

29 November 2021

Tess

By email: fyi-request-17030-df12623c@requests.fyi.org.nz

Dear Tess

Official Information Act Request: COVID-19 genome sequencing

On 4 October 2021 you sent a request for information under the Official Information Act 1982 to ESR as follows:

- "1. Are you obtaining your genome sequencing from supplied positive PCR samples? If so, what is the average CT value? and if not, how are you obtaining your material/data to work with?
- 2. Out of all of the positive COVID19 results in New Zealand, how many have been genome sequenced?
- 3. Of all of the genome sequenced results, how many are a direct match to COVID19 (all variants)?
- 4. From the positive test results that were genome sequenced, how many variants have been found? and which variants were these?"

Our response to your request:

1. Are you obtaining your genome sequencing from supplied positive PCR samples? If so, what is the average CT value? and if not, how are you obtaining your material/data to work with?

Yes, whole genome sequencing (WGS) uses the sample taken for the PCR diagnostic test. For any positive PCR test the remaining sample is forwarded to ESR for WGS. Diagnostic testing in New Zealand is undertaken using several different platforms, it is therefore not possible to provide a meaningful average CT value. WGS is most likely to be successful on samples with a CT value under 30.

2. Out of all of the positive COVID19 results in New Zealand, how many have been genome sequenced?

As of 29/11/2021, whole genome sequencing has been attempted on 6236 cases and sequence data has been obtained from 5338 cases.

3. Of all of the genome sequenced results, how many are a direct match to COVID19 (all variants)?

All 5338 of the sequences obtained are COVID-19 genomes. Sequence data is compared for samples from NZ and with data obtained from COVID-19 samples worldwide. These have been deposited in a public database, GISAID (https://www.gisaid.org/).



4. From the positive test results that were genome sequenced, how many variants have been found? and which variants were these?

SARS-COV-2 VARIANTS IN NEW ZEALAND - SUMMARY

(Source: Microreact 'covid genomic analysis' project 09.00 am, 29 November 2021)

WHO nomenclature	Pango lineage	Confirmed cases	Report date of last confirmed case
VARIANTS OF CONCERN (VOC)			
Alpha	B.1.1.7	178	06 Aug 2021
Beta	B.1.351	33	27 Jun 2021
Gamma	P.1	8	01 Jun 2021
Delta	B.1.617.2 (and AY sublineages, excluding AY.4.2*)	3797	23 Nov 2021
Omicron	B.1.1.529	<u>O</u>	-
VARIANTS UNDER INVESTIGATION (VUI)			
Delta*	AY.4.2*	5	04 Nov 2021
Eta	B.1.525	8	08 Jun 2021
Theta	P.3	3	20 Mar 2021
Карра	B.1.617.1	5	09 Apr 2021
	B.1.617.3	4	11 Apr 2021
-	C.36.3	4	12 Jun 2021
Lambda	C.37	0	-
Mu	B.1.621**	1	19 Jun 2021

^{*} AY.4.2 is a sub-lineage within Delta that has been assigned as a distinct VUI

^{**} The case of the Mu variant detected in New Zealand was lineage B.1.621.1, a sub-lineage of B.1.621 which has all the key spike mutations of concern found in lineage B.1.621



Your right to seek a review

You have the right to seek an investigation and review by the Ombudsman of this decision. Information about how to make a complaint is available at www.ombudsman.parliament.nz or freephone 0800 802 602.

Thank you for your request.

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Yours sincerely

Jill Vintiner

Joint General Manager Health and Environment Group – Health ESR