Review of: "SARS-CoV-2 infectivity by viral load, S gene variants and demographic factors and the utility of lateral flow devices to prevent transmission"

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This is a statistics study about infectivity and viral load, the B.1.1.7 variant and household contact in 2,474,066 contacts of 1,064,004 SARS-CoV-2 cases. And the author try to assess the feasibility of infection detection with lateral flow devices. The principal findings were that cases with high viral loads, household, older age and B.1.1.7 variant are the most infectious and the best performing LFDs detect most infectious cases.

There are a number of concerns with this study which include the following:

1. SARS-CoV-2 infectivity is associated with index case viral load, but the conclusion is not effectively instructive because it is almost impossible to quarantine contacts based on viral load. There are great differences in viral load in different periods after SARS-CoV-2 infection. Patients with low viral load may still infect contacts, which is related to many factors, such as the immune status of patients and contacts. Therefore, isolation of contacts is the most effective way to quickly block the epidemic. In my opinion, if the author can analyze the change of viral load with time after infection, and at which time SARS-CoV-2 is more likely to be transmitted to people in contact, such research is more meaningful.
2. Although the most sensitive LFDs would detect 89.5% (89.4-89.6%) of cases with PCR-positive contacts, the sensitivity of LFD is relatively low compared to that of RT-PCR.
3. The author mentioned "Index cases with SGTF had lower Ct values", my question is that whether there is significiant difference between cases with SGTF and cases without SGFT in terms of Ct?
4. The method of collecting swabs is also an important factor. Whether there is the possibility that the location of sampling site and other situations where some patients may have obvious cough, sneeze and other stress reactions during the sampling could result in the inconsistency between the actual viral load and PCR detection results. And this inconsistency could affect the reliability of the research.