

Extraintestinal pathogenic *Escherichia coli* in camels: Characteristics and sources of infection

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Introduction

Escherichia coli is a common Gram-negative bacterium colonizing human and animal intestines. Some strains can harbour various virulence factors and thus belong to the major causative agents of human and animal infections. Extraintestinal pathogenic *E. coli* (ExPEC) cause infections ranging from common cystitis to life-threatening septicemia. ExPEC strains encode for various combinations of virulence factors, which increase their virulence and their ability to survive in extraintestinal environments. In camel husbandry, *E. coli* is responsible for diarrheal conditions, and may also cause camelid uterine infections, resulting in spontaneous abortions and increased neonatal mortality.

Bacteriocins are peptides or proteins produced by various bacteria with antimicrobial activity. Bacteriocins have a narrow spectrum of activity as they kill only related bacteria to the bacteriocin producer. Owing to their antimicrobial activity, they are used in food preservation and they have also promising potential in human and veterinary medicine.

Although, camel intestinal pathogenic *E. coli* is well studied, a little is known about ExPEC causing deadly sepsis in camel calves. The aim of this study was to characterize set of extraintestinal pathogenic *E. coli* (ExPEC) from camels and compare their characteristics with commensal *E. coli*.

Methodology



CVRL

Central Veterinary Research Laboratory (Dubai)

ExPEC strains
n = 207

Fecal
E. coli strains
n = 139

PCR screening

- Phylogenetic groups Clermont et al. 2013
- Virulence determinants (n = 35) Bosák et al. 2023
- Serotypes (n = 162) Iguchi et al. 2013
- Bacteriocin determinants (n = 36) Bosák et al. 2019

References

Clermont O, Christenson JK, Denamur E, Gordon DM. The Clermont *Escherichia coli* phylotyping method revisited: improvement of specificity and detection of new phylo-groups. *Environ Microbiol Rep.* 2013 Feb;5(1):58-65.

Bosák J, Kohoutová D, Hrala M, Křenová J, Morávková P, Rejchrt S, Bureš J, Šmajš D. *Escherichia coli* from biopsies differ in virulence genes between patients with colorectal neoplasia and healthy controls. *Front Microbiol.* 2023 Apr 13;14:1141619.

Iguchi A, Iyoda S, Seto K, Morita-Ishihara T, Scheutz F, Ohnishi M; Pathogenic *E. coli* Working Group in Japan. *Escherichia coli* O-Genotyping PCR: a Comprehensive and Practical Platform for Molecular O Serogrouping. *J Clin Microbiol.* 2015 Aug;53(8):2427-32.

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Results

Phylogenetic groups of *E. coli*

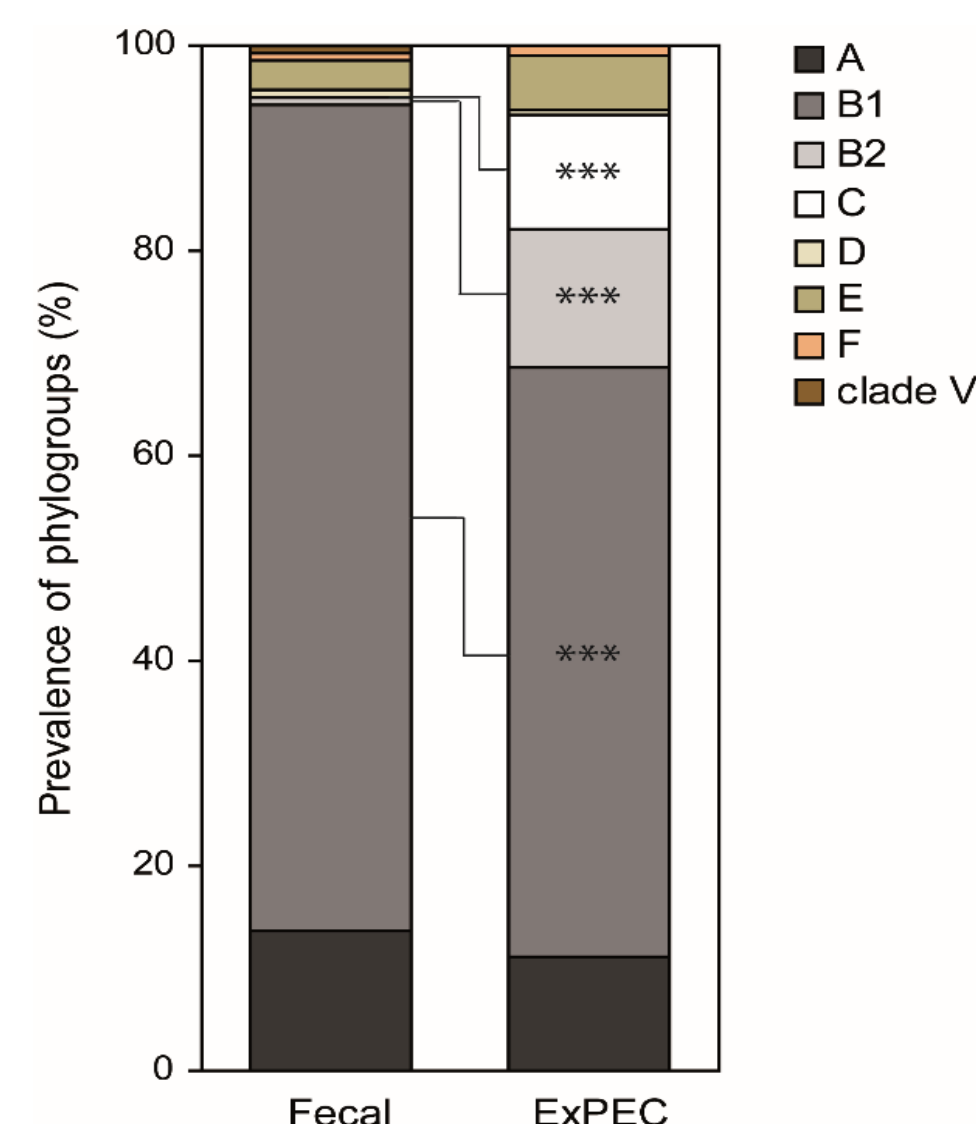


Fig. 1: Distribution of phylogenetic groups between ExPEC (n = 207) and fecal (n = 139) *E. coli* from camels.

Virulence determinants

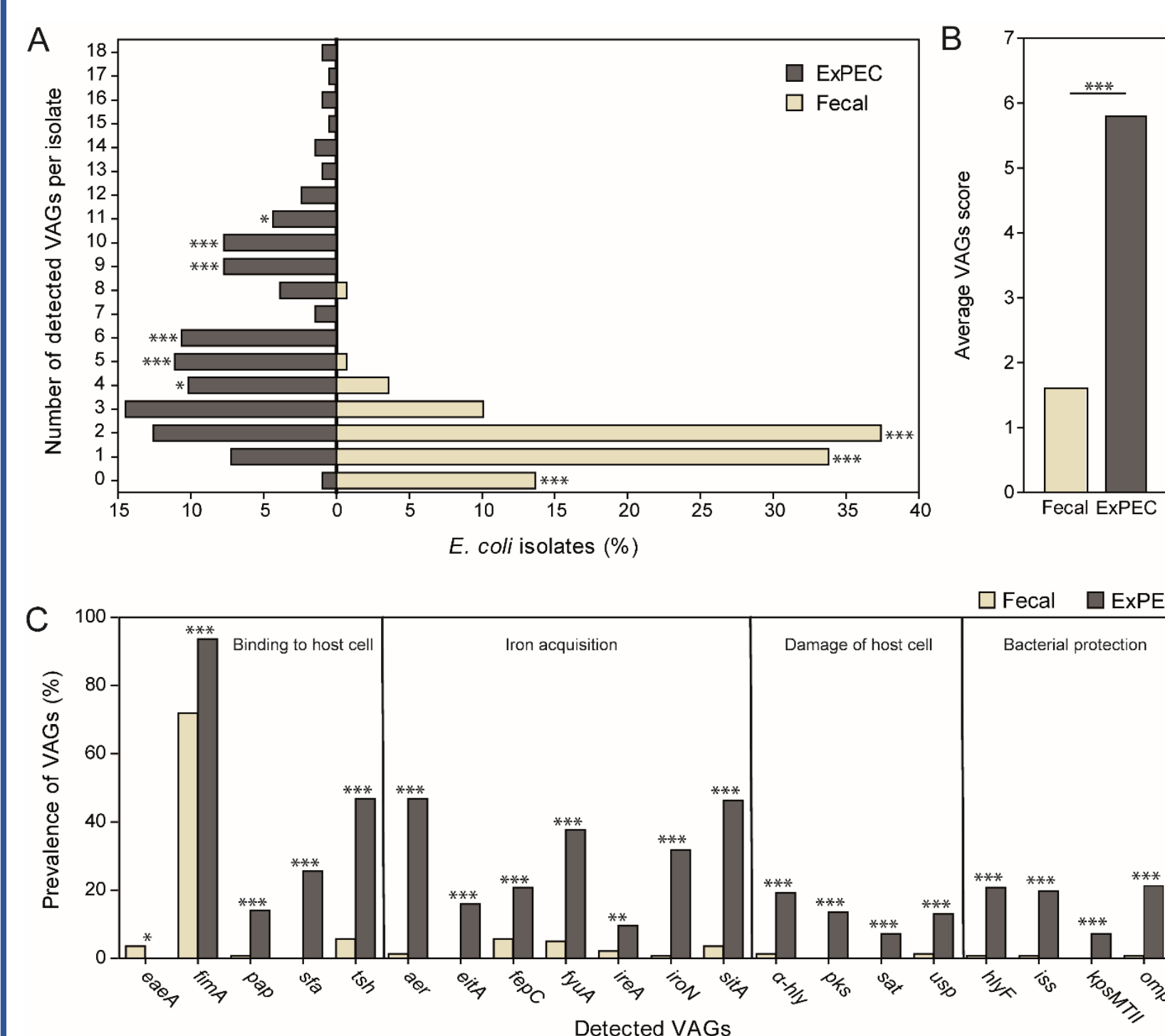


Fig. 2: Distribution of VAGs among ExPEC (n = 207) and fecal (n = 139) *E. coli* from camels. Compared to fecal *E. coli*, ExPEC isolates harbored significantly more virulence factors (A, B). Out of 35 tested VAGs, the prevalence of twenty VAGs differed between analyzed *E. coli* sets (C); all except *eaeA* showed increased prevalence in pathogens.

Serotypes

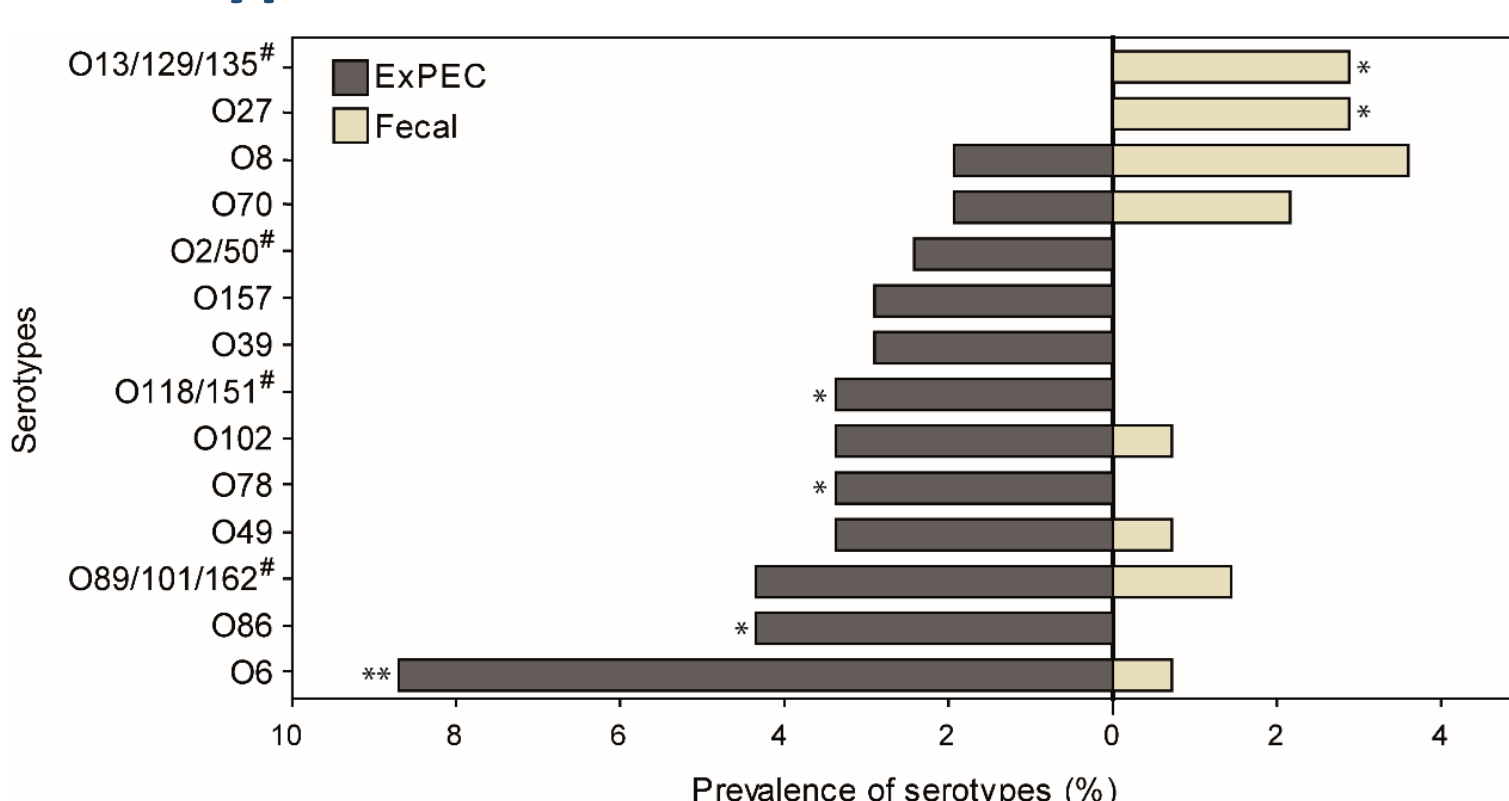


Fig. 3: Distribution of the most prevalent O serotypes (> 2% in camel *E. coli*) in pathogenic (n = 207) and fecal (n = 139) *E. coli* from camels. Serotypes O6, O78, O86 and O118/O151 were associated with ExPEC isolates.

Correspondence analysis

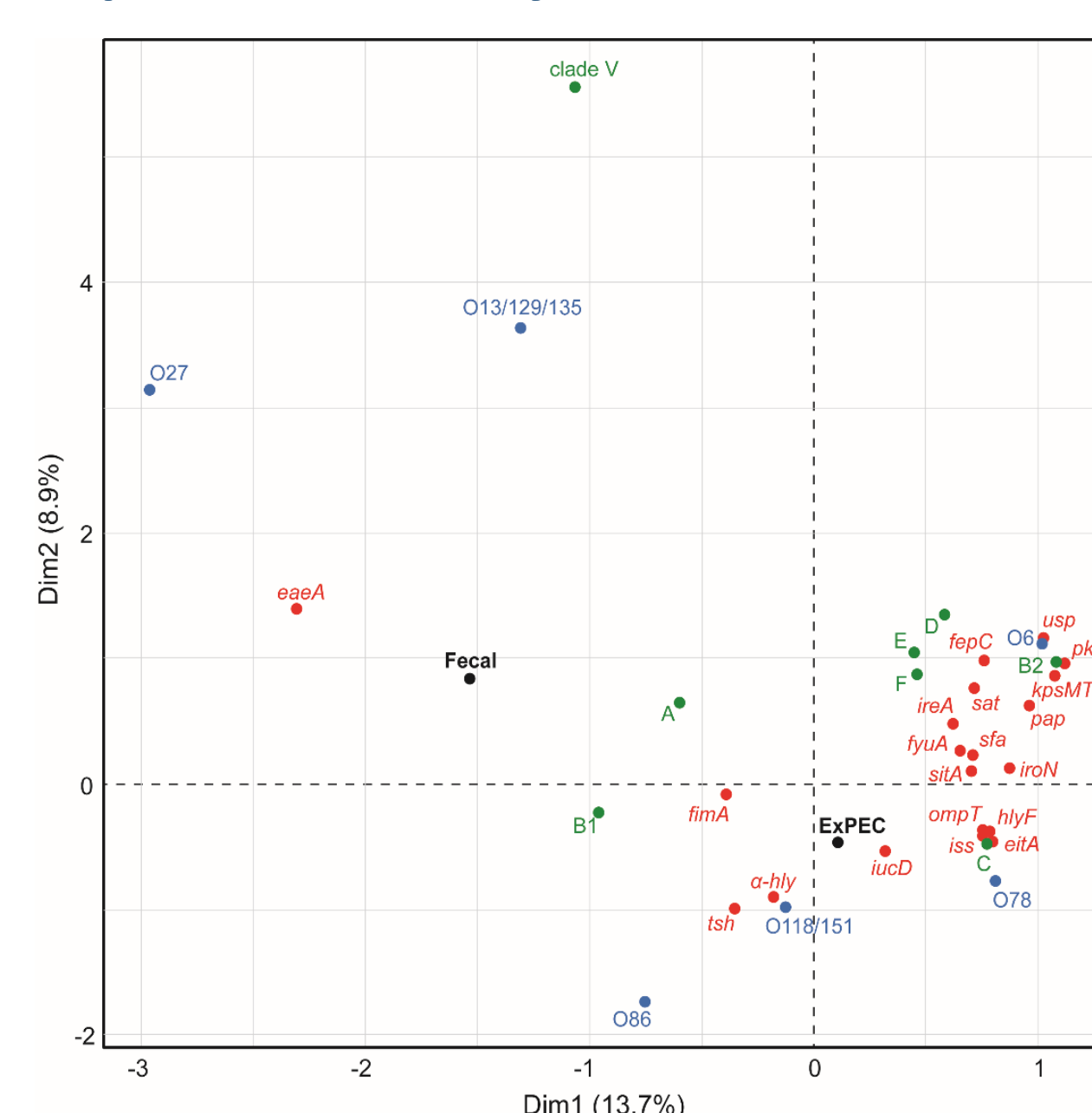


Fig. 4: Correspondence analysis of all camel *E. coli* isolates (n = 346) and their characteristics. ExPEC strains form distinct group which correlates with majority of virulence factors. Two sets of pathogenic and fecal isolates are highlighted in black, phylogenetic groups are shown in green, serotypes in blue, and virulence determinants in red. Only significantly different characteristics were used in this analysis.

Bacteriocin prevalence

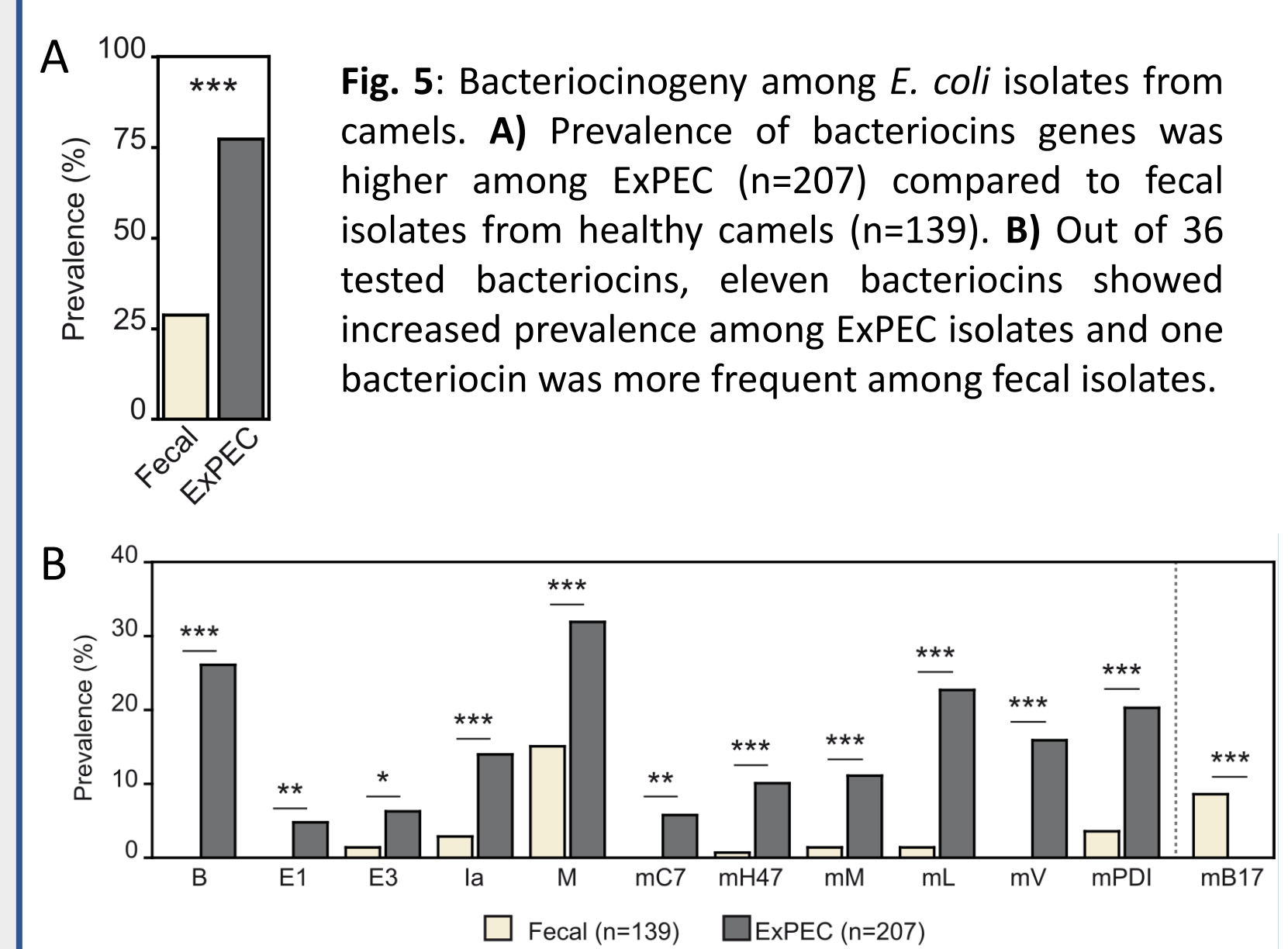


Fig. 5: Bacteriocinogeny among *E. coli* isolates from camels. A) Prevalence of bacteriocins genes was higher among ExPEC (n=207) compared to fecal isolates from healthy camels (n=139). B) Out of 36 tested bacteriocins, eleven bacteriocins showed increased prevalence among ExPEC isolates and one bacteriocin was more frequent among fecal isolates.

Correspondence analysis

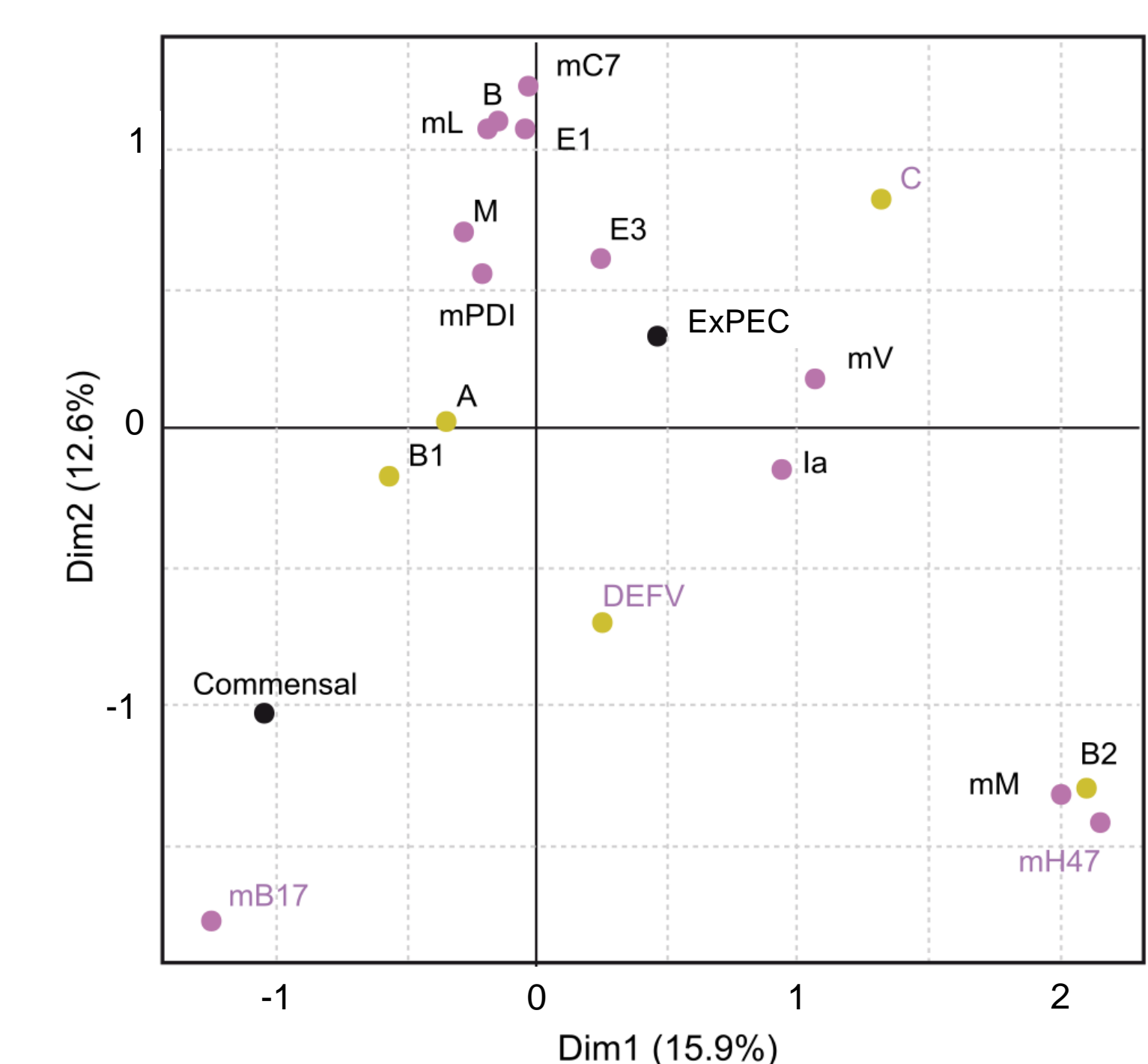
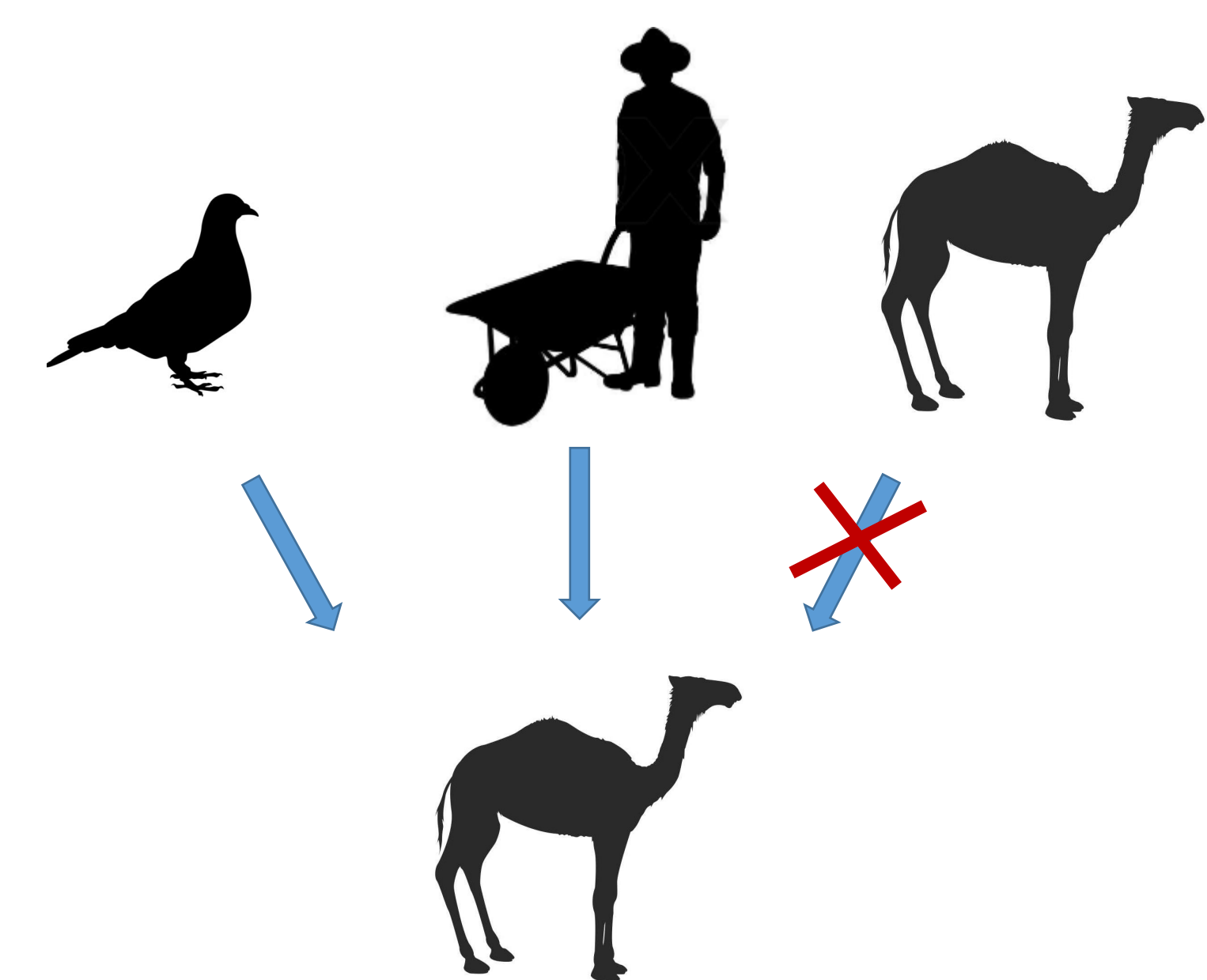


Fig. 1: Schematic distribution of phylogenetic groups and twelve bacteriocins associated with pathogens (from Fig. 5B).

Discussion

Tracing the origin of infections



Based on identified characteristics, **adult camels are not considered an important reservoir of ExPEC for their calves.**

At the same time, avian-pathogenic *E. coli* and human fecal *E. coli* do share characteristics with camel ExPEC. Therefore, we hypothesize that the source of camel infections is either **wild birds or human keepers.**

Conclusion

In conclusion, this study characterized the largest set of extraintestinal pathogenic *Escherichia coli* isolated from camel calves. We found a positive association between these isolates and various serotypes, phylogenetic groups, virulence factors, and bacteriocins. Moreover, fecal *E. coli* from healthy animals did not resemble ExPEC isolates and were found to form a relatively distinct group in the correlation analyses. Based on the analyzed data, we hypothesize that the source of camel infections is either wild birds or human keepers. This information should help in preventing of septicemic infections of camel calves and should increase the protection of camel herds.