Surveillance report

Surveillance generated by nf-ncov-voc for Lambda variant

Date

This report is generated on 2022-02-02 using 171066 number of genomes collected between 2020-02-25 and 2021-12-29

Pango Lineages

Pango Lineages in this report ['C.37']

Indicator

This table contains key indicators identified

Indicator	Sub-categories from POKAY	Mutations
Transmissibility between humans	transmissibility	
Infection Severity	ACE2 receptor binding affinity, viral load, outcome hazard ratio	p.D614G, p.F490S, p.L452Q
Immunity after natural infection	convalescent plasma escape, reinfection, humoral response durability	p.F490S
Vaccines	vaccine neutralization efficacy	p.D614G
Monoclonal antibodies	monoclonal antibody serial passage escape, pharmaceutical effectiveness	p.F490S
Diagnostics	clinical indicators, antigenic test failure, symptom prevalence	

Mutation Significance

This table contains key functional impacts of mutations identified

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.F490S	ACE2 receptor binding affinity	Among the first selected minor variants in an in vitro evolution experiment for ACE2 binding.	C.37	Zahradnik et al. (2021)	26	T	C	1.0
p.F490S	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows resistence to mAb SARS2-32.	C.37	Liu et al. (2020)	26	T	C	1.0
p.F490S	antibody epitope effects	Complete loss of binding in ELISA by the variant against monoclonal antibody ab8	C.37	Sun et al. (2021)	26	T	C	1.0
p.F490S	convalescent plasma escape	Strong reduction in neutralization capability of all 4 convalescent sera tested (3 ablations).	C.37	Liu et al. (2021)	26	T	C	1.0
p.F490S	monoclonal antibody serial passage escape	Ranked mildly effective mutant against this position in the RBD for highly neutralizing COV2-2496 monoclonal antibody	C.37	Greaney et al. (2020)	26	T	C	1.0
p.F490S	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	C.37	Starr et al. (2021)	26	T	C	1.0
p.F490S	monoclonal antibody serial passage escape	Class 2/3 mAb C603 modestly selected for the emergence of this mutation in vitro.	C.37	Wang et al. (2021)	26	T	C	1.0
p.F490S	pharmaceutical effectiveness	Greater than 10-fold reduction of binding effeiency vs wild type for mAb LY-CoV555.	C.37	Rappazzo et al. (2021)	26	T	C	1.0
p.L452Q	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.07 fold	C.37	Starr et al. (2020)	26	T	A	1.0
p.L452Q	gene expression increase	Experimentally, Spike gene expression increased 0.27 fold	C.37	Starr et al. (2020)	26	T	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	ACE2 receptor binding affinity	In four cell lines (including 293T-hACE2 cells), this mutation combination increases infectivity vs D614G alone	C.37	Li et al. (2020)	26	A	G	1.0
p.D614G	immunosuppression variant emergence	Studying 94 COVID-19 extended infection cases with genomics April 1 to October 17, 2020, one case developed 23 mutations in a 19 day period, including this combination in Spike.	C.37	Landis et al. (2021)	26	A	G	1.0
p.D614G	syncytium formation	Slight increase in Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus.	C.37	Kim et al. (2021)	26	A	G	1.0
p.D614G	tissue specific neutralization	The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: results (only one nasal swab from different previously infected vacinee neutralizing at weeks 3 and 6 against B.1.1.7 and D614G) suggest that vaccinees probably do not elicit an early humoral response detectable at mucosal surfaces even though sera neutralization was observed. They strengthen the hypothesis that some vaccines may not protect against viral acquisition and infection of the oral–nasal region, but may prevent severe disease associated with viral dissemination in the lower respiratory tract.	C.37	Planas et al. (2021)	26	A	G	1.0
p.D614G	trafficking	Circulating variant shown in vitro to not have major defects or enhancement of cell surface protein trafficking (i.e. Spike cleavage or fusion required for cell entry)	C.37	Barrett et al. (2021)	26	A	G	1.0
p.D614G	trafficking	The increased transduction with Spike D614G ranged from 1.3- to 2.4-fold in Caco-2 and Calu-3 cells expressing endogenous ACE2 and from 1.5- to 7.7-fold in A549ACE2 and Huh7.5ACE2 overexpressing ACE2. Although there is minimal difference in ACE2 receptor binding between the D614 and G614 Spike variants, the G614 variant is more resistant to proteolytic cleavage, suggesting a possible mechanism for the increased transduction.	C.37	Daniloski et al. (2021)	26	A	G	1.0
p.D614G	trafficking	No change in infectivity (24h) relative to D614G alone in Caco-2 cells, Vero or Calu-3.	C.37	Kim et al. (2021)	26	A	G	1.0
p.D614G	trafficking	extasciitilde4x more efficient S2 domain cleavage compared to wild type in Caco-2 cells, mid-range of three cell line tested (Vero and Calu-3).	C.37	Kim et al. (2021)	26	A	G	1.0
p.D614G	trafficking	Among S variants tested, the D614G mutant shows the highest cell entry (extasciitilde3.5x wild type), as supported by structural and binding analyses.	C.37	Ozono et al. (2020)	26	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	trafficking	We report here pseudoviruses carrying SG614 enter ACE2-expressing cells more efficiently than wild type (extasciitilde9-fold). This increased entry correlates with less S1-domain shedding and higher S-protein incorporation into the virion. D614G does not alter S-protein binding to ACE2 or neutralization sensitivity of pseudoviruses. Thus, D614G may increase infectivity by assembling more functional S protein into the virion.	C.37	Zhang et l. (2020)	26	A	G	1.0
p.D614G	vaccine neutralization efficacy	Pseudotyped D614G virus has reduced neutralization activity vs wild type: 1.2x (37 sera Pfizer median 9 days post 2nd dose, 37 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA.	C.37	Garcia-Beltran et al. (2021)	26	A	G	1.0
p.D614G	vaccine neutralization efficacy	Using a lentivirus virus pseudotyped with D614G Spike, sera from vaccinated individuals who received the second dose (9–11 days post-second dose of Pfizer) exhibited a robust neutralizing potential, with a mean NT50 value of 99,000. This was an average of a 2-fold increase, relative to sera drawn from the individuals who received one dose of vaccination—mean NT50 dilution of 51,300. Importantly, a 6-fold increase in mean NT50 dilution was obtained when sera from the first vaccination dose was compared to convalescent sera from cohort with severe disease (NT50 51,000 vs 8,700) 21 to 63 days post-onset.	C.37	Kuzmina et al. (2021)	26	A	G	1.0
p.D614G	viral load	Hamsters infected with SARS-CoV-2 expressing spike(D614G) (G614 virus) produced higher infectious titres in nasal washes and the trachea, but not in the lungs, supporting clinical evidence showing that the mutation enhances viral loads in the upper respiratory tract of COVID-19 patients and may increase transmission.	C.37	Plante et al. (2020)	26	A	G	1.0
p.D614G	virion structure	Estimated free energy change (ddG) for this variant is 2.5 kcal/mol (i.e. stabilizing relative to wild type)	C.37	Spratt et al. (2021)	26	A	G	1.0
p.D614G	virion structure	Negative stain EM shows increased proportion of "one-up" trimer conformation of Spike proteins on the surface of virions, where the up conformation is presumed to be more likely to bind ACE2.	C.37	Weissman et al. (2020)	26	A	G	1.0
p.D614G	virion structure	CryoEM shows increased proportion of "one-up" trimer conformation of Spike proteins on the surface of virions, where the up conformation is presumed to be more likely to bind ACE2.	C.37	Yurkovetskiy et al. (2020)	26	A	G	1.0

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p.D614G	virion structure	Based on pseudotyped virus experiments, D614G may increase infectivity by assembling more functional S protein into the virion.	C.37	Zhang et al. (2020)	26	A	G	1.0

The results here are in whole or part based upon data hosted at the Canadian VirusSeq Data Portal: https://virusseq-dataportal.ca/.We wish to acknowledge the following organisations/laboratories for contributing data to the Portal: Canadian Public Health Laboratory Network (CPHLN), CanCOGGeN VirusSeq and the list of labs available at https://virusseq-dataportal.ca/acknowledgements)