Article

SARS-CoV-2 Variants of Concern and Clinical Severity in the Mexican Pediatric Population

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Supplementary data

Table S1. Viral activity effects reported in high-frequency mutations associated with pediatric sequences in Mexico.
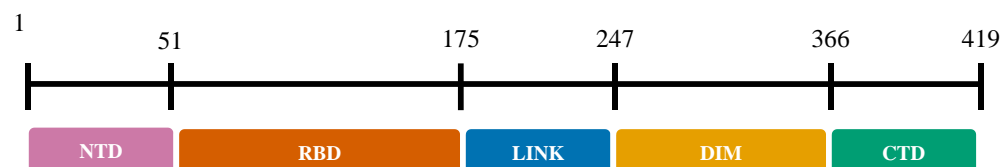
Gen/Mutation	Associated VOCs [a]	Effects in Viral Activity		
		Transmissibility	Immunity	Severity
Envelope				
T9I	o			Virulence decreased [41]
Nucleocapsid				
P13L	o		Decreased T cell recognition [42]	Decreased pathogenicity [43,44]
Spike				
T478K	δ o	Increase ACE2 affinity [45] Increased potential transmission [46]	Reduced affinity and antibody response [47,48] Increased antibody escape [45,49]	Increase virulence [45] Increased severity [50]
P681H	α o	Increase ACE2 binding [51] Increase infectivity and transmission [52]	Reduced affinity and antibody response [53,54]	Increased virulence [55] Increase replication, viral load [42]
G142D	o		Decrease antibody binding [41]	
H655Y	ɣ o	Increase ACE2 binding [51]		
L452R	δ o		Reduced affinity and antibody response [47]	
N679K	o	Increase ACE2 binding [51]		
N969K	o	Decrease infectivity [56]		
Q954H	o	Decrease infectivity [56]		
N764K	o			Increase virulence [57]
G339D	o		Increase antibody escape [58]	
S375F	o	Increased potential transmission [46]	Increase antibody escape [58]	
S373P	o	Increased potential transmission [46]	Increase antibody escape [58]	
N501Y	α β ɣ o	Increase infectivity and transmission [46,58]	Reduced affinity and antibody response [47,58]	

[a] Variants of Concern (α) Alpha, (β) Beta, (ɣ) Gamma, (δ) Delta, and (o) Omicron.
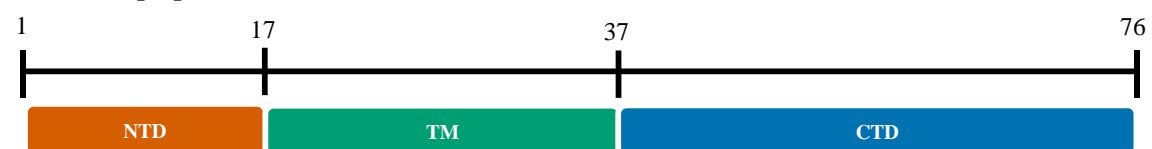
D. Spike protein

C. Nucleocapsid protein
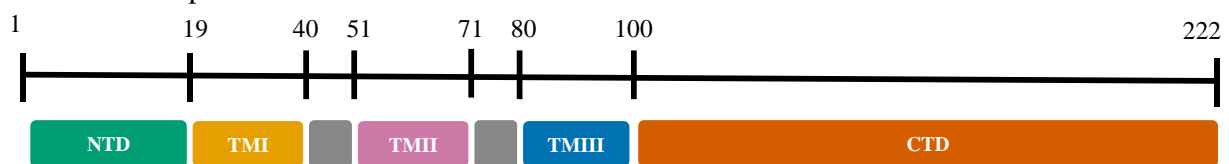

B. Envelope protein

A. Membrane protein

Figure S1. A schematic illustration of the structural proteins of SARS-CoV-2. (**A**) S protein; (S1A) S1A domain, (S1B) S1B domain, (S1C) S1C Domain, (S1D) S1D domain, (PCS) protease cleavage site, (CβS) Central β-strand. (**B**) N protein; (NTD) N-Terminal, (RBD) Receptor Binding domain, (LINK) Predicted central linker, (DIM) Dimerization domain, (CTD) C-Terminal. (**C**) E protein; (NTD) N-Terminal, (TM) Transmembrane (CTD) C-Terminal. (**D**) M protein; (NTD) N-Terminal, (TMI) Transmembrane I domain, (TMII) Transmembrane II domain, (TMIII) Transmembrane III domain, (CTD) C-Terminal.
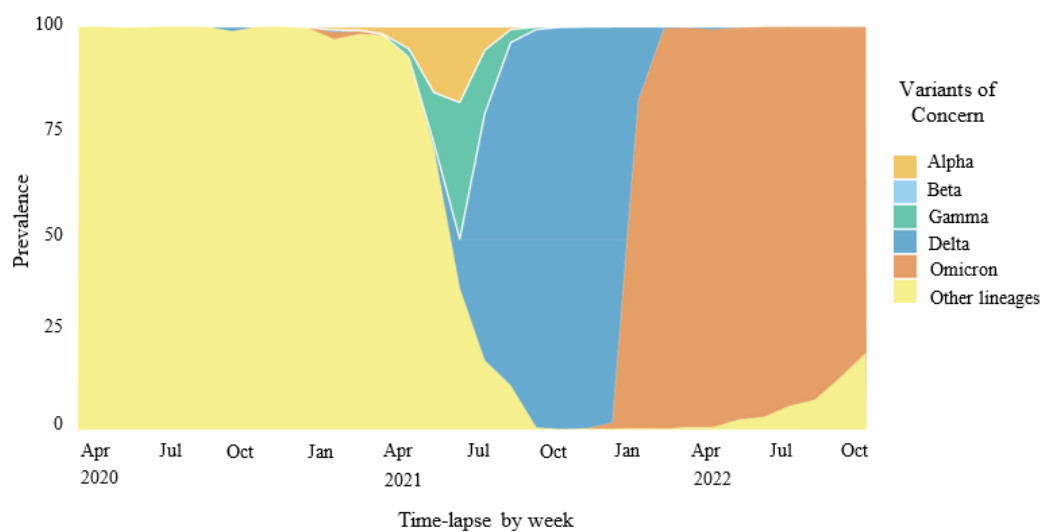
Figure S2. Analysis of prevalence distribution across Variants of concern (VOCs) in Mexico (*n* = 75,348).
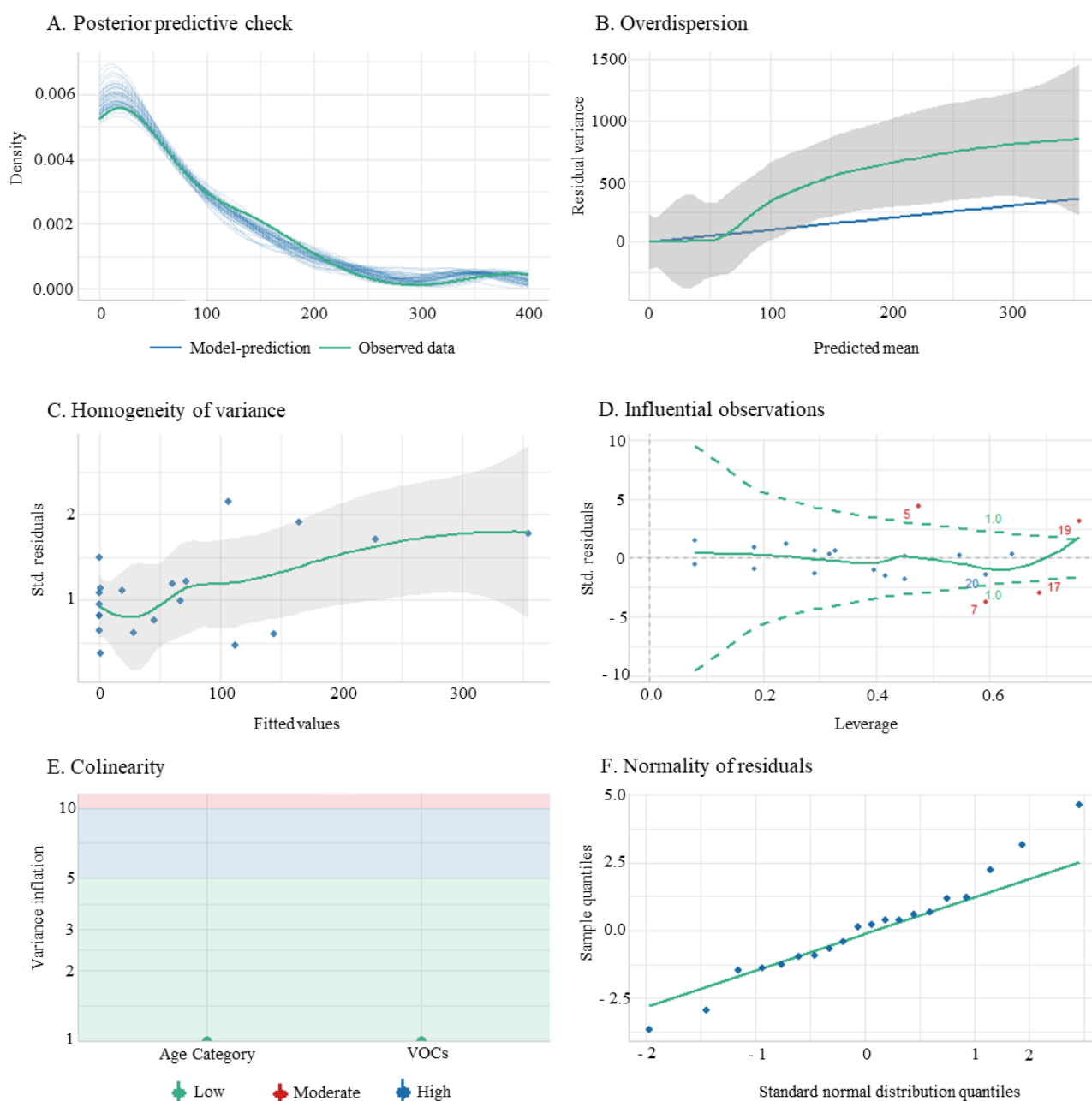
Figure S3. Evaluations assessments plots for the clinical pediatric severity logistics models. (**A**) Posterior predictive check; model-predicted lines should resemble observed data line. (**B**) Overdispersion and zero-inflation; observed residual variance (green line) should follow predicted residual variance (blue line). (**C**) Homogeneity of variance; reference line should be flat and horizontal. (**D**) Influential observations; points should be inside the contour lines. (**E**) Collinearity; High collinearity (VIF) may inflate parameter uncertainty. (**F**) Normality of residuals; dots should fall along the line.