

Abacwaningi bathi igciwane le-COVID-19 lingase liguquke kancane, kwenze ukuthuthukiswa komgomo kube lula

ST Communications

I-Genomic Diversity kanye ne-Hotspot Mutations kuma-30,983 SARS-CoV-2 Genomes:

Ukuqhubekela Emgomeni Wamazwe Omhlaba “Wegciwane Elivalekile”?

Abstract

Impathamhlaba i-COVID-19 belulokhu luqhubeka kusukela lwaqala ngasekupheleni kukaNovemba 2019 eWuhan, eChina.

Ukuqonda nokuqapha ukuguquguquka kofuzo kwegciwane, izici zalo zendawo, nokuzinza kwalo kubaluleke kakhulu ekulawuleni ukusabalala kwesifo futhi ikakhulukazi ekuthuthukisweni komgomo wendawo yonke ohlanganisa zonke izinhlobo ezibhebhethekayo.

Kulo mbono, sihlaziye izinhlobo zofuzo ze-SARS-CoV-2 eziphelele ezingama-30,983 ezivela emazweni angama-79 akumazwekazi ayisithupha futhi saqoqwa kusukela zingama-24 kuZibandlela wezi-2019, kuya kumhla ziyi-13 kuNhlaba wezi-2020, ngokusho kwesizindalwazi se-GISAID.

Ukuhlaziya kwethu kuveze ubukhona kwezindawo ezihlukile ze-3206, ezinokusabalalisa okufanayo kwezinhlobo zokuguqulwa kwezakhi ezindaweni ezihlukene.

Ngokuphawulekayo, imvamisa ephansi yokuguqulwa kwezinguquko eziphindaphindiwe iye yabonwa; izinguquko eziyi-169 kuphela (5.27%) zande ngo-1% kwama-genomes.

Nokho, izindawo eziyishumi nane ezinezinguquko zegciwane kakhulu (<10%) sezikhonjiwe ezindaweni ezingafani ezihambisana ne-genome yegciwane; ayisishiyagalombili ku-ORF1ab polyprotein (ku-nsp2, nsp3, isizinda se-transmembrane, i-RdRp, i-helicase, i-exonuclease, ne-endoribonuclease), ama-nucleocapsid protein, kanye ne-protein ngayinye kwamathathu:

i-Spike, i-ORF3a, ne-ORF8.

Ngaphezu kwalokho, ukuguqulwa okungafanii okungu-36 kukhonjwe esizindeni sokubopha i-receptor-binding (RBD) yephrotheni ye-spike enokwanda okuphansi (<1%) kuwo wonke

ama-genome, mane kuphela angathuthukisa ukubophezela kwe-SARS-CoV-2 yephrotheni ye-spike kumamukeli we-ACE2 wabantu.

Le miphumela kanye nokuhluka kwe-intra-genomic ye-SARS-CoV-2 kungakhombisa ukuthi ngokungafani negciwane lomkhuhlane noma amagciwane e-HIV, i-SARS-CoV-2 inenani eliphansi lokuguquka okwenza ukuthuthukiswa komgomo osebenzayo womhlaba wonke kube maningi kakhulu amathuba.

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Ngo-2020, abacwaningi babone izinguquko ezincane kwi-genome ye-SARS-CoV-2 isabhebhethaka emhlabeni wonke.

Ososayensi bathe uma igciwane liba nezinguquko ezimbalwa ngokuhamba kwesikhathi, ukwenza umgomo owodwa we-COVID-19 kungaba lula.

Ngaleso s'khathi, igciwane le-COVID-19, SARS-CoV-2, belibhebhethaka ngokushesha futhi libulala abantu, ososayensi bebesebenza kanzima ukwakho umgomo osebenzayo.

Balalndele izinguquko kwi-genome yegciwane babheka ukuthi zishesha kangakanani ezindaweni ezihlukene.

Ulwazi beluhlose ukubasiza ngokugada isifo se-COVID-19 kangcono, nokwakha umgomo ongasebenza kuzo zonke izinguquko zegciwane.

Kulolu cwaningo, abacwaningi bahlaziye izinguquko ze-genome ye-SARS-CoV-2 ezindaweni ezahlukene emhlabeni.

Baphinde babheka amathuba okwenza umgomo ozolwa nazo zonke izinguquko ze-SARS-CoV-2 emhlabeni wonke.

Abacwaningi baqoqe imininingwane ephela ye-SARS-CoV-2 emazweni awu-79 emazwenikazi awu-6 base bewahlaziya.

Bahlaziye inhlobo nezinguquko ezivamile kwe-genome ngayinye.

Abacwaningi baphinde baqhathanisa ama- genomes e-SARS-CoV-2 emazweni ahlukene base bebheka ubuhlobo kulezi zinguquko.

Imiphumela yabo iveze izinguquko ezincane kuma-genomes e-SARS-CoV-2 emazweni acwaningiwe.

Amasampula am'balwa (5.27) abenoshintsho adlula u-1% kuwo onke ama-genome.

Kuwo onke amazwekazi ayi-6, abacwaningi babike izehlakalo ezidale izinguquko ezenzeka endaweni eyodwa kwi-genome yegciwane.

Ososayensi bathi izinguquko eziningi zivela endaweni eyodwa kwi-genome, izinhlobo zegciwane ezitsha zingavela.

Abacwaningi babike ukuthi u-67.96% wazo zonke izinguquko zamagenomes abazobonile ekuhlaziyeni kwabo kungaba nomthelela ekulandelaneni kwamaphrotheni egciwane, kodwa kungashintshi ukusebenza kwayo.

Ingxenye eyodwa yezinguquko ezintathu ingaba nomthelela esakhiweni sephrotheni yegciwane le-COVID-19.

Abacwaningi bathole izinguquko ezi-2 kuphela kwi-genome yegciwane zivame emazwenikazi ayi-6; ezinye bezihlukile emazwenikazi.

Imiphumela yabo iveze nokuthi izinhlobo zegciwane e-Afrika bezihlobene eduze nalezi zamanye amazwekazi, zonke izinhlobo ezisemazwenikazi zavela e-Asia.

Izinhlobo zaseNyakatho neMelika, iNingizimu neMelika, nezase-Afrika zivela eYurophu, ezinye izinhlobo beziseYurophu kuphela.

Abacwaningi bathe izinguquko zokulandelana kofuzo entweni ebizwa nge 'S protein' azibi namthelela esakhiweni futhi ngeke zibe nomthelela omkhulu wokusebenza komgomo.

Ososayensi banentshisekelo ku-'S protein' uma benza imigomo ngoba iyiphrotheni esetshenziswa igciwane ukungena kumaseli womuntu.

Ucwaningo luveze ukuthi ngokungafani negciwane lomkhuhlane noma i-HIV, i-SARS-CoV-2 genome ayizange ishintshe ngokushesha, obekungenza kube lula kososayensi ukuthi bakhe umuthi wokugomela i-COVID-19 womhlaba wonke.

Abacwaningi batuse ukubhekwa okuqhubekayo kwezinguquko ze-SARS-CoV-2 ezi-genomic