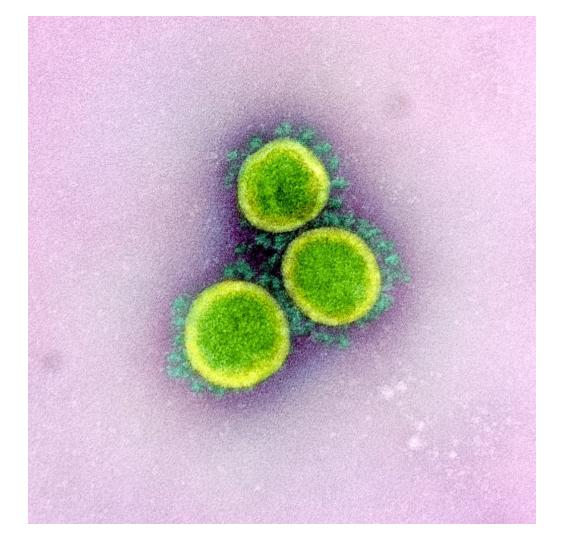
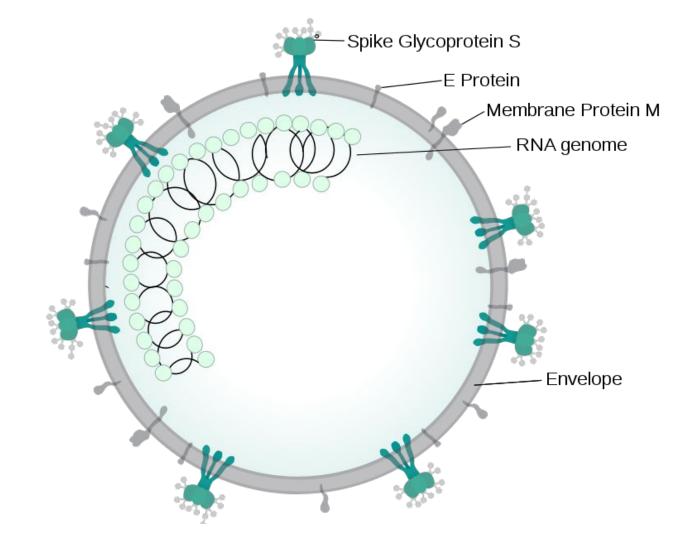
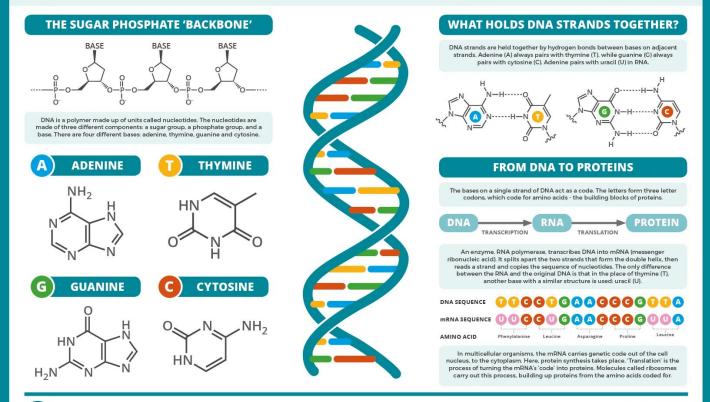
A SMALL PEEK INTO SARS-COV-2 GENOMICS

Melih Yıldız Middle East Technical University





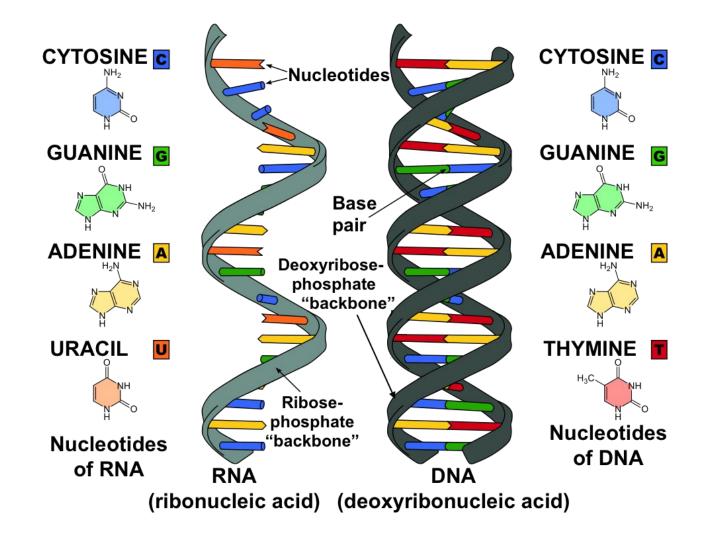
THE CHEMICAL STRUCTURE OF DNA

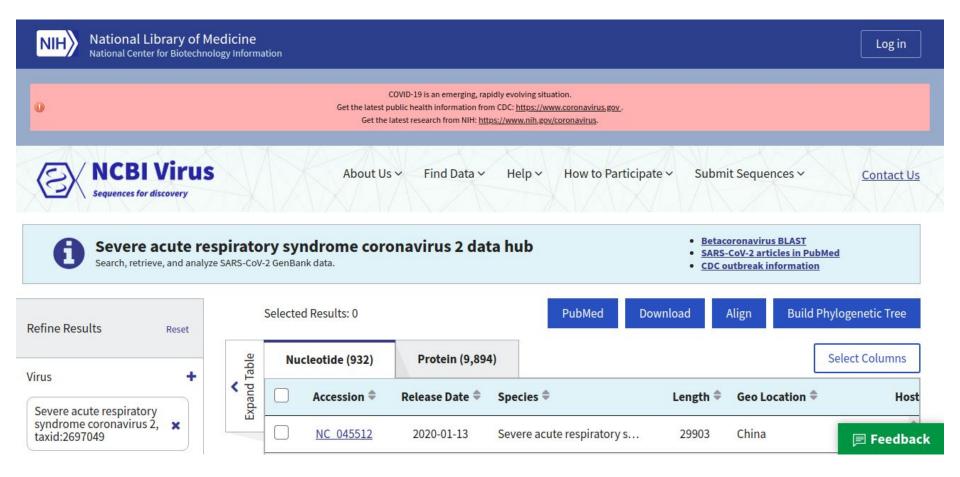


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Ci



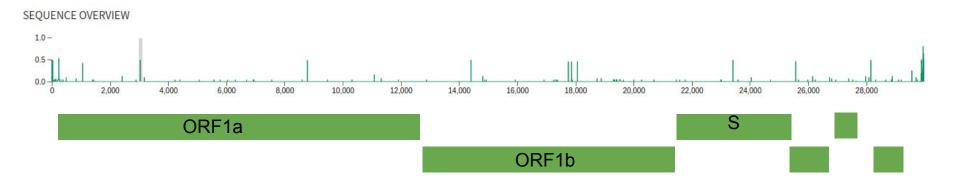




668 complete genome sequences from 21 countries

including one genome sequence from Turkey

CAACTGAAATCTATCAGGCCGGTAGCACCCTTGTAATGGTGTTGAAGGTTTTAATTGTT GAGTAGTAGTACTTTCTTTTGAACTTCTACATGCACCAGCAACTGTTTGTGGACCTAAAA AGTCTACTAATTTGGTTAAAAAACAAATGTGTCAATTTCAACTTCAATGGTTTAACAGGCA CAGGTGTTCTTACTGAGTCTAACAAAAAGTTTCTGCCTTTCCAACAATTTGGCAGAGACA TTGCTGACACTACTGATGCTGTCCGTGATCCACAGACACTTGAGATTCTTGACATTACAC CATGTTCTTTTGGTGGTGTCAGTGTTATAACACCAGGAACAAATACTTCTAACCAGGTTG CTGTTCTTTATCAGGGTGTTAACTGCACAGAAGTCCCTGTTGCTATTCATGCAGATCAAC TTACTCCTACTTGGCGTGTTTATTCTACAGGTTCTAATGTTTTTCAAACACGTGCAGGCT GTTTAATAGGGGCTGAACATGTCAACAACTCATATGAGTGTGACATACCCATTGGTGCAG GTATATGCGCTAGTTATCAGACTCAGACTAATTCTCCTCGGCGGGCACGTAGTGTAGCTA GTCAATCCATCATTGCCTACACTATGTCACTTGGTGCAGAAAATTCAGTTGCTTACTCTA ATAACTCTATTGCCATACCCACAAATTTTACTATTAGTGTTACCACAGAAATTCTACCAG TGTCTATGACCAAGACATCAGTAGATTGTACAATGTACATTTGTGGTGATTCAACTGAAT GCAGCAATCTTTTGTTGCAATATGGCAGTTTTTGTACACAATTAAACCGTGCTTTAACTG ACAAAACACCACCAATTAAAGATTTTGGTGGTTTTAATTTTTCACAAATATTACCAGATC CATCAAAACCAAGCAAGAGGTCATTTATTGAAGATCTACTTTTCAACAAAGTGACACTTG CAGATGCTGGCTTCATCAAACAATATGGTGATTGCCTTGGTGATATTGCTGCTAGAGACC TCATTTGTGCACAAAAGTTTAACGGCCTTACTGTTTTGCCACCTTTGCTCACAGATGAAA TGATTGCTCAATACACTTCTGCACTGTTAGCGGGTACAATCACTTCTGGTTGGACCTTTG GTGCAGGTGCTGCATTACAAATACCATTTGCTATGCAAATGGCTTATAGGTTTAATGGTA GTGCTATTGGCAAAATTCAAGACTCACTTTCTTCCACAGCAAGTGCACTTGGAAAACTTC AAGATGTGGTCAACCAAAATGCACAAGCTTTAAACACGCTTGTTAAACAACTTAGCTCCA ATTTTGGTGCAATTTCAAGTGTTTTAAATGATATCCTTTCACGTCTTGACAAAGTTGAGG CTGAAGTGCAAATTGATAGGTTGATCACAGGCAGACTTCAAAGTTTGCAGACATATGTGA CTCAACAATTAATTAGAGCTGCAGAAATCAGAGCTTCTGCTAATCTTGCTGCTACTAAAA TGTCAGAGTGTGTGCTTGGACAATCAAAAAGAGTTGATTTTTGTGGAAAGGGCTATCATC TTATGTCCTTCCCTCAGTCAGCACCTCATGGTGTAGTCTTCTTGCATGTGACTTATGTCC CTGCACAAGAAAAGAACTTCACAACTGCTCCTGCCATTTGTCATGATGGAAAAGCACACT TTCCTCGTGAAGGTGTCTTTGTTTCAAATGGCACACACTGGTTTGTAACACAAAGGAATT

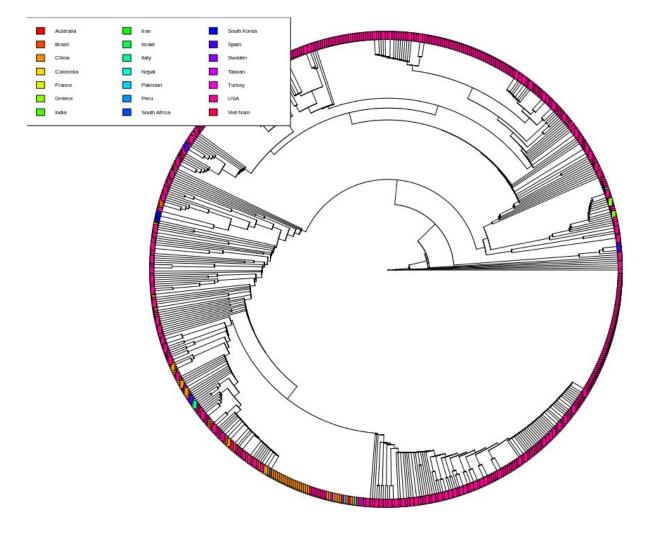


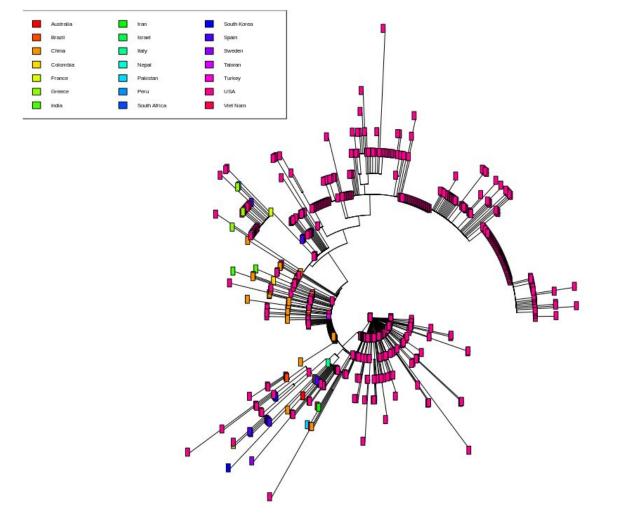
Total of 10 genes, some are marked

Phylogenetic Relationships of Virus Isolates

Two phylogenetic tree methods:

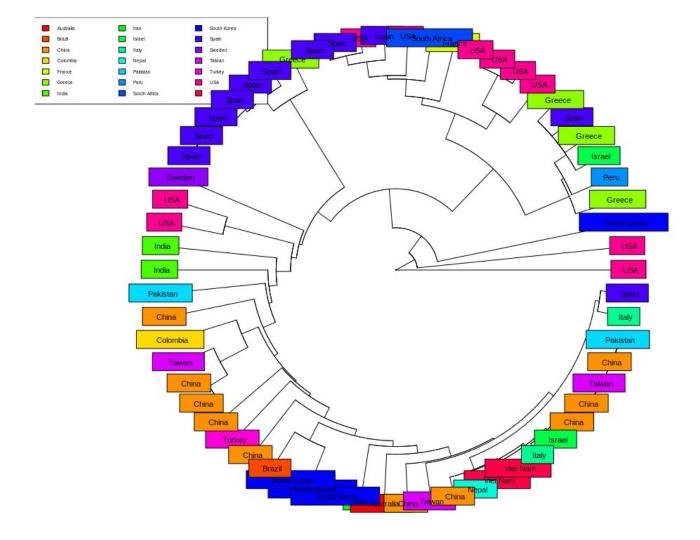
- UPGMA
- Neighbor-Joining

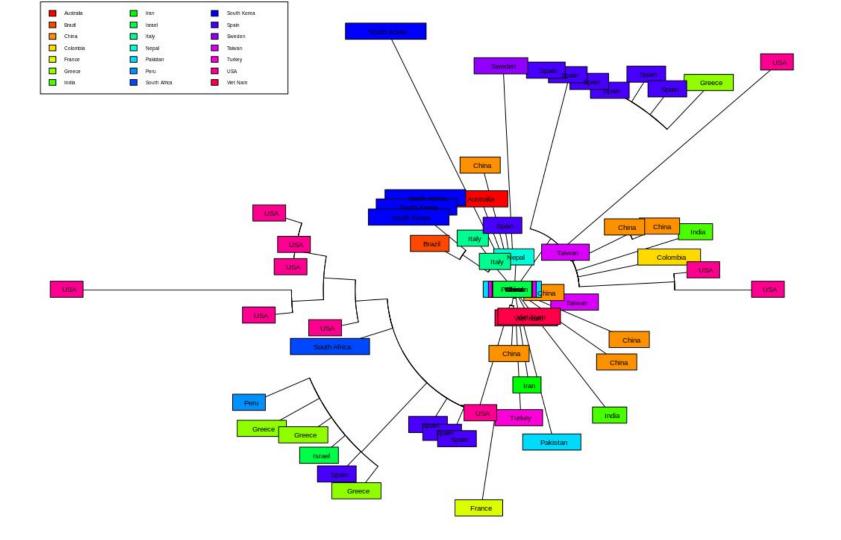




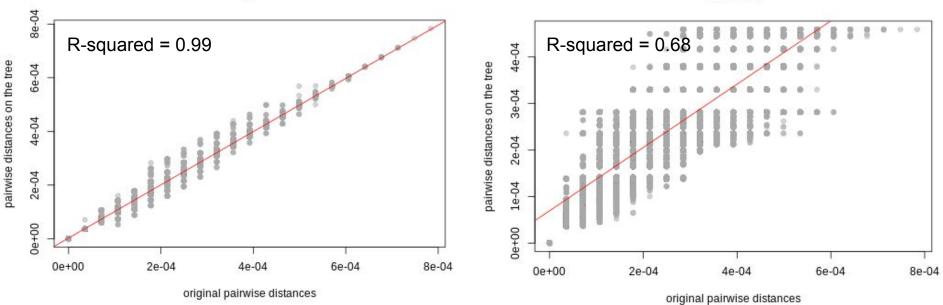
Country of Sequence Origin	Number of Sequences	Country of Sequence Origin	Number of Sequences
USA	564	Australia	1
China	61	Brazil	1
Spain	11	Colombia	1
Greece	4	France	1
South Korea	4	Iran	1
Taiwan	3	Nepal	1
India	2	Peru	1
Isreal	2	South Africa	1
Italy	2	Sweden	1
Pakistan	2	Turkey	1
Vietnam	2		

 Table 1: Number of full genome sequences used in the analysis.



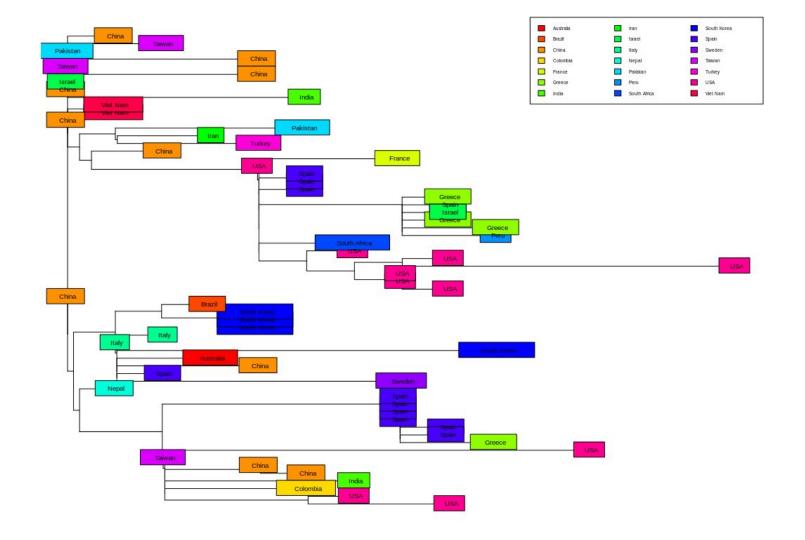


WHICH TREE IS BETTER?



NJ

UPGMA



Further Directions

- Observing evolution of the virus in real time
- Identification of present virus subtypes in different regions
 *Important for qPCR, diagnostics and possibly vaccine development
- Analysis of conservation, drift and positive selection on viral genes.

Thank you!

Reference

• NCBI Virus Database(<u>https://www.ncbi.nlm.nih.gov/labs/virus/vssi/#/</u>)

 Wu, F., Zhao, S., Yu, B., Chen, Y.-M., Wang, W., Song, Z.-G., ... Zhang, Y.-Z. (2020). A new coronavirus associated with human respiratory disease in China. *Nature*, *579*(7798), 265–269. doi: 10.1038/s41586-020-2008-3

• <u>https://www.khanacademy.org/science/high-school-biology/hs-molecular-genetics/hs-</u> <u>rna-and-protein-synthesis/a/hs-rna-and-protein-synthesis-review</u>