Conjugative transfer of ESBL and aminoglycoside antibiotic resistance genes in *Extraintestinal E. coli*: implications for multidrug resistance evolution.

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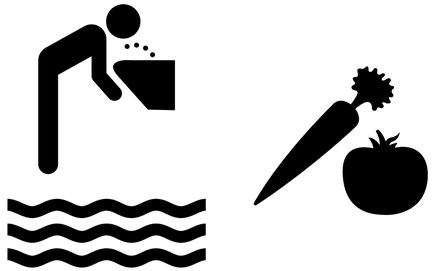
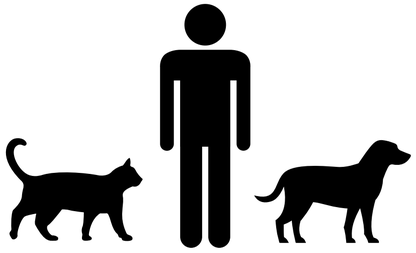
Introduction

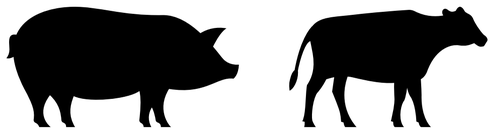
Soil
Water



Human
Companion animals



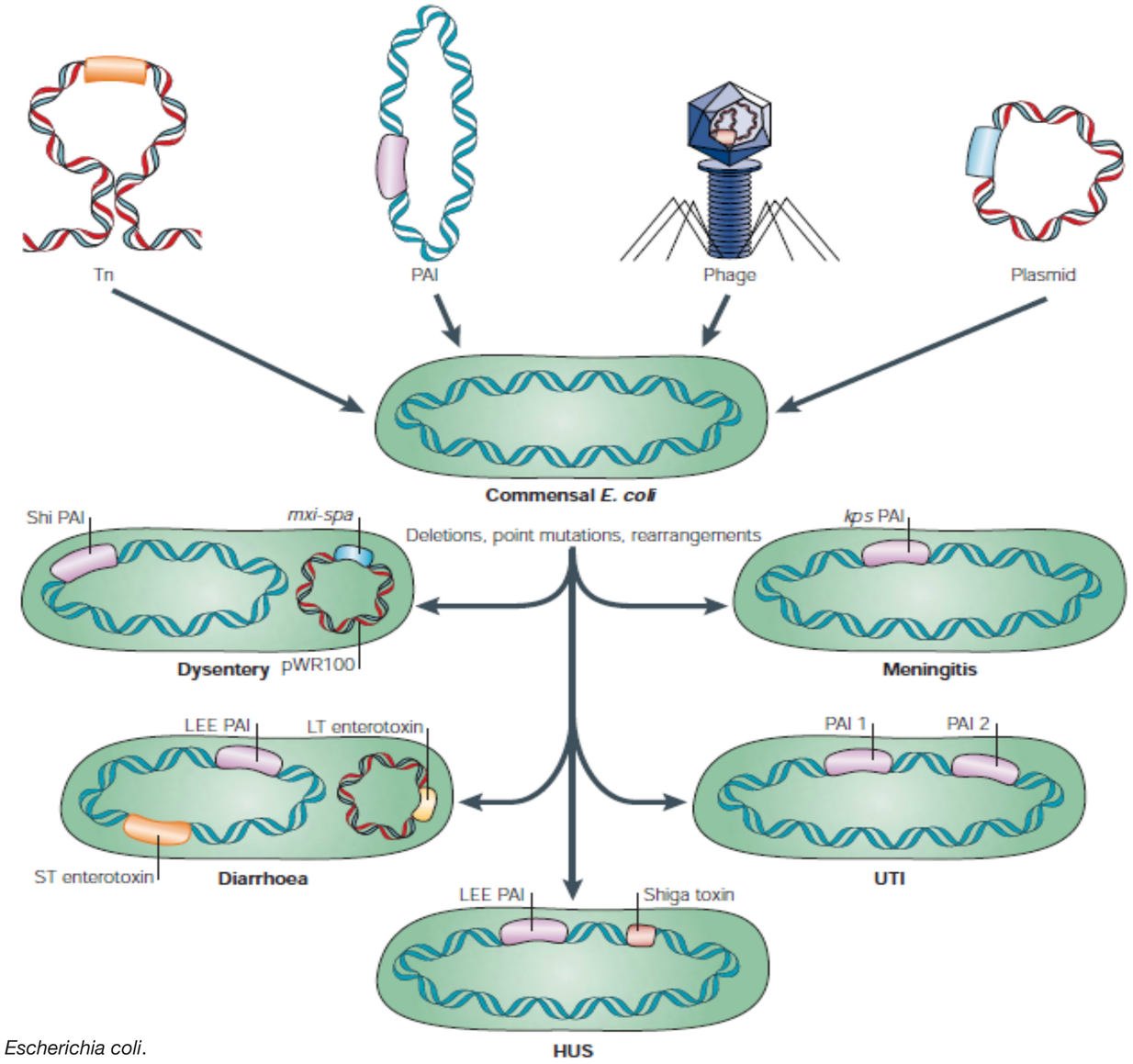
Escherichia coli



Food-producing animals

Food

Pathogenic and multidrug-resistant ExPEC



Mobile genetic elements by

Conjugation

Kaper JB, Nataro JP, Mobley HL. Pathogenic *Escherichia coli*.
Nat Rev Microbiol. 2004 Feb;2(2):123-40.
doi: 10.1038/nrmicro818. PMID: 15040260.

Aim

- To investigate the linkage and potential for horizontal transfer of a limited number of clusters of antibiotic resistance genes that dominate the Extended-Spectrum Beta-Lactamase antibiotic resistance gene landscape in samples of Extraintestinal *E. coli* recovered from two West Coast hospitals in the USA.

Materials and methods

Strains

39 from the **University of Washington** collection

100 from the **UC Merced** collection

139 ExPEC

CG1: *aac(3)-IIa*, *aac(6')-Ib-cr*, bla_{OXA-1}
CG2: *aac(3)-IId*, bla_{TEM-1A} and $bla_{CTX-M-14b}$

Kim et al., unpublished paper.

Conjugation

Carbenicillin and Rifampicin selection

Recipient: *E. coli* LMB100 (lac- and Rif-resistant)

Tranconjugants

- **PFGE-S1** (number and size)
- Plasmid DNA purification
- Resistance genes by **PCR**

Donors and Tc

Analisys

Results and Discussion

Table 1. Prevalence of conjugation.

Conjugative* n=62		Non-conjugative n=77	
44%		56%	
UW	UCM	UW	UCM

*Conjugation efficiency was above 10^{-5} %.

$$CE = \frac{Tc}{R} x100$$

CE: conjugation efficiency
Tc: number of transconjugants
R: number of recipients
and multiplying by 100 (to obtain efficiency value per 100 recipient cells)

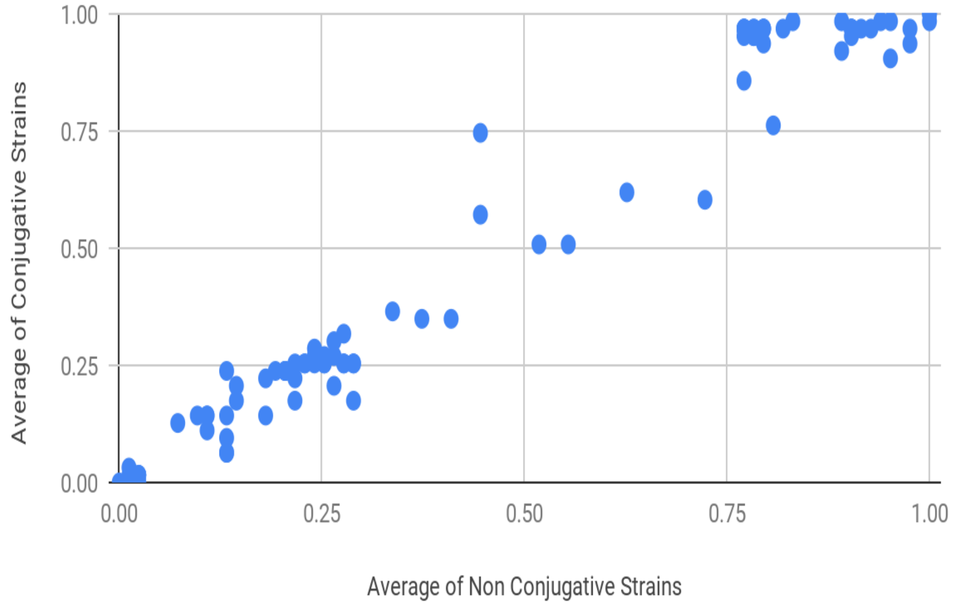


Figure 1. Number of times conjugation genes are present, comparing conjugating or non-conjugating strains. Each dot represents a gene from our conjugation machinery set.

A subset of genes that is enriched in in conjugating strains.

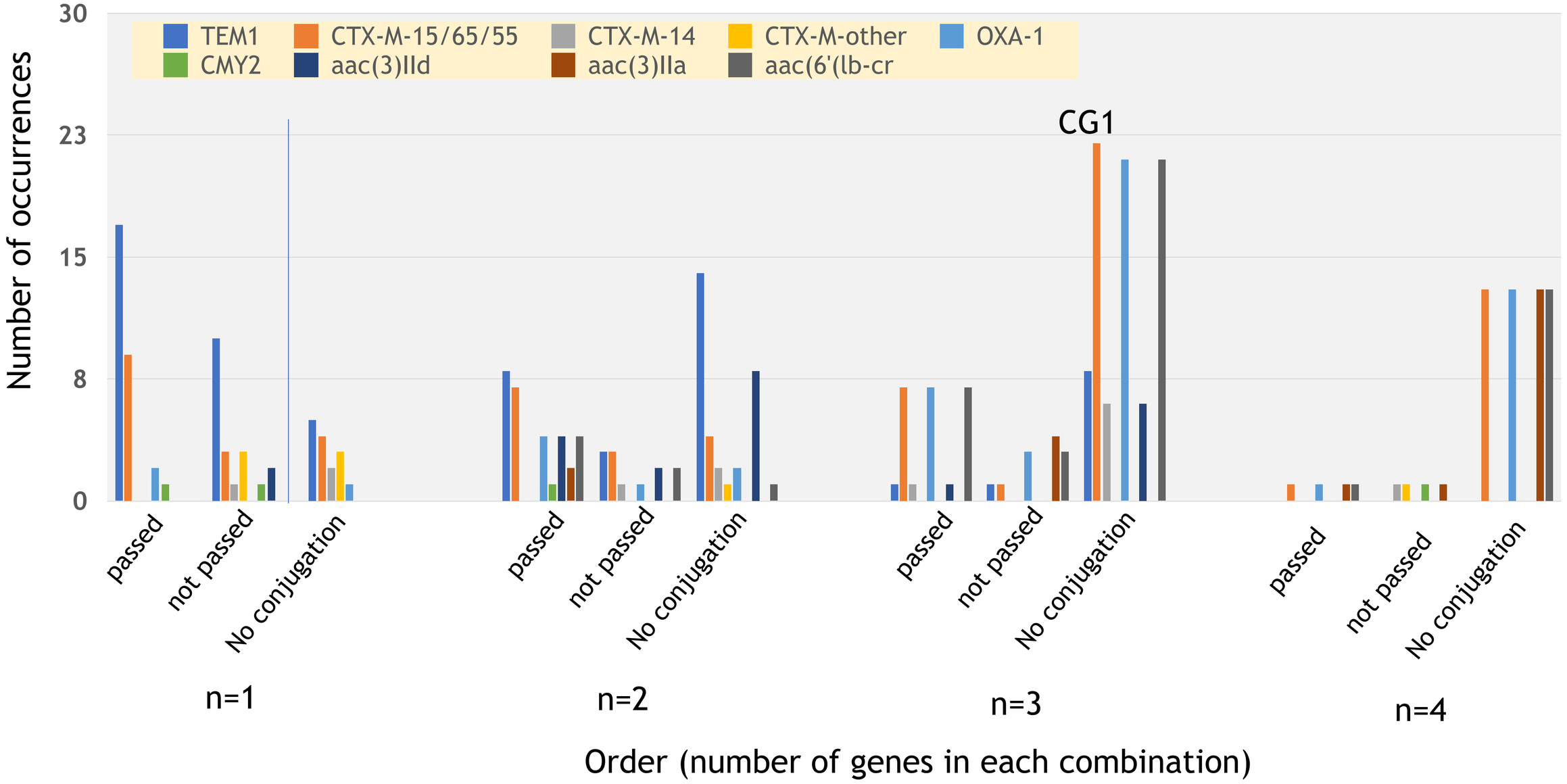
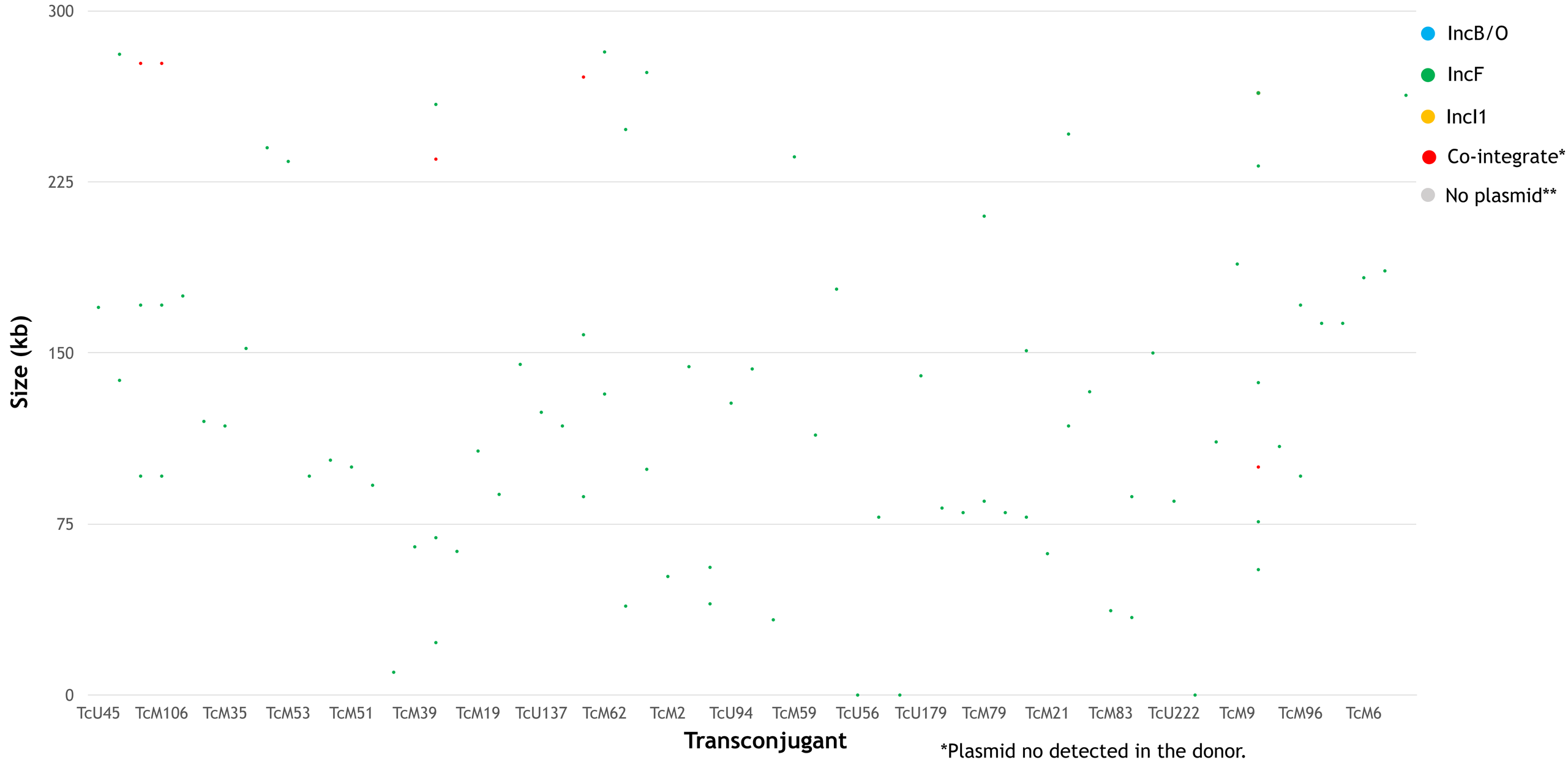


Figure 2. Distribution of all relevant genes by order.



*Plasmid no detected in the donor.
**Plasmid no detected in the transconjugant, it's size was considered zero.

Figure 3. Plasmids transferred by conjugation to recipient strain LMB100.

Conclusions

1. β-lactamase-bearing conjugative plasmids largely (95%) belonged to the IncF plasmid incompatibility group and 97% of these have combinations of IncF replicons.

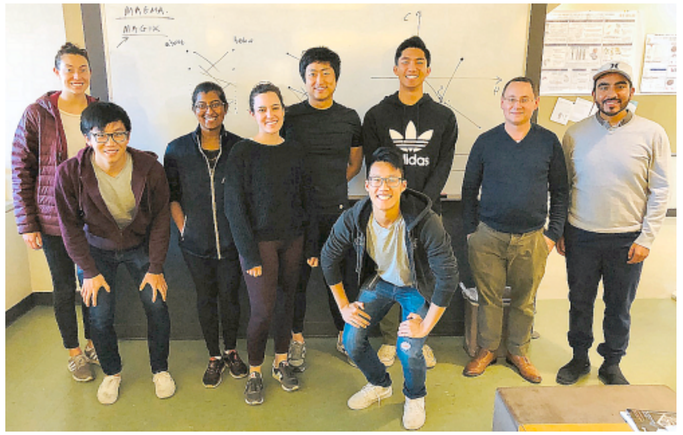
2. AG1 and AG2 gene combinations can spread by conjugation but this is not consistently the case; higher-order combinations tend to appear in non-conjugating strains.

3. The observed patterns of conjugation transfer of CG1 and CG2 genes suggest that conjugation plays an important role in the early stages of evolution of multidrug resistance, making genes available for the generation of adaptive solutions.

4. These adaptive solutions are highly heterogeneous, driven by selection rather than by co-mobilization.

5. Our results suggest that the formation of more complex combinations occurs at the expense of their ability to be mobilized.

Acknowledgments



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