Wuhan-coronavirus homologue map

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Background and Objective

Background: At the beginning of 2020, global risk of infection of coronavirus is spreded. The pandemic started in 2019 and governments announced a state of emergency. In Japan, the government adopted PCR as a diagnosis method of the infection. But the selection of prmers influences the accuracy greatly. Objective: Therefor, I provide a "map" of homological region of coronavirus genome to other viruses and annimals genomes to help the primer design.

Data

Vertebrates:

- Bat (NW_017738920.1 .. NW_017802358.1; 63439frgs)
 Dog (NC_006583.3 .. NC_006621.3; 39chrs)
- Beluga (NW_022097992.1 .. NW_022103895.1; 5904frgs)
- Camel (NC_044511.1 .. NC_044547.1; 37chrs)
- Cat (NC_018723.3 .. NC_018741.3; 19chrs)

Viruses:

- 7554 genomes of viruses or phages
- Ferret (NW_004569142.1 .. NW_004576923.1; 7782frgs)
- Human (NC_000001.4 .. NC_000024.3; 24chrs)
- Mouse (NC_000067.6 .. NC_000087.7; 21chrs)
- Wuhan-corona virus genome (MN908947.3)
- Rabbit (NC_013669.1 .. NC_013690.1; 22chrs)
- Pig (NC_010443.5 .. NC_010462.3; 20chrs)
- Turkey (NC_015011.2 .. NC_015042.2; 32chrs)

Rock Pigeon (NW_004973171.1 .. NW_004988092.1; 14922frgs)

Method

BLAST

DB: makeblastdb -in <<input file>> -out <<DB name>> -dbtype nucl -parse_seqids Query: megablast -d <<DB name>> -i <<query sequence>> -W 10 > <<output file>>

Self-BLAST

Fragmentation: fragment bf=<<input file>> S=25 G=25 cs=1 > <<output file>> DB: same as above. Query: same as above.

Window-fourrier

Fragmentation: 30 fragments; 1000 bases / fragment Conversion: "A" -> 1, "T" -> -1, "G" -> 1, "C" -> -1Fourier transform: Ft (<< each fragment>>)

Selection of frequent homologues Vertebrates: base-hit count >= 5; seq-lenght >= 5

Viruses: base-hit count >= 18; seq-lenght >= 5

Result

No. homologue

The homologues

2	AATTTTA	2047	2007	6	Yes							
	GATGAGGATGAAGAAGAAGGT	3047	3067	O								
C	CTACAAAGAAAACAGTTAC	5866	5884	5	Yes							
A	ATAAATATTATAATTTG	6944	6960	7	Yes							
7	TTGCAT	7425	7430	5	Yes	N	No. I	homologue	start	end	count	in (
(CCATCCATCTTTACTTTGATAAA	7764	7786	7	Yes	1	L5 (CAAGATCTCAATGGTAACTGGTGATT	14 068	14 104	21	Yes
	TTTTTGTTGCTGCTATTTTCTATTTA	8607	8632	9	Yes	1	L6 -	TGGTAATGCTGC	14 775	14786	18	Yes
	ATTTCTCTGTTTGTTTTTGT	11 167	11 186	7	Yes			ACAAAACGTAATGTCATCCCTACTATAACTCAAATGAATCTTAAGTATGCCATTAGTGCAAAGAATAGAGCTCGCACCGTAGCTGGTGTCTCTAT	15 031	15 125	32	Yes
	AAAAGT	12 198	12 203	5	Yes			CTTATGGGTTGGGATTATCCTAAATGTGATAGAGCCATGCCTAA	15 280	15 323	37	Yes
	ATAAAATAGAAGAA	19 121	19 134	6	Yes			GATGCCACAACTGCTTATGCTAATAGTGTTTTTAACAT	15 490	15 527	19	Yes
	TGTTTGTTTTTCTTGTTTTATTGC	21 564	21 587	14	Yes			CAAAACAATGTTTTTATGTCTGAAGCAAAATGTTGGACTGAGACTGACCTTACTAAAGGACCTCATGAATTTTGCTCTCAACATACA	15 805	15 891	26	Yes
.2 1	TATTAAAATATAATGAA	22 389	22 405	5	Yes	2	21 (GGTTGTGATGGCAGTTTGTATGTAAATAAACATGCATTCCACACACC	19 276	19 325	27	Yes
.3 7	TTTTCT	26 495	26 500	5	No	2	22	TATGAGAGTTATACATTTTGGTGCTGGTTCTGATAAAGGAGTTGCACCAGGTAC	20 850	20 903	21	Yes
4 (CCTAA	29 375	29 379	5	Yes	2	23 (CCGAGGCCACGCGGAGTACGAGTGTACAG	29 732	29 764	32	No
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