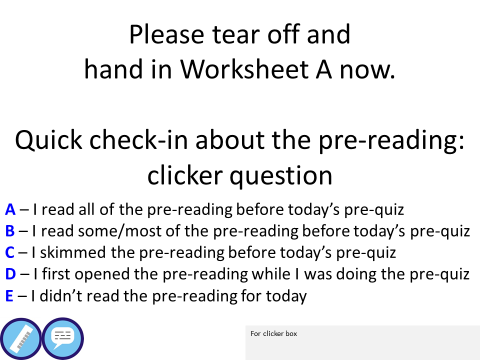
# **Concepts first, jargon second improves student articulation of understanding**

Lisa McDonnell, Megan Barker, and Carl Wieman

# **Supplemental Material**



**Figure S1.**  **Clicker question asked in class to identify students who had completed the pre-reading quiz.** Only those who chose option A were included in our analysis. Those that chose option E were analyzed as a control for the effects of completing the pre-class reading.

**Table S1: Sample of pre-class reading given to the treatment (concepts-first) and control (jargon + concepts) groups.** Text in pre-reading figures were similarly modified as appropriate for concepts-first group.

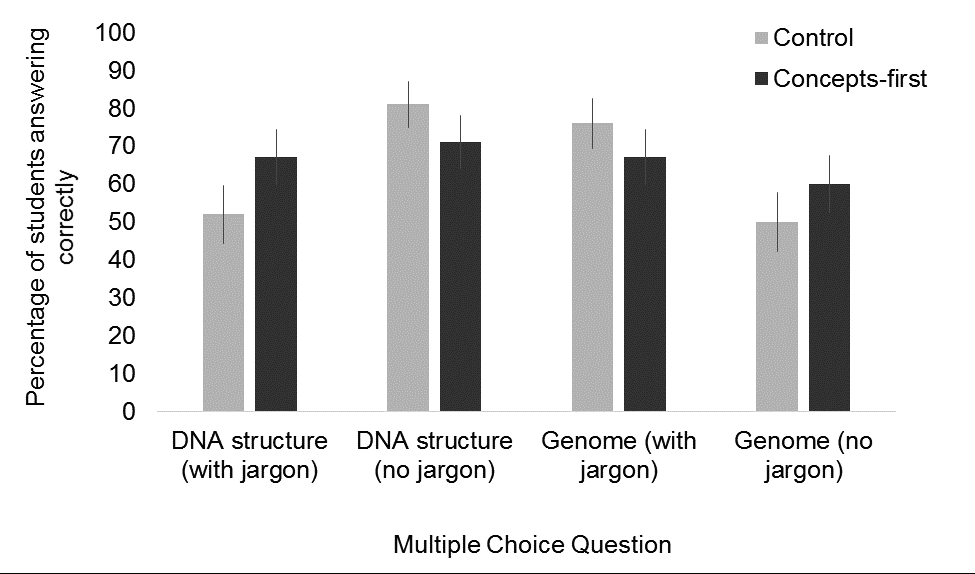
|  |  |
| --- | --- |
| **Passage from Control Group (jargon + concepts)** | **Passage from Treatment Group (concepts-first, jargon removed)** |
| Cells today have four different ribonucleotides, each of which contains a different nitrogenous base. These bases, diagrammed in **Figure 1C**, belong to structural groups called **purines** and **pyrimidines**. Ribonucleotides include the **purines** adenine (A) and guanine (G), and the **pyrimidines** cytosine (C) and uracil (U). | Cells today have four different RNA monomers, each of which contains a different base. These bases, diagrammed in **Figure 1C**, are either large (two rings) or small (one ring). RNA monomers include the large bases A and G, and the small bases C and U. |
| A genome is an organism’s complete set of hereditary DNA molecules. In humans, a copy of the entire **genome**—more than 3 billion DNA base pairs—is contained in all cells that have a nucleus (actually most of our cells are diploid, meaning we have two copies of the genome). There can be as few as 1 to more than 100 chromosomes in a eukaryotic genome. | All of the DNA sequence that is passed on from one generation to the next is considered the **total hereditary genetic material** of a haploid cell. This hereditary DNA material consists of *all* DNA sequences. In humans, the total hereditary genetic material —DNA sequences that total more than 3 billion DNA base pairs—is contained in all cells that have a nucleus (actually most of our cells are diploid, meaning we have two sets of hereditary genetic material). Eukaryotic hereditary genetic material can be as few as 1 to more than 100 chromosomes. |

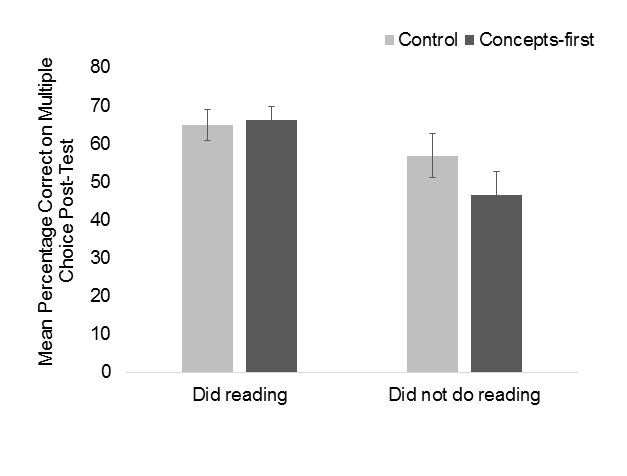
**Table S2: Post-test questions**

|  |  |
| --- | --- |
| **Question description** | **Question text**  (\* correct answers for multiple choice questions; Rubrics for free-response questions in Table S2) |
| DNA structure topic; multiple choice with jargon | 1. In normal double-stranded DNA, why are purines base-paired with pyrimidines?   * 1. Because a purine-purine pair would be too small, and a pyrimidine-pyrimidine pair would be too large   2. Because the number of A must equal the number of T and the number of G must equal the number of C   3. Because the strongest stacking interactions are found between purines and pyrimidines, making the DNA more stable   4. Because purine-pyrimidine pairs maximize the number of hydrogen bonds, making the DNA more stable.   5. (\*) Because complementary purine-pyrimidine base pairs have the same geometries |
| DNA structure topic; multiple choice without jargon | 2. Why does double-stranded DNA have a regular, uniform structure?   * 1. Because a regular structure allows the bases to pack on top of each other   2. Because the bases can make non-covalent interactions both between strands, and within the same strand   3. (\*) Because complementary base pairs always cause the same distance between DNA backbones   4. Because the number of A must equal the number of T & the number of G must equal the number of C   5. Because the hydrogen-bonding is the same in all base pairs containing one large base with one small base |
| Genome topic; multiple choice with jargon | 3. You are comparing the genetic material of two species. Species A has 100 million base pairs in one of its haploid cells. Species B has 96 million base pairs in one of its haploid cells. From this data, you can conclude that:   * 1. (\*) The genome of species A is larger than the genome of species B.   2. Species A has more genes than species B.   3. The genome of species B is larger than the genome of species A.   4. Species B has more genes than species A.   5. None of the above can be concluded based on this data. |
| Genome topic; multiple choice without jargon | 4. Examine the data in the table below:   |  |  |  | | --- | --- | --- | | Species | Amount of DNA in a haploid cell (base pairs) | Number of base-pairs that code for proteins | | A | 8,000,000 | 8,000 | | B | 200,000,000 | 19,000 | | C | 19,000,000 | 500,000 |   Based on this information, which statement is true? The hereditary genetic material:   * 1. of species A is the largest.   2. (\*) of species B is the largest.   3. of species C is the largest.   4. of species B contains the most genes.   5. None of the above can be concluded based on this information. |
| DNA structure topic – free response | 5. A double-stranded DNA molecule is shown below, with a portion of its sequence written out. There are several non-complementary base pairs, highlighted.    The overall **stability** of this DNA molecule is **less** **than** a normal double-stranded DNA molecule. **Explain why** in 1-2 brief sentences. |
| Genome topic – free response | 6. You are researching a newly-discovered plant, and you want to determine all of the DNA sequences (genes and the non-coding sequences in-between genes) in this plant.  **What genetic material** should you determine the sequence of? **Explain why**, in 1-2 short sentences. |

**Table S3: Free-response questions scoring rubrics**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Question 5** | **Rubric** | **Concept 1 (Inter-strand size/distance altered)** | | | **Concept 2 (Interactions affected)** | **Jargon: “Stacking interactions”**  **Score 1 or 0** | **Jargon: “Hydrogen bonds”**  **Score 1 or 0** | **Jargon: “Purine/Pyrimidine”**  **Score 1 or 0** |
| **Argument 1: Size of bases and/or base-pairs.**  **Score 1 or 0** | **Argument 2: Changes fit/distance between strands.**  **Score 1 or 0** | | **Argument 3: Interactions are affected (described effects to hydrogen bonds or hydrophobic interactions)**  **Score 1 or 0** |
| **Question 6** | **Rubric** | **Concept 1(Genome is all of the genetic material in a cell, including coding and non-coding sequences)** | | | | **Concept 2 (heritability of the genome)** | | **Jargon: Genome Score 1 or 0** |
| **Argument 1: The genome is all the genetic material/DNA sequences in a cell** | | **Argument 2: Genome includes all coding and non-coding sequences** | | **Argument 3: Genome is inherited/hereditary**  **Score 1 or 0** | |

**Figure S2. Multiple Choice Scores.** Multiple choice questions within each topic are isomorphic (containing or not containing jargon). No significant differences were observed between groups on the same question (Chi squared test, all p>0.06). Error bars are standard error of the mean for binomial data.

****

**Figure S3. Student scores on multiple-choice questions of post-test.** Comparing students who did the pre-reading and students who did not complete the pre-class reading. Students who did not complete the pre-reading performed significantly worse on the multiple-choice post-test items (t-test, p<0.001). Error bars are standard error.

**Table S3: Number of arguments given in post-test free response questions**. Comparing arguments between students who did the pre-reading and student who did not complete the pre-class reading. The number of student responses that included 0, 1, 2, or 3 correct arguments on the free response post-test items.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | *DNA structure* | | | | *Genomes* | | | |
| *Number of correct arguments* | *Did not do reading* | | *Did reading* | | *Did not do reading* | | *Did reading* | |
| *Control* | *Concepts-first* | *Control* | *Concepts-*  *first* | *Control* | *Concepts-first* | *Control* | *Concepts-*  *first* |
| 0 | 8 | 7 | 26 | 18 | 20 | 15 | 31 | 22 |
| 1 | 10 | 13 | 8 | 15 | 2 | 7 | 9 | 9 |
| 2 | 3 | 2 | 6 | 4 | 0 | 0 | 2 | 10 |
| 3 | 1 | 0 | 2 | 5 | 0 | 0 | 0 | 1 |

**Table S4:Statistical comparison of the number of arguments given in free-response questions.** These values were calculated from the counts in Table S3 using a Chi squared test. For students who did not complete the reading there was no difference between the control and treatment group. Students who did not complete the pre-reading had significantly fewer arguments than those that did complete the pre-reading. These three comparisons combined indicate that 1) the reading has an impact on learning, and 2) the inclusion of jargon in the reading has an impact on learning.

|  |  |  |
| --- | --- | --- |
| *Comparison* | *Chi-squared p-value, within this topic* | |
| *DNA structure* | *Genomes* |
| Did not do reading control vs.  Did reading control | < 0.0001 | < 0.005 |
| Did not do reading concepts first vs. Did reading concepts-first | < 0.005 | < 0.005 |
| Did reading control vs.  Did reading concepts-first | < 0.005 | < 0.0005 |