## Teaching Notes

### By *Nik Tsotakos*

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**Course Information**

Department: Biology

Level: **Upper Undergraduate**

Course type: **Both**

Students: **Majors**

Number of Students: 22

**Module Information**

Original Module Name: Understanding COVID-19 Biology to Design a Vaccine

Link to Original: https://qubeshub.org/qubesresources/publications/1904/1

Adapted Module Name: COVID-19: On the way to a vaccine

Link to Adapted Module]

Modified Module Name:

Files associated: Class Handouts

Modification Learning Goals:

Following the completion of the module, the students should be able to:

* retrieve protein and nucleic acid sequences from public repositories
* align sequences using open license software
* explain similarities and differences between aligned sequences
* construct phylogenetic trees and explain principles of molecular evolution
* design primers and probes for a qPCR assay
* make use of resources that are relevant to gene expression (i.e. NCBI Gene database, GTEx)
* explore molecular interactions by visualizing available 3D protein models with freely available software

**Teaching Notes**

*This module was delivered to an upper-level undergraduate Genetics class. Most of the students would go on to graduate at the end of the semester, but there were a few juniors in the classroom. Importantly, the class met in a computer lab and was very heavy on hands-on analyses and primary literature readings.*

Part I:

This activity was adapted from the Newman et al paper. It was performed prior to the publication of the paper by Andersen et al in Nature Medicine (found at https://www.nature.com/articles/s41591-020-0820-9). The viral sequences were pulled from www.viprbrc.org. Since the selection of the genomes took place so early in the pandemic (February 2, 2020, approx. a month prior to the stay-at-home orders in the USA), some of them have likely been deprecated.

The assignment at the end of part I is related to literature previously studied in the class, but it can be connected to COVID-19, since surfactant protein A has immunomodulatory properties in the lung.

Part II:

This part was delivered to the students following a presentation on qPCR and primer design. They were given the paper by Thornton & Basu as supplemental material. The in silico PCR tool of the UCSC genome browser (found [here](https://genome.ucsc.edu/cgi-bin/hgPcr)) is a helpful tool to quickly assess students’ answers. The actual sequences used by the CDC-approved kits, as shown in the relevant document, were not given to students, and used only for assessment purposes.

Part III:

This activity was introduced following the shift to remote instruction in the Spring 2002 semester. However, the students had prior experience with using both databases from earlier meetings in the classroom. This part can be assigned as homework, followed by discussion when the class meets (in person or remotely). A good, succinct summary of findings re: ACE2 and TMPRSS2 can be found [here](https://www.jwatch.org/na51115/2020/03/18/ace2-sars-cov-2-receptor-required-cell-entry).

Part IV:

When this discussion was initiated in classroom, there were some news articles, but the TIME article linked [here](https://time.com/5829202/covid-19-gender-differences/) was not yet available. Students worked in small groups, and came up with interesting ideas (X-inactivation and genes escaping it, hormones (later discussed here: <https://www.sciencemag.org/news/2020/06/why-coronavirus-hits-men-harder-sex-hormones-offer-clues>.

Parts V and VI:

These parts were delivered to the class unchanged from the original module, despite the fact that they were written targeting a lower-level undergraduate audience. The students at this point were familiar with PDB, iCn3D, and BLAST, but the activities remained unchanged for two reasons: i) to ease off the difficulty of the activities, as many students were heavily stressed due to pandemic measures/personal problems/upcoming graduation, etc., and ii) to streamline grading of the assignments.

These activities can deifinitely be presented more succinctly to students who are familiar with the databases used.