Perevaryukha A. Yu.(Saint-Petersburg, Russia)**Hybrid model of COVID waves taking into account the aspect of stochastic evolution.**

A new hybrid model of COVID-19 waves is proposed taking into account the stochastic evolution of the virus and incompletely deterministic confrontation with unevenly distributed population immunity specified by susceptibility gradation groups. Random mutations in the S-protein of the virus and strict factors of evolutionary selection form a series of changes in the activity of competing virus lineages. We will define the description of the activation of a new COVID wave in a hybrid structure with probable transitions $P(A_f)$ based on the gradation of the affinity of binding of the S-protein to the receptor. Taking into account the stochastic perturbation τ_1 by a random variable γ in the range $\gamma(\omega) \in [1, 2]$ with a perturbed uniform random variable delay $(t - \tau_1\gamma)$, we describe the transition to a new form of COVID waves for a more affine variant of the S-protein when occurs $\Delta A_f > 0.1$:

$$\begin{cases} \frac{dY}{dt} = R_2 Y(t) \exp(-\varsigma Y(t - \gamma\tau) - \varepsilon\sqrt{(J - N^2(t - \tau))}, P_1(A_f) \\ \frac{dN}{dt} = R_1 N(t) \ln\left(\frac{\mathcal{K}}{N(t - \tau\gamma)}\right) - \frac{\delta N^2(t - \tau_1\gamma)}{(J - Y(t - \psi))^2} - \varphi Y(t), P_2(A_f)\delta > q. \end{cases} \quad (1)$$

Structure (1) takes into account the effect of activation of a new wave of COVID-19 with an increase in the probability of a sufficient number of random mutations. For $Y(0) < J < \mathcal{K}$, $N(t) \to 0 + \epsilon$, the wave attenuation mode will change. The position of the oscillation extrema $N(t) \to N_*(t), \max N_*(t) < J$, $\min N_*(t)$ depends on the delay perturbation. Evolution is preserved with sufficient affinity $A_f > \bar{A}_f$. **Theorem 1.** *There exists $R_1 = \bar{R}$, such that for the event $\lim_{t \to \bar{t}} N(t; \bar{R}_1\tau) = 0$ the probability $P > 0$ and $\exists \hat{R}_1 > \bar{R}_1, t < \infty$ for this event $P = 1$.* $\hat{R}_1$ is the maximum reproductive number of the virus. The hybrid structure describes the influence of the accumulation of adaptive mutations on the transition to a new regime of epidemic oscillations.

REFERENCES

1. *Perevaryukha A. Yu.* "A Continuous Model of Three Scenarios of the Infection Process with Delayed Immune Response Factors Biophysics, 2021, V. 66, Iss. 2, 327–348.