Reply to cai et al regarding "vertical transmission of coronavirus disease 2019: a systematic review and meta-analysis"

We appreciate Cai et al for their letter to the editor and for expressing interest in our work. We would like to thank them for the points raised and would like to take the opportunity to respond with regard to our article.[1]

First, we would like to thank Cai et al for pointing out a small typo, ie, 68 studies instead of what should be 69 studies in the 'search strategy' section. However, throughout the rest of the manuscript including the 'Search Results' and 'Systematic Review' sections, it is clearly stated that "69 studies fulfilled the eligibility criteria and were included in the qualitative synthesis" and in accordance "69 studies included in qualitative synthesis" are also noted in the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) flowchart (Figure 1). Out of those 69 studies, 30 case reports and 39 cohort studies or case series were selected for the quantitative synthesis. Notably, the meta-analysis part of the paper was performed on the nasopharyngeal (NP) swab results, and as stated, "38 of 39 cohort or case series studies of pregnant women with COVID-19 infection had information on neonatal NP swab testing results." Therefore, 38 studies were included in the meta-analysis and not 39 as Cai et al suggest. We explicitly state in our manuscript, in the PRISMA flowchart (Figure 1), and in Tables 2 and 3 that the number of cohort or case series studies incorporated into our meta-analysis is 38. This can also be noted from the Forest plot (Figure 3) listing the 38 studies included in the meta-analysis.

Second, we thank Cai et al for pointing out that 2 small case series from China potentially had some duplicate reporting with 2 other case series studies from the same hospitals[2–5] based on the overlapping periods of data acquisition. Although we generally agree that duplicate reporting must be avoided, we cannot realistically exclude duplicate patients as we have no access to the list of patients used by Yu et al, Hu et al, Yang et al, and Chen et al.[2–5] We believe that this is beyond us and exemplifies the consequences of publishing duplicate datasets. Ultimately, the inclusion of these data does not change the conclusion of the meta-analysis, as noted by the authors of this letter and our own subanalyses. Specifically, if we removed these 4 studies from our Chinese cohort or case series meta-analysis, ie Yu et al ($n=3$; weight, 0.41), Hu et al ($n=7$; weight, 0.82), Chen et al ($n=6$; weight, 0.72), and Yang et al ($n=5$; weight, 0.62), this would remove 21 out of 397 neonates, which is approximately 5.5% of the neonates included in our meta-analysis of the studies from China. These 4 studies account for a mere 2.57% out of the 100% total weight of the meta-analysis, which would not appreciably change our results. In addition, in the article, we analyzed the cohort or case series studies from China and from outside China separately. Notably, this tandem analysis produced similar vertical transmission estimates of 2.0% and 2.8%, respectively. Hence, potentially removing these 4 studies would not change the general conclusion of our paper that vertical transmission is possible and occurs in a very small minority of patients.

Given the rapidly emerging data surrounding COVID-19 infection at the time and the volume of new reports, we wished to provide as inclusive an estimate of vertical transmission as was available at that time. With the ongoing emergence of additional data, future studies will ultimately further refine our initial estimates. ■

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The authors report no conflict of interest.

This manuscript did not receive any funding

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https://doi.org/10.1016/j.ajog.2021.09.029