

Universiteit Utrecht





Plasmid transfer is more efficient between phylogenetically closer related bacteria: a literature review

Jesse B. Alderliesten^{1*} | Egil A.J. Fischer¹ | Arjan Stegeman¹ | Arjan de Visser² | Sarah Duxbury² | Mark Zwart³

1 Utrecht University, Faculty of Veterinary Medicine. Utrecht, the Netherlands * Contact: j.b.alderliesten@uu.nl 2 Wageningen University & Research, Laboratory of Genetics. Wageningen, the Netherlands 3 NIOO-KNAW, Department of Microbial Ecology. Wageningen, the Netherlands

Background

- Antimicrobial resistance (AMR) in bacteria
- Clinical and economical problems
- AMR-genes on plasmids can be transferred between bacteria (Figure 1).
- Possible transfer from commensal to pathogenic bacteria

Aim

To quantify the influence of phylogenetic relatedness between donor *E. coli* and recipient bacteria on the efficiency of plasmid transfer

Methods

- Searched PubMed, CAB Abstracts, and references from Hunter (2008)¹
- Quantitative data on plasmid transfer
- *E. coli* as donor
- Liquid broth as medium

Records	Records	Records
from	from CAB	from Hunter
PubMed	Abstracts	(2008)1
(n = 3921)	(n = 1514)	(n = 34)



Figure 1. Plasmid transfer from an *E. coli* donor (left) to a recipient (right)³.

Results

- 284 data points from 18 studies

- 85 non-*E. coli* recipients: median distance to *E. coli* 0.07 (range 0.02 - 0.30; Figure 2)
- Plasmid transfer is more efficient between phylogenetically closer related bacteria (Table 1)

- Also affected by donor origin, plasmid incompatibility type, and used temperature

 Table 1. Estimates of plasmid transfer

 frequencies from a multivariable model





Figure 2. Phylogenetic tree based on 16S rRNA sequences² of the Bacteria, with Archaea as outgroup. Bacteria which appear as recipients in the data are shown in red, with their distance to *E. coli* indicated. Most recipients belong to the phylum Proteobacteria, for which the lines denote individual species. The remaining part of

	Da poi	Data points		Multivariable analysis			
Variable	n	%	Esti- mate	2.5%	97.5%		
Intercept							
	284	100	-4.26	-5.08	-3.58		
Phylogeneti	c distai	nce to	E. coli				
Intercept	284	100	Reference				
Slope	284	100	-13.90	-20.12	-6.54		
Origin of donor bacterium							
Labstrain	255	89.8	Reference				
Human	16	5.6	-1.47	-3.07	0.16		
Chicken	5	1.8	1.36	-1.03	3.66		
Mice	4	1.4	-3.27	-5.37	-1.43		
Wastewater	4	1.4	3.55	1.06	5.93		
Incompatibi	lity typ	e of p	lasmid				
F	82	28.9	Reference				
A/C/E	10	3.5	-2.26	-3.29	-1.02		
Н	69	24.3	-2.13	-3.11	-0.81		
I-complex	5	1.8	-0.49	-1.87	1.26		
L/M	10	3.5	0.03	-1.01	1.28		
N	5	1.8	-0.71	-2.34	0.85		
Р	48	16.9	1.18	0.10	2.59		
Т	8	2.8	-0.40	-1.92	1.30		
V	3	1.1	-1.76	-3.96	0.64		
W	3	1.1	0.12	-1.70	2.17		
Х	3	1.1	1.15	-0.86	3.36		
NR	38	13.4	-1.68	-2.44	-0.57		
Temperatur	e used	(°C)					
35-37	125	44.0	Reference				
5	4	1.4	0.57	-1.42	2.15		
20-30	138	48.6	0.62	0.03	1.11		
43-47	12	4.2	-1.11	-2.17	-0.16		
NR	5	1.8	2.07	-0.12	4.36		

the tree is less detailed, with both lines denoting phyla.

Data extraction

- Bacteria (origin, phylogenetic distance to *E. coli*², growth phase)
- Plasmid (incompatibility type)
- Experimental conditions (medium, culture type, pH, temperature, duration, ratio donor per recipient)

Model

- Log(plasmid transfer frequency) as dependent variable
- StudyID as random intercept

'Univariable' selection

- <15% missing data
- p-value < 0.2 for Log(plasmid transfer frequency) = Variable + (1 | StudyID)
 Model selection on remaining variables
- Akaike information criterion

References

- ¹ Hunter PR, Wilkinson DC, et al. Appl. Environ. Microbiol. 74:6085-90 (2008).
- ² Cole JR, Wang Q, *et al*. *Nucleic Acids Res.* 42:D633-42 (2014)

³ Reece JB, Urry LA, *et al. Campbell Biology*. Pearson Education (2011). Figure 27-12.

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Conclusion

Efficiency of plasmid transfer decreases with increasing phylogenetic distance, but transfer to more distantly related bacteria is possible. Given the large number of gut bacteria, they will share plasmids and AMR genes over larger phylogenetic distances.