

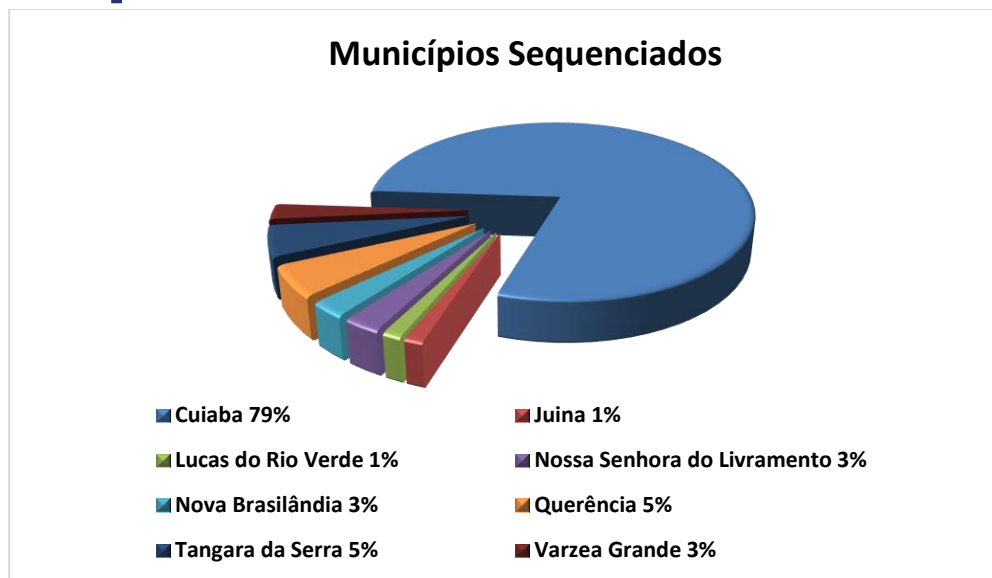
**17º RELATÓRIO REFERENTE AO
SEQUENCIAMENTO DE NOVA GERAÇÃO DAS
AMOSTRAS DE SARS-CoV-2 POSITIVAS
REALIZADO NO LACEN-MT PARA
IDENTIFICAÇÃO E MONITORAMENTO DAS
VARIANTES CIRCULANTES NO ESTADO DE
MATO GROSSO**

O SARS-CoV-2 é um vírus RNA de fita simples (+ ssRNA), polaridade positiva e não segmentada, sentido positivo, 5'-cap, 3'-poliadenilado e tamanho surpreendentemente grande, variando de 27 a 32 quilobases (2), pertencem à família *Coronaviridae*, gênero *betacoronavirus*, sendo designado como SARS-CoV-2, vírus que está relacionado à síndrome respiratória aguda (SRAG) e com alto teor de dispersão (1). O genoma do SARS-CoV-2 codifica proteínas não estruturais e quatro proteínas estruturais como: espícula [S], envelope [E], membrana [M], nucleocapsídeo [N] e várias proteínas acessórias (3, 4).

O método de sequenciamento genético permite realizar a leitura dos genomas virais com o objetivo de identificar novos patógenos e aprimorar a compreensão das origens e da transmissão de vírus emergentes. É válido ressaltar que um dos propósitos do sequenciamento genético é acompanhar, monitorar e identificar a circulação das linhagens e sublinhagens de SARS-CoV-2 em todo Estado, tendo em vista que o vírus continua a sofrer mutações que diferem da estirpe original de Wuhan. Além de atender aos seguintes critérios estabelecidos pela Vigilância Epidemiológica: suspeitas e/ou contatos de VOC (do inglês *Variants of concern*, variantes de preocupação) e VOI (do inglês *Variants of interest*, variantes de interesse), óbitos, casos graves e com rápida evolução, amostras com carga viral alta, além de pacientes com diagnóstico positivo para SARS-CoV-2.

No período de 17 a 28 de Abril de 2023, a equipe do LACEN-MT, a fim de entender melhor o vírus causador da COVID-19 circulante no Estado de Mato Grosso, selecionaram 100 amostras positivas do SARS-CoV-2, das quais 77 apresentaram quantidade suficiente de DNA para serem sequenciadas após a PCR. O sequenciamento foi realizado em 77 genomas de pacientes com sintomas da doença que foram diagnosticados como positivos para o SARS-CoV-2, com valores de CT (cycle threshold) variando entre 15 e 30.

As amostras sequenciadas foram de oito municípios de Mato Grosso: Cuiabá (60 amostras), Juína (1 amostra), Lucas do Rio Verde (1 amostra), Nossa Senhora do Livramento (2 amostras), Nova Brasilândia (2 amostras), Querência (4 amostras), Tangara da Serra (4 amostras) e Várzea Grande (2 amostras) (ver Figura 1).



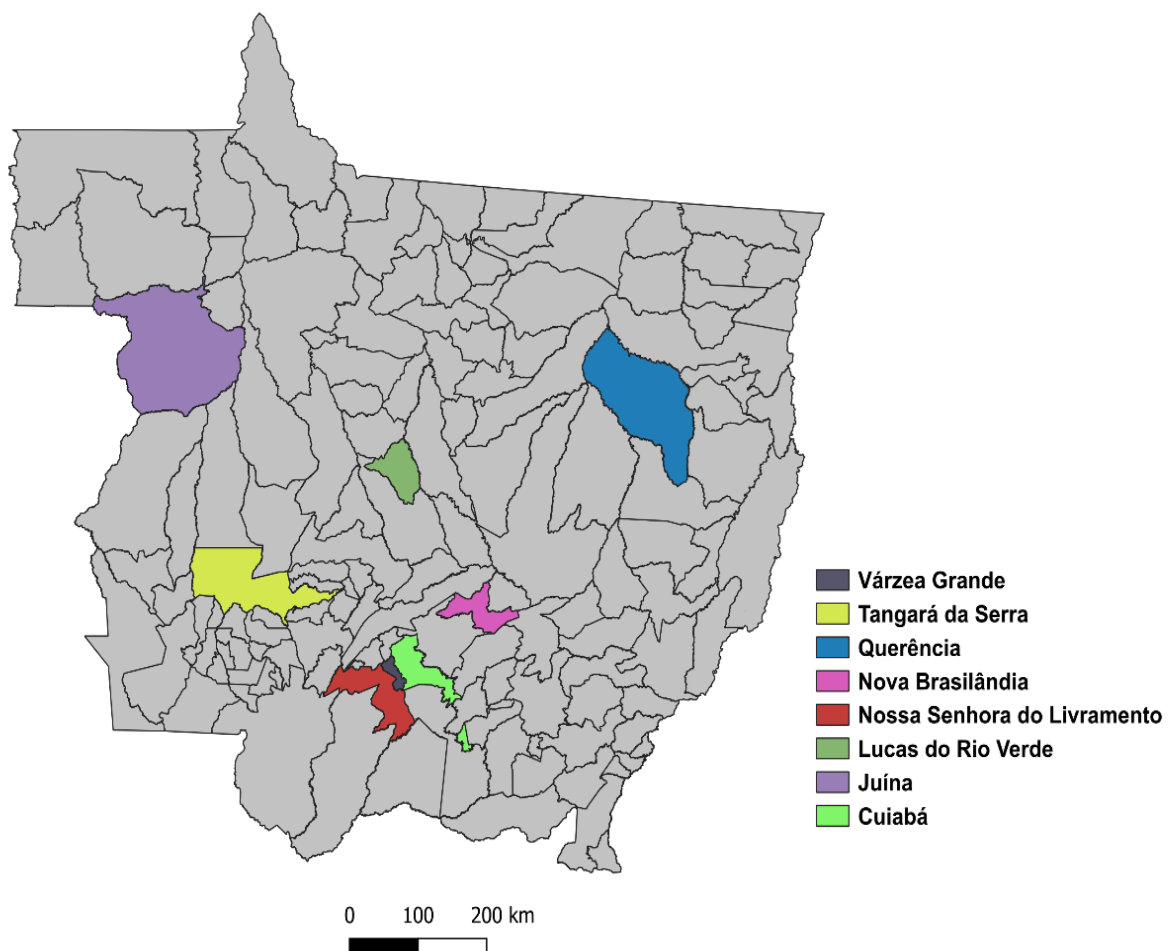
Os genomas foram sequenciados utilizando a tecnologia desenvolvida pela Thermo Fisher Scientific (Ion Genestudio S5 Plus), apresentando valores de cobertura superior a 70% do genoma total (**Tabela 1**).

As sequências genômicas obtidas foram analisadas utilizando o software *Genome Detective - Coronavirus Typing Tool*, disponível online em: (<https://www.genomedetective.com/app/typingtool/virus/>) (5).

A avaliação da linhagem foi realizada utilizando duas ferramentas *Phylogenetic Assignment of Named Global Outbreak LINEages* disponível em: (<https://github.com/hCoV-2019/pangolin>) e Nextclade (<https://clades.nextstrain.org/>) seguindo a recente classificação dinâmica proposta por Rambaut e colaboradores (**Figura 2**) (7).

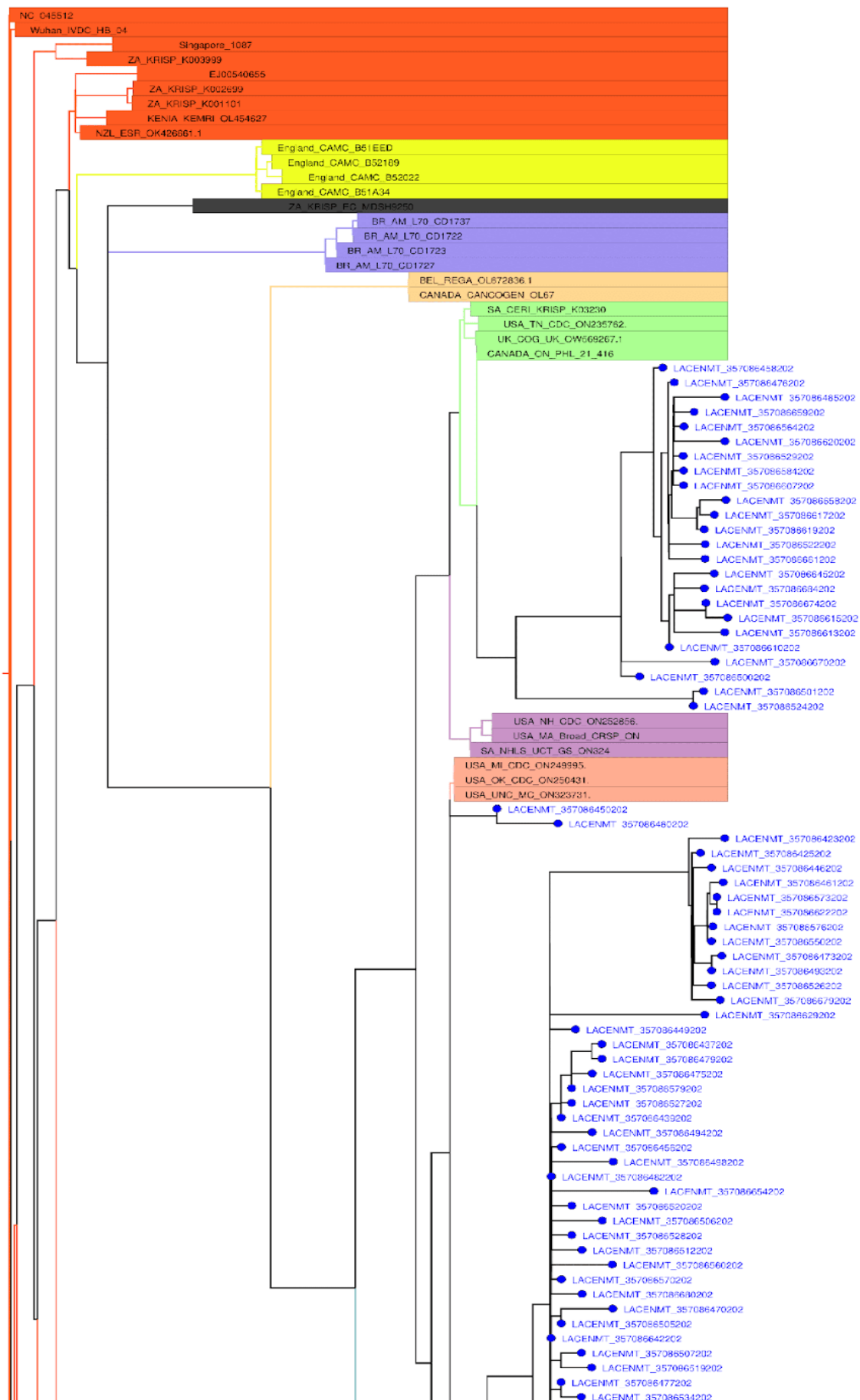


Figura 1: Mapa do Estado de Mato Grosso, destacando os municípios onde foram obtidas e caracterizadas as novas sequências genômicas do SARS-CoV-2.



BarCode	Assignment	Coverage	Lineages	Nº Interno	ID-Sequencia	ID_Amostra	Requisição_GAL Sequenciamento	LACEN	CT
BarCode251	Severe acute respiratory syndrome-related coronavirus	89%	BQ.1.1.31	98260	hCoV-19/Brazil/MT-LACENMT-357086423/2023	357086423	230101000658	LACEN-MT	32,26,28
BarCode252	Severe acute respiratory syndrome-related coronavirus	91%	BQ.1.1	98264	hCoV-19/Brazil/MT-LACENMT-357086425/2023	357086425	230101000659	LACEN-MT	31,25,27
BarCode253	Severe acute respiratory syndrome-related coronavirus	60%	BE.10	98294	hCoV-19/Brazil/MT-LACENMT-357086430/2023	357086430	230101000661	LACEN-MT	33,28,29
BarCode254	Severe acute respiratory syndrome-related coronavirus	91%	BQ.1	98297	hCoV-19/Brazil/MT-LACENMT-357086437/2023	357086437	230101000662	LACEN-MT	32,27,28
BarCode255	Severe acute respiratory syndrome-related coronavirus	84%	BQ.1	98315	hCoV-19/Brazil/MT-LACENMT-357086439/2023	357086439	230101000664	LACEN-MT	30,24,26
BarCode256	Severe acute respiratory syndrome-related coronavirus	81%	BQ.1.1	98329	hCoV-19/Brazil/MT-LACENMT-357086446/2023	357086446	230101000666	LACEN-MT	30,25,28
BarCode244	Severe acute respiratory syndrome-related coronavirus	93%	BQ.1.1	98393	hCoV-19/Brazil/MT-LACENMT-357086449/2023	357086449	230101000668	LACEN-MT	31,31,28
BarCode245	Severe acute respiratory syndrome-related coronavirus	93%	BA.5.1	98459	hCoV-19/Brazil/MT-LACENMT-357086450/2023	357086450	230101000669	LACEN-MT	19,21,24
BarCode246	Severe acute respiratory syndrome-related coronavirus	89%	BA.5.3.1	98461	hCoV-19/Brazil/MT-LACENMT-357086454/2023	357086454	230101000670	LACEN-MT	17,19,24
BarCode247	Severe acute respiratory syndrome-related coronavirus	90%	BQ.1.1	98463	hCoV-19/Brazil/MT-LACENMT-357086456/2023	357086456	230101000671	LACEN-MT	22,23,27
BarCode248	Severe acute respiratory syndrome-related coronavirus	91%	XBB.1.18	98467	hCoV-19/Brazil/MT-LACENMT-357086458/2023	357086458	230101000672	LACEN-MT	17,20,23
BarCode249	Severe acute respiratory syndrome-related coronavirus	91%	BA.5.3.1	98468	hCoV-19/Brazil/MT-LACENMT-357086460/2023	357086460	230101000673	LACEN-MT	23,24,27
BarCode250	Severe acute respiratory syndrome-related coronavirus	92%	BQ.1.1	98471	hCoV-19/Brazil/MT-LACENMT-357086461/2023	357086461	230101000674	LACEN-MT	21,21,26
BarCode237	Severe acute respiratory syndrome-related coronavirus	92%	BQ.1.24	98474	hCoV-19/Brazil/MT-LACENMT-357086462/2023	357086462	230101000675	LACEN-MT	22,23,28
BarCode238	Severe acute respiratory syndrome-related coronavirus	92%	BA.5.3.1	98475	hCoV-19/Brazil/MT-LACENMT-357086467/2023	357086467	230101000676	LACEN-MT	26,27,30
BarCode239	Severe acute respiratory syndrome-related coronavirus	90%	BQ.1	98476	hCoV-19/Brazil/MT-LACENMT-357086469/2023	357086469	230101000677	LACEN-MT	16,18,22
BarCode240	Severe acute respiratory syndrome-related coronavirus	91%	BQ.1.1	98480	hCoV-19/Brazil/MT-LACENMT-357086470/2023	357086470	230101000678	LACEN-MT	20,21,24
BarCode241	Severe acute respiratory syndrome-related coronavirus	88%	BQ.1.1	98485	hCoV-19/Brazil/MT-LACENMT-357086473/2023	357086473	230101000680	LACEN-MT	26,27,29
BarCode242	Severe acute respiratory syndrome-related coronavirus	88%	BQ.1.1.11	98500	hCoV-19/Brazil/MT-LACENMT-357086475/2023	357086475	230101000681	LACEN-MT	27,29,32
BarCode243	Severe acute respiratory syndrome-related coronavirus	68%	XBB.1.18.1	98541	hCoV-19/Brazil/MT-LACENMT-357086476/2023	357086476	230101000682	LACEN-MT	28,29
BarCode229	Severe acute respiratory syndrome-related coronavirus	84%	BQ.1.1	98551	hCoV-19/Brazil/MT-LACENMT-357086477/2023	357086477	230101000683	LACEN-MT	23,22
BarCode230	Severe acute respiratory syndrome-related coronavirus	94%	BQ.1.1	98552	hCoV-19/Brazil/MT-LACENMT-357086479/2023	357086479	230101000684	LACEN-MT	25,24
BarCode231	Severe acute respiratory syndrome-related coronavirus	75%	DL.1	98553	hCoV-19/Brazil/MT-LACENMT-357086480/2023	357086480	230101000685	LACEN-MT	17,18
BarCode232	Severe acute respiratory syndrome-related coronavirus	91%	BQ.1.1	98555	hCoV-19/Brazil/MT-LACENMT-357086482/2023	357086482	230101000686	LACEN-MT	20,20
BarCode233	Severe acute respiratory syndrome-related coronavirus	91%	XBB.1.18	98556	hCoV-19/Brazil/MT-LACENMT-357086485/2023	357086485	230101000687	LACEN-MT	23,22
BarCode234	Severe acute respiratory syndrome-related coronavirus	76%	BQ.1.1	98579	hCoV-19/Brazil/MT-LACENMT-357086493/2023	357086493	230101000688	LACEN-MT	24,22
BarCode235	Severe acute respiratory syndrome-related coronavirus	76%	BQ.1.1.11	98580	hCoV-19/Brazil/MT-LACENMT-357086494/2023	357086494	230101000689	LACEN-MT	28,28
BarCode236	Severe acute respiratory syndrome-related coronavirus	81%	BQ.1	98582	hCoV-19/Brazil/MT-LACENMT-357086496/2023	357086496	230101000690	LACEN-MT	27,27
BarCode221	Severe acute respiratory syndrome-related coronavirus	92%	BQ.1.1	98586	hCoV-19/Brazil/MT-LACENMT-357086498/2023	357086498	230101000691	LACEN-MT	22,21
BarCode222	Severe acute respiratory syndrome-related coronavirus	92%	XBB.2	98594	hCoV-19/Brazil/MT-LACENMT-357086500/2023	357086500	230101000692	LACEN-MT	22,21
BarCode223	Severe acute respiratory syndrome-related coronavirus	89%	BN.3.1	98595	hCoV-19/Brazil/MT-LACENMT-357086501/2023	357086501	230101000693	LACEN-MT	24,23
BarCode225	Severe acute respiratory syndrome-related coronavirus	77%	BQ.1.1	98643	hCoV-19/Brazil/MT-LACENMT-357086505/2023	357086505	230101000695	LACEN-MT	23,25,29
BarCode226	Severe acute respiratory syndrome-related coronavirus	84%	BQ.1	98644	hCoV-19/Brazil/MT-LACENMT-357086506/2023	357086506	230101000696	LACEN-MT	21,24,28
BarCode227	Severe acute respiratory syndrome-related coronavirus	93%	BQ.1.1	98645	hCoV-19/Brazil/MT-LACENMT-357086507/2023	357086507	230101000697	LACEN-MT	19,21,26
BarCode228	Severe acute respiratory syndrome-related coronavirus	93%	XBJ.2	98646	hCoV-19/Brazil/MT-LACENMT-357086509/2023	357086509	230101000698	LACEN-MT	20,22,27
BarCode213	Severe acute respiratory syndrome-related coronavirus	83%	BQ.1.1	98653	hCoV-19/Brazil/MT-LACENMT-357086512/2023	357086512	230101000699	LACEN-MT	25,26,31
BarCode214	Severe acute respiratory syndrome-related coronavirus	93%	BQ.1.1	98655	hCoV-19/Brazil/MT-LACENMT-357086519/2023	357086519	230101000700	LACEN-MT	23,25,30
BarCode215	Severe acute respiratory syndrome-related coronavirus	46%	BQ.1.1	98656	hCoV-19/Brazil/MT-LACENMT-357086520/2023	357086520	230101000701	LACEN-MT	20,22,27
BarCode216	Severe acute respiratory syndrome-related coronavirus	91%	XBB.1.18.1	98658	hCoV-19/Brazil/MT-LACENMT-357086522/2023	357086522	230101000702	LACEN-MT	22,23,27
BarCode217	Severe acute respiratory syndrome-related coronavirus	94%	BN.3.1	98684	hCoV-19/Brazil/MT-LACENMT-357086524/2023	357086524	230101000703	LACEN-MT	25,26,30
BarCode218	Severe acute respiratory syndrome-related coronavirus	93%	BQ.1.1.11	98686	hCoV-19/Brazil/MT-LACENMT-357086526/2023	357086526	230101000704	LACEN-MT	22,22,27
BarCode219	Severe acute respiratory syndrome-related coronavirus	92%	BQ.1	98689	hCoV-19/Brazil/MT-LACENMT-357086527/2023	357086527	230101000705	LACEN-MT	21,23,28
BarCode220	Severe acute respiratory syndrome-related coronavirus	94%	BQ.1.1.31	98690	hCoV-19/Brazil/MT-LACENMT-357086528/2023	357086528	230101000706	LACEN-MT	17,19,24
BarCode206	Severe acute respiratory syndrome-related coronavirus	89%	XBB.1.18	98691	hCoV-19/Brazil/MT-LACENMT-357086529/2023	357086529	230101000707	LACEN-MT	20,22,26
BarCode207	Severe acute respiratory syndrome-related coronavirus	50%	BQ.1.1	98692	hCoV-19/Brazil/MT-LACENMT-357086534/2023	357086534	230101000708	LACEN-MT	22,24,28
BarCode208	Severe acute respiratory syndrome-related coronavirus	89%	BQ.1.1	98695	hCoV-19/Brazil/MT-LACENMT-357086469/2023	357086469	230101000709	LACEN-MT	23,24,28
BarCode209	Severe acute respiratory syndrome-related coronavirus	45%	XBB.1.18.1	98707	hCoV-19/Brazil/MT-LACENMT-357086564/2023	357086564	230101000710	LACEN-MT	21,20,24
BarCode210	Severe acute respiratory syndrome-related coronavirus	91%	BE.9	98708	hCoV-19/Brazil/MT-LACENMT-357086567/2023	357086567	230101000711	LACEN-MT	24,27,30
BarCode211	Severe acute respiratory syndrome-related coronavirus	90%	BQ.1	98709	hCoV-19/Brazil/MT-LACENMT-357086573/2023	357086573	230101000712	LACEN-MT	22,24,28
BarCode212	Severe acute respiratory syndrome-related coronavirus	92%	BQ.1	98711	hCoV-19/Brazil/MT-LACENMT-357086576/2023	357086576	230101000713	LACEN-MT	23,26,30
BarCode201	Severe acute respiratory syndrome-related coronavirus	92%	BA.5.3.1	98713	hCoV-19/Brazil/MT-LACENMT-357086583/2023	357086583	230101000715	LACEN-MT	21,23,28
BarCode202	Severe acute respiratory syndrome-related coronavirus	88%	XBB.1.18	98715	hCoV-19/Brazil/MT-LACENMT-357086584/2023	357086584	230101000716	LACEN-MT	23,25,29
BarCode203	Severe acute respiratory syndrome-related coronavirus	93%	BQ.1	98723	hCoV-19/Brazil/MT-LACENMT-357086550/2023	357086550	230101000719	LACEN-MT	18,18,23
BarCode204	Severe acute respiratory syndrome-related coronavirus	84%	BQ.1.1.5	98733	hCoV-19/Brazil/MT-LACENMT-357086560/2023	357086560	230101000721	LACEN-MT	32,26,26
BarCode205	Severe acute respiratory syndrome-related coronavirus	94%	BQ.1.1	98737	hCoV-19/Brazil/MT-LACENMT-357086570/2023	357086570	230101000722	LACEN-MT	30,24,24
BarCode267	Severe acute respiratory syndrome-related coronavirus	92%	BQ.1	98766	hCoV-19/Brazil/MT-LACENMT-357086579/2023	357086579	230101000723	LACEN-MT	28,24,26
BarCode258	Severe acute respiratory syndrome-related coronavirus	94%	BA.5.3.1	98767	hCoV-19/Brazil/MT-LACENMT-357086586/2023	357086586	230101000724	LACEN-MT	29,26,27
BarCode259	Severe acute respiratory syndrome-related coronavirus	80%	XBB.1.18.1	98774	hCoV-19/Brazil/MT-LACENMT-357086607/2023	357086607	230101000727	LACEN-MT	26,23,25
BarCode260	Severe acute respiratory syndrome-related coronavirus	93%	BQ.1.1.31	98778	hCoV-19/Brazil/MT-LACENMT-357086622/2023	357086622	230101000728	LACEN-MT	26,22,25
BarCode261	Severe acute respiratory syndrome-related coronavirus	76%	BQ.1.1	98784	hCoV-19/Brazil/MT-LACENMT-357086629/2023	357086629	230101000730	LACEN-MT	29,26,28
BarCode262	Severe acute respiratory syndrome-related coronavirus	94%	BQ.1.1	98810	hCoV-19/Brazil/MT-LACENMT-357086680/2023	357086680	230101000731	LACEN-MT	25,26,28
BarCode263	Severe acute respiratory syndrome-related coronavirus	96%	BQ.1	98813	hCoV-19/Brazil/MT-LACENMT-357086679/2023	357086679	230101000732	LACEN-MT	27,25,30
BarCode264	Severe acute respiratory syndrome-related coronavirus	93%	BQ.1.1	98895	hCoV-19/Brazil/MT-LACENMT-357086642/2023	357086642	230101000735	LACEN-MT	31,27,29
BarCode265	Severe acute respiratory syndrome-related coronavirus	94%	XBB.1.5	98947	hCoV-19/Brazil/MT-LACENMT-357086645/2023	357086645	230101000737	LACEN-MT	27,36,31
BarCode266	Severe acute respiratory syndrome-related coronavirus	90%	XBB.1.5	99648	hCoV-19/Brazil/MT-LACENMT-357086684/2023	357086684	230101000738	LACEN-MT	19,23,22
BarCode267	Severe acute respiratory syndrome-related coronavirus	93%	BQ.1.1.23	99663	hCoV-19/Brazil/MT-LACENMT-357086654/2023	357086654	230101000740	LACEN-MT	21,28,24
BarCode268	Severe acute respiratory syndrome-related coronavirus	90%	XBB.1.18.1	99731	hCoV-19/Brazil/MT-LACENMT-357086658/2023	357086658	230101000741	LACEN-MT	17,18,17
BarCode269	Severe acute respiratory syndrome-related coronavirus	93%	XBB.1.18.1	99746	hCoV-19/Brazil/MT-LACENMT-357086659/2023	357086659	230101000742	LACEN-MT	23,23,23
BarCode270	Severe acute respiratory syndrome-related coronavirus	93%	XBB.1.18	99753	hCoV-19/Brazil/MT-LACENMT-357086661/2023	357086661	230101000743	LACEN-MT	21,21,21
BarCode272	Severe acute respiratory syndrome-related coronavirus	93%	XBB.1.5	99810	hCoV-19/Brazil/MT-LACENMT-357086670/2023	357086670	230101000746	LACEN-MT	21,20,20
BarCode273	Severe acute respiratory syndrome-related coronavirus	93%	XBB.1.5	99813	hCoV-19/Brazil/MT-LACENMT-357086610/2023	357086610	230101000747	LACEN-MT	25,26,24
BarCode274	Severe acute respiratory syndrome-related coronavirus	92%	XBB.1.5	99823	hCoV-19/Brazil/MT-LACENMT-357086674/2023	357086674	230101000748	LACEN-MT	27,33,29
BarCode275	Severe acute respiratory syndrome-related coronavirus	76%	XBB.1.5	99857	hCoV-19/Brazil/MT-LACENMT-357086461/2023	357086461	230101000751	LACEN-MT	20,25,23
BarCode276	Severe acute respiratory syndrome-related coronavirus	89%	XBB.1.5	99858	hCoV-19/Brazil/MT-LACENMT-357086615/2023	357086615	230101000752	LACEN-MT	17,20,19
BarCode277	Severe acute respiratory syndrome-related coronavirus	87%	XBB.1.18.1	99893	hCoV-19/Brazil/MT-LACENMT-357086617/2023	357086617	230101000753	LACEN-MT	18,24,23
BarCode278	Severe acute respiratory syndrome-related coronavirus	48%	XBB.1.18.1	99895	hCoV-19/Brazil/MT-LACENMT-357086619/2023	357086619	230101000754	LACEN-MT	17,22,22
BarCode279	Severe acute respiratory syndrome-related coronavirus	90%	XBB.1.18.1	99897	hCoV-19/Brazil/MT-LACENMT-357086620/2023	357086620	230101000755	LACEN-MT	18,23,24

Tabela1: Informações sobre as amostras sequenciadas e as respectivas linhagens identificadas do vírus SARS-CoV-2



International A_B Diversity

Alpha (B.1.1.7 I20)

Beta (B.1.351 20H)

Gamma (P.1 20J)

Delta (B.1.617.2 21A,21L)

Omicron (BA.1 21K)

Omicron (BA.2 21L)

Omicron (BA.1/BA.2)

Omicron (BA.4 22A)

Omicron (BA.5 22B)

Figura 2: Filogenia do vírus SARS-CoV-2 reconstruída utilizando as sequências genômicas isoladas em Mato Grosso (em azul) e sequências de referência presentes no banco de dados da ferramenta *Genome Detective- Coronavirs Typing Tool*, disponível online (CLEEMPUT, et al., 2020).

Ao realizar o sequenciamento dos 77 genomas, todos os casos apresentaram a variante Ômicron do SARS-CoV-2, indicando sua presença em 100% das amostras analisadas. Este fato sugere uma possível relação entre a alta transmissibilidade da variante e o número de infecções registradas no Estado de Mato Grosso, bem como a ocorrência de eventos de importação e disseminação do vírus. Além disso, a ausência de medidas preventivas para conter a disseminação do vírus pode ter contribuído para a disseminação da variante Ômicron.

Foram identificadas várias variantes em diferentes proporções. A sublinhagem BQ.1 foi a mais prevalente, representando 30% das amostras analisadas, seguida por XBB.1.18.1 (12%), XBB.1.5 (9%), BQ.1.1.31 (4%), BQ.1.1.11 (4%), BA.5.3.1 (6%), XBB.1.18 (6%), BN.3.1 (2%), BQ.1 (14%), BE.10 (1%), BQ.1.24 (1%), BQ.1.1.5 (1%), BE.9 (1%), DL.1 (1%), XBB.1.18 (1%), XBB.1.18.1 (1%), XBB.2 (1%), e XBJ.2 (1%). **(Figura 3).**

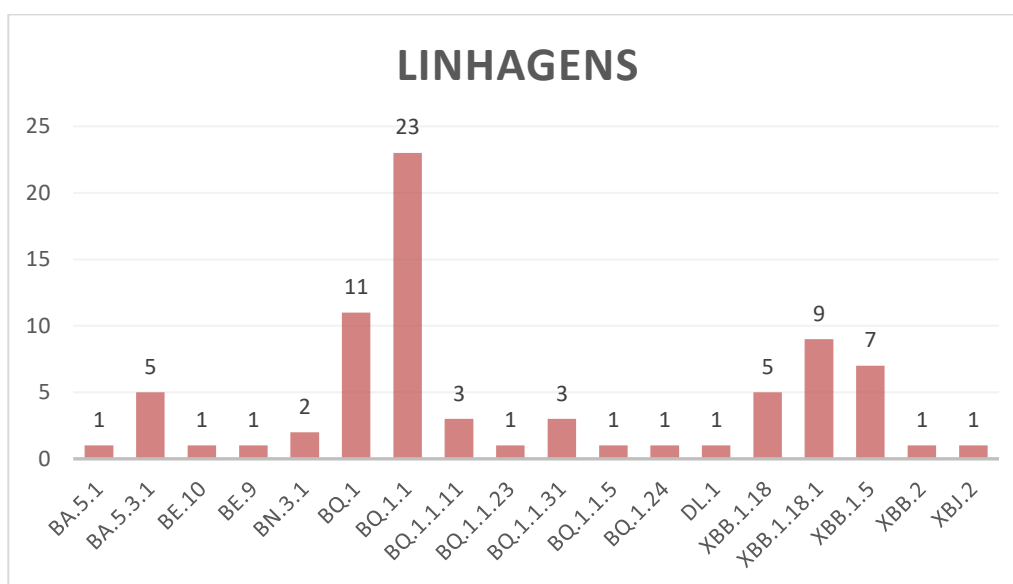


Figura 3: Quantidade das sublinhagens obtidas das sequências genômicas do SARS-CoV-2.

Ao desvendar o histórico do SARS-CoV-2, autoridades e pesquisadores podem adotar medidas adequadas para tentar conter sua disseminação, além de realizar inferências filogenéticas mais detalhadas sobre a dispersão do vírus no Estado. Por fim, ratificamos que a mobilidade humana representa um fator crucial para a dispersão do SARS-CoV2, portanto, medidas preventivas continuam sendo essenciais para minimizar a circulação deste patógeno



no Estado de Mato Grosso.

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