Using Ct Values to Predict the Future Trajectory of COVID-19 New Daily Cases: A Multicenter Cross-Sectional Study

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Abstract

Introduction: Proactive prediction of the epidemiologic dynamics of viral diseases and outbreaks of the likes of COVID-19 has remained a difficult pursuit for scientists, public health researchers, and policymakers. It is unclear whether RT-PCR Cycle Threshold (Ct) values of COVID-19—or any other virus—as indicator of viral load, could represent a possible predictor for underlying epidemiologic changes on a population level. The objective of this study is thus to investigate whether population-wide changes in SARS-CoV-2 RT-PCR Ct values over time are associated with the daily fraction of positive COVID-19 tests, and to analyse the factors that may influence the Ct values.

Methods: A retrospective cross-sectional study was conducted on 63,879 patients from May 4, 2020 to September 30, 2020, in all COVID-19 facilities in the Kingdom of Bahrain. Data collected included number of tests and newly diagnosed cases, as well as Ct values, age, gender nationality, and symptomatic status.

Results: Ct values were found to be negatively and very weakly correlated with the fraction of daily positive cases in the population [r = −0.06, CI95% −0.06 to −0.05; p=0.001). The R-squared for the regression model (adjusting for age and number of daily tests) showed an accuracy of 45.3%. Ct Values showed an association with nationality (p=0.012). After the stratification, the association between Ct values and the fraction of daily positive cases was only maintained for the female gender and Bahraini-nationality. Symptomatic presentation was significantly associated with lower Ct values (higher viral loads). Ct values do not show any correlation with age (p=0.333) or gender (p=0.522).

Conclusion: We report one of the first and largest studies to investigate the epidemiologic associations of Ct values with COVID-19. Ct values offer a potentially simple and widely accessible tool to predict and model epidemiologic dynamics on a population level. More population studies and predictive models from global cohorts are necessary.