



# Typing of *vtx* genes

**FLEMMING SCHEUTZ**

**STATENS SERUM INSTITUT**

**The International *Escherichia* and *Klebsiella*  
Centre (WHO)  
Copenhagen**





# Main groups

Stx1/VT1 and VT2

## Subtypes

Suffixed with small Arabic letters

Stx1: Shiga toxin from *Shigella stx1a*

VT1: *E. coli* Verocytotoxins      *vtx1b* to *vtx1d*

VT2: *vtx2a* to *vtx2h*

## Variant designations

Subtype - first published O group - strain No.

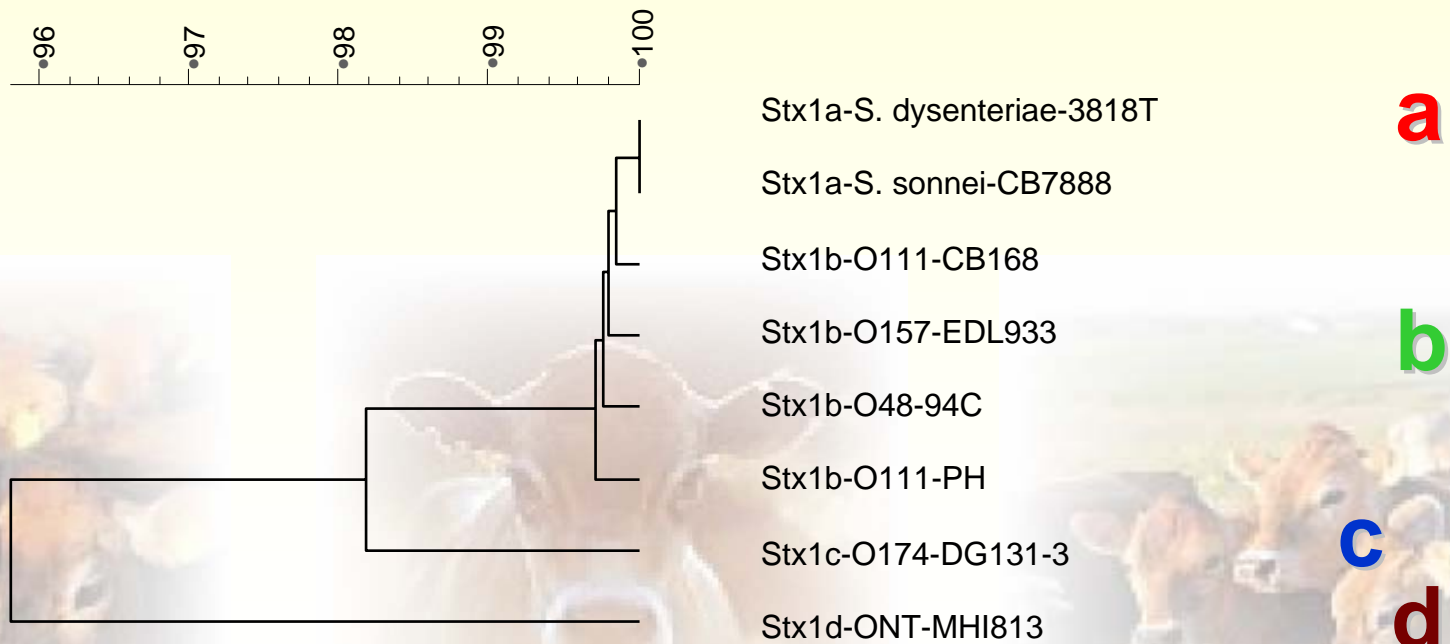
Phylogenetic sequence based nomenclature for the combined A- and B-subunits

SP	A <sub>1</sub>	A <sub>2</sub>	SP	B
----	----------------	----------------	----	---



# Stx1 : 4 subtypes a - d 7-8 variants

Pairwise (OG:100%,UG:0%) (FAST:2,10) Gapcost:0%  
VT1 translated sequences

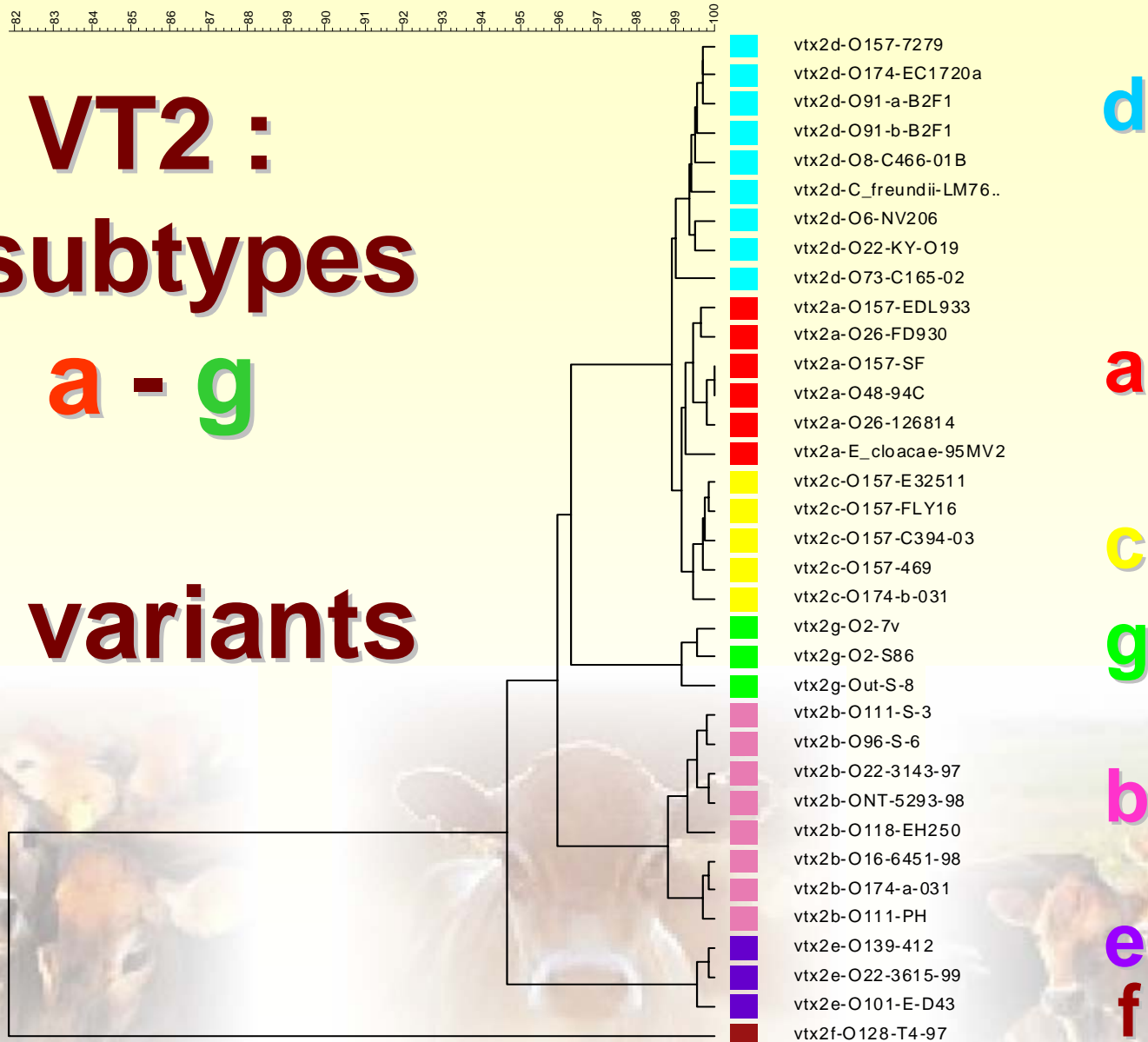




# VT2 : 7 subtypes

a - g

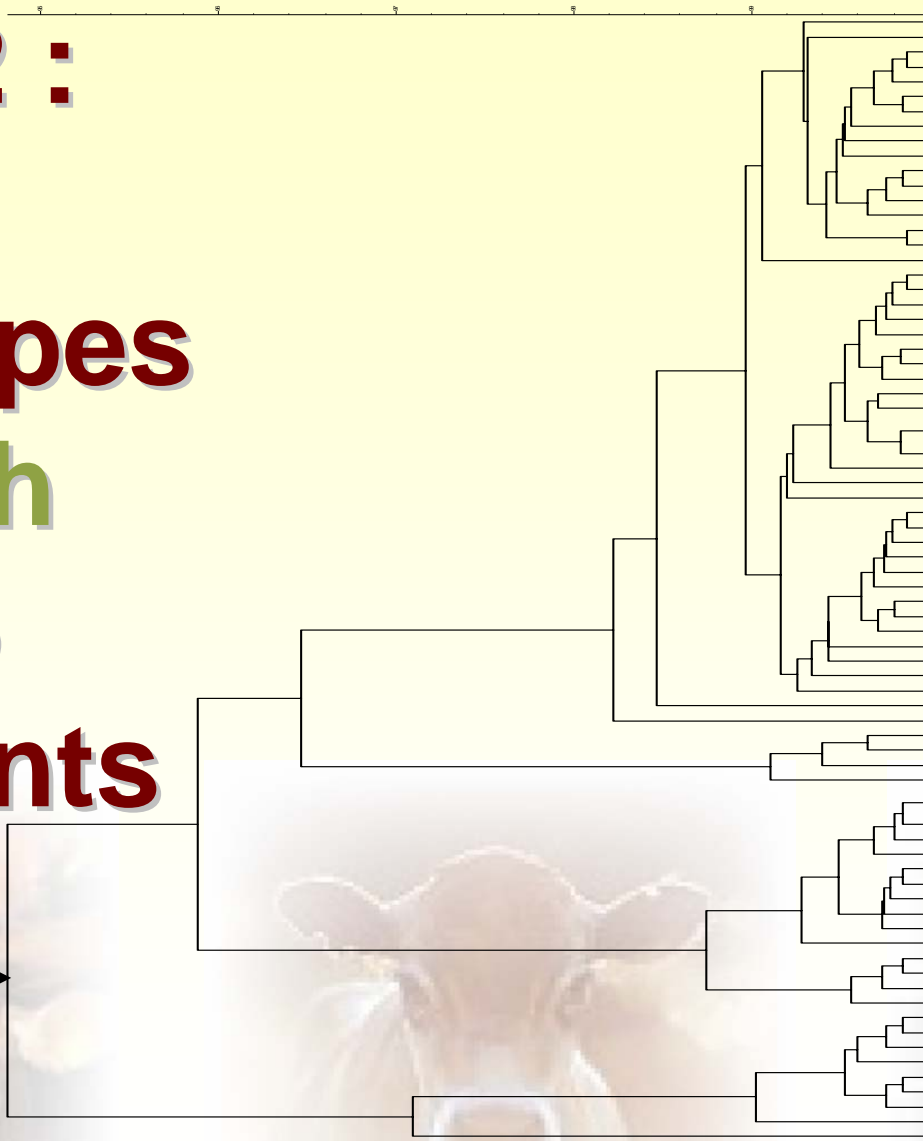
# 36 variants





Pairwise (100-100% (JG:0%)) (FAST2:10) Gaps excluded  
vtx\_TRANSLATED (m in us space)

**VT2 :**  
**8**  
**subtypes**  
**a - h**  
**76**  
**variants**



- vtx2d-C\_freundli-LM 76
- vtx2d-O 55-5905 NEW
- vtx2d-O 157-7279
- vtx2d-O 174-E C 173b
- vtx2c-O 174-E C 1720a
- vtx2d-O 91-B2F1-a
- vtx2d-O NT-EB C 2 75
- vtx2d-O NT-EC 1 671a
- vtx2d-O 91-B2F1-b
- vtx2d-O 8-C 466-01B
- vtx2h-O 2-E C 604a
- vtx2h-O 28-H28
- vtx2h-O 22-KY-O 19
- vtx2h-O 6-NV 206
- vtx2a-O 8-V TB 178
- vtx2a-O 104-G 5506
- vtx2h-O 73-C 165-02
- vtx2a-O 157-ED L933
- vtx2a-O 136-V TB 601
- vtx2a-A\_cinetobacter haemolyticus NEW
- vtx2a-O 111-928-91 NEW
- vtx2a-O 157-93-111 NEW
- vtx2a-O 113-DL-3 NEW
- vtx2a-O NT-IB 581 NEW
- vtx2a-O 157-A 397
- vtx2a-O NT-pEH EC 400
- vtx2a-O NT-EB C 2 17
- vtx2a-O 157-S F-258-98
- vtx2a-O 48-94C
- vtx2a-O 26-126814
- vtx2a-O 26-FD 930
- vtx2a-O NT-EB C 2 10 NEW
- vtx2a-E\_cloacae-95M V 2
- vtx2c-O 157-E 32511
- vtx2c-O 157-FLY 16
- vtx2c-O 171-EBC 287
- vtx2c-O 157-C 394-03
- vtx2c-O 177-06-5121 NEW
- vtx2c-O 157-Y350-1
- vtx2c-O 157-469
- vtx2c-O 157-A 75
- vtx2c-O 157-310
- vtx2c-O 174-031-b
- vtx2c-O 157-G 5101
- vtx2c-O 157-V 20
- vtx2c-O NT-EB C 2 19
- vtx2d-O 103-pVTEC 7
- vtx2c-O NT-pVTEC 9
- vtx2g-O 2-HI-11 NEW
- vtx2g-O 2-S 86
- vtx2g-O 2-7v
- vtx2g-O ut-S 8
- vtx2b-O 40-5293-98
- vtx2b-O 93-S 5
- vtx2b-O 22-3143-97
- vtx2b-O ut-HI-N
- vtx2b-O 8-S 9
- vtx2b-O 96-S-10
- vtx2b-O 96-S-6
- vtx2b-O 111-S-2
- vtx2b-O 96-S-7
- vtx2b-O 111-S-3
- vtx2b-O 118-EH 250
- vtx2b-O 16-6451-98
- vtx2b-O 174-031-a
- vtx2b-O 111-PH
- vtx2b-O NT-IT 606 NEW
- vtx2e-O 139-S 1191
- vtx2e-O 22-3615-99
- vtx2e-O NT-2771
- vtx2e-O 101-E D 42 NEW
- vtx2e-O 101-E D 43 NEW
- vtx2e-O 101-E D 68 NEW
- vtx2e-O 101-E D 53 NEW
- vtx2e-O 26-R 107 NEW
- vtx2e-O 7-FHI-1106-1092
- vtx2f-O 128-T4-97 **f**

**d**

**h**

**a**

**c**

**g**

**b**

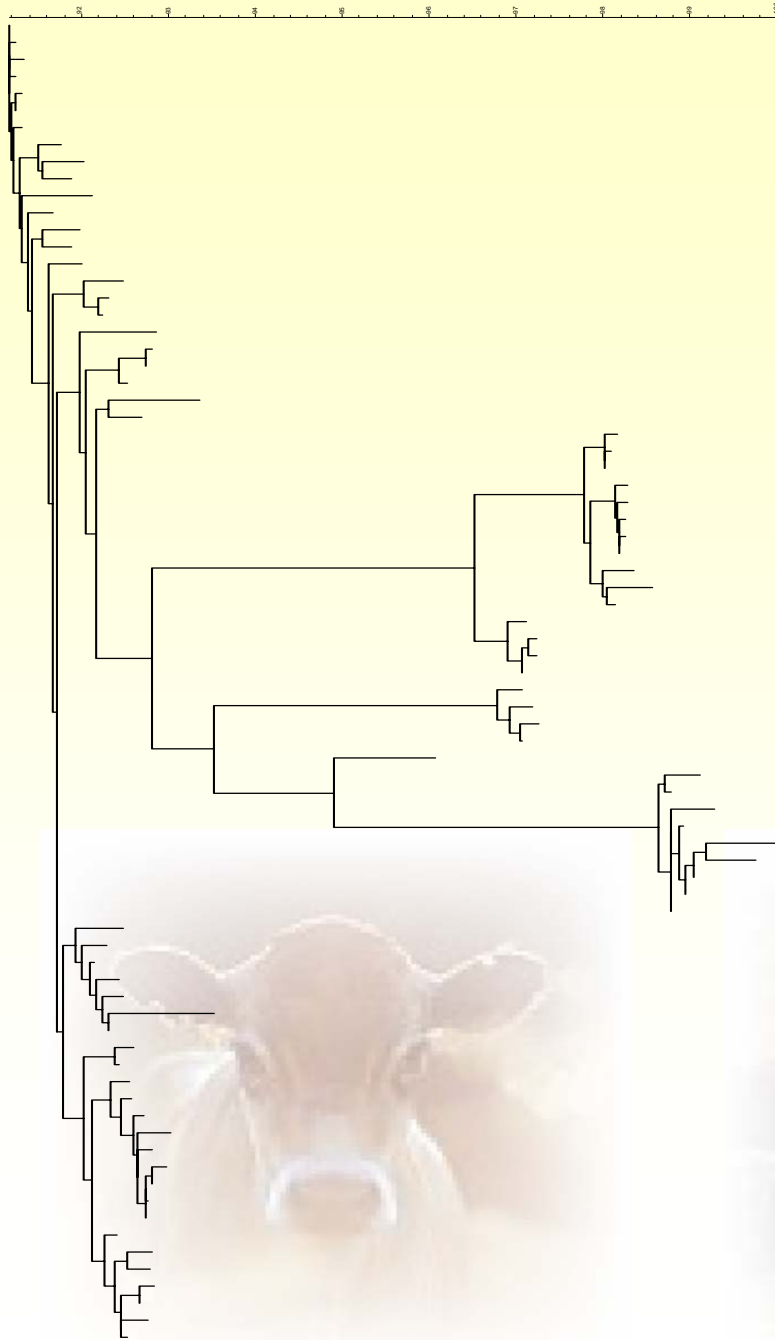
**e**



# *vtx2* : 8 sub- types a - h

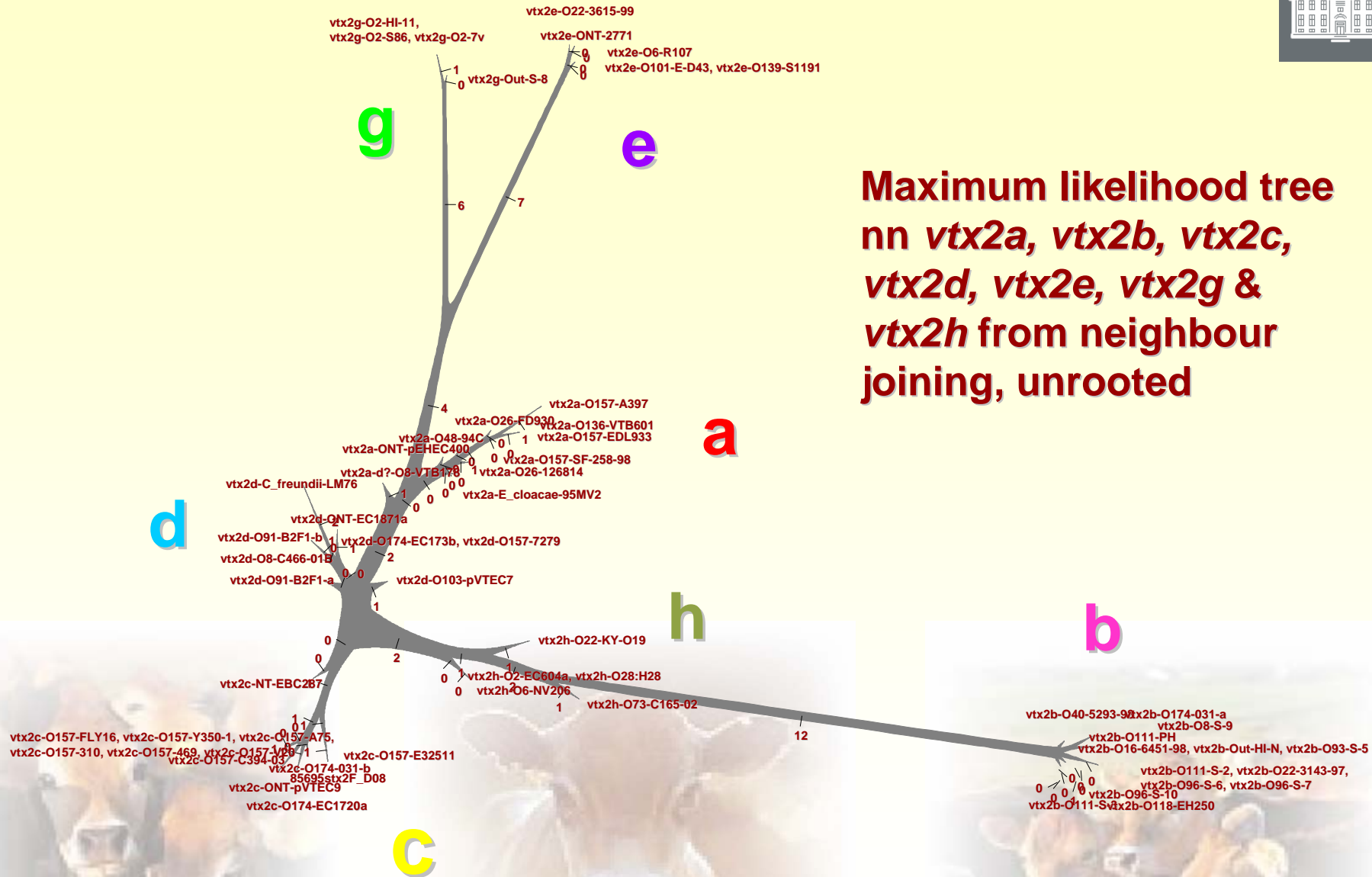
# 78 variants

GenBank sequences



- Vtx2c-O157-FLY16
- Vtx2c-O157-C394-03
- Vtx2c-O157-V20
- Vtx2c-O157-Y350-1
- Vtx2c-O157-A75
- Vtx2c-O157-310
- Vtx2c-O157-469
- Vtx2c-O174-EC172
- Vtx2c-ONT-EBC219
- Vtx2c-O177-06-5121
- Vtx2c-ONT-pVTEC9
- Vtx2c-O157-E32511
- Vtx2c-O157-G5101
- Vtx2c-O174-031-b
- Vtx2c-O171-EB C287
- Vtx2c-ONT-EBC289
- Vtx2d-ONT-EBC275
- Vtx2d-O91-B2F1-a
- Vtx2d-O55-5905
- Vtx2h-O6-NV206
- Vtx2h-O2-EC604a
- Vtx2h-O28:H28
- Vtx2h-O73-C165-0
- Vtx2h-O22-KY-O19
- Vtx2b-O8-S-9
- Vtx2b-OuI-HI-N
- Vtx2b-O93-S-5
- Vtx2b-O111-S-3
- Vtx2b-O96-S-10
- Vtx2b-O111-S-2
- Vtx2b-O96-S-7
- Vtx2b-O96-S-6
- Vtx2b-O22-3143-9
- Vtx2b-O118-EH250
- Vtx2b-O40-5293-98
- Vtx2b-ONT-I7606
- Vtx2b-O111-PH
- Vtx2b-O174-031-a
- Vtx2b-O16-6451-98
- Vtx2g-OuI-S-8
- Vtx2g-O2-7v
- Vtx2g-O2-HI-11
- Vtx2g-O2-S86
- Vtx2e-O?-FH1-106-1092
- Vtx2e-O101-E-D42
- Vtx2e-O22-3615-99
- Vtx2e-O26-R107
- Vtx2e-O101-E-D43
- Vtx2e-O121-NP962
- Vtx2e-ONT-2771
- Vtx2e-O101-E-D53
- Vtx2e-O101-E-D68
- Vtx2e-O139-S1191
- Vtx2d-O103-pVTEC7
- Vtx2d-ONT-EC1871a
- Vtx2d-O174-EC173b
- Vtx2d-O8-C466-01B
- Vtx2d-O91-B2F1-b
- Vtx2d-C\_freundii-LM76
- Vtx2d-O157-7279
- Vtx2a-O104-G5506
- Vtx2a-O8-VT.B.178
- Vtx2a-O157-A397
- Vtx2a-ONT-I6581
- Vtx2a-O136-VTB601
- Vtx2a-ONT-EBC210
- Vtx2a-O26-FD930
- Vtx2a-Acinetobacter haemolyticus
- Vtx2a-O157-93-111
- Vtx2a-O111-928-91
- Vtx2a-O157-EDL933
- Vtx2a-O113-CL-3
- Vtx2a-O48-94C
- Vtx2a-ONT-EBC217
- Vtx2a-O26-126814
- Vtx2a-O157-SF-258-98
- Vtx2a-E\_cloacae-95MV2
- Vtx2a-ONT-pEHEC400





Maximum likelihood tree  
nn *vtx2a*, *vtx2b*, *vtx2c*,  
*vtx2d*, *vtx2e*, *vtx2g* &  
*vtx2h* from neighbour  
joining, unrooted







**Maximum likelihood tree of  
*vtx2a*, *vtx2c*, *vtx2d* & *vtx2h*  
from neighbour joining,  
unrooted**



# "Semi" Draft Proposal

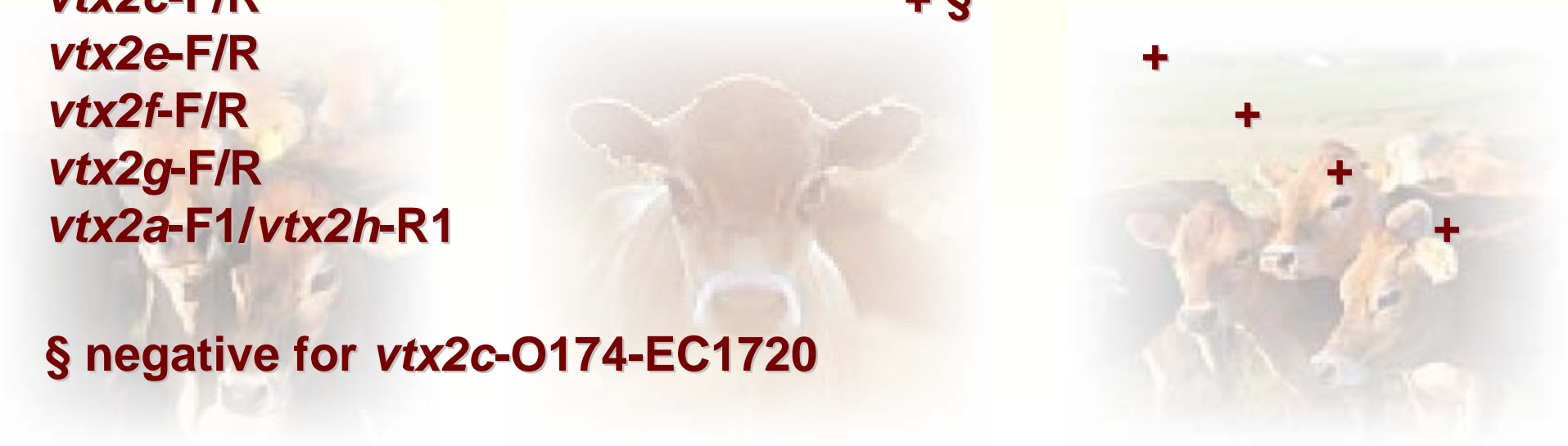
Primer pairs	Subtype <i>vtx2a</i>	<i>b</i>	<i>c</i>	<i>d</i>	<i>e</i>	<i>f</i>	<i>g</i>
F4 / R1	+	+	+	+			+
F4f / R1e-f					+	+	
GK3/GK4	+		+	+			+
Stx2-a/Stx2-b	2/6!!						
Stx2c-a/Stx2c-b			+	2/9			
VT2cm/VT2f		+					
128-1/128-2						+	
209F /781R							+



# Prototype *vtx2* specific PCR

Primer pairs	Subtype	<i>vtx2</i>	a	b	c	d	e	f	g	h
F4 / R1			+	+	+	+			+	+
F4f / R1e-f							+	+		
<i>vtx2a</i> -F1/R1/R2			+							
<i>vtx2b</i> -F/R				+						
<i>vtx2cd</i> -F/R					+	+				
<i>vtx2c</i> -F/R					+	§				
<i>vtx2e</i> -F/R							+			
<i>vtx2f</i> -F/R								+		
<i>vtx2g</i> -F/R									+	
<i>vtx2a</i> -F1/ <i>vtx2h</i> -R1										+

§ negative for *vtx2c*-O174-EC1720





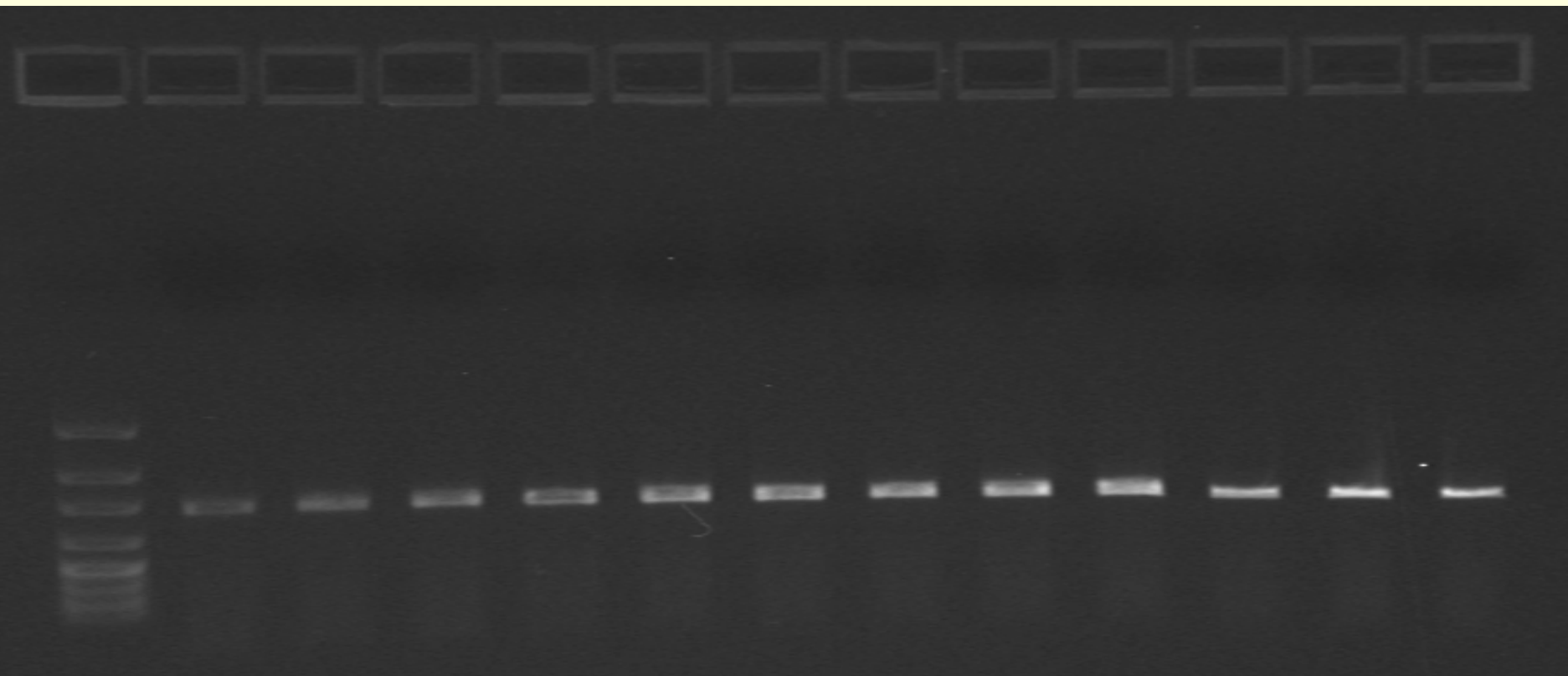
**Primers: *vtx2a*-F1/*vtx2h*-R1**

**Gradient PCR as of Wednesday 50-62°C**

*vtx2h* using variant *vtx2h*-O73-C165-02

°C 50 51.1 52.2 53.3 54.4 55.5 56.6 57.7 58.9 60 61 62

**M**







# Future testing

## Association between *eae* and VT subtype in 503 Danish VTEC strains

