

Risk ranking of STEC dairy isolates after characterisation by WGS

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Study (unpublished, keep it confidently, please)

- Main goal: Risk ranking of 40 STEC dairy isolates after FAO/WHO scheme (2018)
- 40 STEC dairy isolates:
 - From Swiss raw milk intended for raw milk cheese produkction
 - From cheeses from the Swiss market (of raw milk, 1x of past milk, cow and goat)
 - 7 isolates from Cantonal Labs (thanks to M. Storari & M. Peier)
- Illumina sequencing
 - EURL WGS PT pipeline & CGE vir
 - *stx*-subtyping-PCR in case of <100% match
- Creation of risk rank table

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Results I (unpublished, keep it confidently, please)

Risk level	Trait (genes)	¹ Potential for:	n (%)	Top6Sero	aggR	eae	ehxA	astA	espP	st/lt	efa1
1	stx _{2a} + eae or aggR	D/BD/HUS	0 (0)	-	-	-	-	-	-	-	-
2	stx _{2d}	D/BD/HUS ²	10 (25.0)	_	-	-	5	-	7	-	-
3	stx _{2c} + eae	D/BD ³	1 (2.5)	_	-	1	1	1	1	-	-
4	stx _{1a} + eae	D/BD ³	11 (27.5)	5x O26 2x O145	-	11	11	11	10	-	8
5	Other <u>stx</u> subtypes	D	18 (45.0)	1x O145	-	-	10	6	3	5	-
		Tot	al: 40	8	0	12	27	18		5	8

estimated potential to cause D: diarrhoea, BD: bloody diarrhoea, HUS: haemolytic uraemic syndrome, depending on host susceptibility and other factors; e. g. antibiotic treatment.

- Almost half of isolates in the lowest risk group and none in the highest
- Classical STEC O26 only with stx1a (NOT stx2a); no O80:H2

- No aggR-containing hybrid strains found, other hybrids/mosaics present (STEC-ETEC...)
- Two with stx2a & 2d (eae-neg, O22:H16 and O113:H21) => Most virulent ones?

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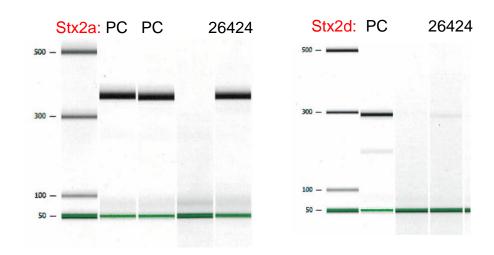
² association with HUS dependent on stx2d variant and strain background

³ some subtypes have been reported to cause BD, and on rare occasions HUS



Results II (unpublished, keep it confidently, please)

- Mostly very high agreement between stx-subtyping-PCR and WGS
- stx-subtyping-PCR useful especially when more than one of the same stx-subtype is present (e.g. stx2a & stx2d), WGS indicating «mixed» results
- Isolate FAM 26424 (O8:H9, ST23, cheese made from goats milk): *stx*-subtyping-PCR caused false positive results for *stx2a* and *stx2d* (interfering with risk evaluation)!



WGS (ARIES): *stx2e* (99.76%)

WGS (CGE after Dec 2022): stx2/ (100%)

This is already known from DK (EFSA 2019):

Stx2e-O8-FHI-1106-1092 => stx2h => new: stx2l

- Not clinically relevant or just diarrhea (NOR)
- O8:H9, ST23, stx2l from raw mutton and humans (Yang et al, 2022)

Thanks for updating the databases!
We need help with reference strains & PCR-protocols for the new variants!

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