Blastocystis seqeunce types found in pig study

>ST5a(2)

AGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAACGTTGTTGCAGTTAAAAAGCTCGTAGTTGAAAT

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CTAGTGCGAAAGCATTTACCAAGGATGTTTTCATTAATCAAGAACGAAAGCTAC

>ST5b(60)

AGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAACGTTGTTGCAGTTAAAAAGCTCGTAGTTGAAAT

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CTAGTGCGAAAGCATTTACCAAGGATGTTTTCATTAATCAAGAACGAAAGCTAA

>ST5c(8)

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>ST5d(8)

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TATTAATTTATTTGTAATAAGAATTGGTCATTTACTGTGAGAAAATTAGAGTGTTCAAAGCAGGCATTTGCT

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>ST5e(27)

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>ST5f(129)

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>ST1a(49)

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>ST1b(55)

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>ST3a(3)

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TGCTTGAATATATTAGCATGGAATAATCATGTATGATTTTCATGATGTATTTGATTGGTTTGGTTCATGAGA

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>ST3b(5)

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TGAGTATTAATTTACTTGTATATGTATTTAGACATTTACTGTGAGAAAATTAGAGTGTTCAAAGCAGGCATT

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>ST15

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TTTTTTTATAGATTATTATATATTATATTAATTTATAGTATATAATATATATCTATAATCATTTACAGTGAG

AAAATTAGAGTGTTCAAAGCAGATTTTTTATGTTTGAATATATTAGCATGGAATAATACTATAAGATTTTAA

ATTTCTTATATTT-TATTGGTTTTATAATAATTTAAAATAATGATTAATAGGGACAGTTGTGGGTATTCATA

TTCAATTGTCAGAGGTGAAATTCTCGGATTTATGGAAGATGAACTAATGCGAAAGCATTTACCAAGGATGTT

TTCATTAATCAAGAACGAAAGTTA

Table ?

|  |  |  |  |
| --- | --- | --- | --- |
| Subtype | Sequence type | Number of pigs positive | Examples of closest matches to reference DNA sequence entry (accession no.) in NCBI database |
| ST5 | ST5a | 2 | AB107966 (cattle, Japan) (99.76%)  AB070998 (pig, Japan) (99.76%)  MK801415 (pig, Austria) (99.76%) |
|  | ST5b | 60 | AB107964 (pig, Japan) (100%)  MH104976 (pig, Thailand) (100%)  MK801372 (pig, Germany) (100%) |
|  | ST5c | 8 | AB107966 (cattle, Japan) (100%)  AB070998 (pig, Japan) (100%)  MK801415 (pig, Austria) (100%) |
|  | ST5d | 8 | MK375237 (human, Thailand) (99.76%)  MK801375 (pig, Germany) (99.76%)  MK375227 (pig, China) (99.76%) |
|  | ST5e | 27 | KT819615 (pig, Thailand) (100%)  MK375229 (pig, China) (110%) |
|  | ST5f | 129 | MK375237 (pig, China) (100%)  MK801375 (pig, Germany) (100%) |
| ST1 | ST1a | 49 | AB107961 (pig, Japan) (99.76%) |
|  | ST1b | 55 | AB107962 (human, Japan) (100%)  KU719525 (human, Iran) (100%)  MK801400 (pig, Germany) (100%) |
| ST3 | ST3a | 3 | AB070986 (human, Japan) (100%)  MT330276 (human, Thailand) (100%)  AM779042 (human, Turkey) (100%)  MK801389 (pig, Germany) (100%) |
|  | ST3b | 5 | KM216257 (human, Thailand) (100%)  LC414152 (human, Iran) (100%)  MK418914 (macaque, China) (100%) |
| ST15 | ST15\* | NA\* | MK801393 (pig, Germany) (99.34%)  KC148211 (gibbon, zoo) (99.12%)  KC148210 (camel, Egypt) (97.81%) |

\* = due to the low number of sequence read per positive samples, sequence reads were pooled and one consensus sequence was generated from those few sequences that did not exhibit any gaps in the middle.

NA = not applicable.

For Discussion:

Note: The two different ST1 seqeunces are identical to sequences sharing the Allele 4 – hence, the allele system might not be sufficiently discriminative to discern strains of cryptic host specificity.