Human Associated *E. coli* Clonal Complexes CC73, CC95, CC131

The Talk:

- Common *E. coli* lineages in humans
- Temporal stability of lineages
- Lineage substructure and temporal variability
- Gene content differences
- Host distribution of the clonal complexes
- Poultry as a source of ExPEC strains

Human Associated Lineages

- MLST reveals low levels of diversity in humans
- Typically a B2 isolate represents 1 of 9 STs
  - 7 studies, 3 countries

B2	131	73	95	127	141	144	12	14	372	UA
N=1061	39%	25%	15%	5%	2%	< 1%	4%	2%	< 1%	7%

- ST69 represents ≈ 40 % of D isolates
- ST10 perhaps single most abundant ST
  - poorly defined – encompasses ‘most’ yja+ A strains

Clonal Complexes in Canberra 2002 vs 2014

- Canberra Hospital Microbiology Lab
  - basically same methods and people
- Sequential samples from faeces, urine and blood
- 2002 faecal, urine and blood isolates (650+ hosts)
- 2014 faecal, urine and blood isolates (750+ hosts)

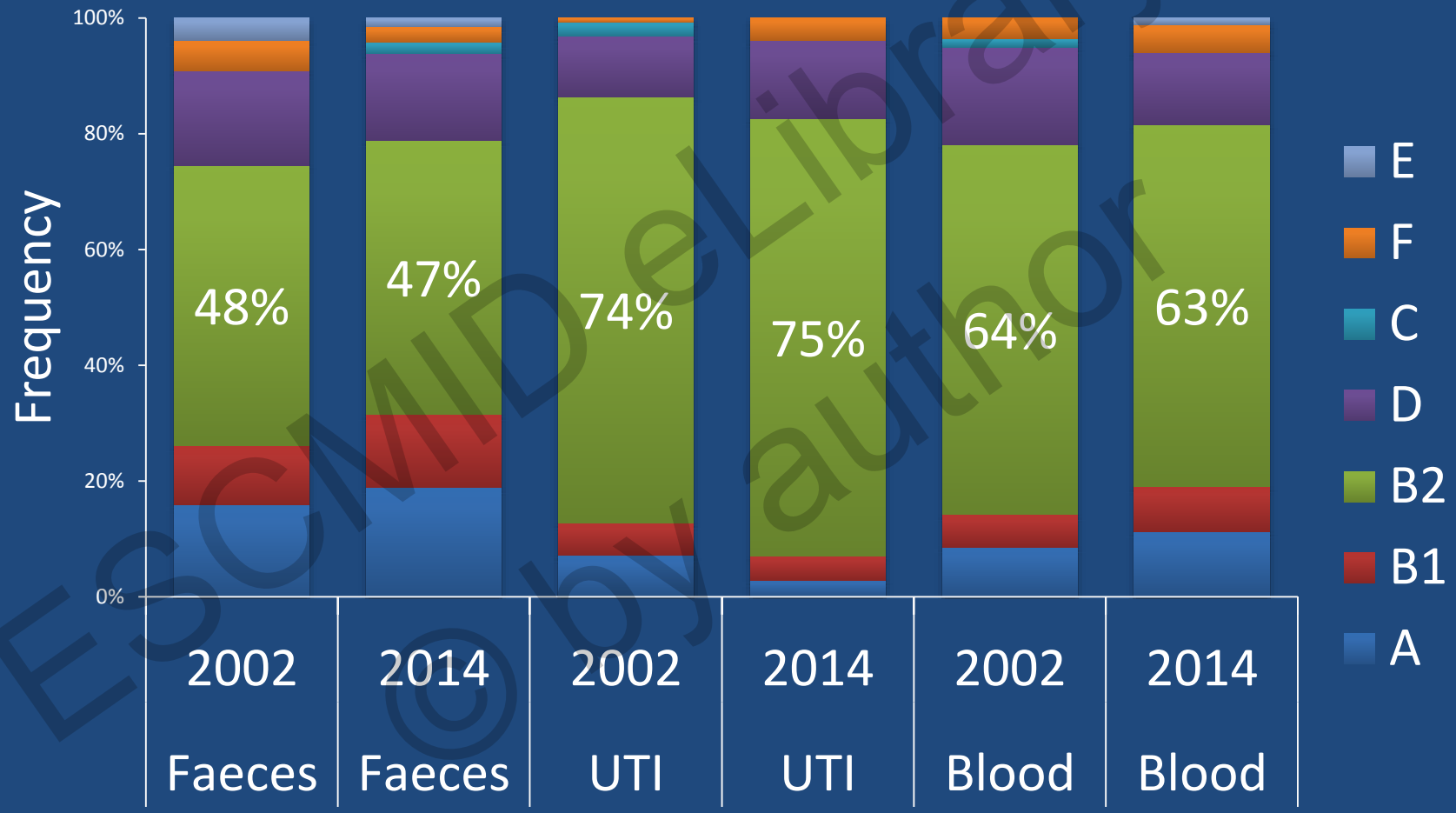
Clonal Complexes in the UK 2001 - 2012

- Bacteraemia Resistance Surveillance Programme
  - 11 hospitals
  - 2001-2011
  - 1st 10 isolates of the year
  - 1094 isolates

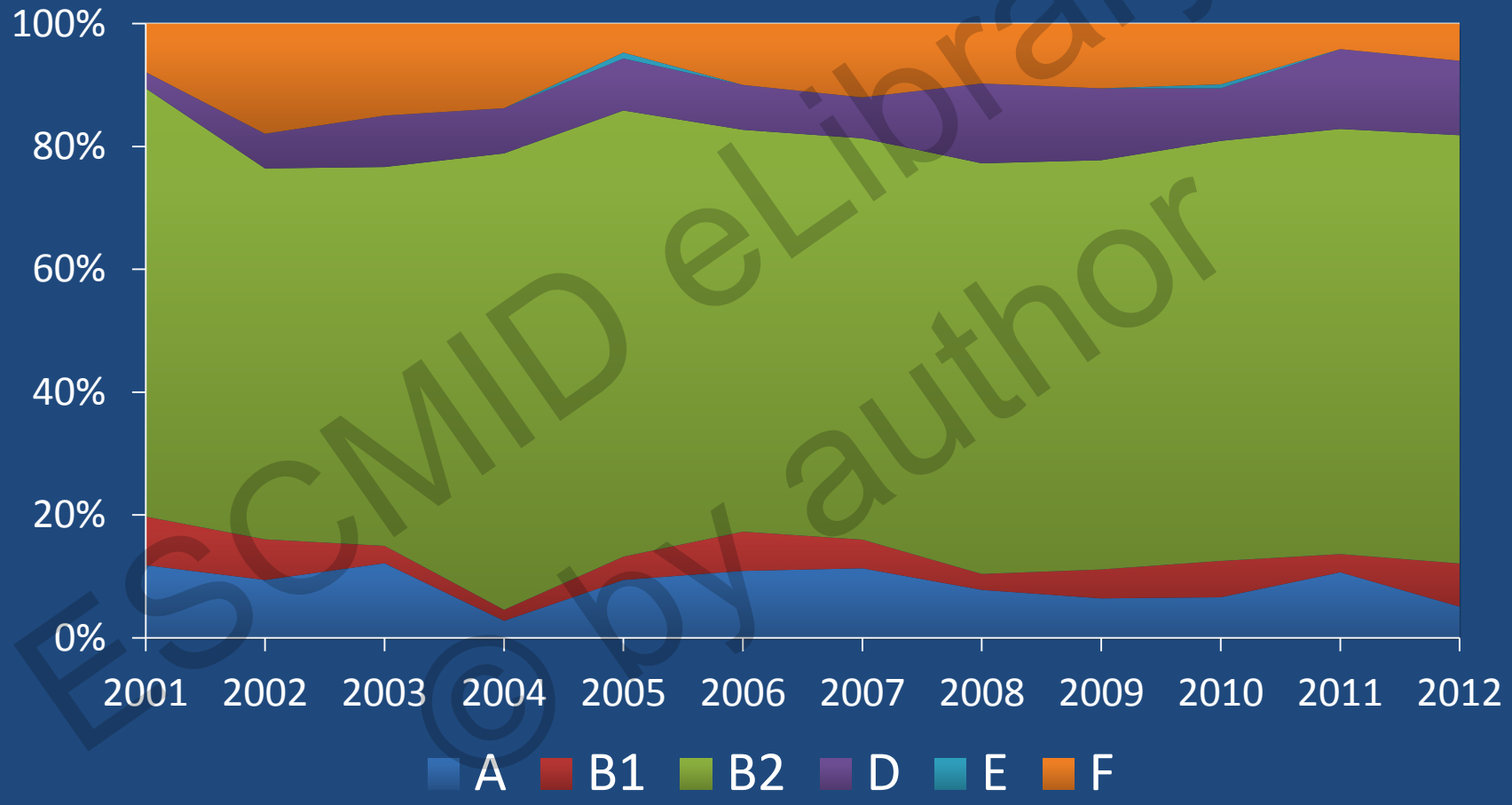
- Diagnostic laboratory at the Cambridge University Hospitals
  - 2006-2012
  - Every 3rd isolate
  - 415 isolates

- Teemu Kallonen, Hayley J. Brodrick, Simon R. Harris, Jukka Corander, Nicholas M. Brown, Veronique Martin, Sharon J. Peacock, and Julian Parkhill Systematic longitudinal survey of invasive *Escherichia coli* in England demonstrates a stable population structure only transiently disturbed by the emergence of ST131 Genome Research 2017.

Phylogroup Abundance - Canberra

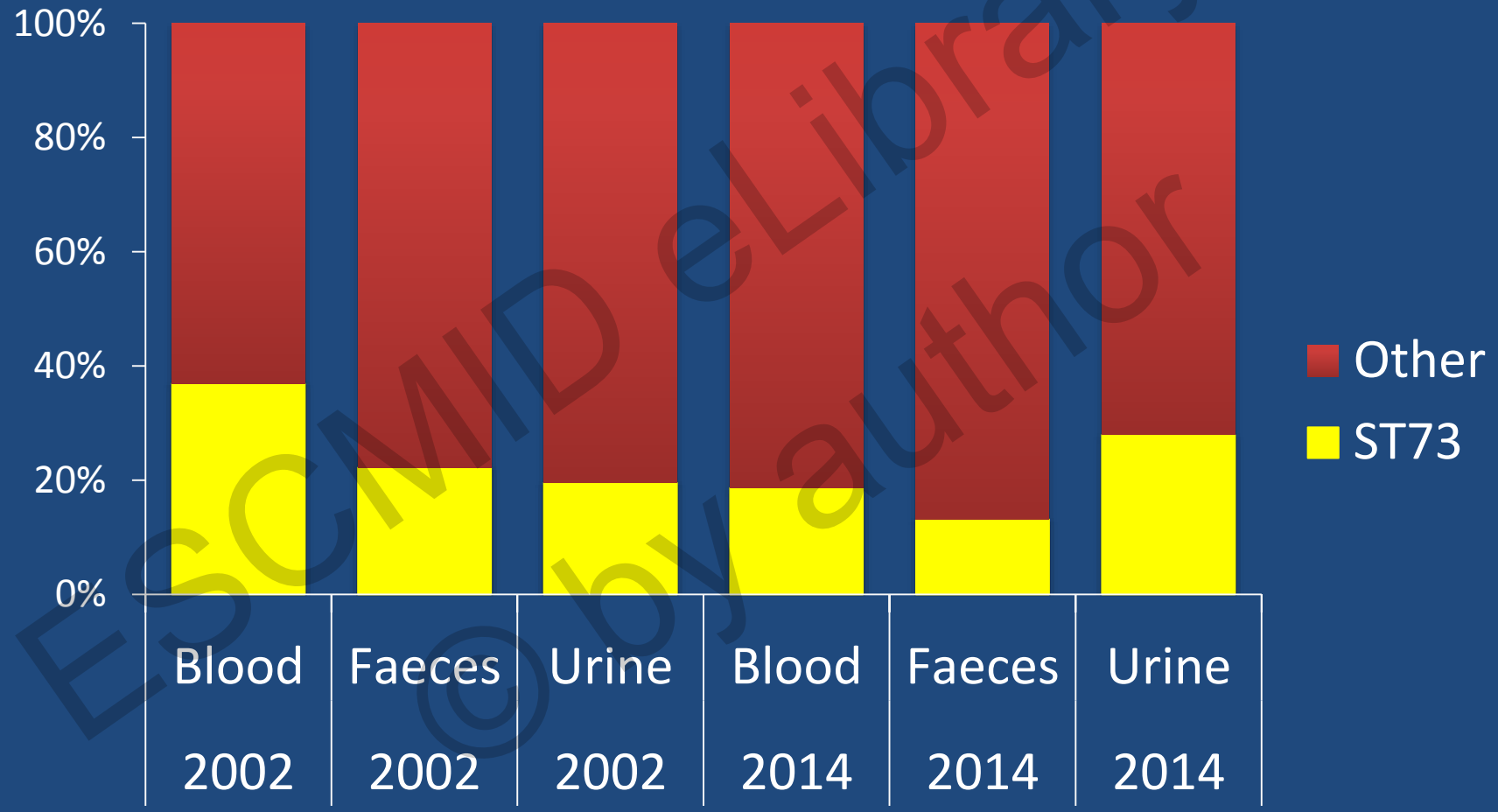


Phylogroup Abundance - UK



CC73 - Canberra

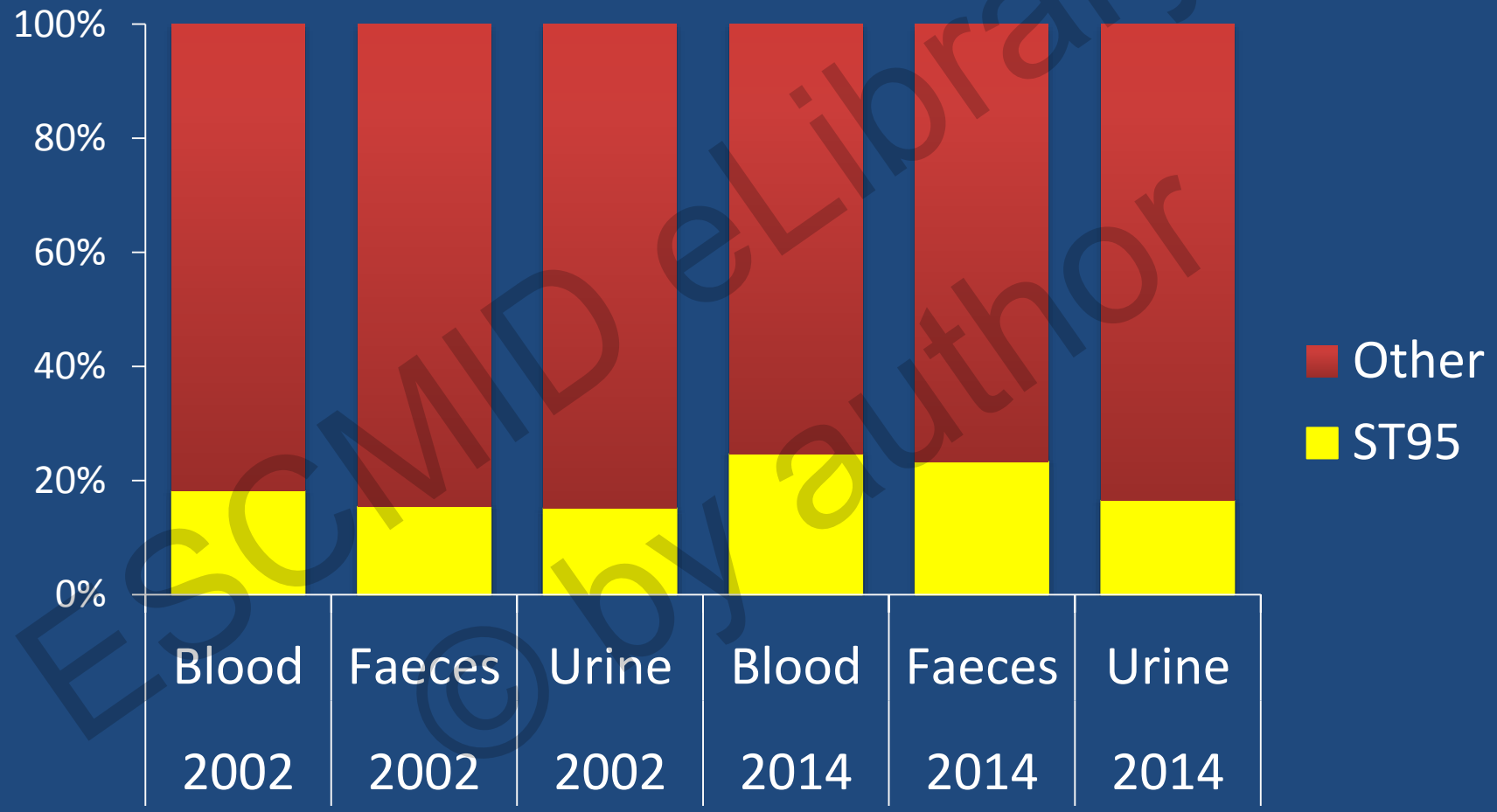
2002:13.2% 2014:10.5%



CC95 - Canberra

2002:8.2%

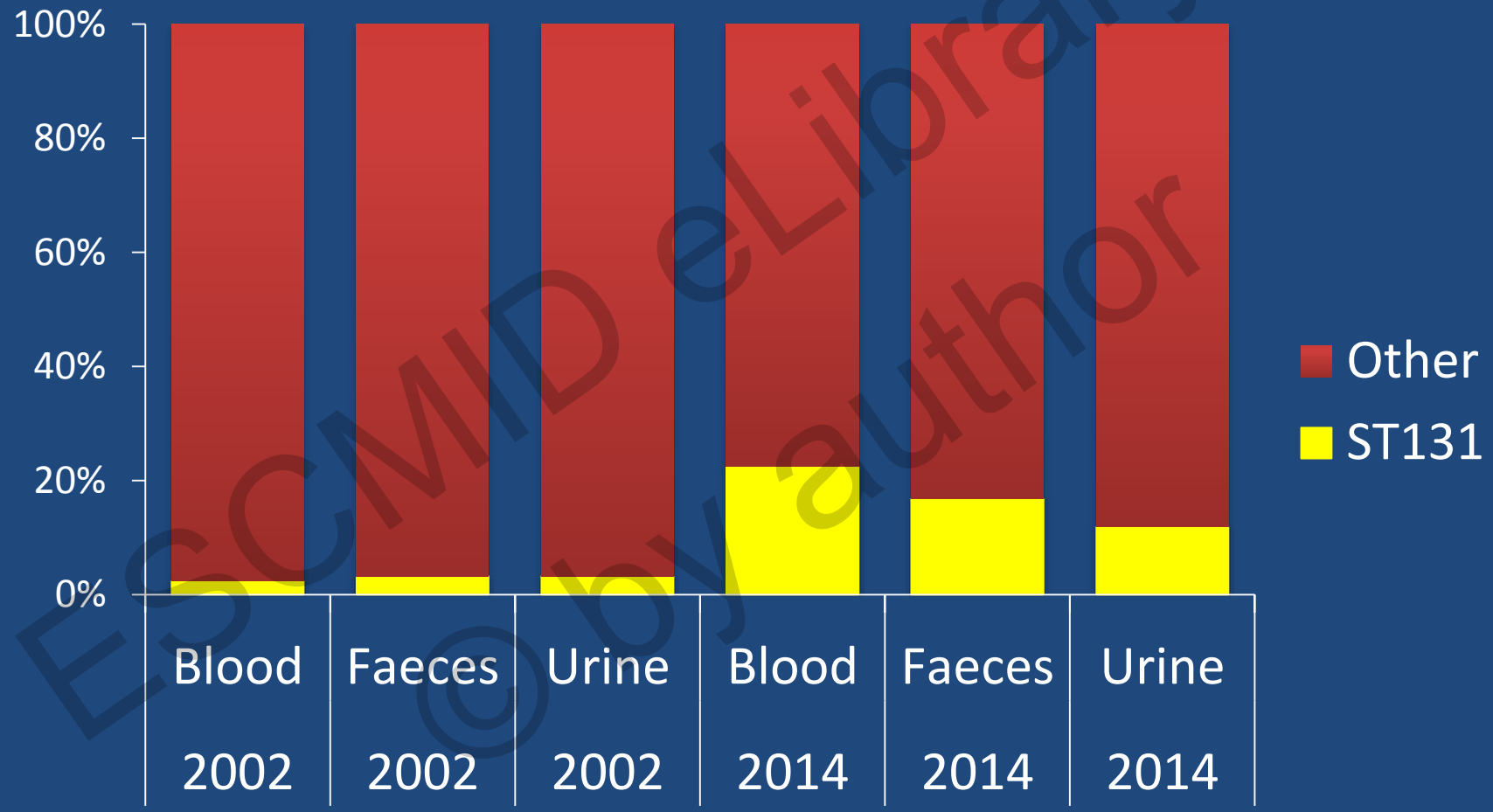
2014:10.5%



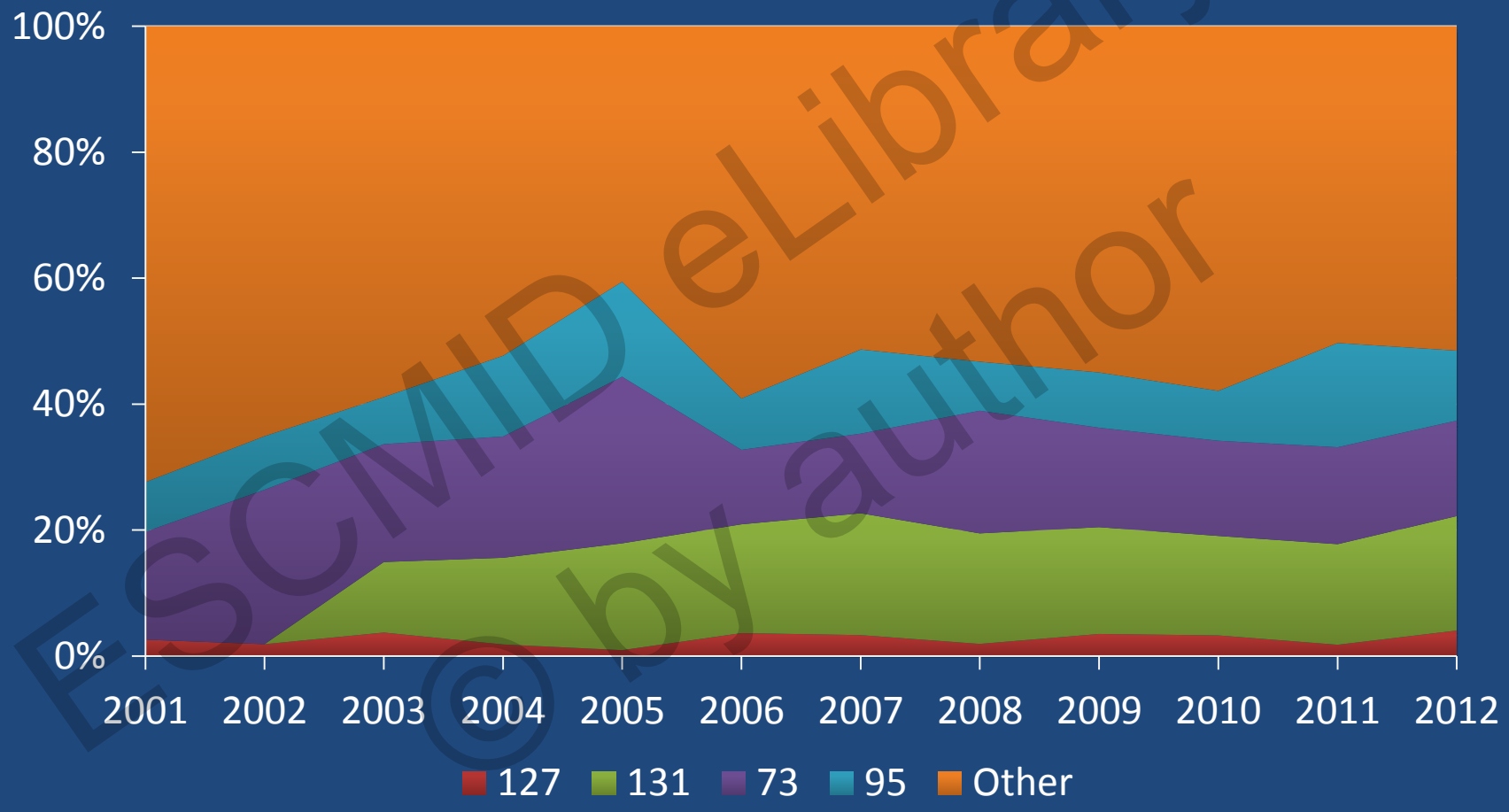
CC131- Canberra

2002:1.5%

2014:8.3%



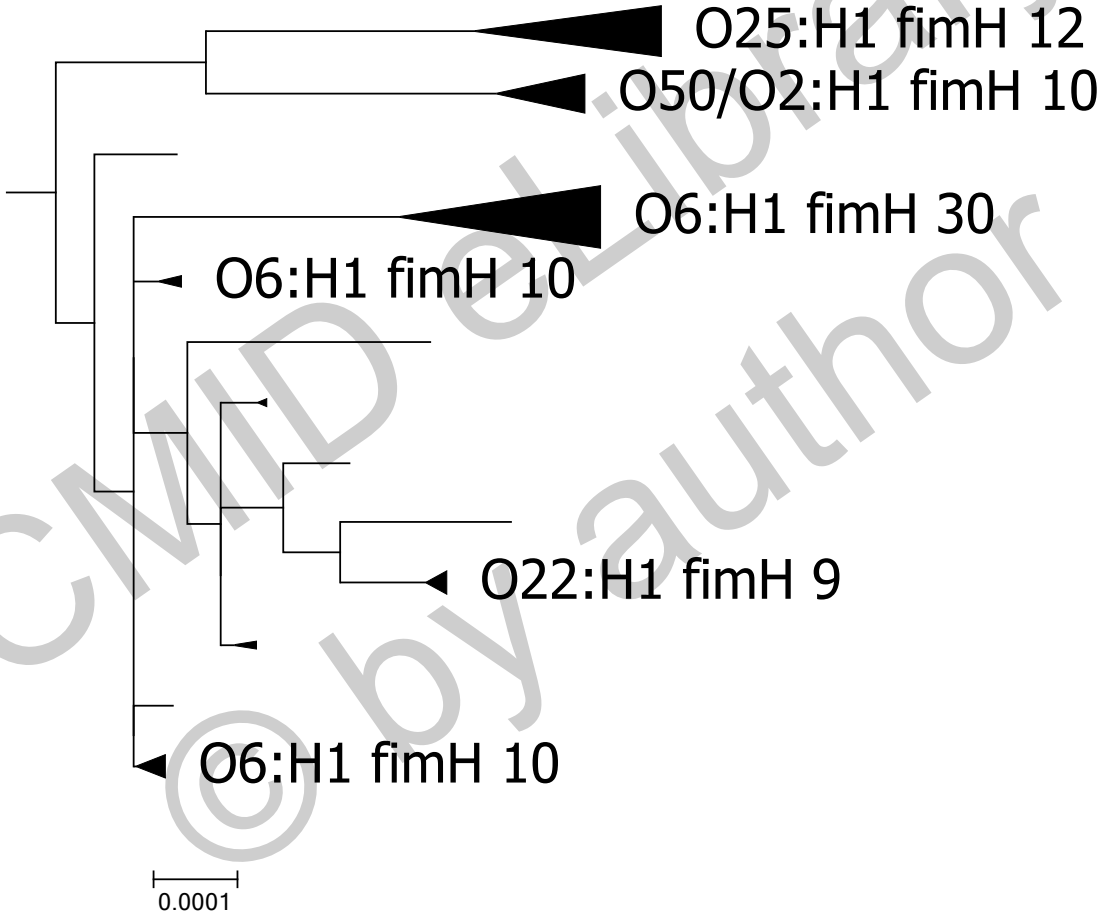
UK Extra-intestinal St Abundance



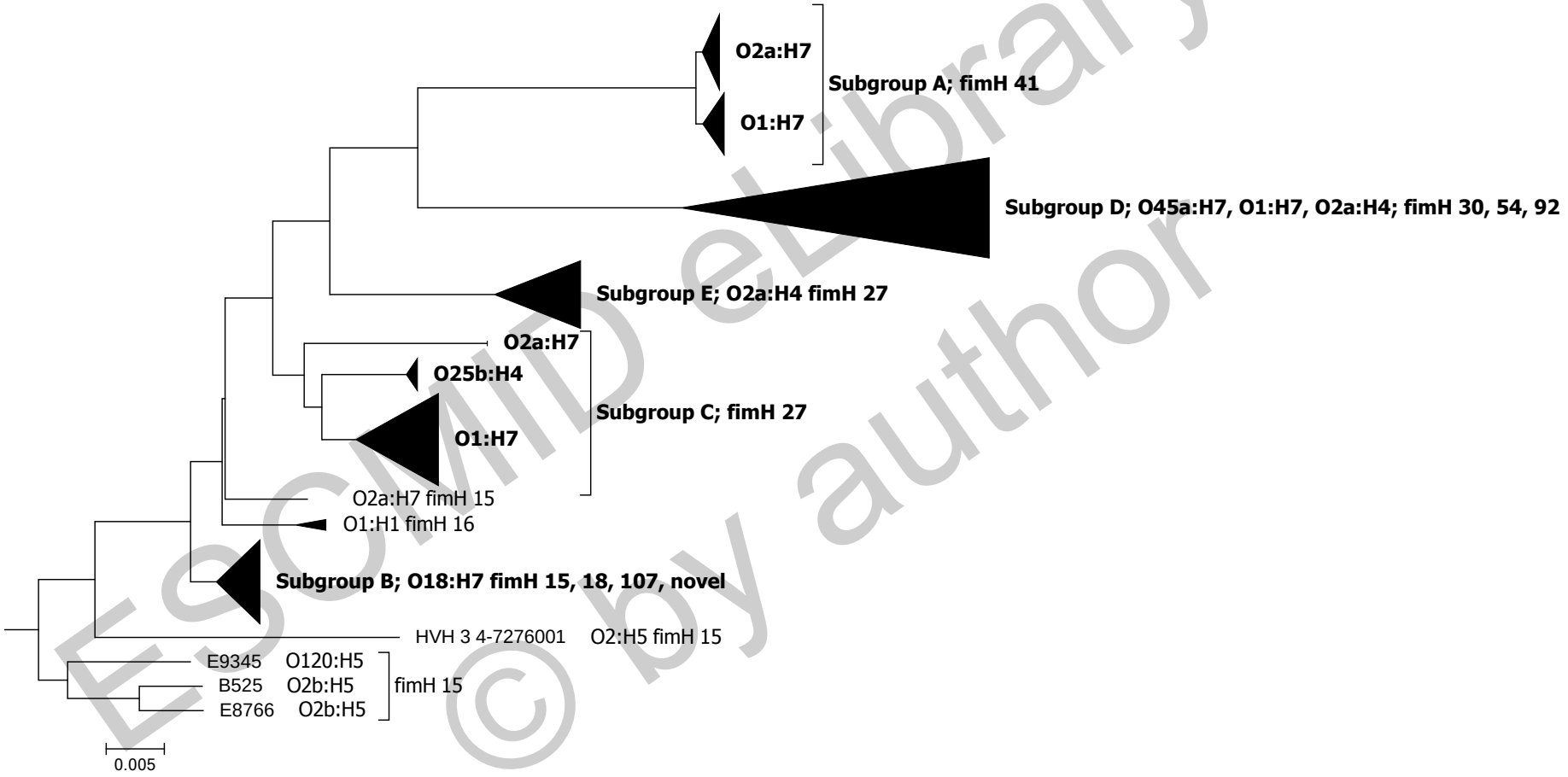
UC Berkley USA – Urine isolates

Clonal Complex	1999/2000 n = 225	2016/2017 n = 233
73	10.2%	13.7%
95	15.1%	16.7%
127	10.7%	15.9%
131	3.1%	5.2%

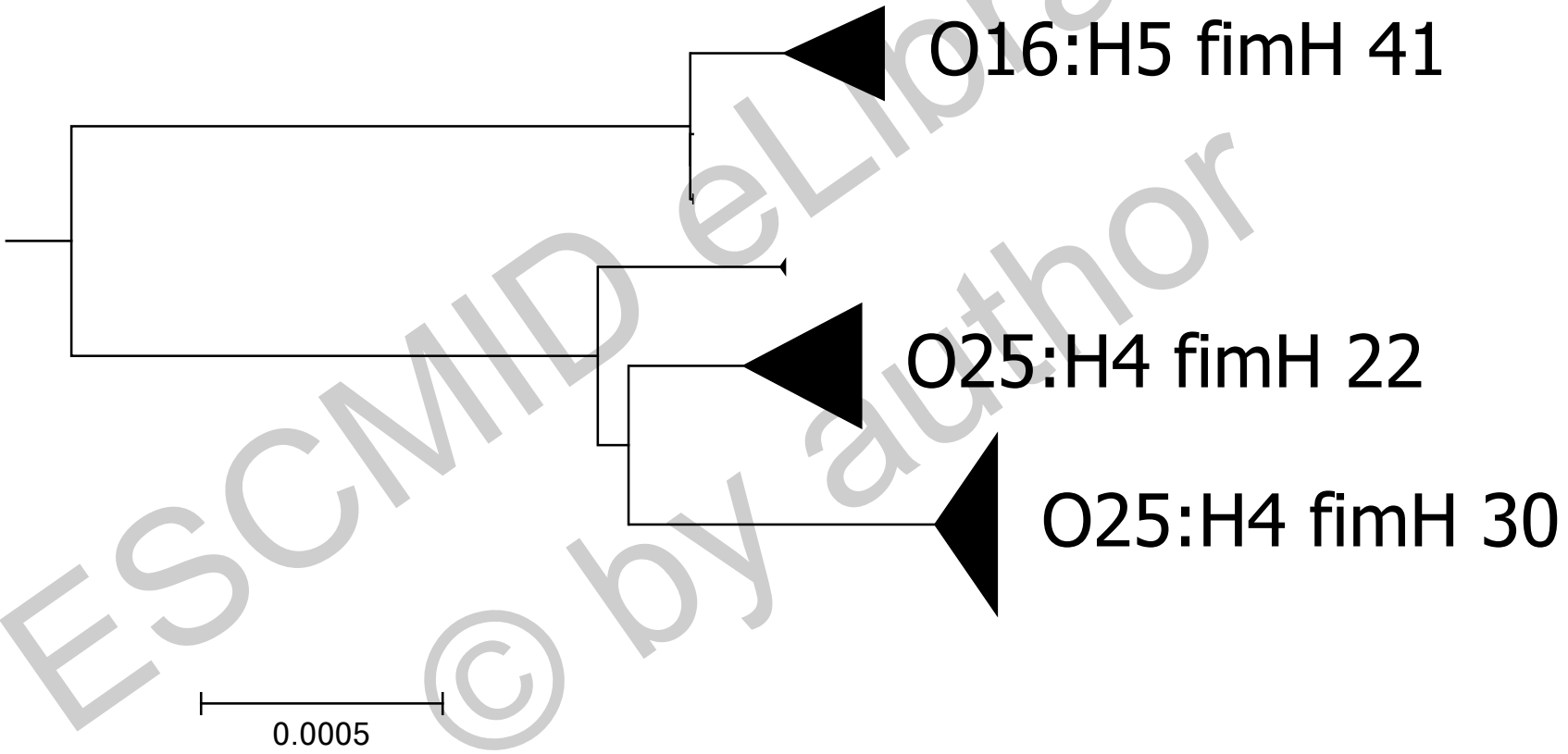
CC73 Substructure



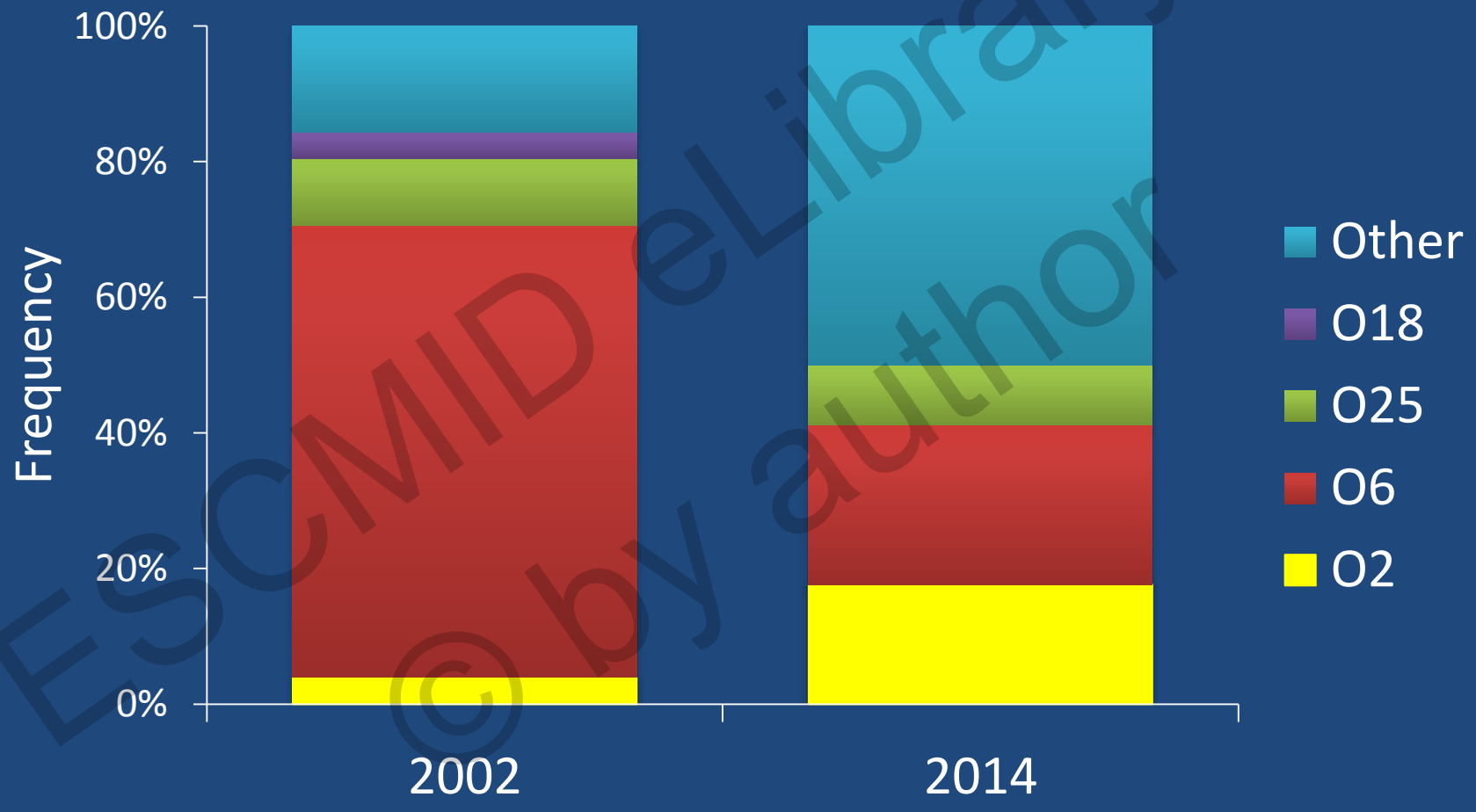
CC95 Substructure



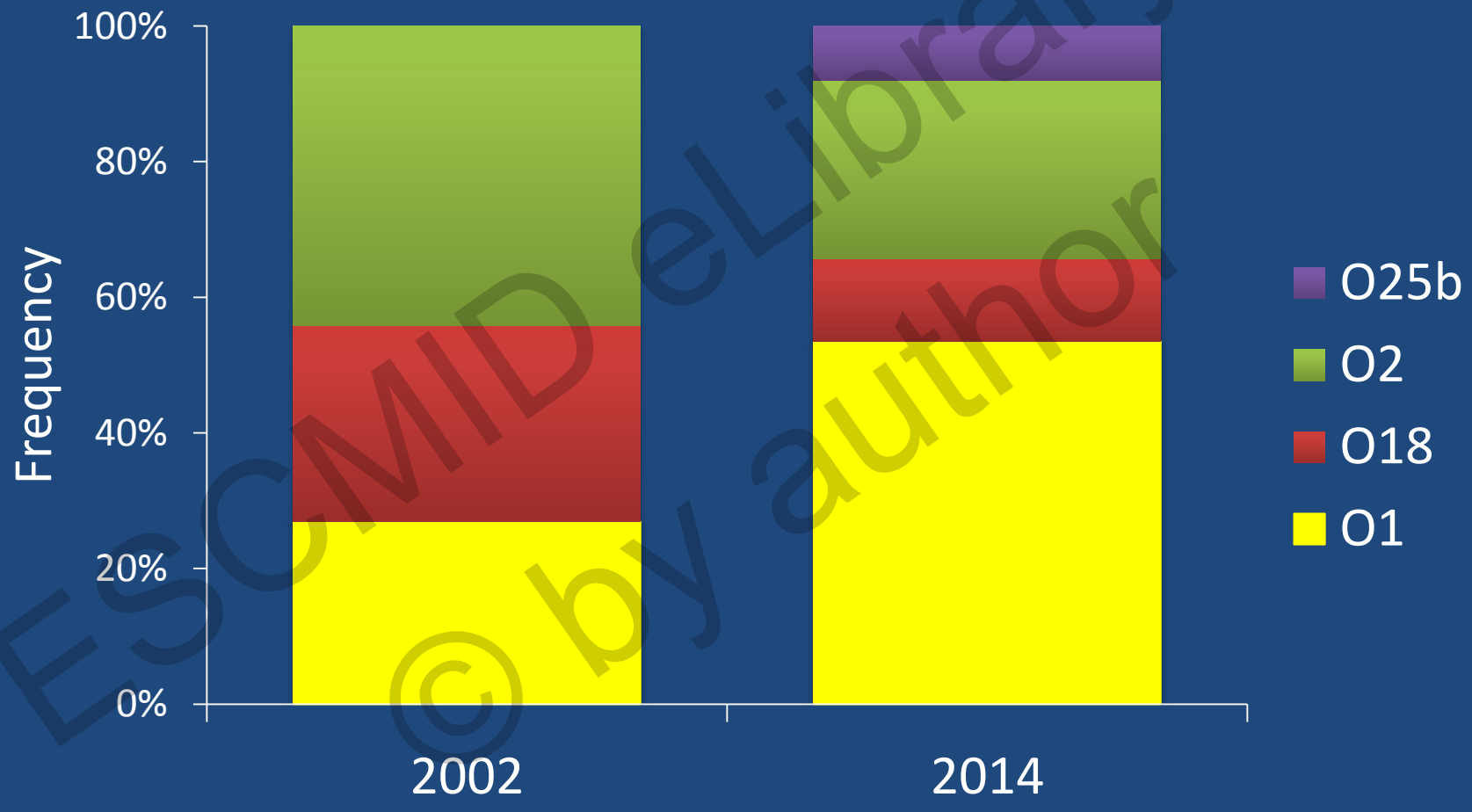
CC131 Substructure



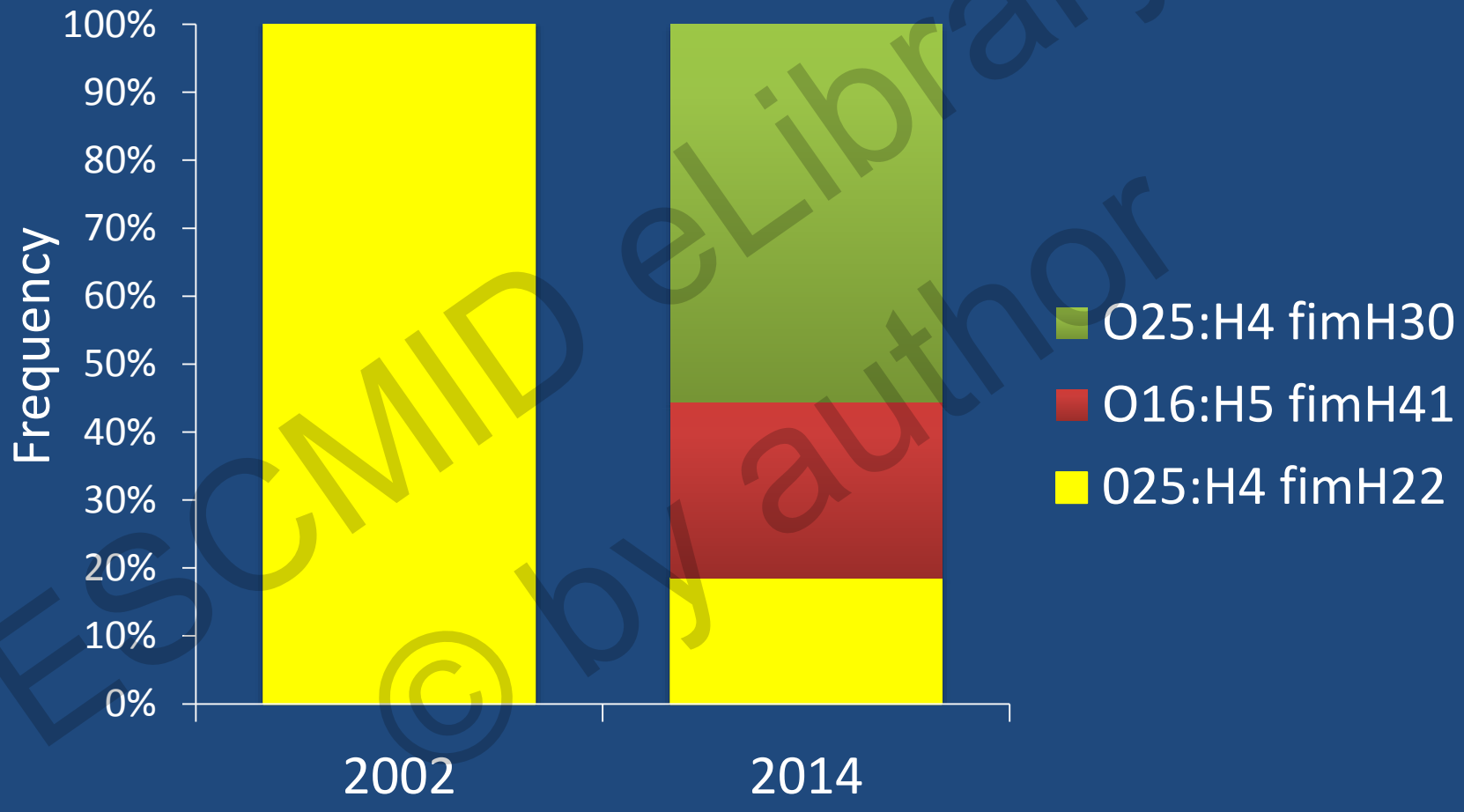
CC73 O types - Canberra



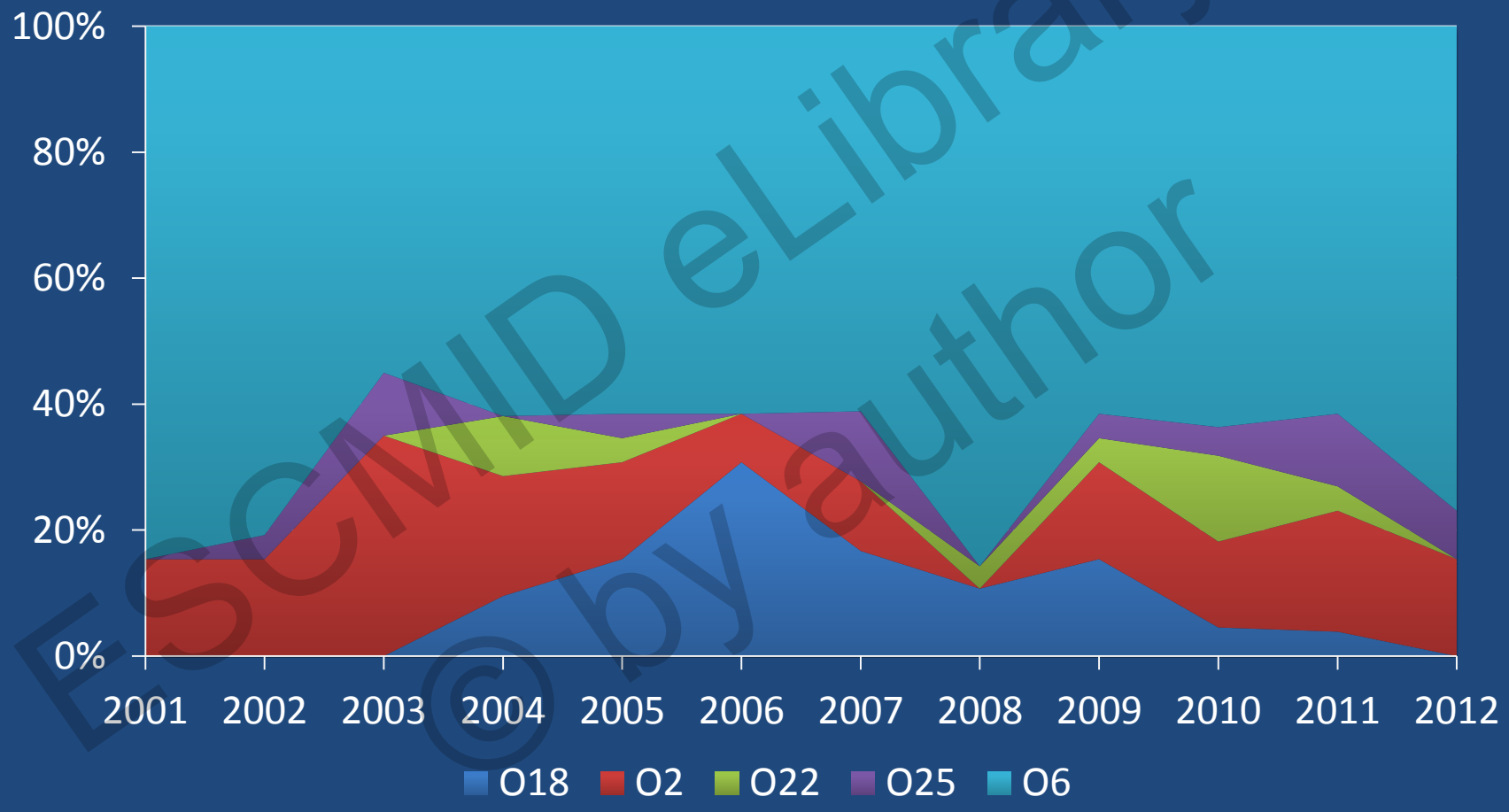
CC95 O types - Canberra



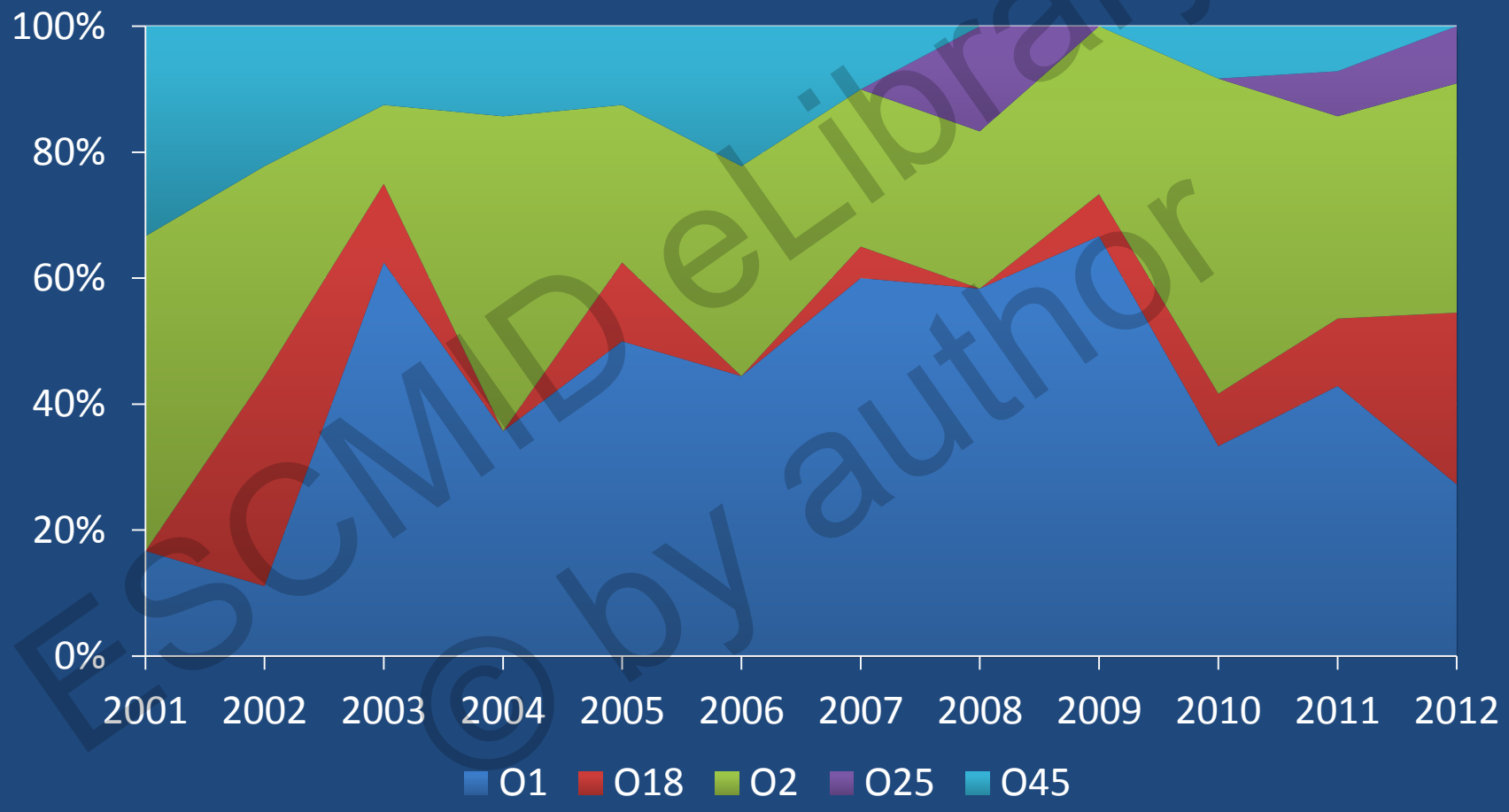
CC131 subtypes - Canberra



O Types ST73 - UK



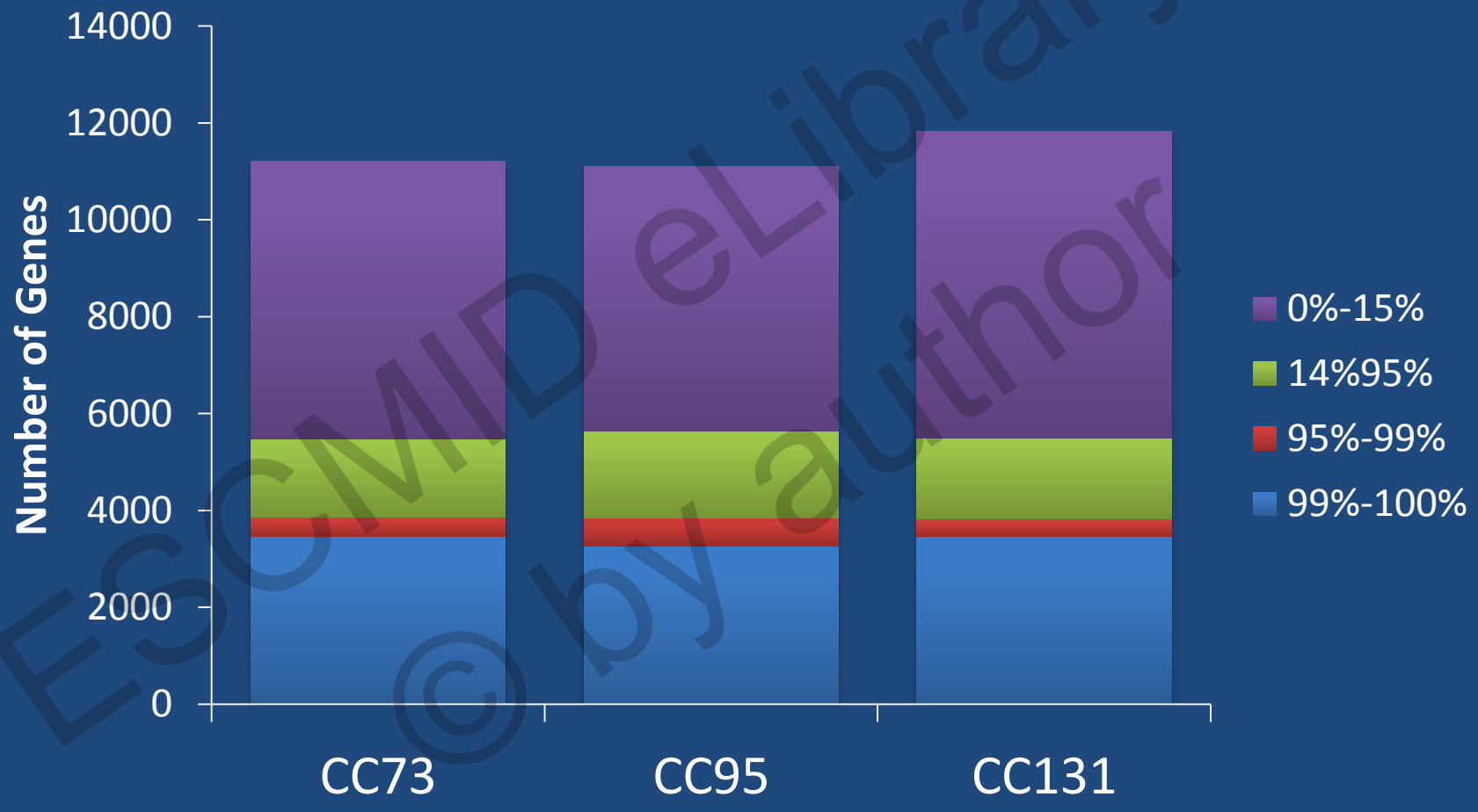
CC95 O types - UK



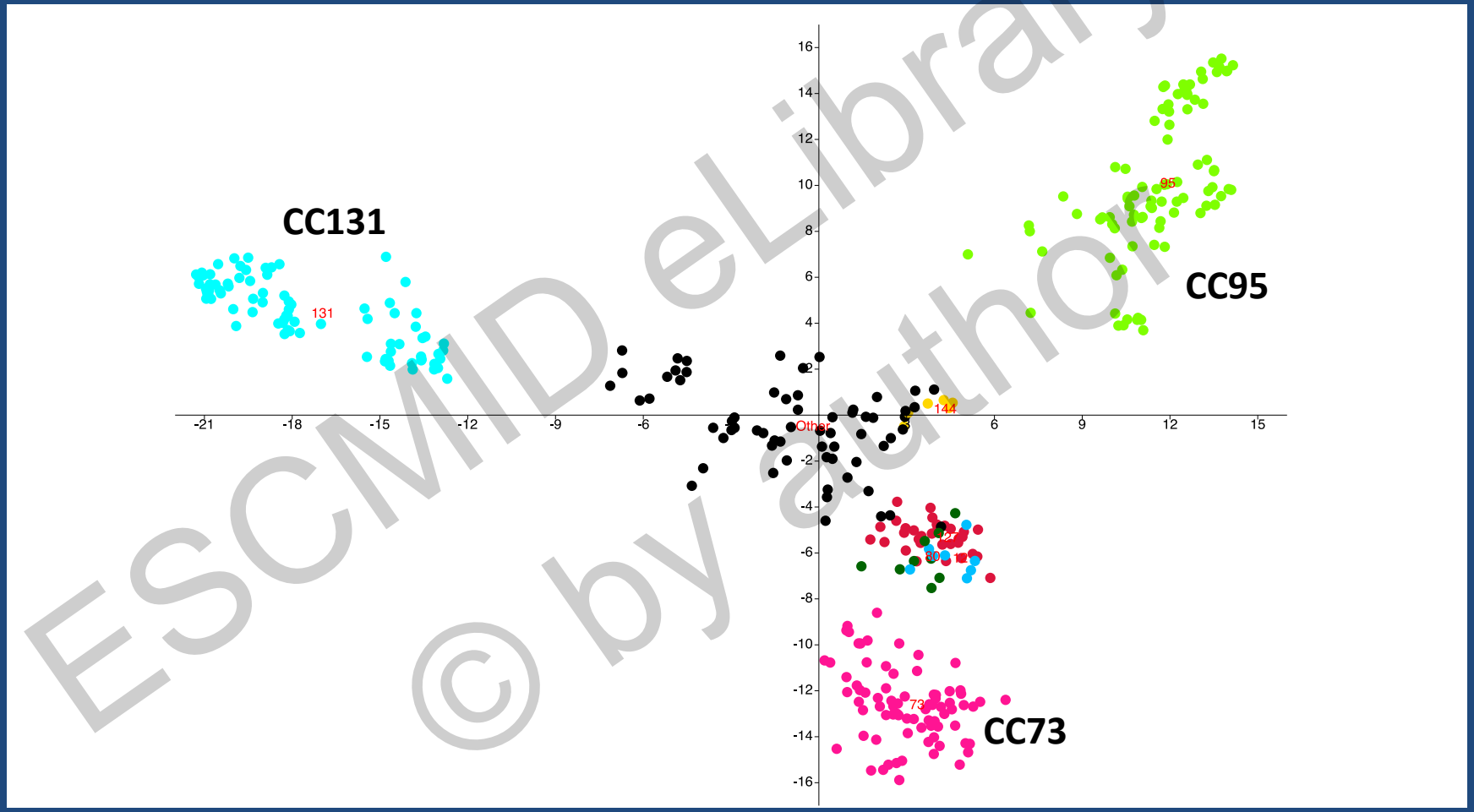
CC131 Subtypes - UK

Variable Gene Content of the Clonal Complexes

Pan Genome



Variable Gene Content



Co-occurrence of Clonal Complexes

- Two studies in Canberra
  - 24 faecal isolates from 202 hosts
  - 100 gut biopsy isolates from 65 hosts

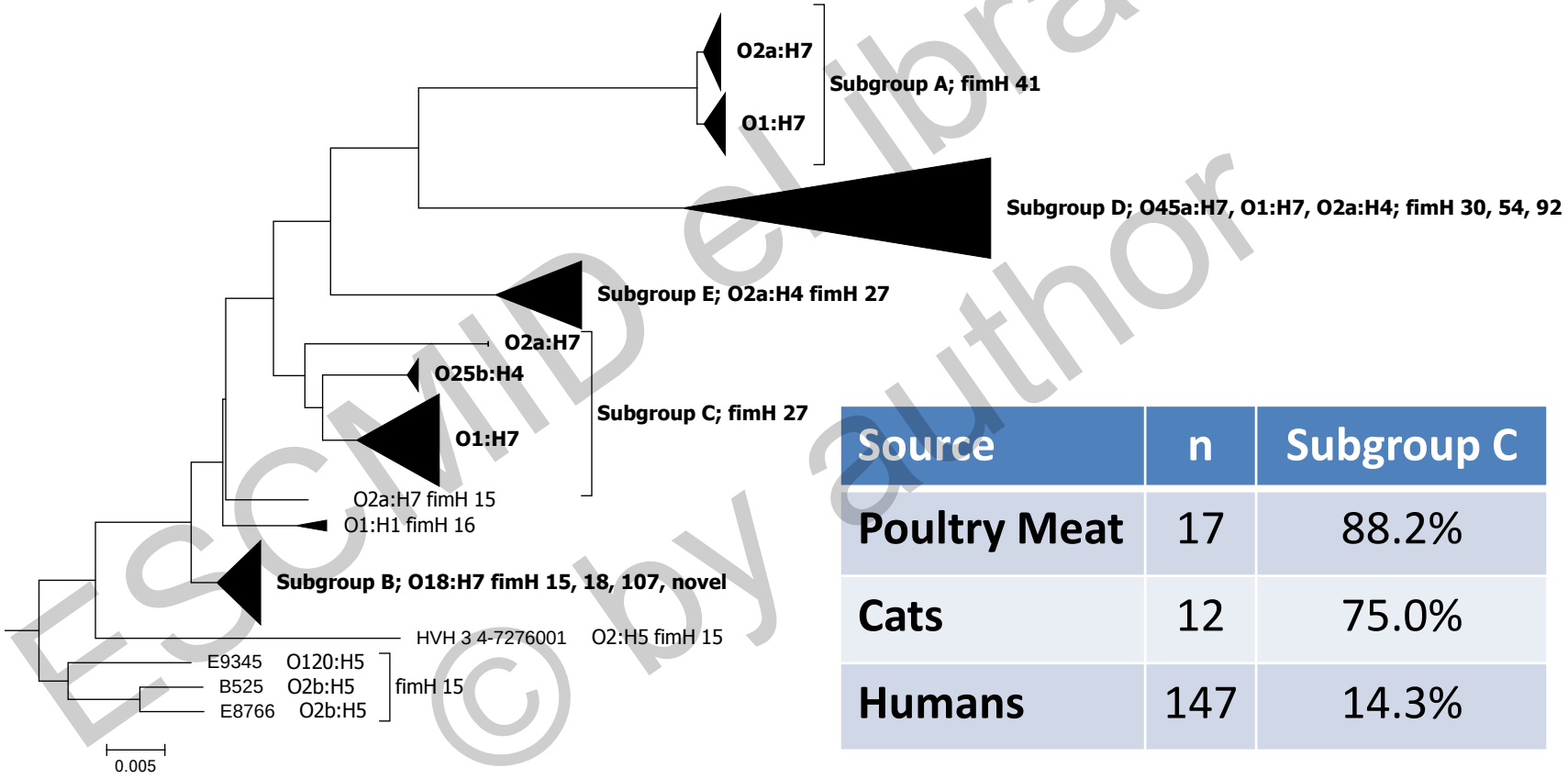
- No instance of CCs, 73, 95, 131 co-occurring

Host Distribution of the Clonal Complexes

Host Distribution of CC95 Australia

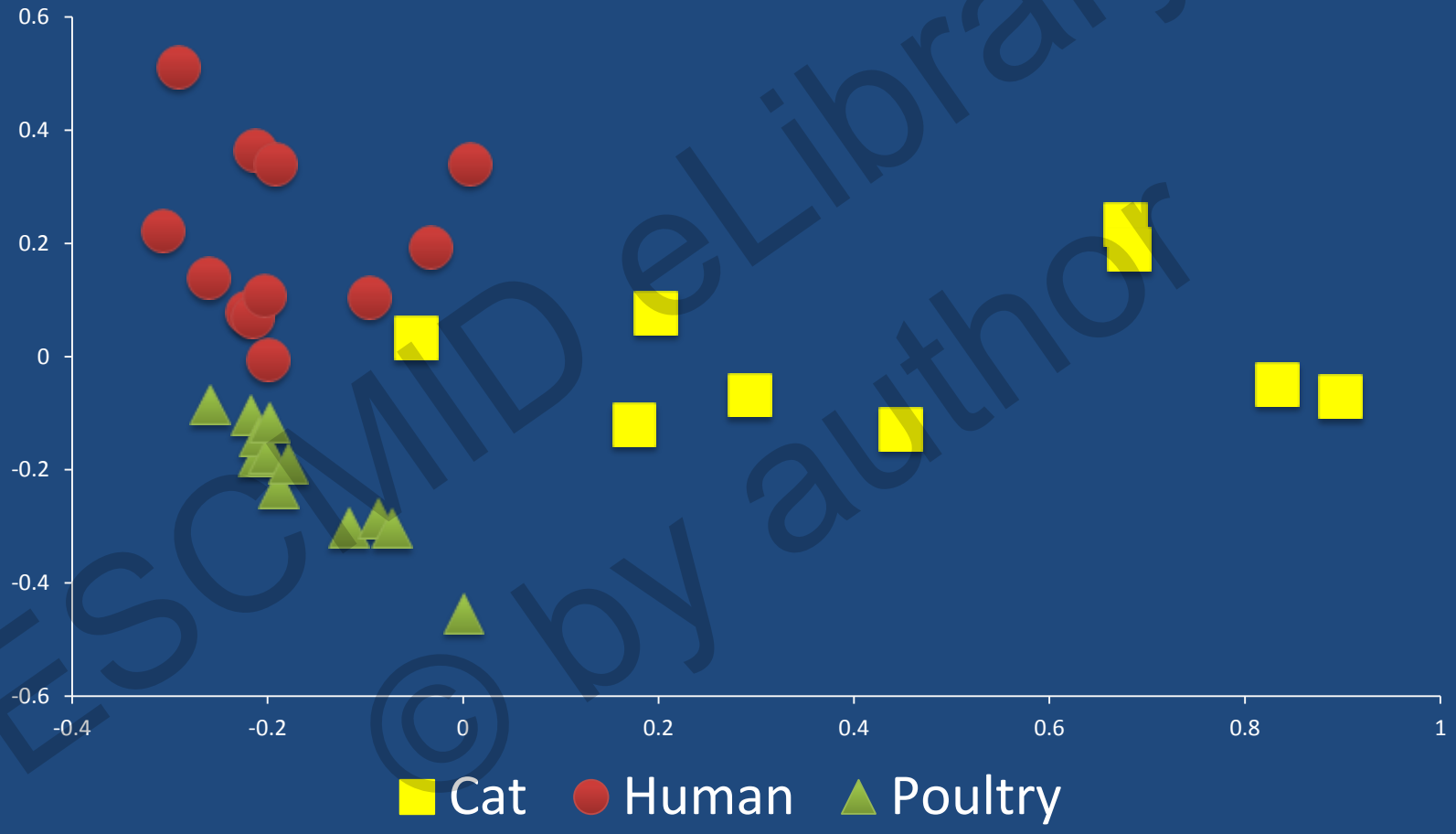
'Host' Group	# 'Hosts' Sampled	CC95	CC73	CC131
Humans	549	9.5%	10.0%	7.8%
Poultry meat	306	5.6%	0%	1.9%
Cats	334	7.2%	19.1%	0.3%
Dogs	203	2.0%	3.9%	1.0%
Native vertebrates	3066	0.06%	0.06%	0.13%
Backyard poultry	278	0%	0%	0%

CC95 Substructure

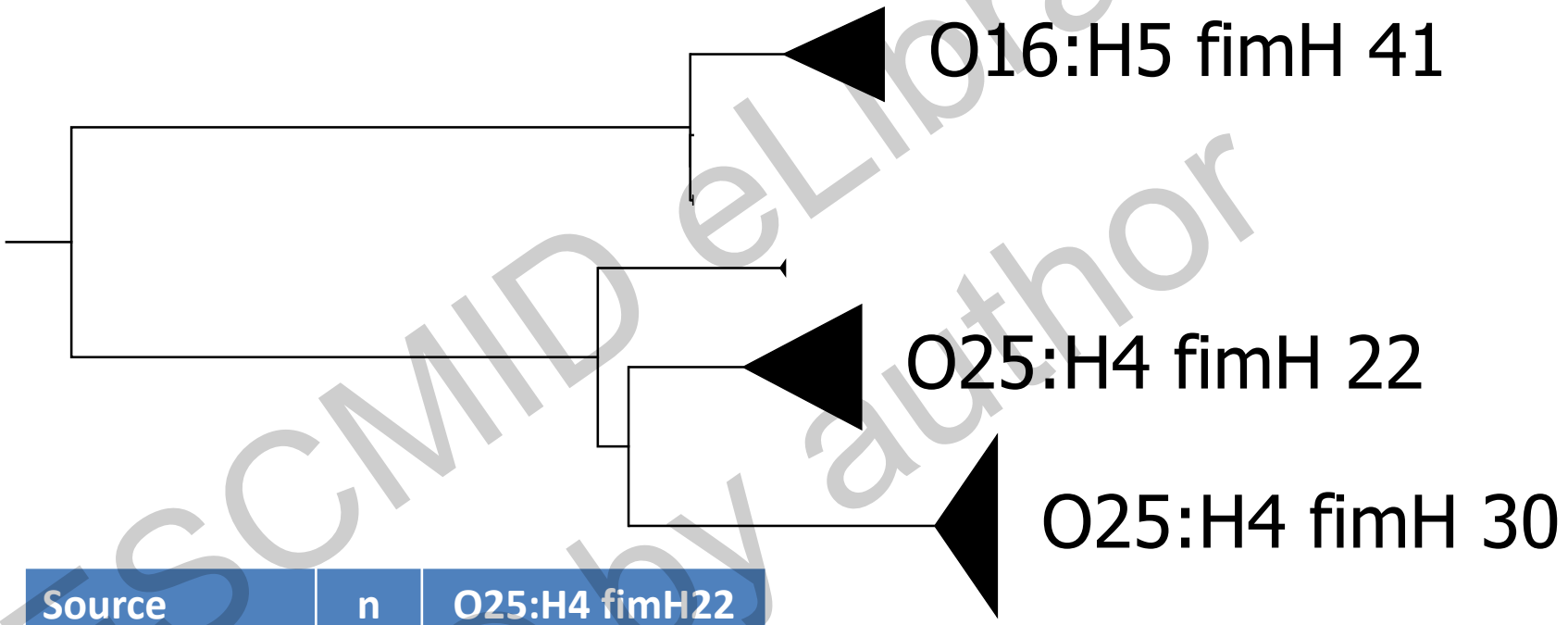


Source	n	Subgroup C
Poultry Meat	17	88.2%
Cats	12	75.0%
Humans	147	14.3%

CC95

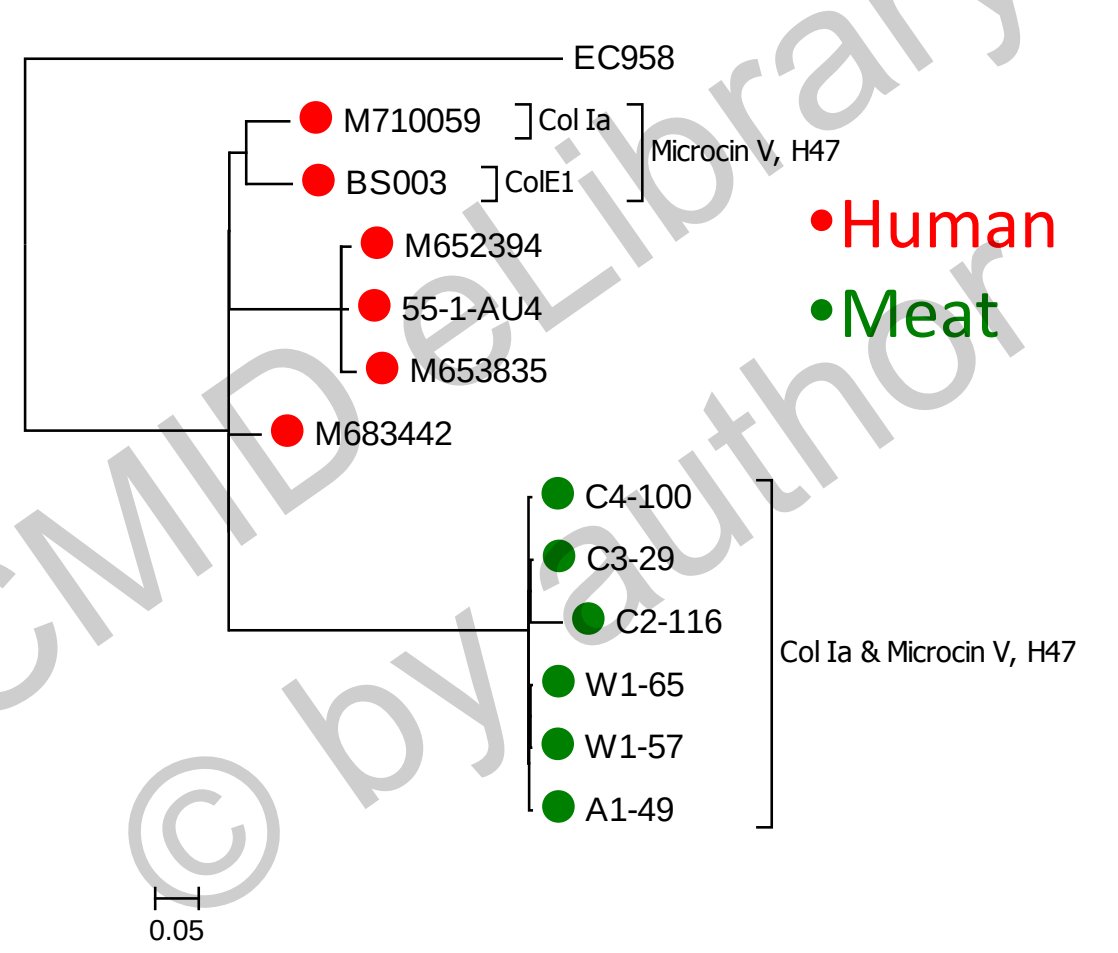


CC131 Substructure

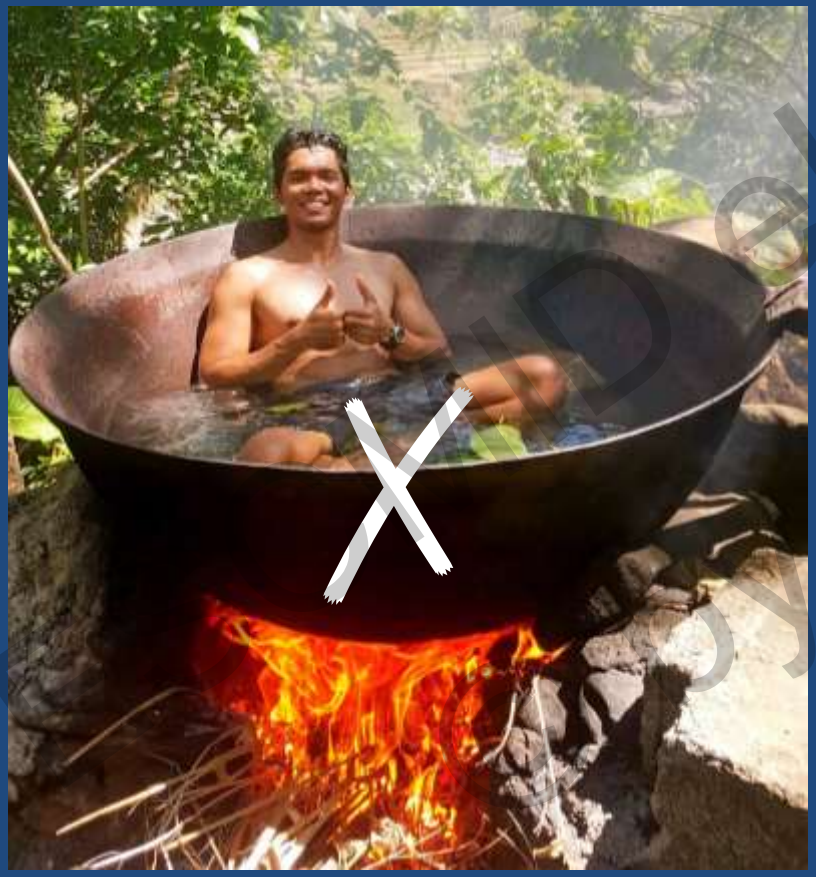


Source	n	O25:H4 fimH22
Poultry Meat	6	100%
Humans	71	17%

ST131 Human vs Poultry



What is the Relative Risk?



Collaborators

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