**Appendices**

**Appendix 1a: Pre/Post-Test**

*Question 1*

*Documents provided*: Excerpt from the article by Watters (2006), "DNA Is Not Destiny: The New Science of Epigenetics", and the definition of epigenetics (Wikipedia, 2023).

*Question*: After reading this article excerpt, which of the following statements do you consider the most valid? (You may choose more than one.)

- These epigenetic modifications have an impact on the phenotype of the mouse pup. *(Correct)*
- These epigenetic modifications are hereditarily transmitted from the pregnant mother to the mouse pup. *(Incorrect)*
- These epigenetic modifications occur in both the pregnant mother and the mouse pup in utero. *(Correct)*
- These epigenetic modifications are not hereditarily transmitted from the pregnant mother to the mouse pup. *(Correct)*

Briefly justify your choice.

*Question 2*

*Document provided*: Transcript excerpts from an interview with Natacha Calestrémé (2021)
CALESTRÉMÉ N. (2021). Interview in "Les 12 dernières minutes", CNEWS. Online: <https://www.youtube.com/@CNEWSofficiel> (accessed October 18, 2021).

*Question*: What would you say about these statements? (One possible answer)

Epigenetics can legitimize psycho-genealogy because it is possible to identify epigenetic modifications transmitted for a specific psychological disorder.

- Epigenetics can legitimize psycho-genealogy because it is possible to identify genetic mutations transmitted for a specific psychological disorder.
- Epigenetics cannot legitimize psycho-genealogy because it is extremely difficult to identify genetic mutations transmitted for a specific psychological disorder.
- Epigenetics cannot legitimize psycho-genealogy because it is extremely difficult to identify epigenetic modifications transmitted for a specific psychological disorder. *(Correct)*

*Question 3*

*Documents provided*: Titles of books or web pages such as:

"Infidelity is hidden in your genes." (Friedman, 2015)

“Why your DNA is not your destiny? Your choices can change your genes and those of your children.” (Cover of Time magazine, January 18, 2010)

*Instructions and questions*:

- Observe the reference document and group the titles that, in your opinion, share common points.
- Justify your classification.
- Based on the messages you read, what new message would you formulate? What message would you like to convey to your readers? Justify your answer.

*Question 4*

*Document provided*:

The French National Consultative Ethics Committee (CCNE), in its Opinion No. 124 (2016), discusses the possibility that whole genome sequencing may become a common medical practice due to increasing technical feasibility and decreasing costs. It also highlights the ethical issues related to integrating such data into medical records.

*Instruction*:

Complete the following sentence. Whole genome sequencing alone... (One possible answer)

- allows for the identification of all current and future diseases of the patient as well as their severity.
- allows for the identification of all current and future diseases of the patient, but not their severity.
- allows for the identification of only certain diseases the patient has or may potentially develop, but never their severity.
- allows for the identification of only certain diseases the patient has or may potentially develop, and in some cases their severity. *(Correct)*
- does not allow for the identification of any diseases the patient has or may potentially develop.

Justify your choice.

**Appendix 1b: Distribution of points by criterion and indicator for each of the four questions in the pre-/post-test**

| | Criteria | Indicators | Maximum Scores | | |
|---|---|---|---|---|---|
| **KNOWLEDGE** | Link between epigenetic modifications and phenotype / distinction from hereditary transmission | **Question 1**<br>Option 1 checked?<br>Yes: 0.5 – No: 0 | 0.5 | 1.5 | 6 |
| | | **Question 1**<br>Options 3 and 4 checked: 1<br>Option 3 or 4 checked: 0.5<br>Neither option checked: 0 | 1 | | |
| | Distinction between epigenetic modifications and mutations | **Question 2**<br>Option 1 or 4 checked: 0.5<br>Option 2 or 3 checked: 0 | 0.5 | 1.5 | |
| | | **Question 3**<br>Two correct groups?<br>Yes: 1 – No: 0 | 1 | | |
| | Expressivity and penetrance | **Question 4**<br>Option 4 checked: 1<br>Other option checked: 0 | 1 | 3 | |
| | | **Question 4**<br>Expressivity mentioned: 0.5 or 1<br>Penetrance mentioned: 0.5 or 1 | 2 | | |
| **MODE OF THINKING** | The student formulates coherent and valid justifications. | **Question 1**<br>Justification OK?<br>About the pregnant mouse: +0.5<br>About the baby mouse: +0.5 | 1 | 2 | 7 |
| | | **Question 3**<br>Justification OK? | 1 | | |
| | The student demonstrates critical thinking | **Question 1**<br>Option 2 checked?<br>No: 1 – Yes: 0 | 1 | 2 | |
| | | **Question 2**<br>Option 3 or 4 checked: 1<br>Option 1 or 2 checked: 0 | 1 | | |
| | The student nuances their statements by considering interconnections and uncertainties/unpredictability. | **Question 3**<br>Interconnections considered:<br>In the proposed title: +0.5<br>In the justification: +0.5 | 1 | 3 | |

| | | | | | |
|---|---|---|---|---|---|
| | | **Question 4**<br>Justification considers interconnections and/or uncertainty/unpredictability:<br>Both: 2<br>One of the two: 1<br>Neither: 0 | 2 | | |

**Appendix 1c: Means and results of the repeated measures ANOVA by evaluation criterion and question component**

| | Criteria | Means | |
|---|---|---|---|
| | | **Pre-test Group A** ***Group B*** (Standard deviation) | **Post-test Group A** ***Group B*** (Standard deviation) |
| **KNOWLEDGE** | Link between epigenetic modifications and phenotype / distinction from hereditary transmission | **0.541** (0.2976) ***0.529*** *(0.2736)* | **0.757** (0.3254) ***0.485*** *(0.3586)* |
| | Distinction between epigenetic modifications and mutations | **0.486** (0.4785) ***0.618*** *(0.5374)* | **0.662** (0.5008) ***0.529*** *(0.5066)* |
| | Expressivity and penetrance | **0.554** (0.5747) ***0.515*** *(0.5837)* | **0.824** (0.7285) ***0.559*** *(0.6486)* |
| **MODE OF THINKING** | The student formulates coherent and valid justifications. | **0.392** (0.3752) ***0.456*** *(0.4500)* | **0.676** (0.5555) ***0.471*** *(0.4072)* |
| | The student demonstrates critical thinking. | **0.650** (0.753) ***0.680*** *(0.727)* | **0.973** (0.6866) ***0.750*** *(0.6990)* |
| | The student nuances their statements by considering interconnections and uncertainties/unpredictability. | **0.297** (0.4481) ***0.412*** *(0.5290)* | **0.865** (0.7514) ***0.500*** *(0,-.6742)* |

The means presented for each criterion are expressed in the unit of the scoring scale specific to that criterion (Appendix 1b).

| | Criteria | Questions related to the criterion | ANOVA Results | | | |
|---|---|---|---|---|---|---|
| **KNOWLEDGE** | Link between epigenetic modifications and phenotype / distinction from hereditary transmission | **Question 1** | $\eta^2 = 0.033$ $p = 0.129$ | $\eta^2 = 0.088$ $p = 0.012$ | $\eta^2 = 0.120$ $p = 0.003$ | $\eta^2 = 0.173$ $p < 0.001$ |
| | | **Question 1** | $\eta^2 = 0.050$ $p = 0.060$ | | | |
| | Distinction between epigenetic modifications and mutations | **Question 2** | $\eta^2 = 0.001$ $p = 0.837$ | $\eta^2 = 0.037$ $p = 0.107$ | | |
| | | **Question 3** | $\eta^2 = 0.053$ $p = 0.052$ | | | |
| | Expressivity and penetrance | **Question 4** | $\eta^2 = 0.000$ $p = 0.856$ | $\eta^2 = 0.022$ $p = 0.212$ | | |
| | | **Question 4** | $\eta^2 = 0.081$ $p = 0.016$ | | | |
| **MODE OF** | The student formulates coherent and valid justifications | **Question 1** | $\eta^2 = 0.000$ $p = 0.914$ | $\eta^2 = 0.049$ $p = 0.064$ | $\eta^2 = 0.115$ $p = 0.004$ | |
| | | **Question 3** | $\eta^2 = 0.070$ $p = 0.026$ | | | |

| | | | | | | |
|---|---|---|---|---|---|---|
| | The student demonstrates critical thinking. | **Question 1** | $\eta^2 = 0.000$<br>$p = 0.919$ | $\eta^2 = 0.024$<br>$p = 0.196$ | | |
| | | **Question 2** | $\eta^2 = 0.059$<br>$p = 0.042$ | | | |
| | The student nuances their statements by considering interconnections and uncertainties/unpredictability. | **Question 3** | $\eta^2 = 0.065$<br>$p = 0.031$ | $\eta^2 = 0.077$<br>$p = 0.019$ | | |
| | | **Question 4** | $\eta^2 = 0.035$<br>$p = 0.118$ | | | |

Green cells indicate statistically significant results obtained from the ANOVA test ($p < 0.05$).

**Appendix 2: Sequence and Didactic Tools for Activity 3**

First, students receive eight articles from various sources (LADEPECHE.fr, Le Point, Ouest France, BFM TV, Pourquoi Docteur, NASA, and Le Figaro) reporting on the DNA changes observed in astronaut Scott Kelly compared to his twin brother who remained on Earth. They are asked to classify these articles into three categories: DNA modified, gene expression modified, or DNA not modified.

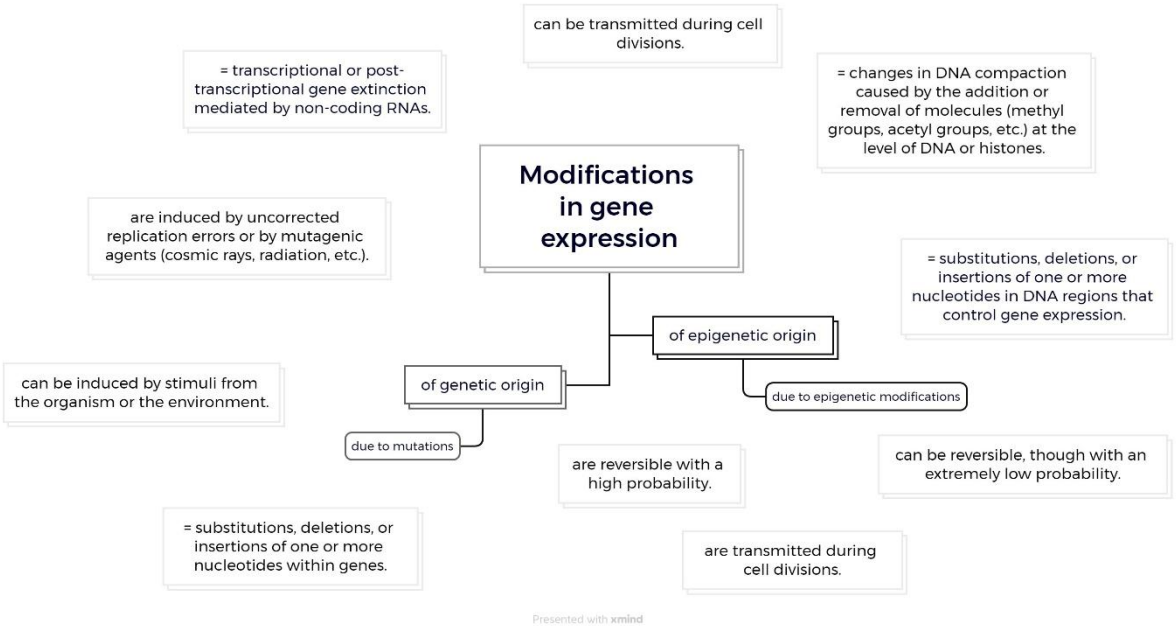
Next, guided by the teacher, students are invited to reflect on the following:

- Some articles claim that Scott Kelly's DNA changed and that his gene expression was modified; they refer to gene expression changes of genetic origin, i.e., mutations.
- Other articles claim that Scott Kelly's DNA did not change, but that his gene expression was modified. What are they referring to?

The teacher explains gene expression changes of epigenetic origin.

The mind map to be constructed (Supplementary Figure 1) includes boxes with characteristics of gene expression changes of either genetic or epigenetic origin. Students must assign each characteristic to the appropriate category.

Supplementary Figure 1: Mind map to be constructed – Characteristics of gene expression changes of genetic or epigenetic origin




Secondly, based on two documents (Documents 1 and 2), students are asked to complete a table.

<u>Document 1: Temperature and fur colour in Siamese cats</u>

Siamese cats have a distinctive coat, darker at the extremities of the paws and muzzle than on the rest of the body. This coloration is due to an enzyme, tyrosinase, produced thanks to the tyrosinase gene. This enzyme enables the production of melanin, a dark pigment derived from the amino acid tyrosine.

Fur colour in relation to temperature

| Body part | Paw extremities | Body |
|---|---|---|
| Temperature | 33°C | 38.5°C |
| Tyrosinase activity | Active (pigment production) | Inactive (no pigment) |
| Fur colour | Brown | White |

Document 2: "You are what you eat"

The morphological and physiological differences between queen and worker bees result from the larva's diet.

Depending on whether the larva is mainly fed royal jelly or bee bread—a mixture of pollen and honey—it will develop into a queen or a worker.

*Royal jelly*, secreted by nurse bees, contains molecules (*protein inhibitors*) capable of inducing *histone* modifications, thereby activating the expression of numerous genes (*DNA off* ↔ *DNA on*).

This nutritional source thus contributes, through distinct mechanisms, to the differentiation between queens and workers.

(Saint-André, 2022, p. 16–17; Kucharski et al., 2008; Spannhoff et al., 2011)

Table to be completed after reading Documents 1 and 2 from Activity 1 of the didactic framework

| | Document 1: Siamese cat | Document 2: Bee larvae |
|---|---|---|
| What *environmental parameter* varies in the example? | | |
| Does the example illustrate the impact of the environment on the *phenotype*? | | |
| Does the example illustrate the impact of the environment on gene expression? If yes, is this impact *genetic* or *epigenetic*? | | |

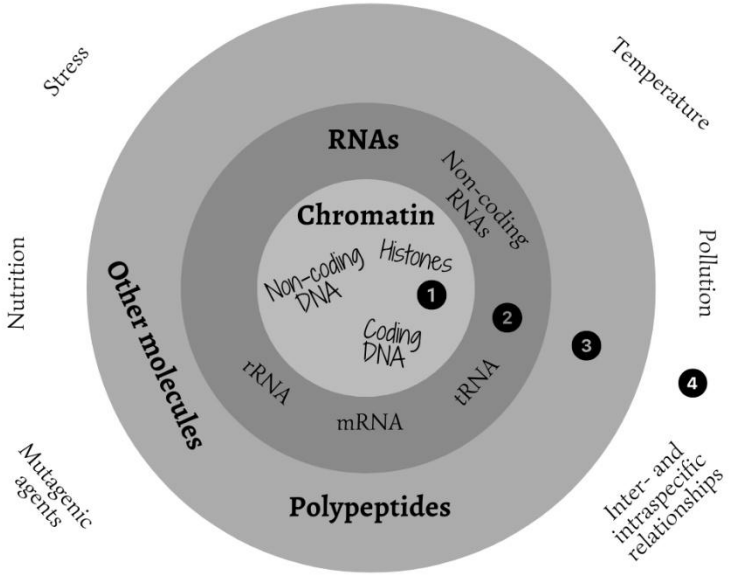
If a change in phenotype is not due to a *mutation*, is it automatically due to an *epigenetic mechanism*? Justify.

Thirdly, students examine the four-level model (Supplementary Figure 2) developed as part of this research. They complete a blank version of the model with the factors influencing fur colour in Siamese cats and another for the development of a bee larva into a queen.

They indicate the connections between these factors and observe whether internal environmental factors (temperature for the cat) or external ones (diet for the larva) impact Level 1 of the model.

Students note that epigenetic mechanisms imply that the environmental factor affects Level 1.

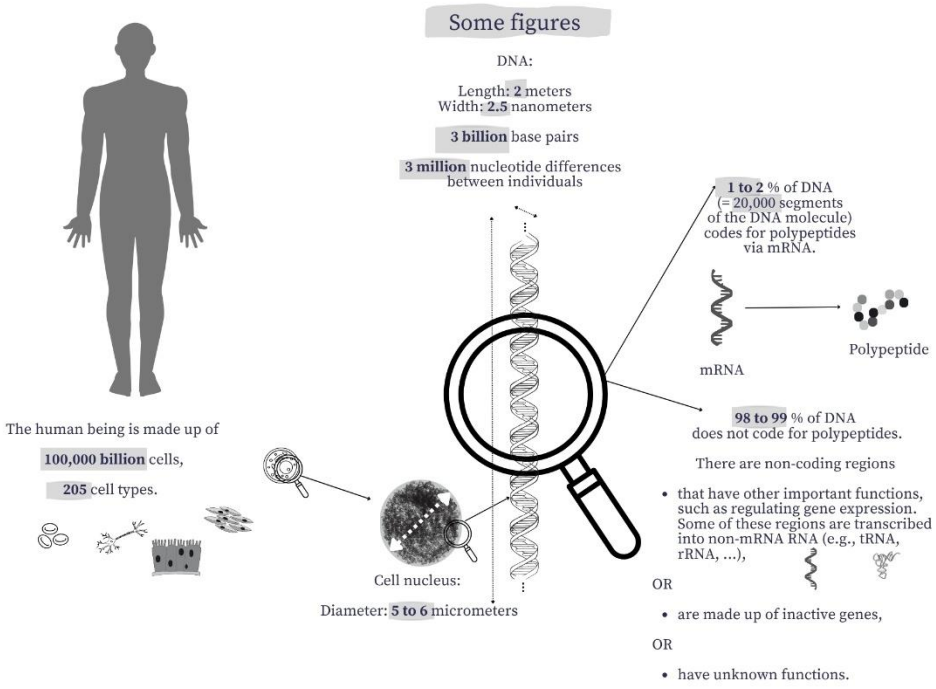
Supplementary Figure 2: Four-level model




A parallel can be drawn between the adult state of the bee larva (worker or queen), which depends on epigenetic modifications caused by its diet, and the adult state of the mouse embryo *in utero* (yellow or grey mouse), which depends on epigenetic modifications caused by the diet of the pregnant mother.

## Appendix 3: “Some Figures” Document

Supplementary Figure 3: “Some Figures” Document



**Appendix 4: Sequence and Didactic Tools of Activity 4**

Based on a document (Document 3), students are asked to answer a question.

Document 3: The worker bee and its evolution over time

"A queen cannot become a worker, nor vice versa: the stability of the epigenetic marks that distinguish queens from workers ensures their long-term identity.

However, some flexibility exists within the worker category, particularly between *nurse bees*, which feed the larvae, and *forager bees*, which collect nectar for the hive.

In response to the experimental removal of nurse bees, *foragers can become nurses*. This change is correlated, at the brain level, with a quantitative modification of DNA methylation in genes involved in behaviour.

The *reversibility* of certain epigenetic marks in the brains of worker bees is therefore associated with this *behavioural plasticity*."

(Saint-André, 2022, p. 19–20)

Question:

Using the example of forager bees that, under certain circumstances and at a given time, can become nurse bees through epigenetic mechanisms, tick the statement you find most valid:

- ○ Analysing the genome is not sufficient to understand both the phenotype and its evolution over time. *(Correct statement)*
- ○ Analysing the genome is sufficient to understand both the phenotype and its evolution over time.
- ○ Analysing the genome is sufficient to understand the phenotype but not its evolution over time.

**Appendix 5: Glossary of Key Concepts in Genetics**

**Genome:** The complete set of genetic material of an individual, encompassing all DNA sequences, including those corresponding to genes.

**Gene:** A sequence of DNA (a sequence of polynucleotides), part of which codes for one or more functional molecules (polypeptide, tRNA, rRNA, or other types of RNA).

**Genetic coding in humans:**

- 1–2% of nuclear DNA (around 20,000 segments) codes for polypeptides via mRNA. A segment may code for one or sometimes several polypeptides. There is a multiplicity of possible alleles for each of these segments (polyallelism).
- 98–99% does not code for polypeptides. These regions have other important functions, such as regulating gene expression. Some of these regions are transcribed into RNA other than mRNA, while others consist of inactive genes or regions with unknown functions.

**Genotype:** The set of alleles of an individual, whether or not they affect the phenotype.

**Phenotype:** The result of interactions between genetic inheritance and factors that influence gene activity.

**Phenotypic plasticity:** The ability of an organism to modify its phenotype in response to environmental variations, allowing flexible adaptation to changing conditions.

**Pleiotropy:** A phenomenon whereby one gene affects several distinct phenotypic traits.

**Phenotypic polygenism:** Most phenotypic traits are polygenic, meaning they result from the combination of alleles from multiple genes that together contribute to the phenotype.

**Phenotypic penetrance:** The probability that a genotype will result in the associated phenotype.

**Phenotypic expressivity:** The variability in the severity of a phenotype caused by the same genotype.

**Modifications in gene expression:**

- **Genetic modifications:** Changes caused by uncorrected replication errors or mutagenic agents that alter the DNA sequence. These are reversible with extremely low probability and are transmitted during cell divisions.
- **Epigenetic modifications:** Changes caused by stimuli from the organism or the environment that do not alter the DNA sequence, are reversible with high probability, and can be transmitted during cell divisions. These modifications result from various mechanisms, often complex and sometimes incompletely characterized (with variable consequences on gene expression), such as chemical modification of DNA bases (e.g., cytosine methylation) or post-translational modification of histones.

**Epigenesis:** The set of epigenetic processes that influence embryonic development. These processes contribute to the progressive establishment of the phenotype from the genotype, in interaction with internal and external conditions.

**Appendix 6: Sequence of Activity 6**

This activity unfolds in several steps, aiming to address the complexity of climate change:

1. Individual preparation (outside the classroom)

Students watch a video from the YouTube channel Nota Bene titled “Has climate change always existed?” (2022), which explores climate from a historical perspective.

Nota Bene (Benjamin Brillaud). (2022, July 4). Has climate change always existed? [Video]. https://www.youtube.com/watch?v=ctXGB_z-Cf4

They answer three questions inspired by the arpentage method (popular education):

a) What did you feel while watching the video?
b) What idea particularly stood out to you?
c) What can you do with what you saw?

2. Small group work

In class, students form small groups to formulate a question based on their personal reflections. These questions are then discussed collectively. The facilitator supports students in precisely formulating the problems and identifying implicit assumptions.

3. Collective discussion

A philosophically oriented discussion is organized, with assigned roles (moderator and observer). Two students are specifically tasked with observing the complexity of the discussion: they identify the knowledge mobilized, the uncertainties, and the need for additional information.

4. Synthesis

The workshop concludes with a collective synthesis.

**Appendix 7: Core Questions for the Semi-Structured Interview**

*The model*

1. Do you remember the model for thinking about knowledge objects with its key terms (overview, interconnections, unpredictability, and emergent properties)? What does it evoke for you?

*Before the didactic framework*

2. On a scale from 1 to 5, how would you rate the complexity of genetics (1: not complex – 5: very complex)? What would you have said before the framework? And now? Can you provide examples or explanations to support your answer?
3. Have you ever encountered other complex topics, in biology or in other disciplines? If so, which ones?
4. How do you spontaneously react to the complexity of these different topics?

*Genetic complexity with expert insight*

5. What mode of thinking should we promote when addressing situations related to genetics? Alternative phrasing: What considerations do you think are essential when dealing with genetic issues? Use concepts and examples discussed during the sessions to support your answer.
6. Which concepts were particularly enlightening for you? Which ones remain difficult to understand? What particularly caught your attention?

*Practicing transfer with an expert*

7. What mode of thinking should we prioritize when addressing the challenges of climate disruption? Alternative phrasing: What considerations do you think are essential in our ecological actions?
8. Which reflections/ideas/concepts were particularly enlightening for you? Which ones remain difficult to grasp? What touched or struck you in particular and motivates you to act in response to climate disruption?

Information generated by Microsoft 365 Copilot in October 2025 and February 2026. (Type of use: text translation)