Growth of D614G Virus : Morgan – Morgan – Finney (MMF) Regression

JAYDIP DATTA (✉ deepjoy1972@gmail.com)

Indian Institute of Chemical Engineers (CRC) , Kolkata ,700032, INDIA <https://orcid.org/0000-0002-0013-5269>

Research Article

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Abstract

In our earlier work [1], a correlation was established between Infection fatality rate (IFR) vs age of the patient by logistic or sigmoid regression model. The regression model shows a more probable IFR with a sigmoid rise after 46 yrs and becoming most significant after 70 yrs and above. In the present study the frequency of infected patient by 'G' type of mutants of SARS-COV-2 with time from Jan, 2020 to June, 2020 for 6.5 months duration of experimental study. The best fit analysis is compared to **Morgan – Morgan – Finney (MMF)** model (3,4) statistics and Polynomial regression model. Both the above model correlates a significant result with Pearson coefficient (r), Probability (p-value). The RBD of D614G (10) interaction with Angiotensin Converting Enzyme-II (ACE2) of host cell can be also correlated to another new spike mutant like N501Y (11) through Pearson coefficient (r) with p-value of significance.

Introduction

The G type of mutants of SARS-COV-2 (2) namely D614G was first discovered in china at the end of Jan, 2020 along with Germany. The quick spreading rate of mutants increasing the susceptibility of infection throughout the Europe. Here the most important epidemiological variants, frequency of 614G infection vs time w.e.f Jan – June, 2020. The goodness of fit analyses two non linear regression like MMF (3,4) and 4th degree polynomial fit. The bioenergetics study(DEL2G) parameters (Figure – X) of newer spike glycoprotein mutants (10,11) D614 type of mutant also shows a good-fit with N501Y (12)mutant .

Methods

The scattered data (2, Figure-I) frequency vs month for 6.5 months retrieved ,are plotted in Excel spreadsheet as well as a distribution of contour with two months interval .The scattered data (2) are executed by Curve Finder (V-1. 4) shows MMF model fit and 4th degree polynomial fit with a significant value of r with p-value(7,8) . In each model the Standard error (s), Root mean standard error (RMSE), Chi-square hypothesis , Covariance matrix support r and p-value . (*Model Curve – 1-3, 5-8*)

The scope of the D type of mutant interaction can be correlated with N type of mutant can be achieved through **Exponential** –goodness of fit with bioenergetics **data** (12, Figure –X) of DEL2G parameters .

Results

MMF MODEL –

Model equation (*Figure – III*) : $y = (ab + cx^d) / (b + x^d)$ —————(1)

$r = 0.99334767$, $s_1 = 0.06152343$, Covariance matrix(6, *Figure V*) = [4 x 4] Sq .

4th Degree Polynomial Fit –

Model equation (*Figure – IV*) : $y = (a + bx + cx^2 + d x^3 +)$ —————(2)

$r = 0.99158899$, $s_2 = 0.0773068$, Covariance matrix(6, *Figure VII*) = [5 x 5] Sq .

The variable y represents frequency of D614G infection and x represents the number of months .

The value of regression coefficients a,b,c, d for this model can be determined from covariance matrix.

$RMSE = \sqrt{[(s_1^2 + s_2^2) / 2]} = 0.06985$ —————(3)

p-value (MMF) < 0.0001 @ 0.01 interval (7,8).

p-value (Polynomial Fit) < 0.0001 (7,8).

Exponential Model Fit (12, Figure –X, XI)– Significant with Pearson coefficient (r) = 1.000 @ Standard Error (s) = 0.0 .

Since in both the cases p-value < 0.01 , Confidence interval (CI) > 95 % .

Conclusion

Both the fit shows the relevant value of r followed by p-value (7,8) shows the infection growth frequency (y) of D614 G type mutant is more significant as the month increases from Jan – June, 2020 . But considering Chi-Sq analysis(Figure –VI) the MMF model is more preferable than 4th Degree- Polynomial model since the tolerance limit = $1 * e^{(-0.006)}$ with 27 iterations(*Figure VIII, 9,10*) is more converged .The exponential goodness(11,12, Figure-XI) also signifies an important bio-energetic interaction of RBD (614G) – ACE 2 with RBD (N501Y) – ACE2 more precisely .

Declarations

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Figures

Figure 1

MMF Model Curve

Figure 2

4th Degree Polynomial Degree Fit

Figure 3

A Contour Distribution For Frequency of D614G Mutant vs Number of Months

Supplementary Files

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