pandemic decimates a large part of the world's population. All players lose half of their population randomly. Return to the **Immunity Space** and wait for the development of a new vaccine, following the space rules.

The Black Plague, caused by the *Yersinia pestis bacillus*, was a pandemic in Europe in the 14th century, decimating ⅔ of the European population. Move to the **Disease Space**.

7. In addition to time and the accumulation of **mutations** over generations, there is a phenomenon that can help rapidly increase the genetic diversity of a population: **gene flows**. As in the previous exercise, suggest students draw diagrams resorting to the game's simplified rules to explain the following cards and the gain in diversity. To do so, they can represent individuals in small circles, including the following steps: original population > effect> resulting population.



8. One of the biggest misconceptions about diversity, which underpins many social tensions, is the association (and limitation) of the understanding of **human population diversity** with **skin color**.

   - We, therefore, suggested a careful approach to this topic, hinging the discussion on the deconstruction of this misconception. Hence, we propose the visualization of the video **"Evo-Ed: History, Genetics, and Human Skin Color"** on the diversity of genes linked to skin color and how some mutations were established in different regions because they conferred an advantage in different environments. Explore the multitude of genes implicated in skin phenotypes, as well.

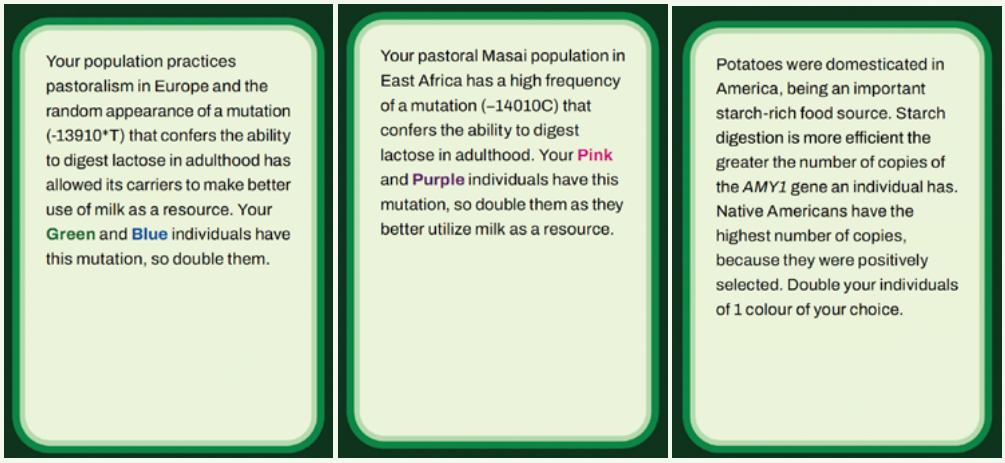
   - Based on the information relayed in the video, discuss the following cards:

- Suggest students read the National Geographic article **"There's no scientific basis for race—it's a made-up label"**. After reading, use the following statement to spur a discussion:

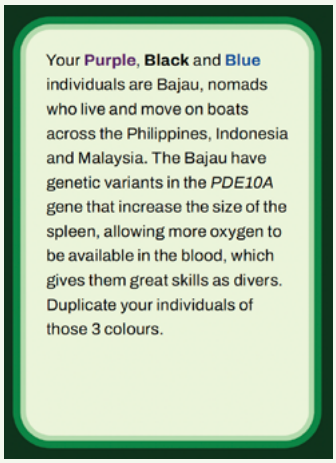
  "There is more genetic diversity within the major human population groups than between these major groups (Africans, Europeans and Asians)."

9. Humans have always developed culturally consolidated technologies for mastering nature, as well as adapting and reconfiguring their environment. According to a few authors, some cultural practices may have led to phenomena of gene/culture co-evolution. These phenomena are highly debated theoretical proposals, so they are usually not addressed from this perspective. On this topic, it is suggested to watch the video **"When Ancient People Changed Their Own DNA"**. This **article** may also be a good prompt for a discussion. This theory is being explored in **contexts** beyond humans', so it is strongly advised to rule out/refute arguments that use Lamarckian logic in discourse construction. In other words, it is paramount to clearly explain that there is no emergence of a new phenotype/genotype due to cultural practices; on the contrary, a given practice (for example, the access to and consumption of milk in culturally pastoral populations) enables milk-tolerant individuals (within the natural diversity of the population) to achieve greater reproductive success and, therefore, the prevalence of this genetic variant increases in the population over generations; in turn, the culture itself may reinforce the preservation of a practice in a positively retroactive / reciprocal way.

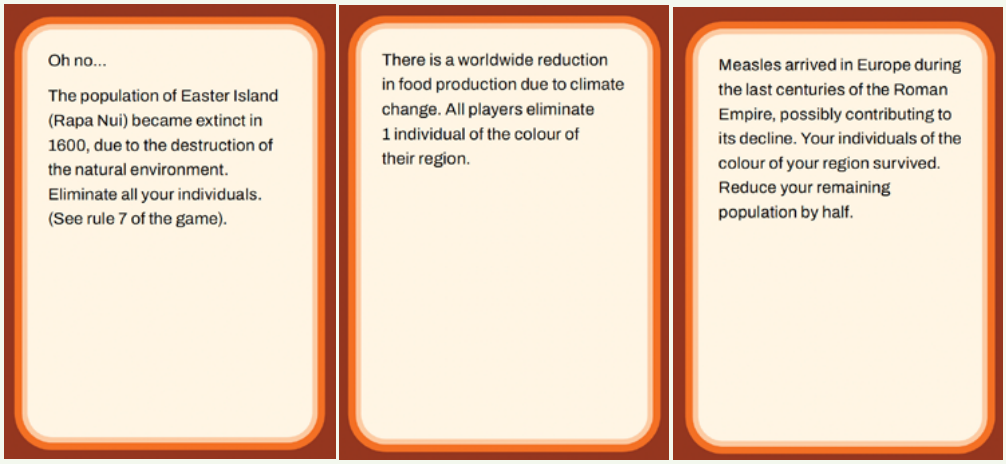
   - Propose to students that they discuss the following cards and how they convey **gene/culture co-evolution**.

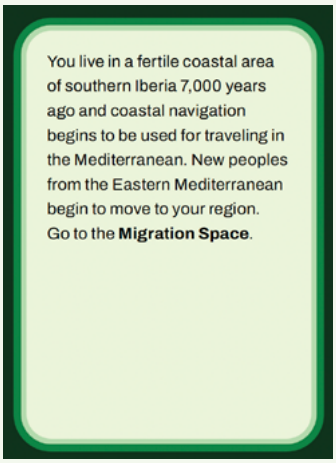


- Within the same framework, it may be suggested to read the article **"'Sea Nomads' Are First Known Humans Genetically Adapted to Diving"** from National Geographic, as well as to watch the video **"Discovering the World of the Bajau Tribe | The Free-Diving Sea Nomads"**. Afterward, the class can debate the **gene/culture co-evolution** concept based on the following card.



10. Suggest reading the cards below for a **"speculative thinking"/ "possible futures"** exercise.



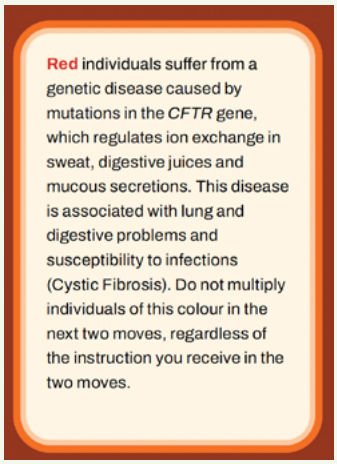


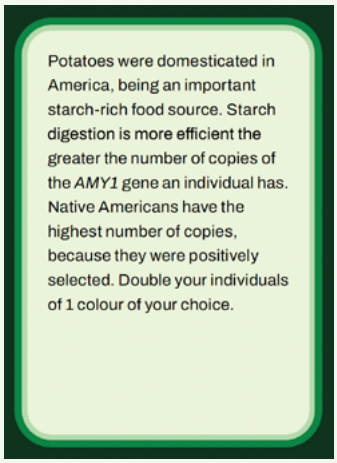
- Propose to students (in groups) that they browse newspapers in search of themes about **current phenomena that may influence the genetics of populations in the future**, such as climate change, water scarcity, food security, population mobility and migration, war conflicts, and pandemics, among others. Wrap it up with a collective discussion about the newspaper articles gathered and guide them to draw/think about possible future scenarios on the reorganization of the society/region in which they live. This speculative exercise should **include social, economic, political and demographic factors**, among others; as well as proposals for solutions to the reconfiguration of this society.

EXPLORATION PROPOSAL: Database browsing

A more complex exploration may be proposed for specific topics broached in a few cards, such as **genes** and **mutations** linked to traits, diseases, or disease resistance. Although this information is often complex, students may be encouraged to pursue independent research on these topics. Some of the examples featured in the cards include **cystic fibrosis, lactose tolerance, sickle cell anemia**, and **thalassemias**.

1. The website **GENECARDS** allows you to search for genes and information about them. You can explore the following cards:

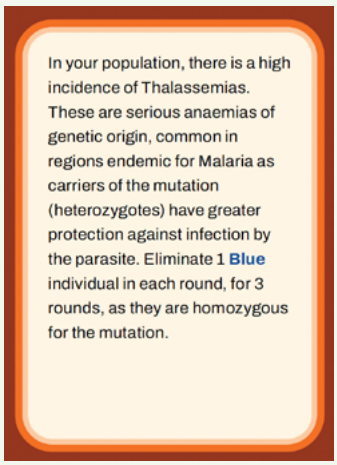


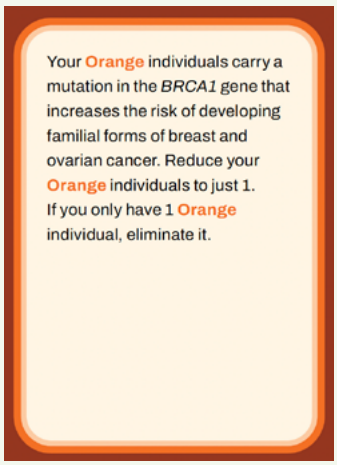


   - Look for the ***CFTR* gene** on the website and identify the type of protein affected by this mutation; which disease is caused by the mutation in this gene and its consequences; the population group in which the disease is most prevalent.

   - On the same website, search for the ***AMY1* gene**. Identify which enzyme is encoded by this gene, the enzyme's function, and in which organs the *AMY1* group proteins are produced.

2. The **MalaCards** website lets you search for diseases and disease-related genes. You can explore the following cards:





- Browse for **Thalassemia** on the website and identify how many genes are identified for this group of diseases; briefly describe the disease characteristics; identify in which regions/populations Thalassemia is frequent.
- On the same website, look for the ***BRCA1* gene** in the Terms area (not diseases). Identify which disease this gene is related to and discuss the importance of knowing family history to prevent this disease.

KEY CONCEPTS

Population Genetics

Population genetics is the area of biology focused on the genetic makeup of populations: organisms of the same species living in the same place at the same time. It is not always easy to determine where populations begin and end, especially in species that move and mix a lot. Population genetics helps measure the differences and changes that exist between populations, however diffuse. It resorts to statistical methods that enable the creation of models to determine whether different versions or variants of genes, called alleles, are more or less common in a population and how their frequency has changed or may change over time.

Genetic Diversity

Genetic diversity translates the variability of a species or population's genetic heritage, and it's investigated through statistical methods that compare genetic similarities and differences, revealing how organisms are related to one another. Some methods allow the establishment of similarity relationships, thus demonstrating how populations, and even species, are genetically related. Other methods and algorithms are able to show the smallest differences between populations and individuals. These also allow for measuring genetic diversity, that is, the genetic differences between individuals in a population.

Genetic Diversity and Adaptation

The greater the variability in a population's genetic heritage, the more easily that population survives and adapts to external (e.g. environmental) challenges. The difference between a population with high genetic diversity and one with low genetic diversity is akin to facing a complex challenge with a single competence versus a set of varied competencies. Similarly, more recent species or populations, or with recent founder effect, regardless of the number of individuals, tend to be less diverse. The same is true when we look at genetic diversity within species themselves. The Iberian lynx, for instance, an endangered species with a reduced number of herds and which has suffered a strong recent bottleneck effect, has a very low genetic diversity of 0.02%. Old and abundant species, on the other hand, usually present greater diversity. For example, the boar has a genetic diversity of 0.45%, and the cat of 0.4%. On the other hand, humans are an abundant species, but compared to others, they have very low genetic diversity, about 0.1%. This happens because we are a young species. Humans, who inhabit any and every part of the world, are in fact genetically very similar (99.9%).

Genetic Heritage

Because the genome of each organism is an integral part of the population's genetic heritage, the fate of each organism - to live, reproduce, die - plays an important role in the future genetic heritage of the population to which it belongs. The genetic heritage of a population is the sum of the entire population's genetic material. The analysis of a population's genetic heritage thus includes the inventory of all alternative versions of genetic sequences, as well as the recording of the frequency with which they arise.

Genetic Drift

Because the genome of each organism is an integral part of the population's genetic heritage, the fate of each organism - to live, reproduce, die - plays an important role in the future genetic heritage of the population to which it belongs. The genetic heritage of a population is the sum of the entire population's genetic material. The analysis of a population's genetic heritage thus includes the inventory of all alternative versions of genetic sequences, as well as the recording of the frequency with which they arise.

Genetic Drift

Fluctuation in the frequencies of different alleles and traits usually occurs by chance, which is at the core of genetic drift. Genetic drift occurs when random events cause certain alleles and/or traits to increase or decrease in a population from one generation to the next. Large and very diverse populations are not as subjected to genetic drift as allele and/or trait frequencies are unlikely to change due to minor random events. Small populations, on the contrary, are much more susceptible to oscillations in the frequency of alleles and/or traits, simply by chance.

Founder Effect

The founder effect has a marked impact on genetic drift. It occurs when a small group of individuals separate from one population and isolate themselves from the others, founding a new population, a phenomenon that has occurred countless times in human history. In a scenario where a few dozen individuals establish a new population in a remote area, isolated from other populations, it is easy to foresee that the resulting population, even if large in number, will also bear very few differences from each other. If no contacts with other populations take place, and there are no new partners to introduce new genes/ alleles/ traits through reproduction, the diversity achieved will always depend on the founders' original genetic heritage. In this scenario, an allele that was rare in an original population can easily become common in a newly formed population.

Bottleneck Effect

Some events can cause drastic reductions in the genetic heritage of a very diverse population - it is the so-called bottleneck effect. The catastrophic loss of many individuals due to an external element can cause the frequency of different alleles to change significantly. The population loses individuals regardless of whether, or not, they are adapted to the environment. In a newly tithed population, the remaining genetic heritage will have a new distribution. About 74,000 years ago, the genetic heritage of modern humans declined significantly; the human population is thought to have been reduced to 3,000 - 10,000 individuals. The exact cause is unknown, but violent volcanic episodes (Mount Toba in Sumatra) are thought to have drastically altered environmental conditions for more than a decade, making it harder for the human species to survive. After this episode, the population quickly recovered. In just a few millennia, human populations have again expanded in number and regained diversity.

Gene Flow

There is another force that can affect allele frequencies in a population with the opposite effect of genetic drift and the bottleneck effect: gene flow. This phenomenon occurs when individuals move and reproduce between different populations, bringing and carrying new alleles, which did not exist in the recipient population.

Mutations

New alleles spontaneously arise in a population as a result of mutations, which are random changes in the genome that can occur naturally due to sporadic errors in the DNA copy. More extensive random changes can also occur, such as when large DNA sequences switch places or even duplicate. These changes, occasional or extensive, may have a detrimental, neutral or useful effect on the survival of the individual, in the short or the long term, for their descendants. As such, the prevalence of these new genetic changes in the population will be conditioned by their effect on the individual.

Modern Human Species

Homo sapiens emerged approximately 300,000-200,000 years ago in Africa. Originally, early humans were a small population with limited genetic diversity. For at least 130,000 years these humans were restricted to the African continent; they multiplied, and spread over the vast territory, migrating, forming various populations and diversifying. In an early stage, these first humans' population groups must have been dispersed, with few individuals and relatively isolated from each other, making way for the genetic heritage to begin to differentiate between populations. With population growth and over tens of thousands of years, new encounters and migrations between groups allowed genetic flows between populations. In time, human genetic heritage became more complex, showing countless gradations. Fossil records evidence that humans moved from Africa to the Middle East on to Asia about 100,000 years ago. These early outflows

from Africa were probably motivated by the rapid population expansion. However, molecular dating of the extreme bottleneck at the origin of all non-Africans is much more recent, indicating that these migratory experiences were unsuccessful.

Human Expansion

Humans ventured out of Africa again about 70,000 years ago. Beginning in the Middle East, humans have remained in warmer climates, spreading across South and East Asia. Approximately 50,000 years ago, they took advantage of the land bridge that at the time connected the Asian continent and present-day Indonesia, and arrived in Australia. With the end of the glacial period, and the emergence of some adaptations preparing them for colder climates, humans eventually spread across Central Asia and Europe approximately 45,000 years ago. But we weren't the first group of hominins to go on this adventure. Along the way, we met other adventurous species that had preceded us. It is now known that crosses with fertile offspring between us and these species occurred, namely with Neanderthals and Denisovans, which left traces (1.5 to 2%) in our genetic heritage. Humans eventually arrived in northern America about 20,000 years ago, something never done by any other hominin species. The two American continents were quickly populated by the newcomers.

Human Ancestry

Evolution occurs at a population level, not individual, so when we talk about ancestry it is important to understand where we come from and how we are related. Science shows that humans are a recent species, hence making us a large family with a fairly common genetic identity. When compared to other mammalian species, humans are very similar to each other. The greatest human diversity is found in Africa, the cradle region in which we lived for our first two hundred thousand years. When humans left Africa, they did so with a small group of founders. Successive founding groups emerged as they moved farther across the globe. Therefore, the genetic diversity of groups existent today outside of Africa is very small, and diversity dwindles the farther the group is from the point of origin.

Inbreeding

Inbreeding results from consanguine coupling, that is, when individuals in a population descend from genetically similar relatives. Inbreeding can occur naturally when the original population has very few individuals. It is common, for example, for endangered species, or very fragmented populations unable to flow between subpopulations, to have a high level of inbreeding. So, when an individual's parents have one or more ancestors in common, i.e., are related to each other, they are said to be consanguineous or inbred. Inbreeding results in the progressive reduction of genetic diversity and the accumulation of several traits in homozygosity in individuals, namely recessive genetic diseases. Inbreeding can also be a product of cultural practices, either in humans themselves when they belong to groups that promote consanguineous marriages, or in domesticated animals/plants over which mating control is exercised to establish characteristics.

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