Probable Pangolin Origin of SARS-CoV-2 Associated with the COVID-19 Outbreak

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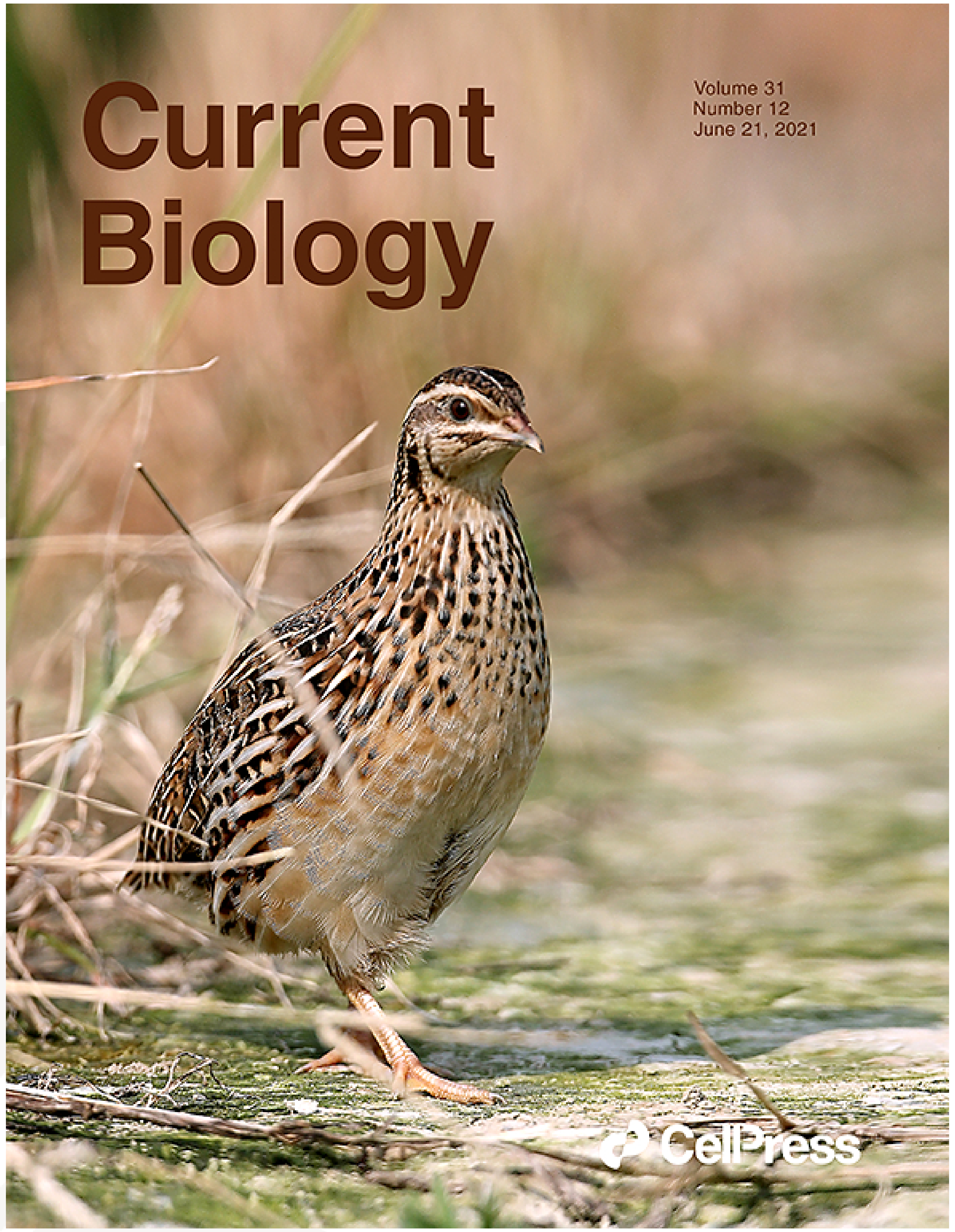
Introduction



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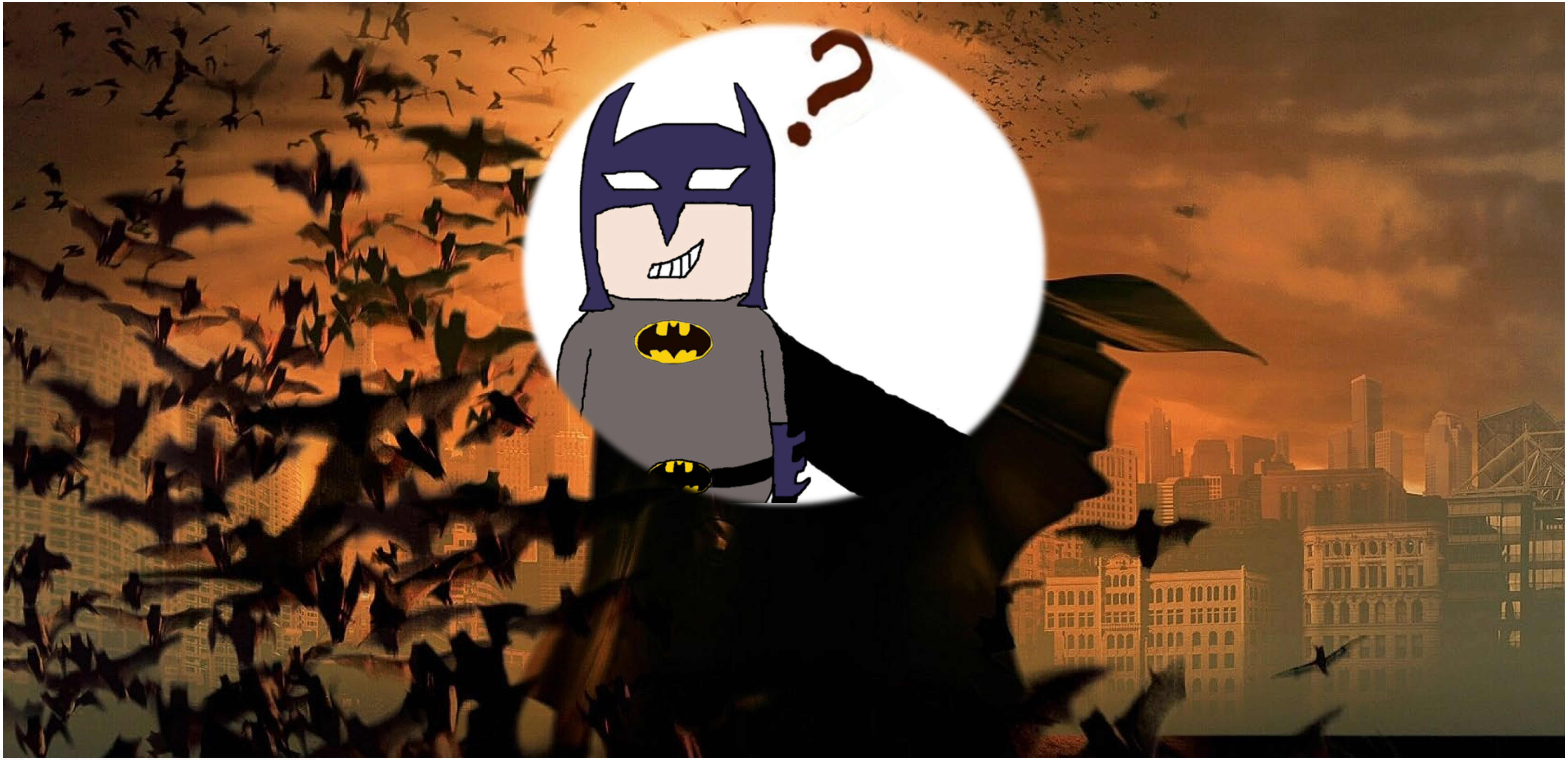
---The above data are from NCBI as of July 4, 2021.



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Researched Questions

- ➢ Assessing the Probability of SARS-CoV-2-like CoV Presence in Pangolin Species.
- ➢ Draft genome of Pangolin-CoV and its genomic characteristics.
- ➢ Phylogenetic Relationships among Pangolin-CoV, RaTG13, and SARS-CoV-2.
- ➢ Dualism of the S protein of Pangolin-CoV.

Assessing the Probability of SARS-CoV-2-like CoV Presence in Pangolin Species

RNA-seq of Pangolin for lung samples.

1882 clean reads mapped to the SARS-CoV-2 and covered 76.02% of the SARS-CoV-2 genome.

De novo assembly of those reads, obtained 36 contigs.

Blast analysis against proteins from 2845 CoV genomes.

22 contigs were best matched to SARS-CoV-2s.

12 contigs matched to bat SARS-CoV-like CoVs.

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Draft genome of Pangolin-CoV and its genomic characteristics

Created a Pangolin-CoV draft genome based on the above 34 contigs.

⇨

Pangolin-CoV shared 91.02% DNA identity with SARS-CoV-2.

⇨

For the spike (S) protein, Pangolin-CoV amino acid sequence identity (97.5%) was higher to SARS-CoV-2 genes than to bat RaTG13 genes (95.5%).

⇙

The high S protein amino acid identity means functional similarity between Pangolin-CoV and SARS-CoV-2.

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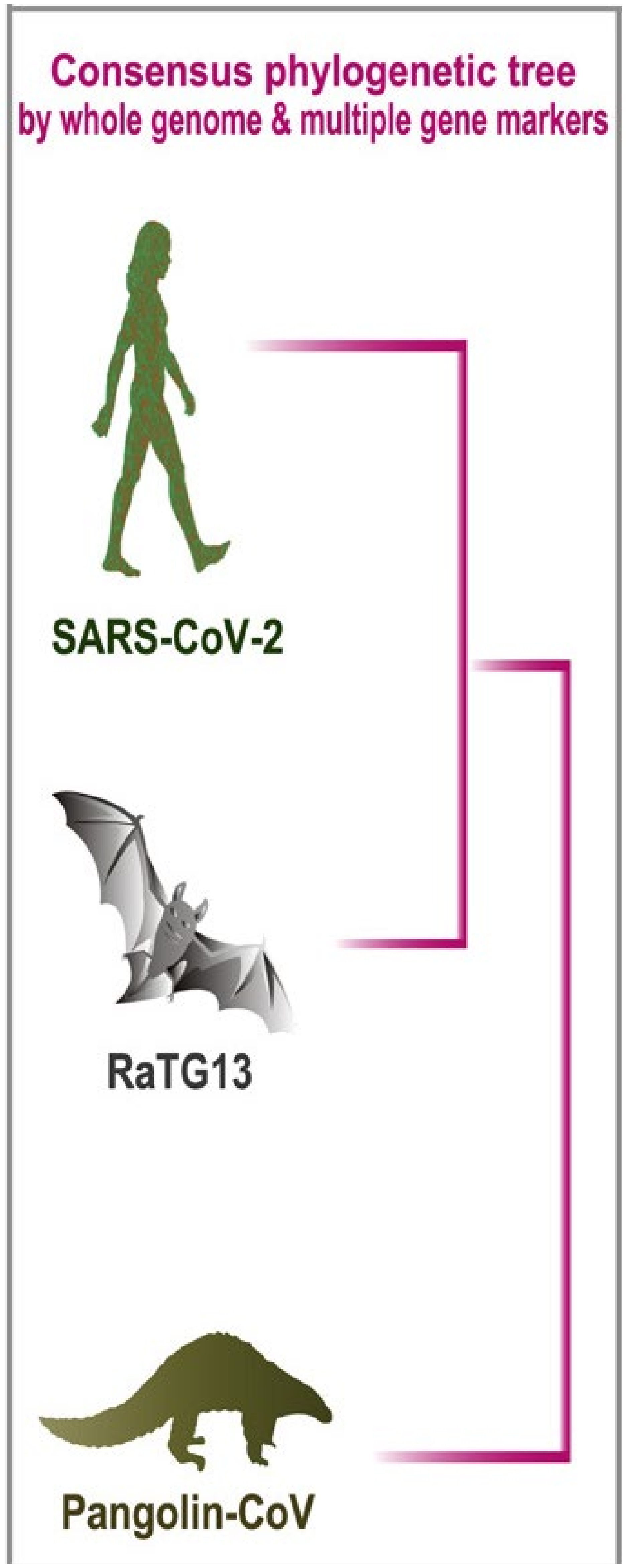
Phylogenetic Relationships among Pangolin-CoV, RaTG13, and SARS-CoV-2



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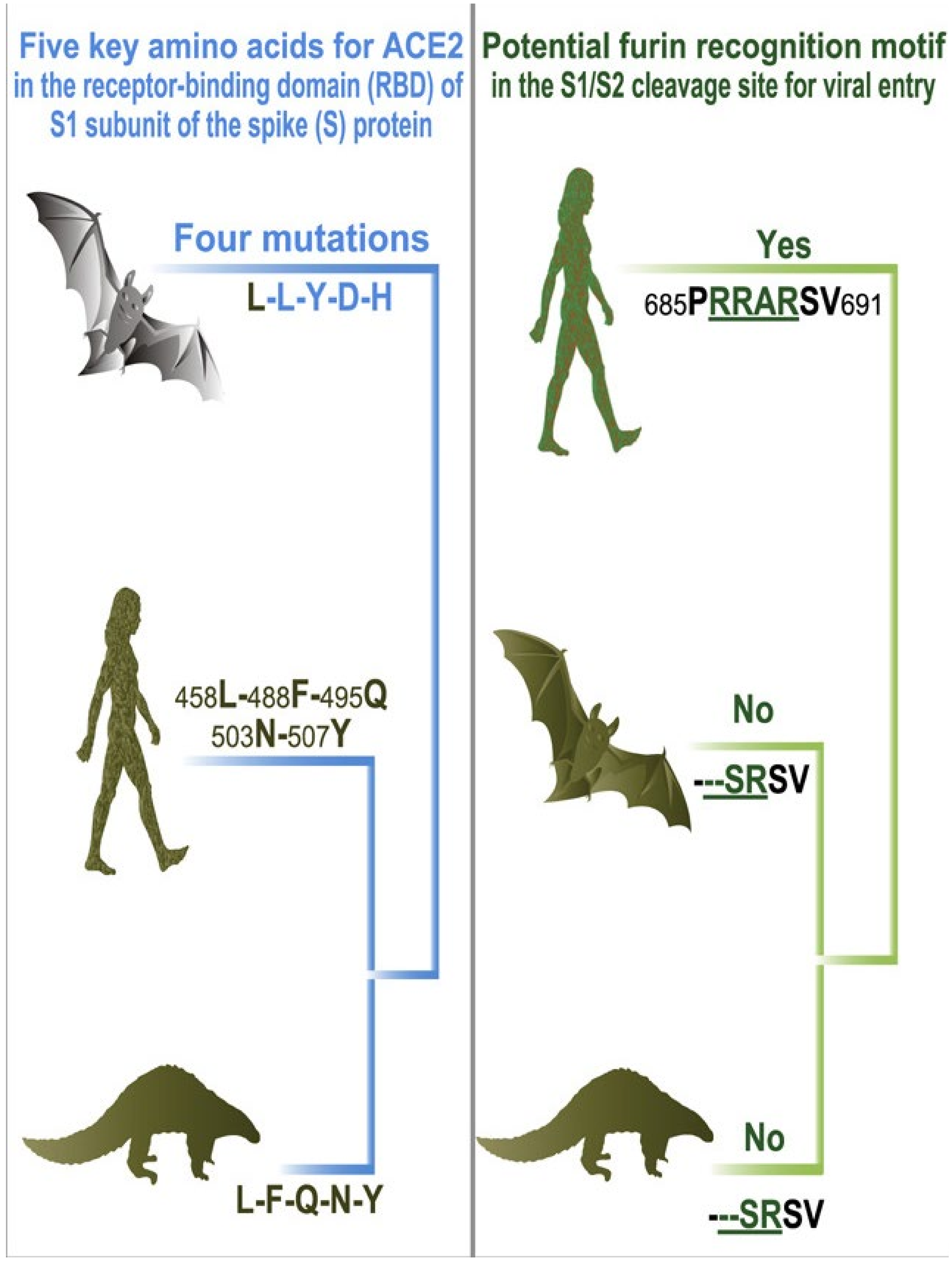
Dualism of the S protein of Pangolin-CoV



Evaluation

Pros:

- The first report on a potential closely related kin (Pangolin-CoV) of SARS-CoV-2.

Cons:

- They have no original lung sample of Pangolin.

Thank You for Your Attention!