

Review of: "Sequence evidence that the D614G clade of SARS-CoV-2 was already circulating in northern Italy in the fall of 2019"

Giorgia Marini¹

¹ Sapienza University of Rome

Potential competing interests: No potential competing interests to declare.

Dear Author,

I have read your draft with great interest. As you mention in the first paragraph, the two “key questions are asked following a viral outbreak, i.e., when and where the zoonotic or lab-leak event occurred.” While the “when” question is “addressed by estimating the viral evolutionary rate and dating the most recent common ancestor (MRCA) of representative viral strains”, the “where” question “is approximated by the location where the earliest viral lineage was sampled.”

I believe your contribution will benefit from explaining why these two questions are so relevant. What are the consequences, if there are any, of knowing “when” and “where”?

Your contribution is extremely accurate and clear in terms of sample sequences. However, you often use expressions such as “already frequent” or “low-probability event” when talking about strains.

I wonder if your paper would benefit from an explicit quantitative estimate/evaluation of such frequencies and probabilities.

Which is your journal target? Do you have in mind a scientific journal or a policy journal? I believe it would be useful to explain why discussing the controversies arising from the set of early SARS-CoV2 sequences so important. And, especially who cares? Policy makers? Doctors?

For both recipient (either policy makers or doctors) it would be important to clarify the policy implications of your question (where?) and the consequences of a “different” where.

Reviewer

