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SARS-CoV-2 Lambda (C.37): An emerging variant of concern?

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ABSTRACT

Many SARS-CoV-2 variants have high infectivity and transmissibility. The viral genome data show that the COVID-19 curves of daily case numbers were shaped by the emergence of the variants, including Alpha 202012/01 GRY (B.1.1.7; the U.K.), Beta GH/501Y.V2 (B.1.351, B.1.351.2, and B.1.351.3; South Africa), Gamma GR/501Y.V3 (P.1, P.1.1, and P.1.2; Japan, Brazil), Eta G/484K.V3 (B.1.525; Nigeria, the U.K.), Delta G/478K.V1 (B.1.617.2, AY.1, AY.2, and AY.3; India), Iota GH/253G.V1 (B.1.526; the U.S.A.), and Kappa G/452R.V3 (B.1.617.1; India). The Lambda (C.37) variant was reported in Peru initially; this has spread to 41 countries in four continents. Seven out of eight mutations in this variant are associated with the viral spike protein, akin to mutations in the other variants. These mutations have implications for effectiveness of the vaccines and neutralizing antibodies in immunized subjects and those previously infected with the virus and are thought to facilitate the viral invasion into host cells and help the virus evade the host immune system. Widespread dissemination of the viral variants may cause severe clinical consequences, lengthy hospitalizations, and unfavorable prognoses. Healthcare systems will be stretched, and health workers will be fatigued. Fast, equitable, and widespread vaccination with strict adherence to hygiene protocols will control the rising curves of the pandemic due to the new variants.

On 17 August 2021, the global statistics of COVID-19 surpassed 227,000,000 positive cases and 4,600,000 fatalities (Worldometer, 2021). Present epidemiological evidence shows that rises in the COVID-19 cases have coincided with the emergence of specific viral variants. Thus, numerous SARS-CoV-2 variants have aggravated the COVID-19 pandemic (Gupta, 2021a, 2021b). The variants have emerged because of the natural viral evolution, which is facilitated by uncontrolled spread of the virus enabling it to become highly transmissible or more infectious than the original lineage reported in Wuhan, China (Bianchi et al., 2021; Cella et al., 2021). Consequently, evolution of the virus has complicated the management of the global health. So far, the variants include Alpha 202,012/01 GRY (B.1.1.7) from the U.K., Beta GH/501Y.V2 (B.1.351, B.1.351.2, and B.1.351.3) from South Africa, Gamma GR/501Y.V3 (P.1, P.1.1, and P.1.2) from Japan and Brazil, Eta G/484K.V3 (B.1.525) from Nigeria and the U.K., Delta G/478K.V1 (B.1.617.2, AY.1, AY.2, and AY.3) from India, Iota GH/253G.V1 (B.1.526) from the U.S.A., and Kappa G/452R.V3 (B.1.617.1) from India (Data available at https://www.gisaid.org/hcov19-variants/ accessed 4 August 2021). By mid-June 2021, the World Health Organization (WHO) initially classified another variant, Lambda (C.37), as a variant of interest (VOI); this variant was first reported in a few countries (The World Health Organization, 2021). However, within a month, the Lambda variant emerged in 41 countries across four continents (https://www.gisaid.org/hcov19-variants/ accessed 3 August 2021).

The VOI Lambda GR/452Q.V1 was initially reported in Peru in August 2021; many South American countries did not have the facilities to genetically track this variant (Romero et al., 2021). Initial genetic analyses have shown that the Lambda variant has seven mutations in the spike protein, like the preceding variants. These mutations include G75V, T76I, del247/253, L452Q, F490S, D614G, and T859N with phenotypic implications, including potentially increased transmissibility or potentially high resistance to neutralizing antibodies (Romero et al., 2021). Other SARS-CoV-2 variants, for example, 501Y.V2 and 501Y.V3, were shown to have a receptor-binding domain with higher affinity for the human receptor, angiotensin-converting enzyme 2, than the wild-type receptor-binding domain, allowing the virus to invade the host cells and evade the human immune system more efficiently (Liu et al., 2021). In addition to amino acid deletions at positions 3675, 3676, and 3677, the Lambda variant carries the S:L452Q mutation, which is the same as that in other VOIs (Baj et al., 2021). Interestingly, the modified spike protein reportedly renders the Lambda variant more infectious than Gamma and Alpha variants, which preceded Lambda (Acevedo et al., 2021). How this specific mutation may affect the effectiveness of the vaccines or that of the neutralizing antibodies is unknown and requires complex genetic, phenotypic, and functional analyses.

1. Lessons for the future

To learn from the emergence of the new variants including Lambda, one should focus on the pathobiological and epidemiological characteristics of the variants. Each variant carries specific mutations which potentially confer a particular advantage to the virus. For example, both D614G and B.1.617 have been associated with higher transmissibility than the parent viral strain (Cherian et al., 2021; Conti et al., 2021). The high transmissibility thus increases the probability that new infections arise during indoor mass-gatherings, causing the upsurge of new positive cases, leading to high numbers of hospitalizations. Furthermore, B.1.1.7 was suspected to be more pathogenic than the other variants (Ramanathan et al., 2021) and can negatively affect the diagnostic

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accuracy of the tests used to rapidly detect the infection in clinical settings (Wang et al., 2020). Finally, the effectiveness of different vaccine formulations may be affected by the variants. Although some vaccine formulations are thought to be unaffected or less affected, some evidence suggests that the prophylactic effects of vaccination could be generally negatively affected (Noh et al., 2021). Thus, urgently establishing robust systems for monitoring the emergence of the variants is necessary in every affected country. Unfortunately, such facilities are unavailable in developing or low-income countries.

2. The Lambda variant: VOI or VOC?

Certain characteristics of the circulating variants allow the WHO Technical Advisory Group on Viral Evolution to classify or reclassify the variants as variants of concern (VOCs) or VOIs. Presently, the Lambda variant has been classified as a VOI, implicating that global monitoring of the epidemiology of this variant, including strict border screening, is necessary especially in those countries that neighbor others with reported cases positive with Lambda. Though we do not understand whether this variant is more pathogenic than other SARS-CoV-2 variants, evidence suggests that it is more transmissible and causes a higher number of cases than the parent strain (Kimura et al., 2021). Thus, urgent and equitable vaccination campaigns together with strict hygiene measures will help to efficiently control the high case numbers of this variant. Generally, the evolving SARS-CoV-2 variants will need to be monitored along with tracking and documenting the success of countermeasures, including antiviral treatments, vaccination, and other epidemiological controls. Finally, Lambda likely is not the last generation of the viral variants. Thus, a firm, consolidated international campaign supported by WHO is required to achieve better outcomes by using the available resources for controlling the pandemic and reducing the fatalities.

Declaration of competing interest

No potential conflict of interest was declared.

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