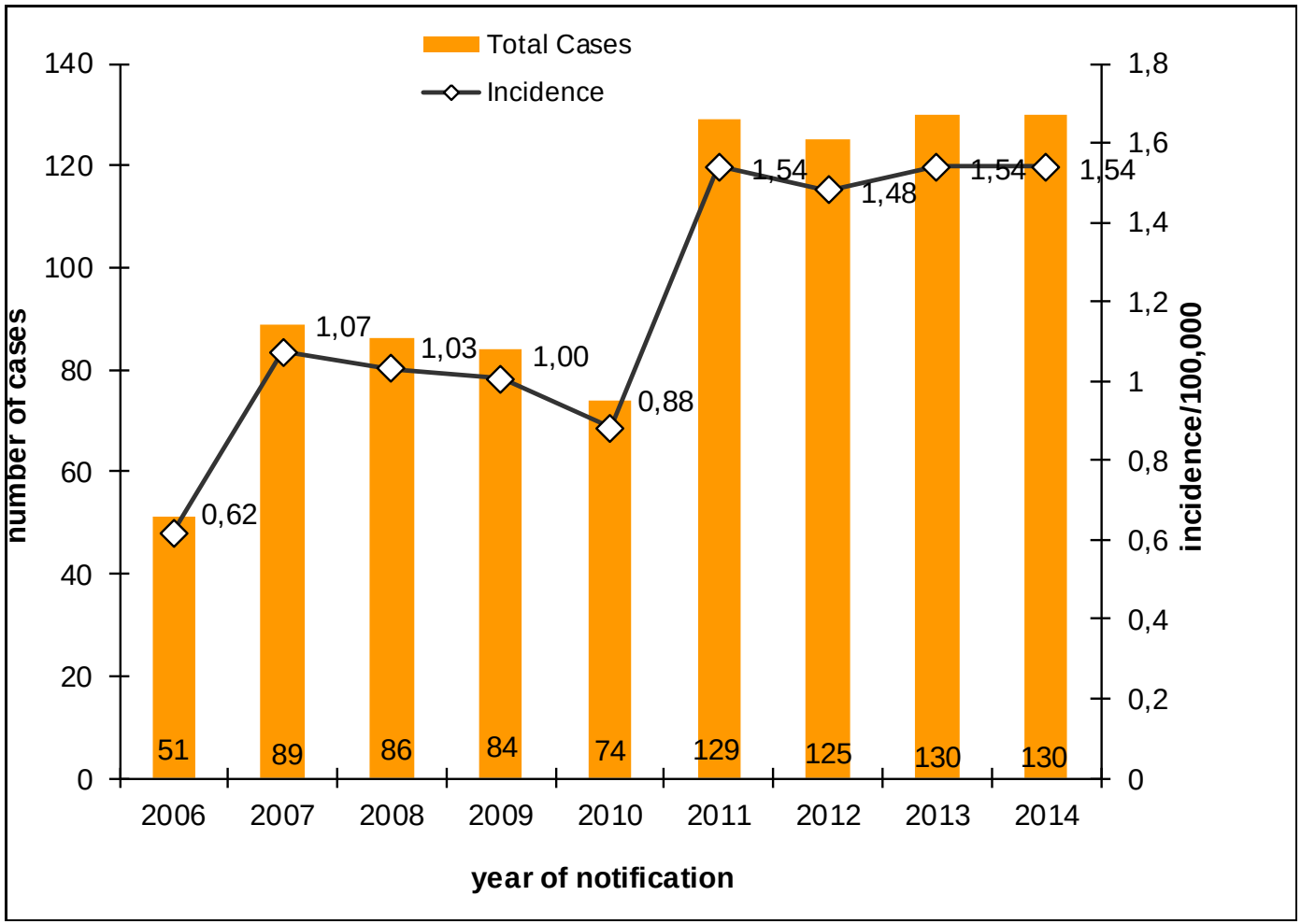
NGS analysis of VTEC O26:H11/HNM isolated in Austria 2009-2014

Sabine Schlager
AGES, IMED-Graz

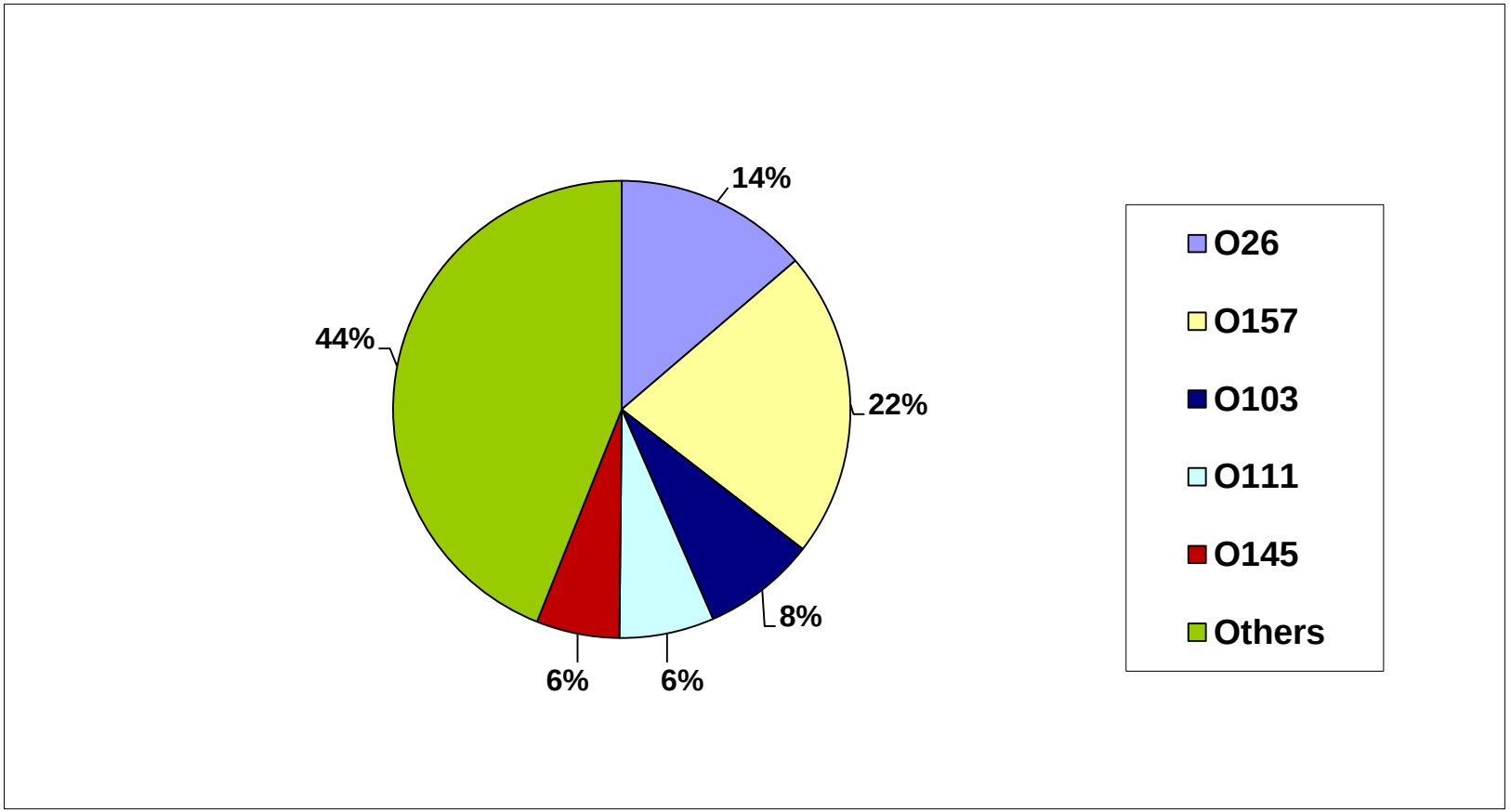
10.11.2016

Incidence of VTEC cases in Austria 2006 - 2014

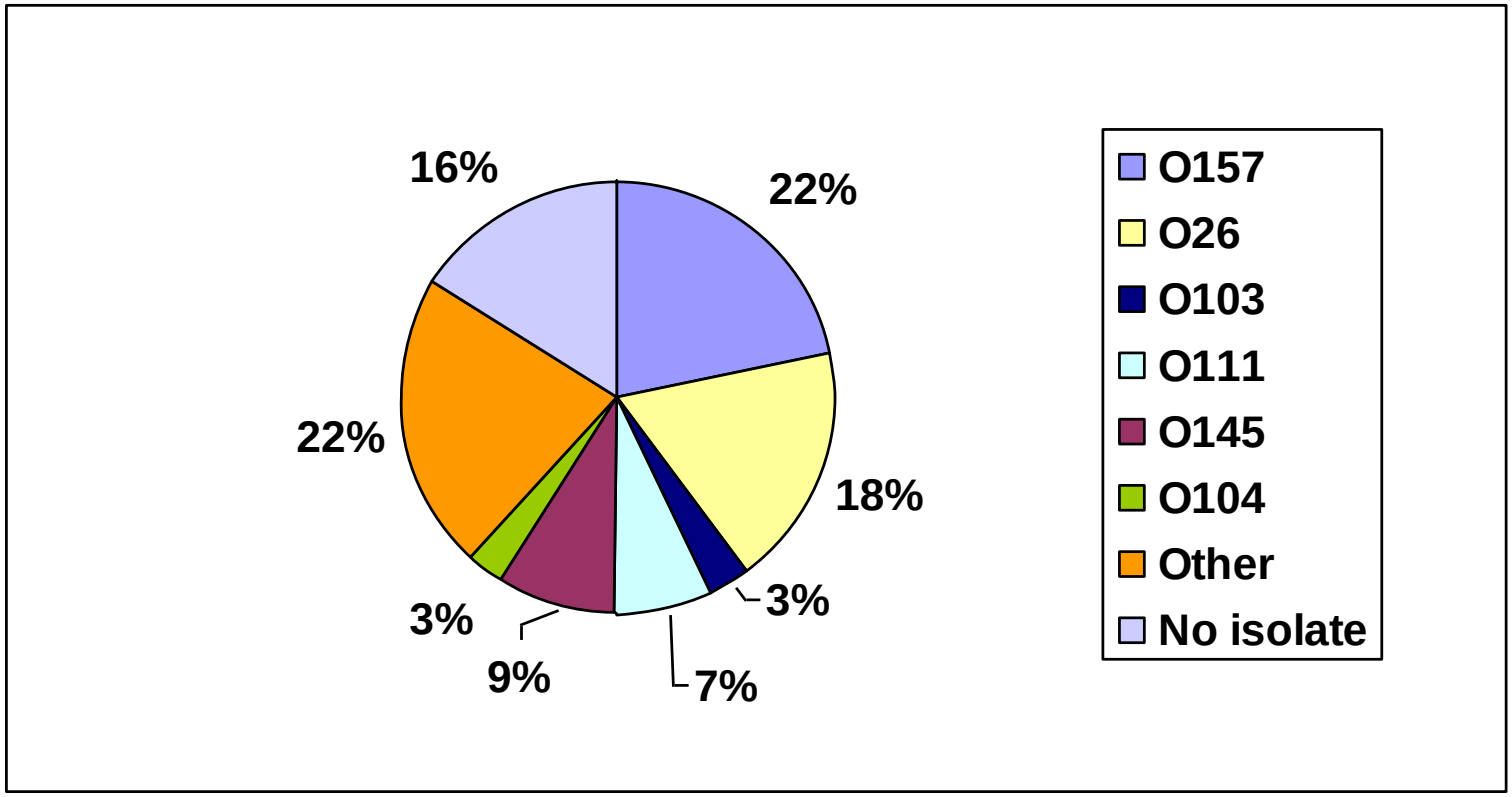


BMG notified cases (2006-2008), EMS data (2009-2014), NRC EHEC-Innsbruck (2006-2009) and NRC VTEC-AGES, Graz (2010-2014)

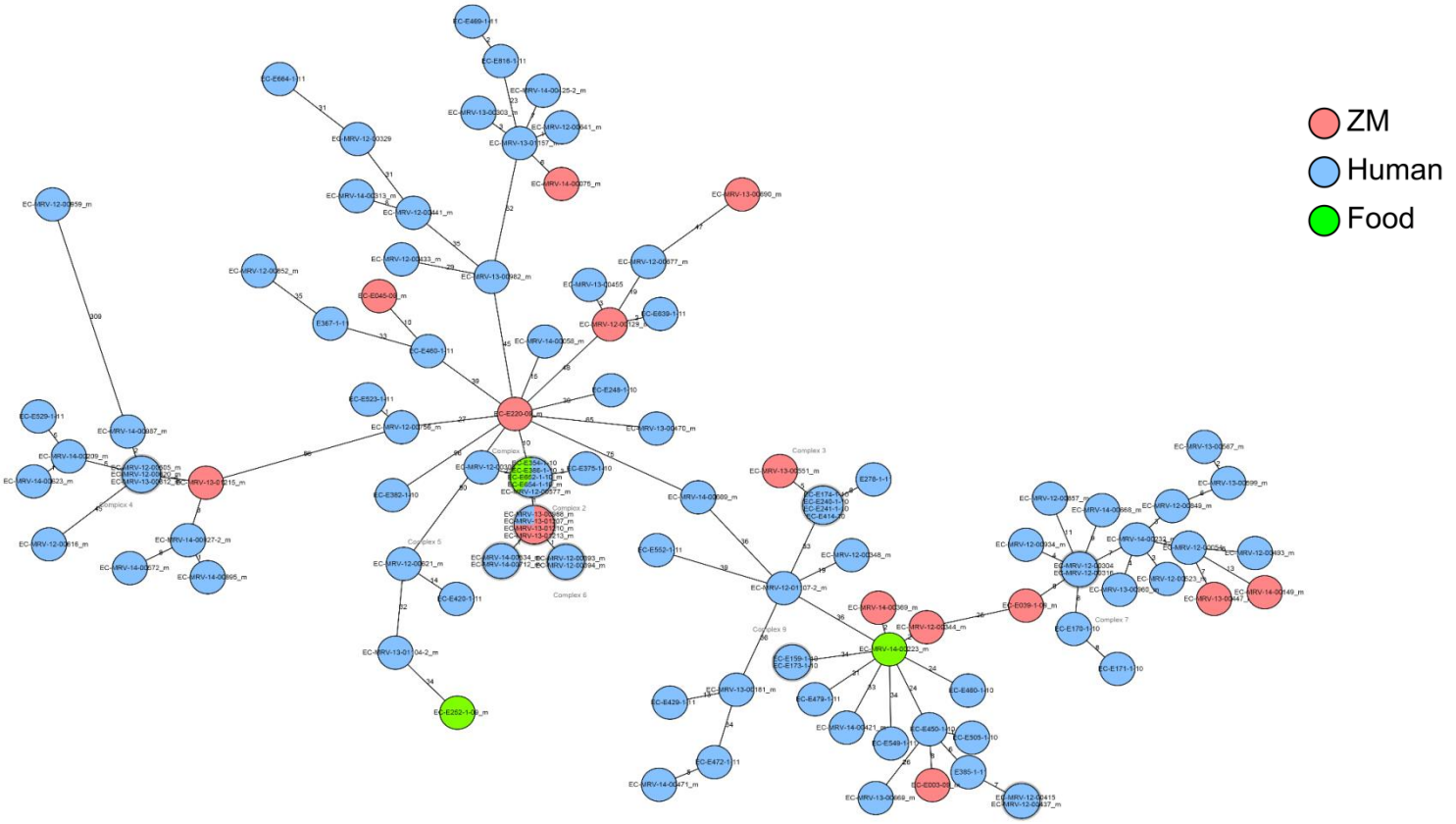
O-serogroups from human VTEC isolates, Austria 2010-2014 (N=612)



VTEC O-serogroups (HUS cases), Austria 2010-2014 (N=68)

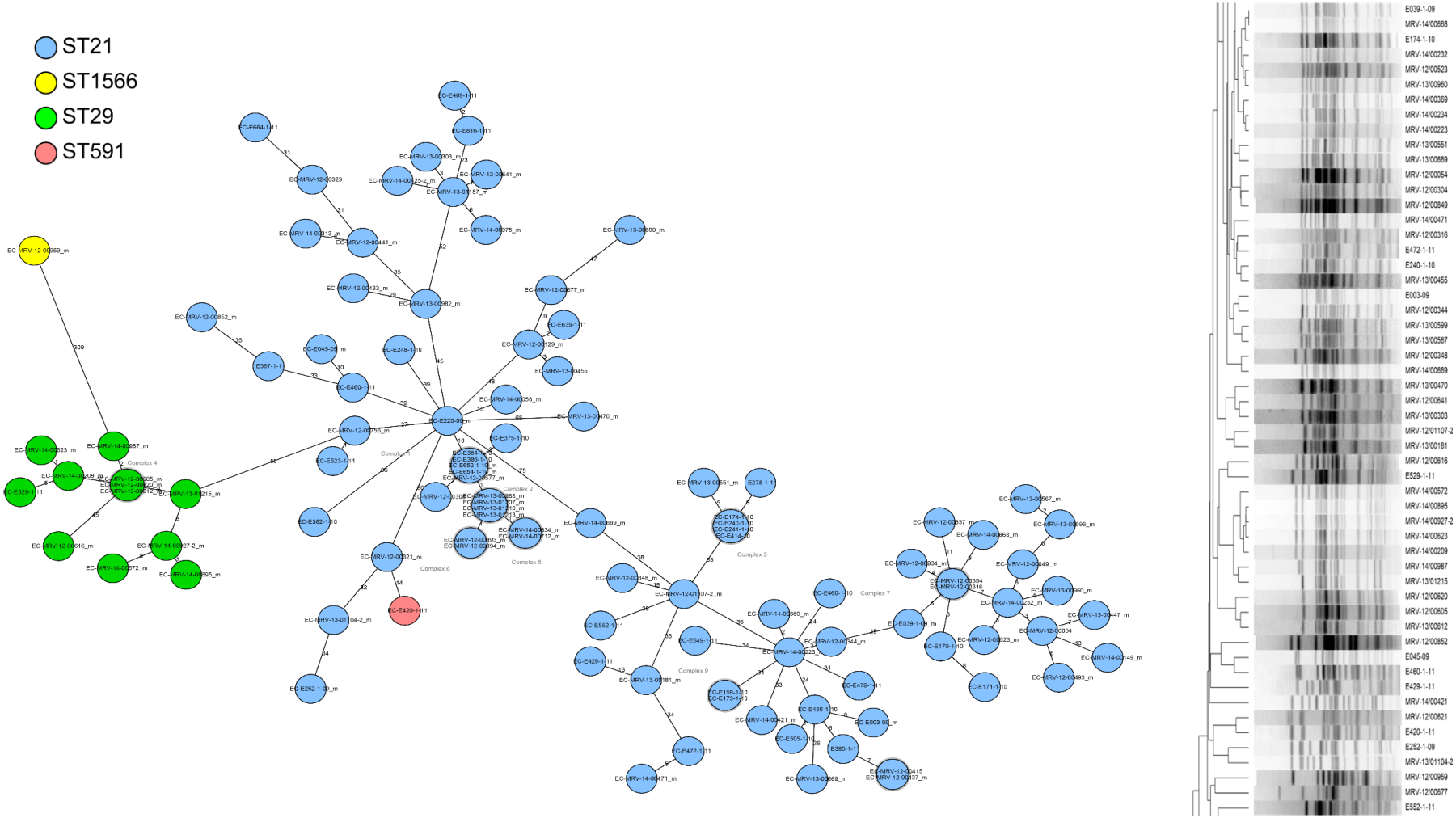


E. coli O26:H11/HNM isolates from human, animal and food, Austria 2009-2014 (N=109)



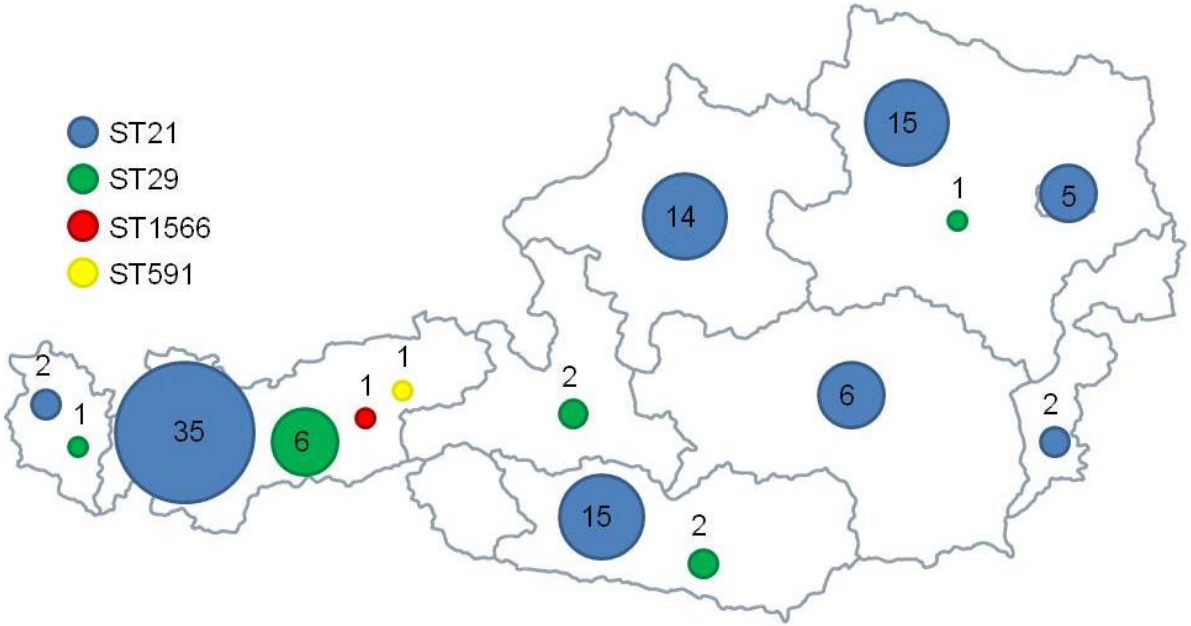
Minimum spanning tree (cgMLST) of the distribution of *E. coli* O26 isolates of different origins. Eighty-nine (81.65%) samples of the collection were of human origin, 4 (3.67%) were isolated from food and 16 (14.68%) were obtained from animals (cattle:N=14; sheep:N=2).

E. coli O26:H11/HNM isolates – MLST Austria 2009-2014 (N=109)



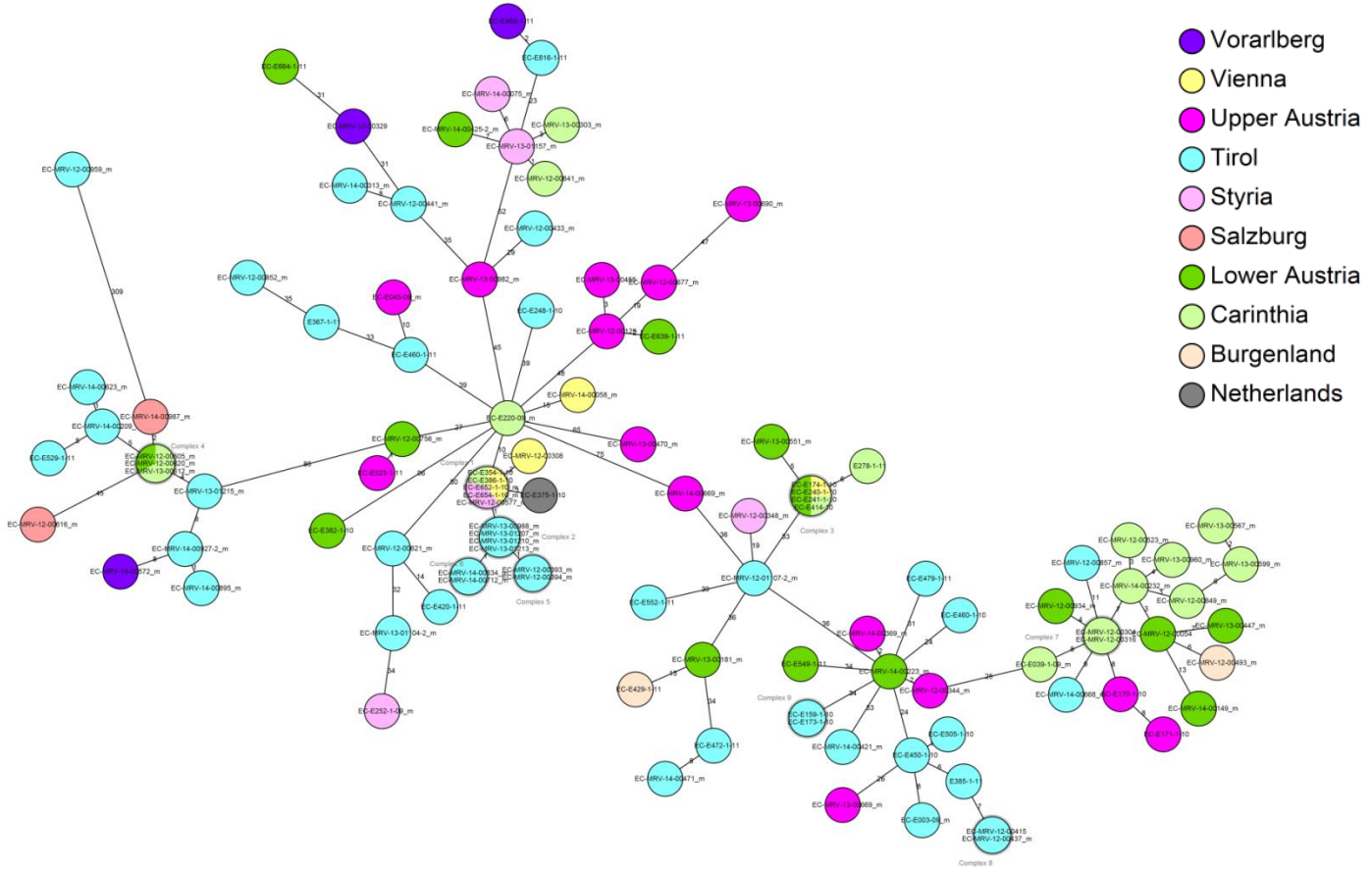
Minimum spanning tree of MLST distribution in Austria. Twelve (11.01%) of 109 *E.coli* O26:H11/HNM belonged to ST29. The remaining samples divided into ST21 (n=95), ST591 (n=1) and ST1566 (n=1).

E. coli O26:H11/HNM isolates – MLST geographical distribution in Austria 2009-2014 (N=109)



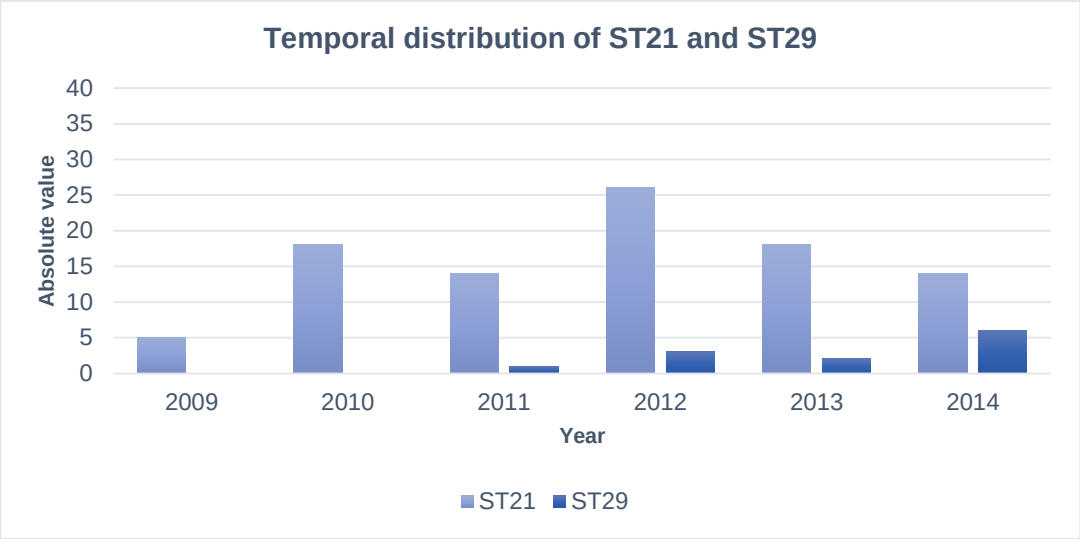
Geographical distribution of *E. coli* O26 strains belonging to ST21, ST29, ST1566 and ST591 in Austrian provinces

E. coli O26:H11/HNM isolates – cgMLST geographical distribution in Austria 2009-2014 (N=109)



Minimum spanning tree (cgMLST) of the prevalence of *E. coli* O26 strains in the Austrians provinces (Vorarlberg (N=3), Tirol (N=43), Salzburg (N=2), Carinthia (N=17), Lower Austria (N=16), Upper Austria (N=14), Vienna (N=5), Styria (N=6) and Burgenland (N=2). One isolate was originated from a Dutch-born person who got ill in Austria (N=1).

Temporal distribution of *E. coli* O26 ST21 vs. ST29 Austria 2009-2014 (N=109)

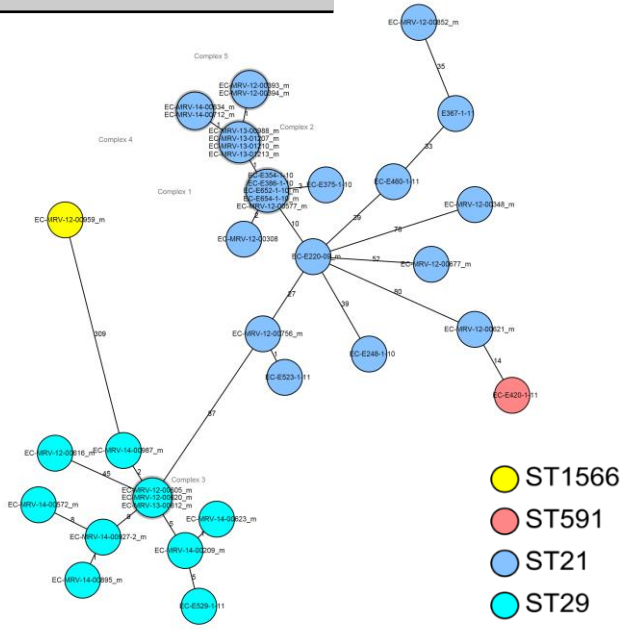


ST (%)	2009	2010	2011	2012	2013	2014
ST21 (%)	5 (100)	18 (100)	14 (87.5)	26 (86.67)	18 (90)	14 (70)
ST29 (%)	0	0	1 (6.25)	3 (10)	2 (10)	6 (30)
ST1566 (%)	0	0	0	1 (3.33)	0	0
ST591 (%)	0	0	1 (6.25)	0	0	0
Total	5	18	16	30	20	20

E. coli O26:H11/HNM – *stx* subtypes Austria 2009-2014 (N=109)

Genotype	ST21	ST29	ST1566	ST591	Strains total
stx1a	61	-	-	-	61
stx1c	1	-	-	-	1
stx2a	25	11	1	1	38
stx2f	1	-	-	-	1
stx1a* + *stx2a	5	-	-	-	5
***stx* negative**	2	1	-	-	3
Strains total	95	12	1	1	109

E. coli O26:H11/HNM strains with different *stx* subtypes based on MLST



NRZ *E. coli* / Schlager

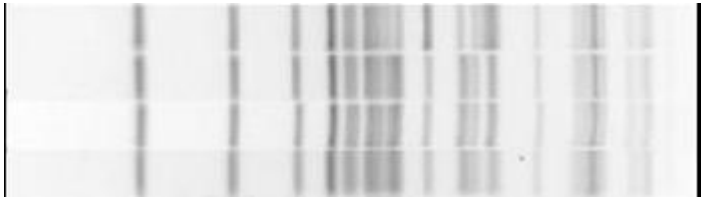
human *E. coli* O26:H11/HNM – clinical outcome Austria 2009-2014 (N=89)

Genotype	Isolate	HUS (n=12 (%))	without HUS (n=77 (%))	Chi-Square	P Value
stx1a	51	1 (1.96)	50 (98.04)		
stx2a (all ST)	32	10 (31.25)	22 (68.75)	14.495[1]	P<0.001
stx2a (ST21)		8 (42.11)	11 (57.89)		
stx2a (ST29)		2 (18.18)	9 (81.82)		
stx2f	1	1 (100)	-	-	-
stx1a+stx2a	4	-	4 (100)	-	-
***stx* negative**	1	-	1 (100)	-	-
Strains total	89	12 (13.48)	77 (86.52)	-	-

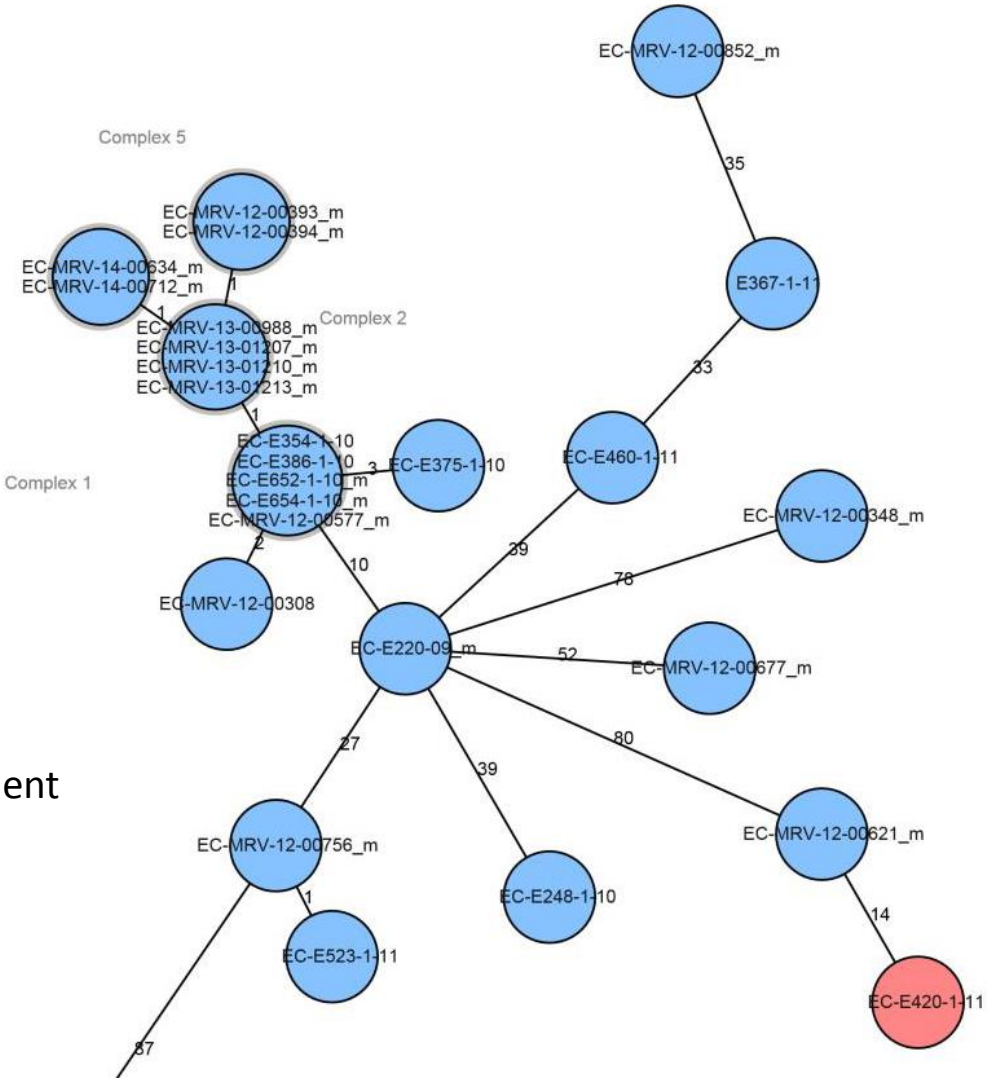
Distribution between *stx* subtypes of *E. coli* O26:H11/HNM isolates and clinical outcomes of infection

[1] Sample size: n=83

Outbreak investigation: VTEC O26:HNM ST21 Austria 2013



cattle 1
cattle 2
cattle 3
indexpatient



NRZ *E. coli* / Schlager

Thank you for your attention!

National Reference Center and National Reference Laboratory for *Escherichia coli* including Verotoxin producing *E.coli,* AGES, IMED Graz

Sabine Schlager
Sabine Neubauer
Nadine Hiden
Birgit Moik
Iris Strutz

Departement of Food Microbiology, AGES, IMED Graz

Claudia Schlagenhaufen

Departement of Veterinary Microbiology, AGES, IMED Graz

Heimo Lassnig

Core Unit Molecular Biology, AGES, IMED Graz

Claudia Mikula

E. coli O26:H11/HNM-Isolate – plasmidkodierte Virulenzfaktoren, Österreich 2009-2014 (N=109)

espP / *etpD* / *ehxA* / *katP*

ST	+/-/+/+	-/+/+/-	-/-/+/-	-/-/+/+	-/-/-/-	Strains total
ST21	81	0	0	12	2	95
ST29	0	11	1	0	0	12
ST1566	0	0	0	0	1	1
ST591	1	0	0	0	0	1
Strains total	82	11	1	12	3	109

Plasmid virulence gene profile of *E. coli* O26:H11/HNM belonging to ST21, ST29, ST1566 and ST591