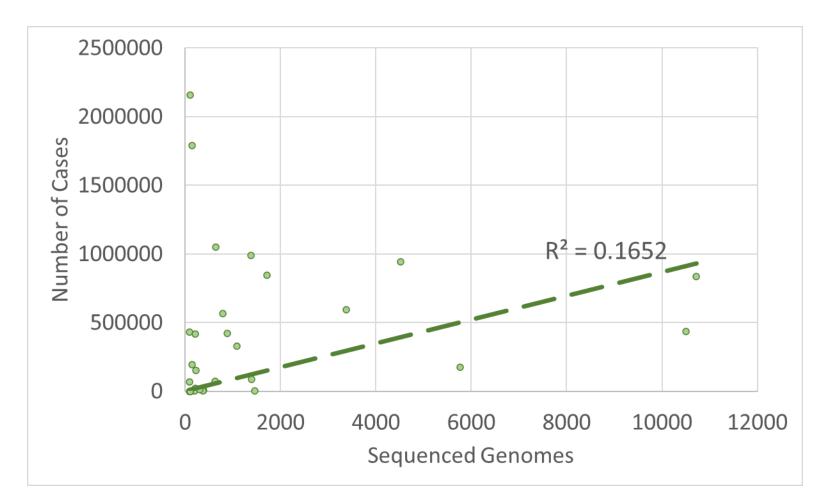
Global Geographic and Temporal Analysis of SARS-CoV-2 Haplotypes Normalized by COVID-19 Cases

23-09-2020

# There is not a correlation between the number of cases and sequenced genomes

Each point represent a month-continent combination



Normalization of frequencies by number of COVID-19 cases

$$NRF_{p} = \frac{\sum_{m,c} (RFP_{m,c} \ x \ NC_{m,c})}{WNC}$$

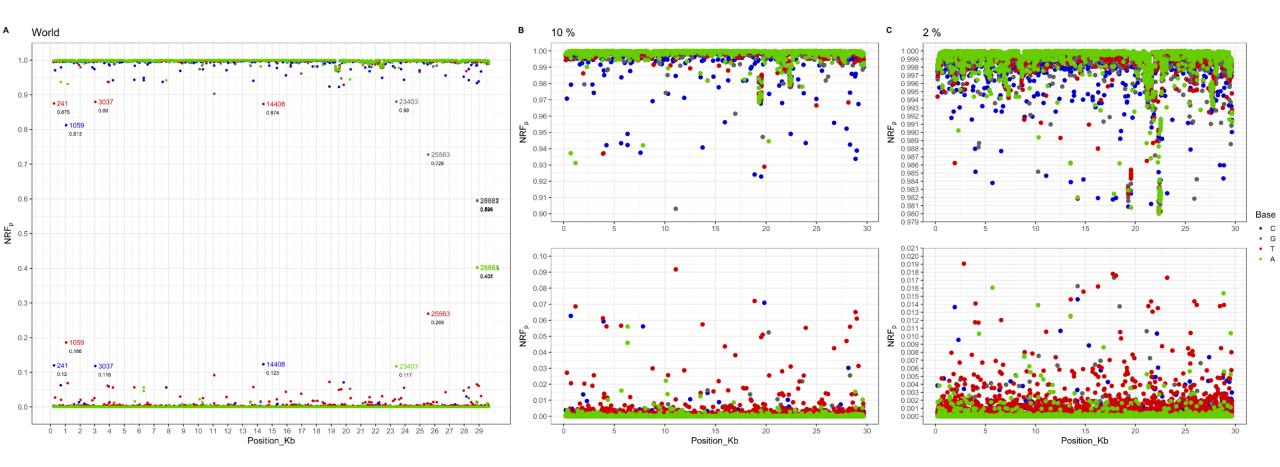
 $RFP_{m,c}$  = Relative Frequency on genomic Position (*p*) in determined month (*m*) and continent (*c*).

- $NC_{m,c}$  = Number of Cases in determined month (*m*) and continent (*c*).
- WNC = World total Number of Cases.

 $NRF_{\mathcal{D}}$ 

= Normalized Relative Frequency on genomic position (p).

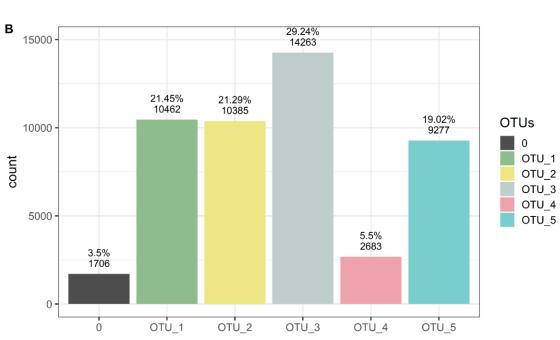
#### NRFp analysis in each SARS-CoV-2 genomic position

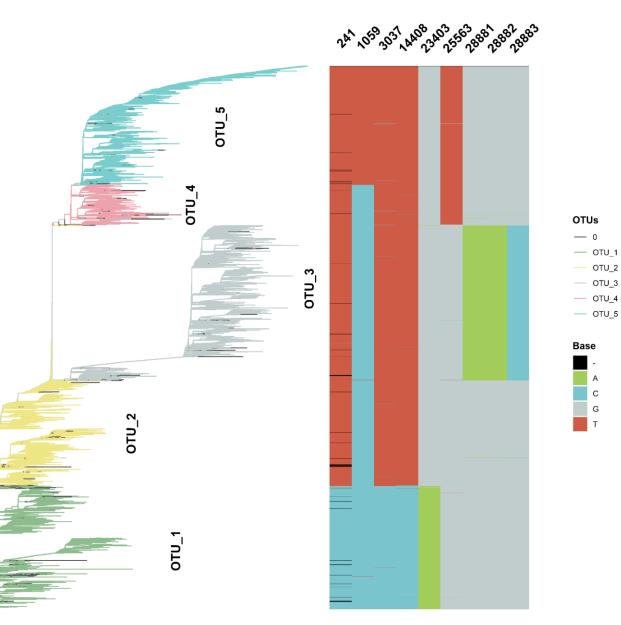


#### Haplotypes identification and phylogenomic análisis of haplotypes

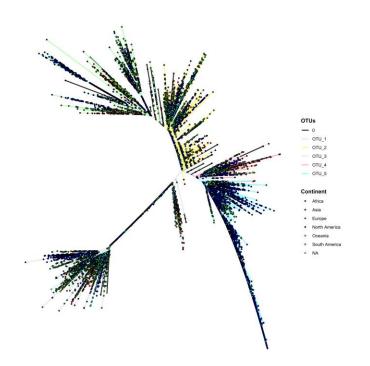
Position	OTU_1	OTU_2	OTU_3	OTU_4	OTU_5	Region	AA_change
241	С	т	т	т	т	5'UTR	
1059	С	С	С	С	т	Nsp2	T85I
3037	С	т	т	т	т	Nsp3	Syn
14408	С	т	т	т	т	Nsp12	P323L
23403	Α	G	G	G	G	S	D614G
25563	G	G	G	т	т	Orf8	S84L
28881	G	G	Α	G	G	N	R203K
28882	G	G	Α	G	G	Ν	R203K
28883	G	G	С	G	G	Ν	G204R

Α

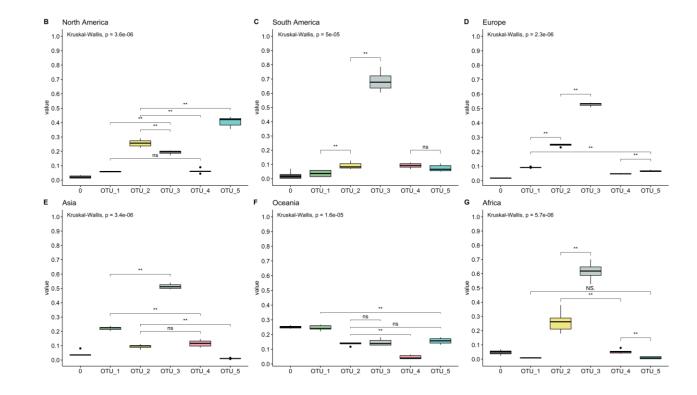




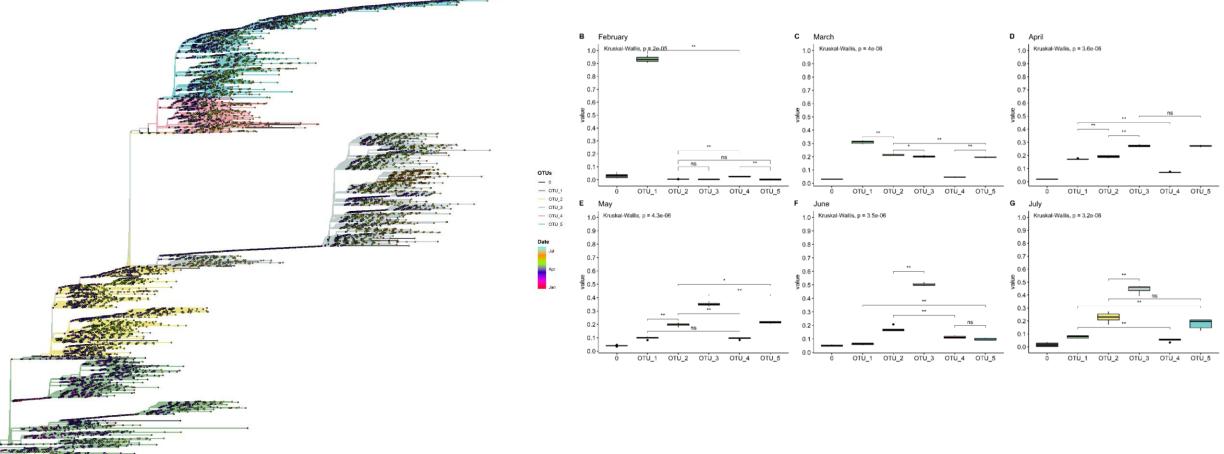
#### Geographical Analysis of Haplotypes



A



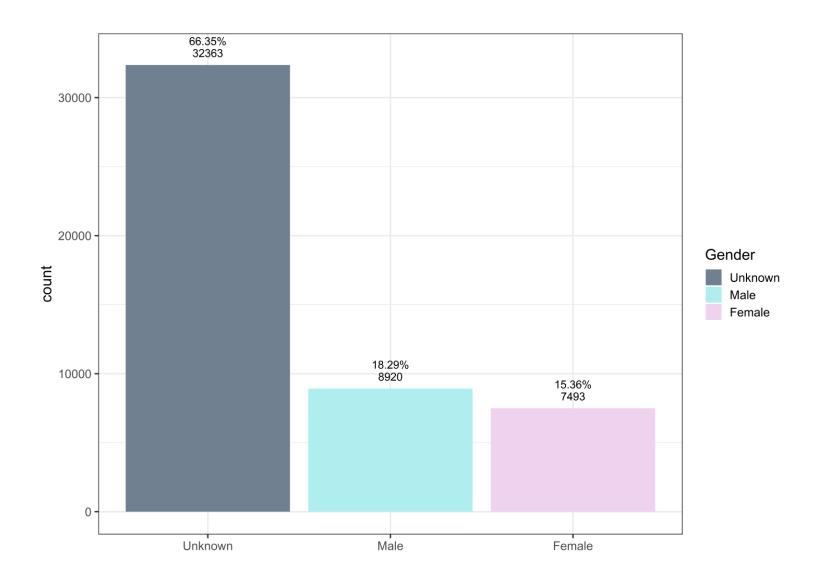
#### Global temporal analysis of haplotypes



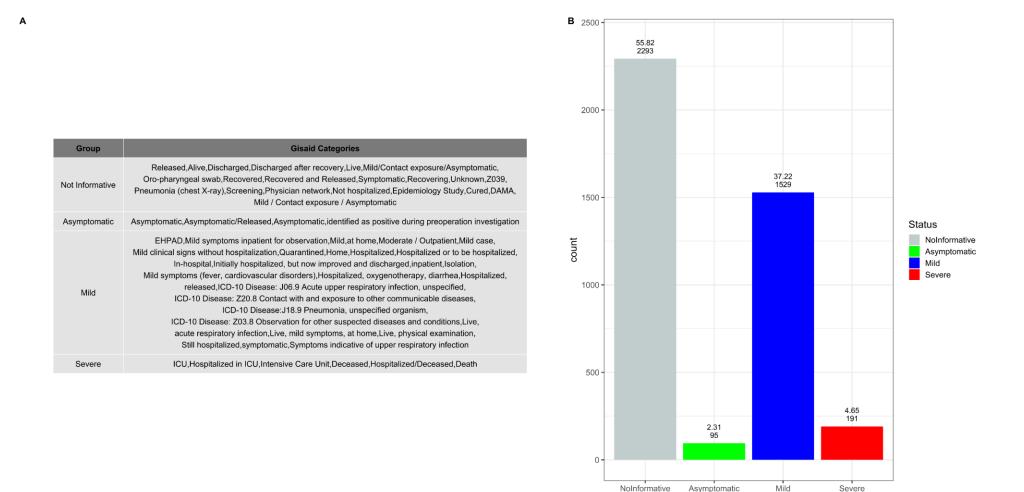
a data a state

Some problems...

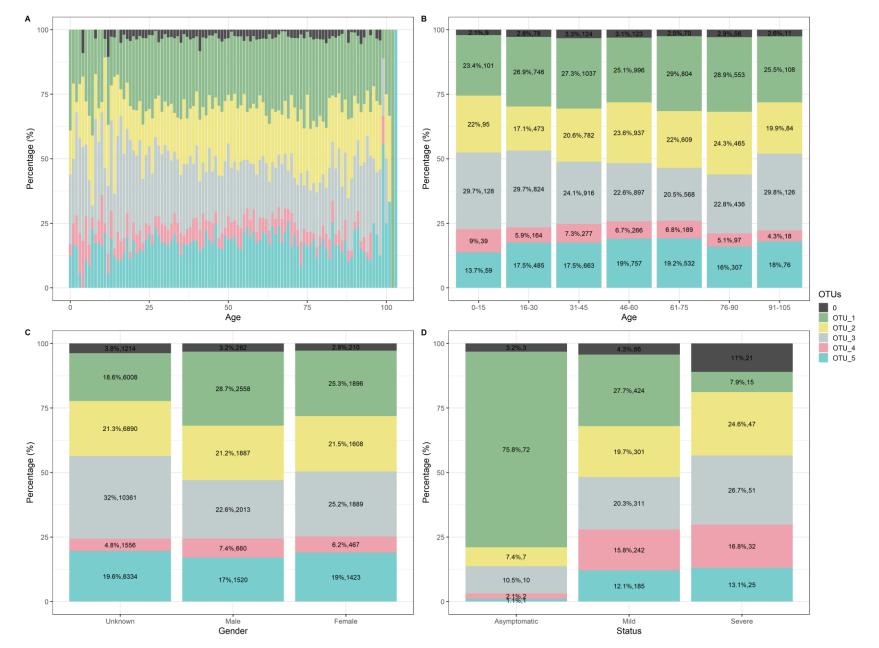
#### Scarce patient data publicly available



#### Incorrectly organized patient status data



#### Relative frequencies of number of genomes by patient data

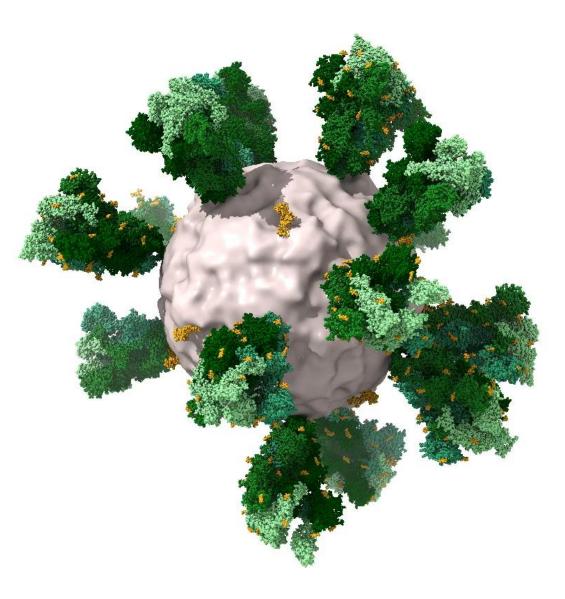


#### Trying to improve the collection of data related to Patient Status

#### We created the web-service:

## SARS-CoV-2 HaploFinder\_URP

http://sarscov2haplofinder.urp.edu.pe/



### Gracias!