

The many clinical advantages of reporting the cycle threshold (Ct) value

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Submitted Mar 02, 2022. Accepted for publication Mar 17, 2022. doi: 10.21037/atm-22-1104 View this article at: https://dx.doi.org/10.21037/atm-22-1104

There is ongoing debate on advantages and limitations of reporting the cycle threshold (Ct) values in clinical specimens testing positive for severe acute respiratory syndrome coronavirus disease 2 (SARS-CoV-2) mRNA. In a recent document published authored by Rhoads *et al.* on behalf of the College of American Pathologists (CAP) Microbiology Committee Perspective (1), the authors concluded that caution shall be used in interpreting the Ct values of SARS-CoV-2 testing. Although we substantially agree that using this means for expressing SARS-CoV-2 viral load in diagnostic samples carries some technical drawbacks, we would like to briefly emphasize here the many other important clinical implications that Ct values reporting may have in coronavirus disease 2019 (COVID-19) diagnostics.

Several lines of evidence now confirm that the Ct value is a significant predictor of emergence and progression of local SARS-CoV-2 outbreaks. This has been clearly demonstrated by Yin *et al.* (2), who showed that the trends of Ct values predict epidemic trajectories in terms of future mean daily positive tests, as well as by Penney *et al.* (3), who demonstrated that the trend of Ct values in SARS-CoV-2 positive samples significantly predicts incident COVID-19 hospitalizations. Besides these important epidemiological implications, mounting evidence reveals that monitoring routine Ct values of SARS-CoV-2 by means of accurate and standardized molecular assays may have substantial clinical implications. To summarize the most important findings, Shah et al. conducted a meta-analysis of studies which explored the association between SARS-CoV-2 viral load and outcome of COVID-19 (4), concluding that patients with low Ct values (i.e., typically <25), display an over 2-fold and a nearly 3-fold higher risk of developing severe COVID-19 illness and death, respectively, compared to those with higher Ct values. In another critical review of the literature, Rao and co-authors concluded that Ct values of SARS-CoV-2 RNA may even anticipate unfavourable changes in some laboratory biomarkers, which are predictive of adverse clinical outcome in patients with SARS-CoV-2 infection (5). Finally, Abu-Raddad et al. demonstrated that systematic assessment of Ct values in patients with COVID-19 vaccine breakthrough are highly predictive of SARS-CoV-2 infectiousness, thus enabling more appropriate planning and establishment of public preventive measures (6).

In conclusion, although we are aware that several pre-analytical (i.e., specimen collection, preservation, storage, transportation, preparation, inactivation and RNA extraction), analytical (e.g., analytical sensitivity and interfering substances, usage of different gene targets and diverse amplification and detection techniques) and postanalytical (e.g., calibration, test results interpretation, correlation with viral load) aspects may bias the importance of reporting the Ct values in SARS-CoV-2 positive samples (7), we firmly believe that the clinical advantages of using accurate and standardized molecular assays fit for this purpose may ultimately offset the limitations (*Table 1*).

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 Table 1 Potential clinical advantages of reporting the Ct value in clinical specimens testing positive for SARS-CoV-2

Predicts emergence and progression of SARS-CoV-2 outbreaks

Predicts the risk of developing severe/critical forms of COVID-19 illness

Predicts SARS-CoV-2 infectiousness, even in in patients with vaccine breakthrough

Ct, cycle threshold; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2; COVID-19, coronavirus disease 2019.

Acknowledgments

Funding: None.

Footnote

Provenance and Peer Review: This article was commissioned by the editorial office, *Annals of Translational Medicine* for the series "Column in Laboratory Medicine". The article did not undergo external peer review.

Conflicts of Interest: Both authors have completed the ICMJE uniform disclosure form (available at https://atm. amegroups.com/article/view/10.21037/atm-22-1104/ coif). The series "Column in Laboratory Medicine" was commissioned by the editorial office without any funding or sponsorship. GL serves as the unpaid Guest Editor of the series. The authors have no other conflicts of interest to declare.

Ethical Statement: The authors are accountable for all aspects of this work in ensuring that questions related to the accuracy or integrity of any part of this work are appropriately investigated and resolved.

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Cite this article as: Lippi G, Plebani M. The many clinical advantages of reporting the cycle threshold (Ct) value. Ann Transl Med 2022;10(7):427. doi: 10.21037/atm-22-1104

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