



Governo de
**Mato
Grosso**

Secretaria de Estado de Saúde de Mato Grosso
Secretaria Adjunta de Atenção e Vigilância em Saúde
Laboratório Central de Saúde Pública de Mato Grosso – LACEN/MT

**RELATÓRIO DE SEQUENCIAMENTO DE NOVA
GERAÇÃO DAS AMOSTRAS DE SARS-COV-2
POSITIVAS 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, variando de 27 a 32 quilobases (2), pertencente à família *Coronaviridae*, gênero *betacoronavirus*, sendo designado como SARS-CoV-2, vírus que está relacionado à síndrome respiratória aguda grave (SRAG) e com alto teor de dispersão (1). O genoma do novo coronavírus codifica proteínas não estruturais e quatro proteínas estruturais sendo: 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 continuam a sofrer mutações que diferem da estirpe original de Wuhan.

Para o sequenciamento utiliza-se os 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.

Para uma compreensão melhor sobre o vírus que causa a COVID-19 circulante no Estado de Mato Grosso, durante o período de 06 de junho a 20 de junho de 2022, a equipe do LACEN-MT realizou o sequenciamento de 63 genomas do SARS-CoV-2, provenientes de pacientes com sintomas da doença, residentes em diferentes municípios do Estado, cujo diagnóstico molecular resultou em positivo para o SARS-CoV-2, com valores de CT (*cycle threshold*) que variaram entre 14 e 25 (**Figura 1**).

Os genomas foram sequenciados utilizando a tecnologia desenvolvida pela Thermo Fisher Scientific (Ion GeneStudio S5 Plus), apresentando valores de cobertura que variam de 82 a 99% do genoma total, cuja amostras foram sobre os respectivos municípios: Cáceres (6), Chapada dos Guimarães (3), Cuiabá (18), Diamantino (1), Guarantã do Norte (4), Juscimeira (1), Matupá (4), Mirassol d'Oeste (1), Nobres (3), Nossa Senhora do Livramento (1), Nova Canaã do Norte





(2), Nova Santa Helena (3), Poconé (1), Rio Branco (3), Salto do Céu (2), Tangará da Serra (4), Várzea Grande (6) (**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 a ferramenta *Phylogenetic Assignment of Named Global Outbreak LINEages* disponível em: (<https://github.com/hCoV-2019/pangolin>), seguindo a recente classificação dinâmica proposta por Rambaut e colaboradores (**Figura 2**) (7).

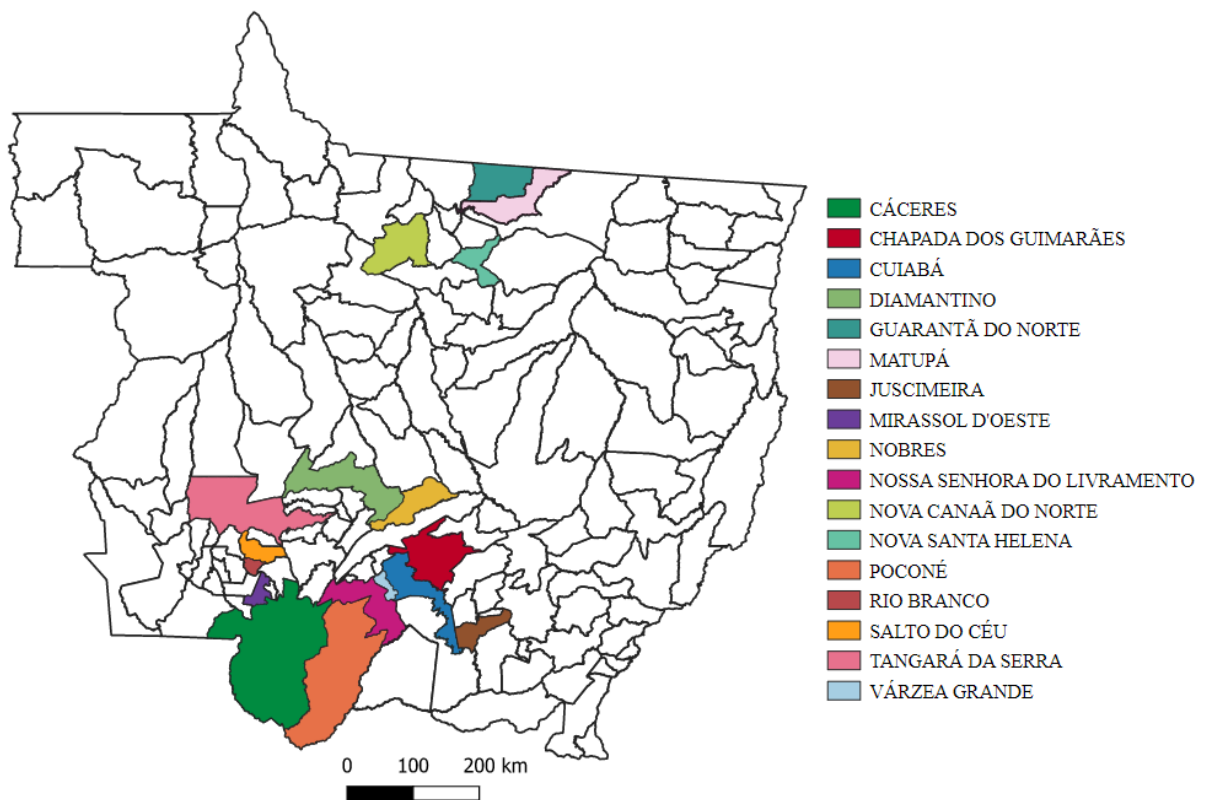


Figura 1: Mapa do Estado de Mato Grosso, destacando os municípios dos hospitais onde foram obtidas e caracterizadas as novas sequências genômicas do SARS-CoV-2.

Barcode	Nº do barcode	Assignment	Contigs	Reads	Coverage	Depth of coverage	Identity NT	Identity AA	Lineages	ID/M/F	ID sequencia	ID Amostra	Requisição GAL_S equenciamento	LACEN	CT (N, ORF_S)
lonCode_0101	BC01	Severe acute respiratory syndrome-related coronavirus	1	1311365	99.8%	8446,8	99.8%	99.6%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510478171/2022	510478171	220101005002	LACEN-MT	21,21
lonCode_0102	BC02	Severe acute respiratory syndrome-related coronavirus	2	739354	99.7%	4666,1	99.8%	99.6%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481171/2022	510481171	220101005750	LACEN-MT	23,23
lonCode_0103	BC03	Severe acute respiratory syndrome-related coronavirus	2	621275	99.7%	3899,8	99.8%	99.7%	BA.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481172/2022	510481172	220101005751	LACEN-MT	23,22
lonCode_0104	BC04	Severe acute respiratory syndrome-related coronavirus	4	266949	99.6%	1642,1	99.8%	99.7%	BA.1.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481177/2022	510481177	220101005752	LACEN-MT	24,24
lonCode_0105	BC05	Severe acute respiratory syndrome-related coronavirus	4	277058	99.7%	1722	99.8%	99.7%	BA.1.14.1	9/51	hCoV-19/Brazil/MT-LACENMT-510481178/2022	510481178	220101005753	LACEN-MT	24,24
lonCode_0106	BC06	Severe acute respiratory syndrome-related coronavirus	6	100666	99.1%	621,9	99.8%	99.7%	BA.1.14.1	9/30	hCoV-19/Brazil/MT-LACENMT-510481179/2022	510481179	220101005754	LACEN-MT	23,23
lonCode_0107	BC07	Severe acute respiratory syndrome-related coronavirus	8	21236	98.8%	131,7	99.8%	99.6%	BA.1.14.1	9/30	hCoV-19/Brazil/MT-LACENMT-510481180/2022	510481180	220101005755	LACEN-MT	24,24
lonCode_0108	BC08	Severe acute respiratory syndrome-related coronavirus	5	251355	99.5%	1522,4	99.8%	99.7%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481182/2022	510481182	220101005757	LACEN-MT	22,22
lonCode_0110	BC10	Severe acute respiratory syndrome-related coronavirus	2	604506	99.7%	3896,5	99.8%	99.7%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481208/2022	510481208	220101005761	LACEN-MT	22,23
lonCode_0111	BC11	Severe acute respiratory syndrome-related coronavirus	2	511423	99.7%	3194,6	99.8%	99.7%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481210/2022	510481210	220101005762	LACEN-MT	22,22
lonCode_0112	BC12	Severe acute respiratory syndrome-related coronavirus	2	644715	99.7%	4177,3	99.8%	99.7%	BA.1.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481212/2022	510481212	220101005763	LACEN-MT	24,24
lonCode_0113	BC13	Severe acute respiratory syndrome-related coronavirus	1	671363	99.8%	4336,4	99.8%	99.6%	BA.1	10/39	hCoV-19/Brazil/MT-LACENMT-510481213/2022	510481213	220101005764	LACEN-MT	23,23
lonCode_0114	BC14	Severe acute respiratory syndrome-related coronavirus	1	633592	99.8%	4080	99.8%	99.6%	BA.1.14.1	11/41	hCoV-19/Brazil/MT-LACENMT-510481214/2022	510481214	220101005765	LACEN-MT	22,22
lonCode_0115	BC15	Severe acute respiratory syndrome-related coronavirus	2	609837	99.7%	3911,7	99.8%	99.7%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481218/2022	510481218	220101005766	LACEN-MT	23,23
lonCode_0116	BC16	Severe acute respiratory syndrome-related coronavirus	4	463896	99.5%	2996,4	99.8%	99.7%	BA.1.1	9/30	hCoV-19/Brazil/MT-LACENMT-510481219/2022	510481219	220101005767	LACEN-MT	26,26
lonCode_0117	BC17	Severe acute respiratory syndrome-related coronavirus	4	937716	99.5%	6024,5	99.8%	99.7%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481310/2022	510481310	220101005768	LACEN-MT	26,26
lonCode_0118	BC18	Severe acute respiratory syndrome-related coronavirus	8	3891	97.9%	24,9	99.8%	99.7%	BA.1.14.1	9/21	hCoV-19/Brazil/MT-LACENMT-510481312/2022	510481312	220101005769	LACEN-MT	30,31
lonCode_0119	BC19	Severe acute respiratory syndrome-related coronavirus	10	1921	97.6%	12,5	99.9%	99.7%	BA.1.14.1	0/18	hCoV-19/Brazil/MT-LACENMT-510481314/2022	510481314	220101005770	LACEN-MT	29,27
lonCode_0120	BC20	Severe acute respiratory syndrome-related coronavirus	4	919718	99.5%	5973	99.8%	99.7%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481316/2022	510481316	220101005771	LACEN-MT	28,27
lonCode_0121	BC21	Severe acute respiratory syndrome-related coronavirus	2	1011136	99.7%	6549,3	99.8%	99.7%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481317/2022	510481317	220101005772	LACEN-MT	26,28
lonCode_0122	BC22	Severe acute respiratory syndrome-related coronavirus	5	255666	99.4%	1669,2	99.8%	99.7%	BA.1.14.1	9/30	hCoV-19/Brazil/MT-LACENMT-510481321/2022	510481321	220101005773	LACEN-MT	30,30
lonCode_0123	BC23	Severe acute respiratory syndrome-related coronavirus	6	834052	99.4%	5392,9	99.8%	99.7%	BA.1.14.1	9/30	hCoV-19/Brazil/MT-LACENMT-510481322/2022	510481322	220101005775	LACEN-MT	28,28
lonCode_0124	BC24	Severe acute respiratory syndrome-related coronavirus	4	722237	99.5%	4667	99.8%	99.7%	BA.1.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481323/2022	510481323	220101005776	LACEN-MT	28,28
lonCode_0125	BC25	Severe acute respiratory syndrome-related coronavirus	5	11004	98.5%	66,6	99.8%	99.7%	BA.1.1	9/24	hCoV-19/Brazil/MT-LACENMT-510481380/2022	510481380	220101005777	LACEN-MT	32,31
lonCode_0126	BC26	Severe acute respiratory syndrome-related coronavirus	3	100352	99.5%	648,5	99.8%	99.6%	BA.2	0/53	hCoV-19/Brazil/MT-LACENMT-510481381/2022	510481381	220101005778	LACEN-MT	29,29,30
lonCode_0127	BC27	Severe acute respiratory syndrome-related coronavirus	1	1824338	99.8%	11762	99.8%	99.6%	BA.2	0/56	hCoV-19/Brazil/MT-LACENMT-510481383/2022	510481383	220101005779	LACEN-MT	25,27,28
lonCode_0128	BC28	Severe acute respiratory syndrome-related coronavirus	5	85226	99.5%	553,3	99.8%	99.7%	BA.1	9/30	hCoV-19/Brazil/MT-LACENMT-510481384/2022	510481384	220101005780	LACEN-MT	32,32
lonCode_0129	BC29	Severe acute respiratory syndrome-related coronavirus	9	20985	98.8%	139,3	99.8%	99.6%	BA.1.14.1	9/30	hCoV-19/Brazil/MT-LACENMT-510481385/2022	510481385	220101005781	LACEN-MT	32,31
lonCode_0130	BC30	Severe acute respiratory syndrome-related coronavirus	4	98684	99.5%	640,8	99.8%	99.7%	BA.1.1	9/24	hCoV-19/Brazil/MT-LACENMT-510481386/2022	510481386	220101005782	LACEN-MT	31,32
lonCode_0131	BC31	Severe acute respiratory syndrome-related coronavirus	5	1129788	99.5%	7298,3	99.8%	99.7%	BA.1.1	9/30	hCoV-19/Brazil/MT-LACENMT-510481387/2022	510481387	220101005783	LACEN-MT	27,27
lonCode_0132	BC32	Severe acute respiratory syndrome-related coronavirus	4	900322	99.5%	5812,8	99.8%	99.6%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481388/2022	510481388	220101005785	LACEN-MT	27,26
lonCode_0101	BC01	Severe acute respiratory syndrome-related coronavirus	3	55967	99.5%	361,4	99.8%	99.7%	BA.1	9/30	hCoV-19/Brazil/MT-LACENMT-510481398/2022	510481398	220101005786	LACEN-MT	25,25
lonCode_0102	BC02	Severe acute respiratory syndrome-related coronavirus	5	188597	99.5%	1168	99.8%	99.7%	BA.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481400/2022	510481400	220101005787	LACEN-MT	28,28
lonCode_0103	BC03	Severe acute respiratory syndrome-related coronavirus	3	128856	99.7%	787,5	99.8%	99.7%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481401/2022	510481401	220101005788	LACEN-MT	28,27
lonCode_0104	BC04	Severe acute respiratory syndrome-related coronavirus	2	604324	99.7%	3813	99.8%	99.6%	BA.1.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481402/2022	510481402	220101005789	LACEN-MT	29,29
lonCode_0105	BC05	Severe acute respiratory syndrome-related coronavirus	1	1029180	99.8%	6659,9	99.8%	99.6%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481403/2022	510481403	220101005790	LACEN-MT	29,30
lonCode_0106	BC06	Severe acute respiratory syndrome-related coronavirus	1	892574	99.8%	5687,7	99.8%	99.6%	BA.1.14.1	9/40	hCoV-19/Brazil/MT-LACENMT-510481404/2022	510481404	220101005791	LACEN-MT	28,27
lonCode_0107	BC07	Severe acute respiratory syndrome-related coronavirus	2	1076538	99.8%	6936,1	99.8%	99.7%	BA.1.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481406/2022	510481406	220101005792	LACEN-MT	28,27
lonCode_0108	BC08	Severe acute respiratory syndrome-related coronavirus	1	1155999	99.8%	7446,3	99.8%	99.6%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481407/2022	510481407	220101005793	LACEN-MT	25,25
lonCode_0109	BC09	Severe acute respiratory syndrome-related coronavirus	4	64589	99.5%	410,7	99.8%	99.7%	BA.1.14.1	9/30	hCoV-19/Brazil/MT-LACENMT-510481413/2022	510481413	220101005794	LACEN-MT	16,15,16
lonCode_0110	BC10	Severe acute respiratory syndrome-related coronavirus	1	492173	99.8%	3169,8	99.8%	99.7%	BA.1.1	9/54	hCoV-19/Brazil/MT-LACENMT-510481415/2022	510481415	220101005795	LACEN-MT	20,20,21
lonCode_0111	BC11	Severe acute respiratory syndrome-related coronavirus	1	594678	99.8%	3828	99.8%	99.6%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481416/2022	510481416	220101005796	LACEN-MT	20,20
lonCode_0112	BC12	Severe acute respiratory syndrome-related coronavirus	1	382724	99.7%	2479,4	99.8%	99.7%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481417/2022	510481417	220101005797	LACEN-MT	21,21
lonCode_0113	BC13	Severe acute respiratory syndrome-related coronavirus	1	506678	99.8%	3297,8	99.8%	99.6%	BA.1.14.1	9/40	hCoV-19/Brazil/MT-LACENMT-510481418/2022	510481418	220101005798	LACEN-MT	21,21
lonCode_0114	BC14	Severe acute respiratory syndrome-related coronavirus	2	384640	99.7%	2493	99.8%	99.7%	BA.1.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481419/2022	510481419	220101005799	LACEN-MT	18,19
lonCode_0115	BC15	Severe acute respiratory syndrome-related coronavirus	1	438447	99.8%	2839	99.8%	99.7%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481420/2022	510481420	220101005800	LACEN-MT	20,20
lonCode_0116	BC16	Severe acute respiratory syndrome-related coronavirus	2	466473	99.6%	3024,6	99.8%	99.7%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481421/2022	510481421	220101005801	LACEN-MT	22,22
lonCode_0117	BC17	Severe acute respiratory syndrome-related coronavirus	1	830197	99.8%	5318,2	99.8%	99.7%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481429/2022	510481429	220101005802	LACEN-MT	18,19,20
lonCode_0118	BC18	Severe acute respiratory syndrome-related coronavirus	7	57129	99%	351,4	99.8%	99.7%	BA.1.14.1	9/30	hCoV-19/Brazil/MT-LACENMT-510481430/2022	510481430	220101005803	LACEN-MT	18,17,18
lonCode_0119	BC19	Severe acute respiratory syndrome-related coronavirus	8	37594	98.9%	241,8	99.8%	99.6%	BA.1.14.1	9/30	hCoV-19/Brazil/MT-LACENMT-510481431/2022	510481431	220101005804	LACEN-MT	20,20,22
lonCode_0120	BC20	Severe acute respiratory syndrome-related coronavirus	4	93831	99.4%	571,7	99.8%	99.7%	BA.1.14.1	9/30	hCoV-19/Brazil/MT-LACENMT-510481432/2022	510481432	220101005805	LACEN-MT	16,16,17
lonCode_0121	BC21	Severe acute respiratory syndrome-related coronavirus	3	406915	99.6%	2543,9	99.8%	99.7%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481433/2022	510481433	220101005806	LACEN-MT	20,21
lonCode_0122	BC22	Severe acute respiratory syndrome-related coronavirus	1	778319	99.8%	5010,8	99.8%	99.7%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481434/2022	510481434	220101005807	LACEN-MT	22,22
lonCode_0123	BC23	Severe acute respiratory syndrome-related coronavirus	2	815511	99.7%	5257,7	99.8%	99.7%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481435/2022	510481435	220101005808	LACEN-MT	20,21
lonCode_0124	BC24	Severe acute respiratory syndrome-related coronavirus	2	929526	99.7%	5993,5	99.8%	99.6%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481436/2022	510481436	220101005809	LACEN-MT	18,18
lonCode_0125	BC25	Severe acute respiratory syndrome-related coronavirus	2	594782	99.7%	3733,9	99.8%	99.6%	BA.1.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481437/2022	510481437	220101005810	LACEN-MT	21,20
lonCode_0126	BC26	Severe acute respiratory syndrome-related coronavirus	2	678348	99.7%	4303,4	99.8%	99.6%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481438/2022	510481438	220101005811	LACEN-MT	20,19
lonCode_0127	BC27	Severe acute respiratory syndrome-related coronavirus	1	759058	99.8%	4889,3	99.8%	99.7%	BA.1.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481439/2022	510481439	220101005812	LACEN-MT	20,20
lonCode_0128	BC28	Severe acute respiratory syndrome-related coronavirus	1	808949	99.8%	5237,8	99.8%	99.7%	BA.1.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481440/2022	510481440	220101005813	LACEN-MT	20,21
lonCode_0129	BC29	Severe acute respiratory syndrome-related coronavirus	1	762143	99.8%	4858,5	99.8%	99.7%	BA.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481441/2022	510481441	220101005814	LACEN-MT	18,18
lonCode_0130	BC30	Severe acute respiratory syndrome-related coronavirus	1	774165	99.8%	4960,8	99.8%	99.6%	BA.1.14.1	9/39	hCoV-19/Brazil/MT-LACENMT-510481442/2022	510481442	220101005815	LACEN-MT	20,20
lonCode_0131	BC31	Severe acute respiratory syndrome-related coronavirus	1	851075	99.8%	5480,1	99.8%	99.7%	BA.1.1	9/48	hCoV-19/Brazil/MT-LACENMT-510481443/2022	510481443</			



Tabela 1: Informações sobre as amostras sequenciadas e as respectivas linhagens identificadas do vírus SARS-CoV-2.

Apenas a Ômicron foi identificada em 100% das amostras sequenciadas, provavelmente relacionado a alta transmissibilidade desta variante, inúmeros eventos de importações e tipagem viral, concomitantes ao elevado número de infecções registrados no Estado além da ausência de medidas preventivas para a dispersão do vírus. A sublinhagem em maior evidência foi a BA.1.14.1 (56 %) seguida pela BA.1.1 (23%), BA.1 (11%), BA.1.14 (5%), BA.2 (3%) e BA.1.14.2 (2%). (Figura 1)

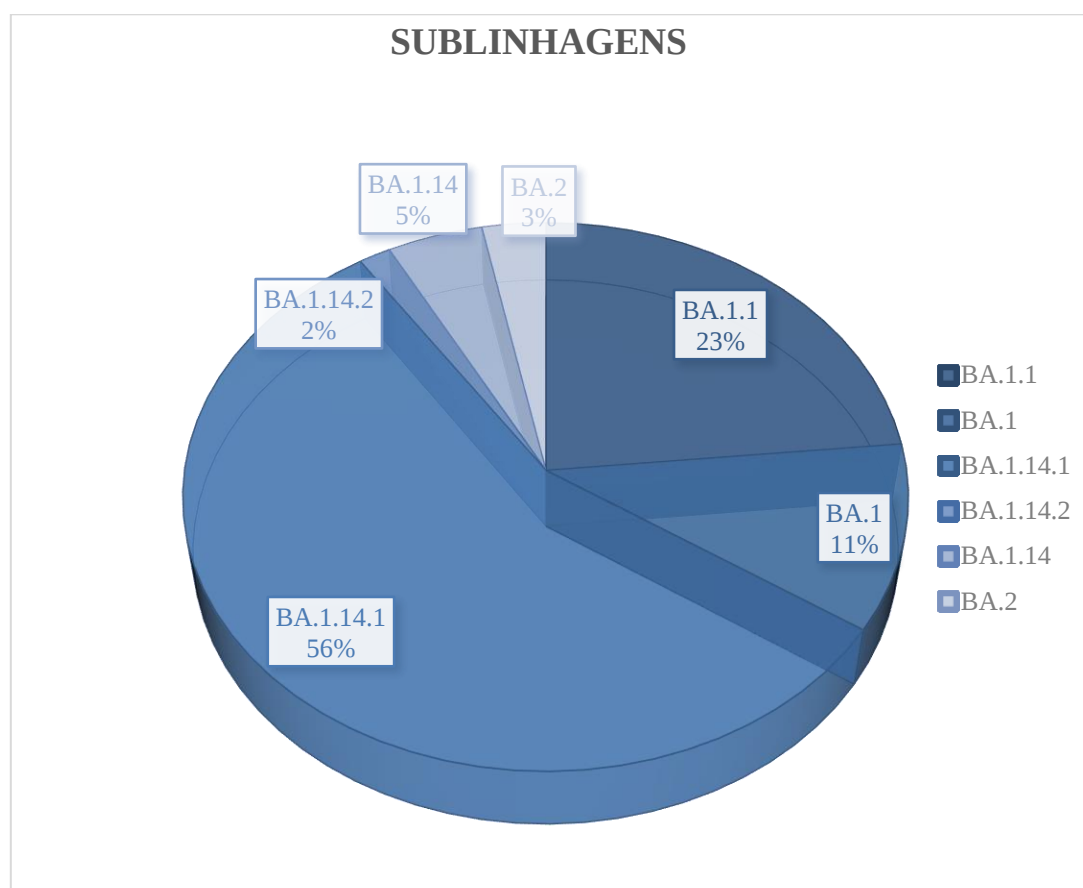


Figura 1: Frequência e porcentagem das sublinhagens do SARS-CoV-2.

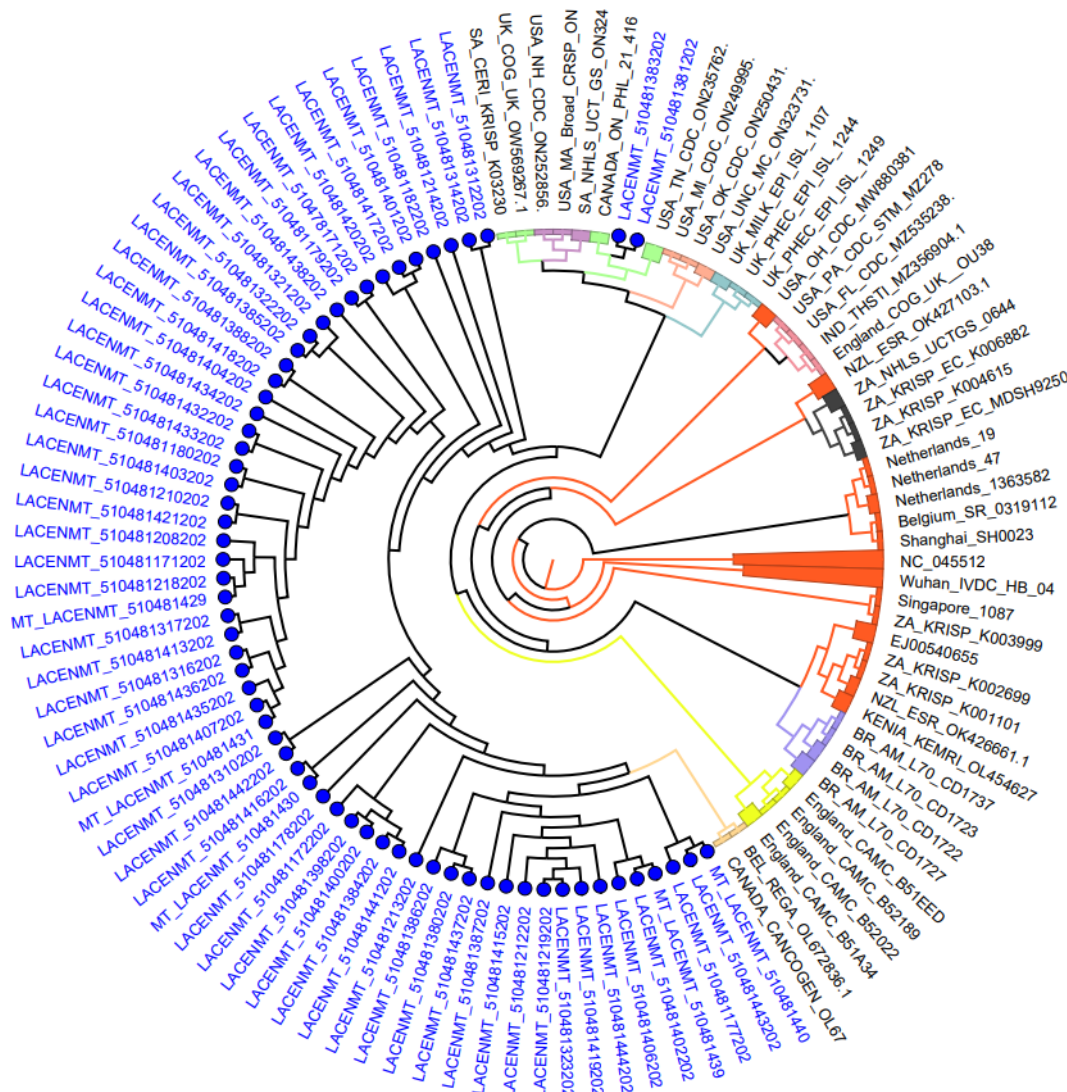


Figura 2: Filogenia do vírus SARS-CoV-2 reconstruída utilizando as sequências genômicas isoladas em Mato Grosso (em azul) e sequências de referência presentes no banco de dados da ferramenta *Genome Detective-Coronavir TypingTool*, disponível online (CLEEMPUT, et al., 2020).

O sequenciamento genético realizado pelo LACEN-MT aponta que as novas linhagens circulantes da variante Ômicron continuam a ganhar espaço no Estado de Mato grosso, favorecendo a ocorrência de casos de COVID-19 em pessoas que já se infectaram pela doença, inclusive os imunizados.

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, o

distanciamento social e medida de restrições ainda continuam sendo essenciais para minimizar a circulação deste patógeno no Estado de Mato Grosso.

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Responsáveis técnicos

Elaine Cristina de Oliveira - Diretora do LACEN-MT
Júlia Deffune Profeta Cidin Almeida
Luana Barbosa da Silva
Luiz Takao Watanabe
Raquel da Silva Ferreira
Stephanni Figueiredo da Silva