Genomic surveillance China

Informatie via VWS attaché Beijing

RT 3 jan 2022

News release by Guangzhou Municipal CDC on 30th Dec 2022

- From October to December 2022, the Guangzhou CDC did the whole genomic sequencing of samples of 848 cases, which all turned out to be Omicron variants:
  - BA.5.2: 814 cases, 96% ; BF.7: 34 cases
- In December, genomic sequencing was made on 23 samples collected from the fever clinics of the sentinel hospitals in the city:
  - All turn out to be BA.5.2 variant, which are highly homologous with the outbreak of in Haizhu district of Guangzhou in October.
  - No other variant was found.

Data from the Frontiers of Medicine Paper 31st Dec 2022

Primary assessment of the diversity of Omicron sublineages and the epidemiologic features of autumn/winter 2022 COVID-19 wave in Chinese mainland

- Genomic sequencing in Shanghai Region autumn/Winter Season 2022:
- Genomic sequencing was carried out on 378 cases randomly sampled from patients in Shanghai, and 369 high quality viral genomes were obtained.
  - Among these genomes, there are 30 Omicron variants registered in GISAID.
  - 355 (95.95%) genomes were Omicron variants: BF.7, BA.5.2, BQ.1 and XBB
  - Cases with Beijing or Guangzhou epidemic are mainly with BF.7 and BA.5.2
  - Cases who enter Shanghai from abroad are mainly with BQ.1 and XBB
  - No new variant has yet been found in these results.

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RESEARCH ARTICLE

Primary assessment of the diversity of Omicron sublineages and the epidemiologic features of autumn/winter 2022 COVID-19 wave in Chinese mainland

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History

NB. Dit lijkt een ander blad dan het Springer blad ‘Frontiers of Medicine’. DOI kan (nog) niet gevonden worden.
Vraag voor full tekst staat uit bij bibliotheek.

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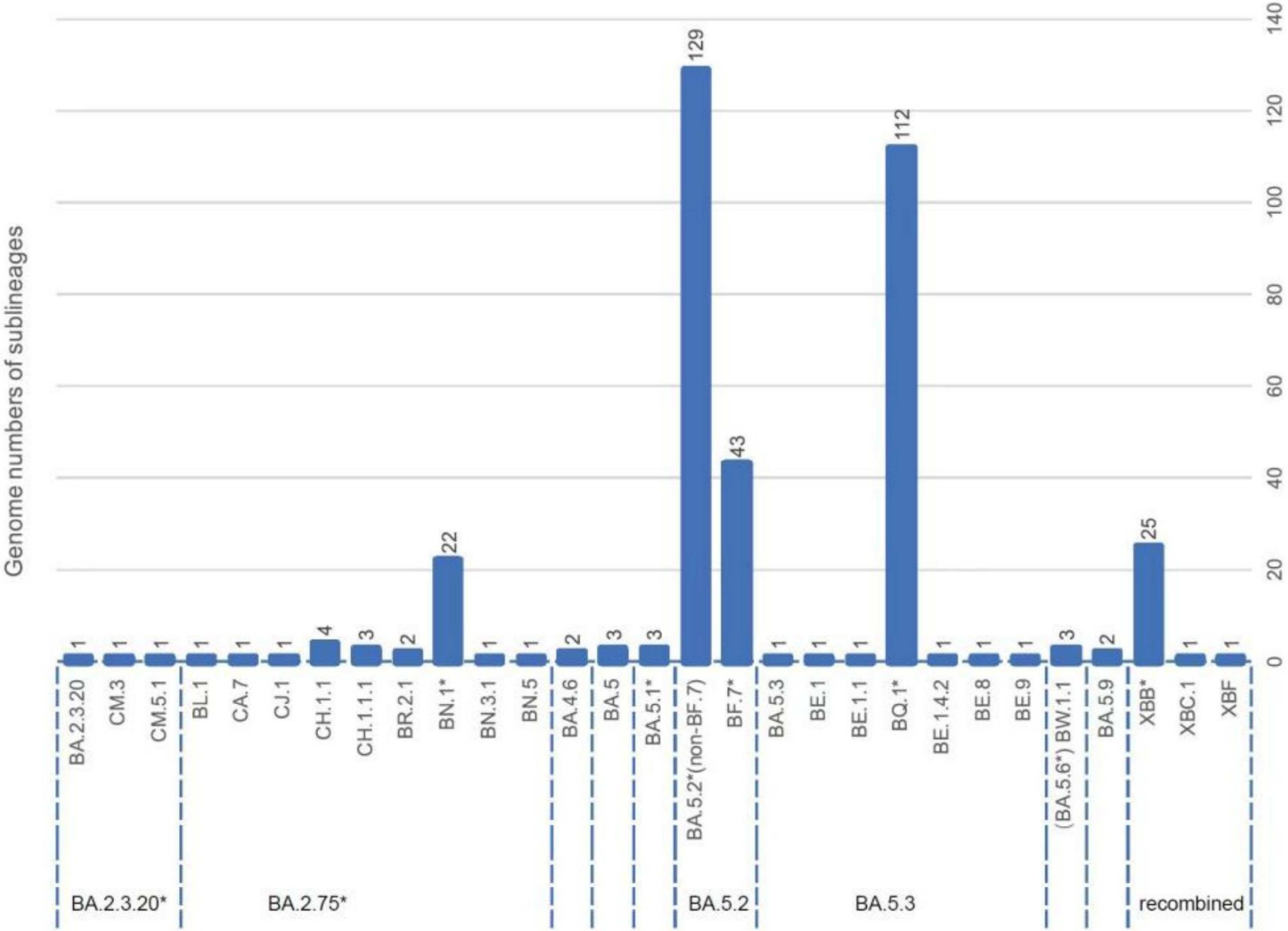
Genome numbers of sublineages
0
20
40
60
80
100
120
140
BA.2.3.20 1
CM.3 1
CM.5.1 1
BL.1 1
CA.7 1
CJ.1 1
CH.1.1 4
CH.1.1.1 3
BR.2.1 2
BN.1* 22
BN.3.1 1
BN.5 1
BA.4.6 2
BA.5 3
BA.5.1* 3
BA.5.2*(non-BF.7) 129
BF.7* 43
BA.5.3 1
BE.1 1
BE.1.1 1
BQ.1* 112
BE.1.4.2 1
BE.8 1
BE.9 1
(BA.5.6*) BW.1.1 3
BA.5.9 2
XBB* 25
XBC.1 1
XBF 1
BA.2.3.20*
BA.2.75*
BA.5.2
BA.5.3
recombined

News release China CDC 13th December

The prevalent variants are still BA.5.2和BF.7.

Vertaalde tekst:

‘Recently, a new variant called BQ.1.1 has appeared in the Internet. The Chinese Center for Disease Control and Prevention said today (December 13) that BQ.1 is the sixth generation subclade of Omicron BA.5 produced by mutation and change of the virus during the epidemic transmission of the population. BQ.1.1 is the first generation subbranch of BQ.1. The pathogenicity of these evolutionary branches is significantly weakened, and the proportion of severe disease and death is significantly lower than that of the early circulating variant strains. The strains circulating in China at this stage are still dominated by BA.5.2 and BF.7 subclades of BA.5’.

Vertaalde tekst deel 2

‘China will continue to strengthen the monitoring of genomic mutations of the Omicron variant circulating globally, imported into China and locally circulating, and timely carry out the assessment of transmissibility, immune evasion capacity and pathogenicity of emerging dominant strains, so as to provide scientific basis for the continuous optimization of vaccine research and development and prevention and control policies’.

Samenvatting

- Openbare/beschikbare informatie over varianten is zeer beperkt.
- Sequenties van kleine sets monsters openbaar. Of ze random zijn is niet bekend.
- Duiding China CDC:
  - BA.5.2 en subvarianten daarvan (BF.7) gaan vooral rond Bejing, en Guangzhou
  - Geïmporteerde gevallen in Shanghai vooral BQ.1 en XBB

  Maar er is ook dit bericht van 13 dec:

  BQ.1 and its subclades were detected in autochthonous cases in 9 provinces (hnr.cn)).

  Keywords: BQ.1 and its subclades were detected in local cases in 9 provinces

Conclusies

- Op basis van beperkte info uit enkele regio's lijkt het erop dat in China dezelfde varianten rondgaan die we ook in de rest van de wereld zien.
- Als er in China echt alleen dergelijke beperkte sequentiedata beschikbaar zijn zal een nieuwe variant in China niet (gemakkelijk) opgepikt kunnen worden.

Is het RT het eens met deze conclusies?