Pathogenic, phylogenetic, and antibiotic-resistant profile of *Escherichia coli* in aquatic environments

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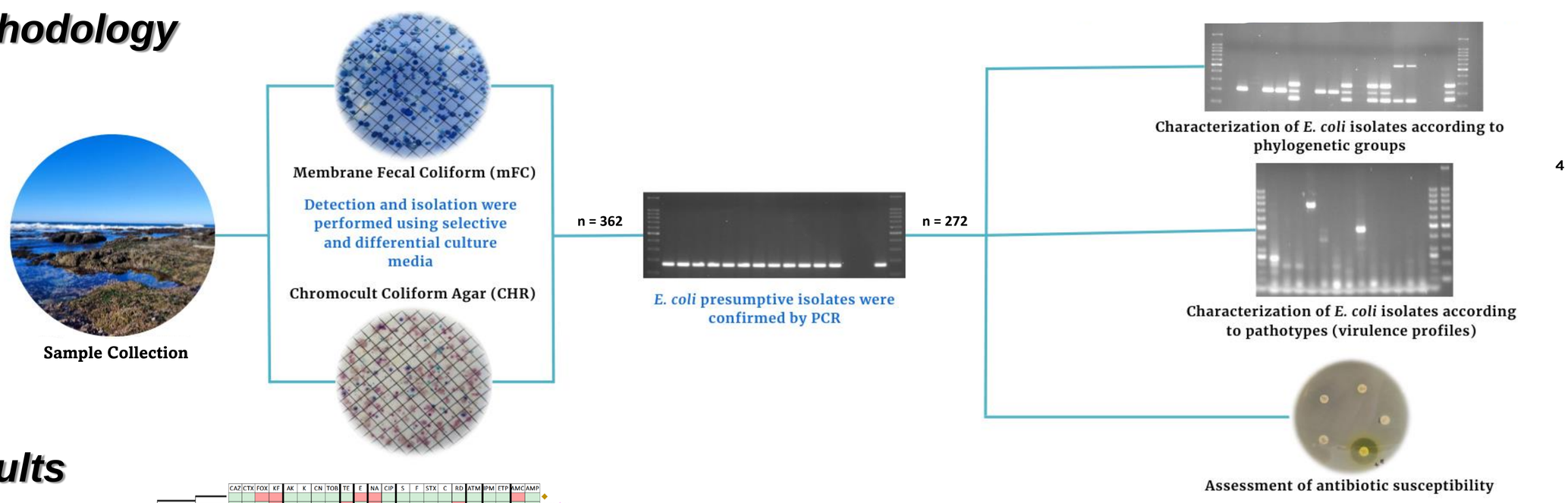
Background

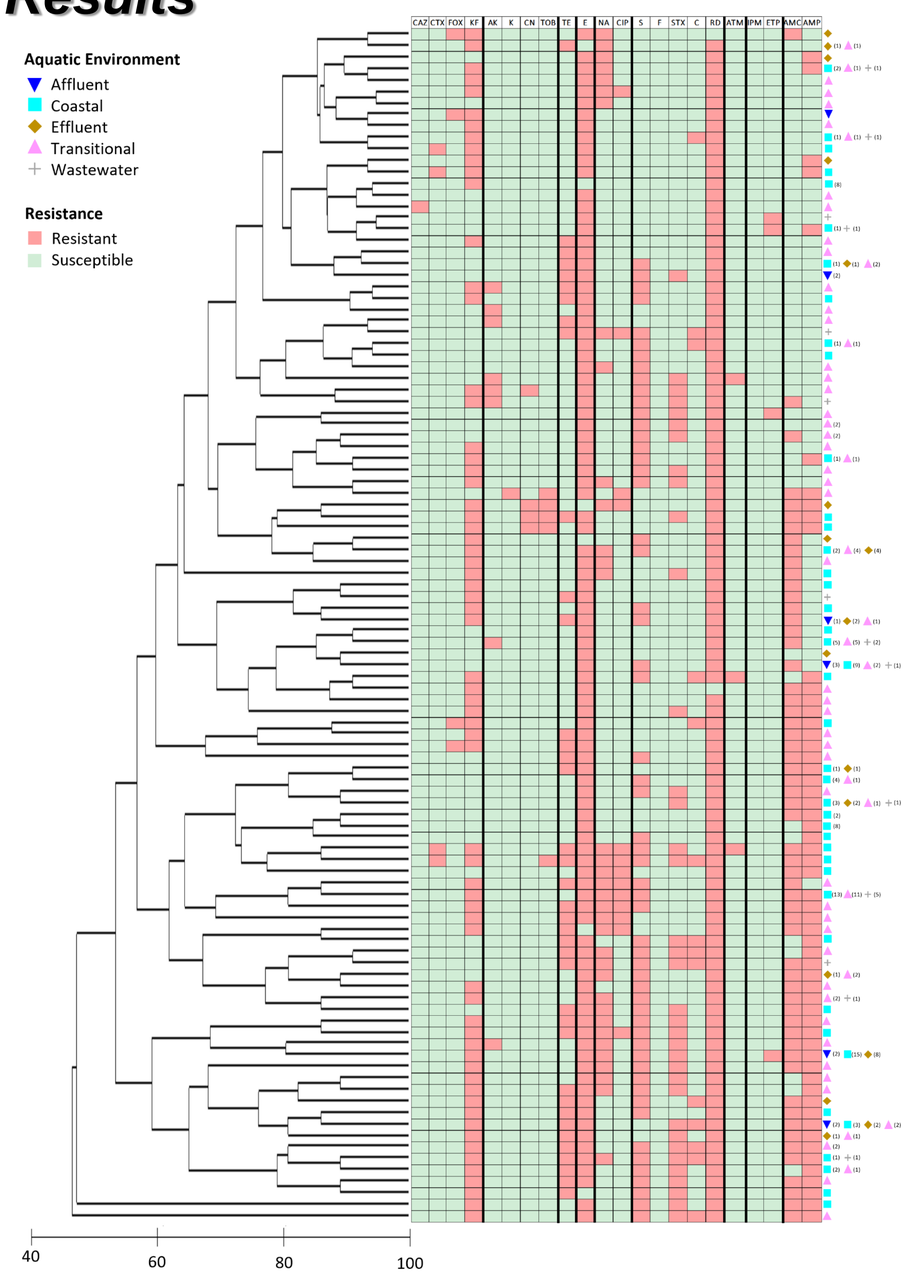
Escherichia coli is a commensal bacterium that inhabits the intestine of humans and other warm-blood animals[1], and thus it is routinely used as a microbiological indicator of fecal contamination[2] in the aquatic environment. Several *E. coli* strains can be pathogenic, causing both extra-intestinal and intestinal diseases in humans, being therefore of public health concern[3].

The aim of this study was to investigate the origin and the pathogenic profile of the fecal indicator bacteria (FIB) *Escherichia coli* in temperate Atlantic recreational waters, and to explore eventual potential implications for public health.

Methodology

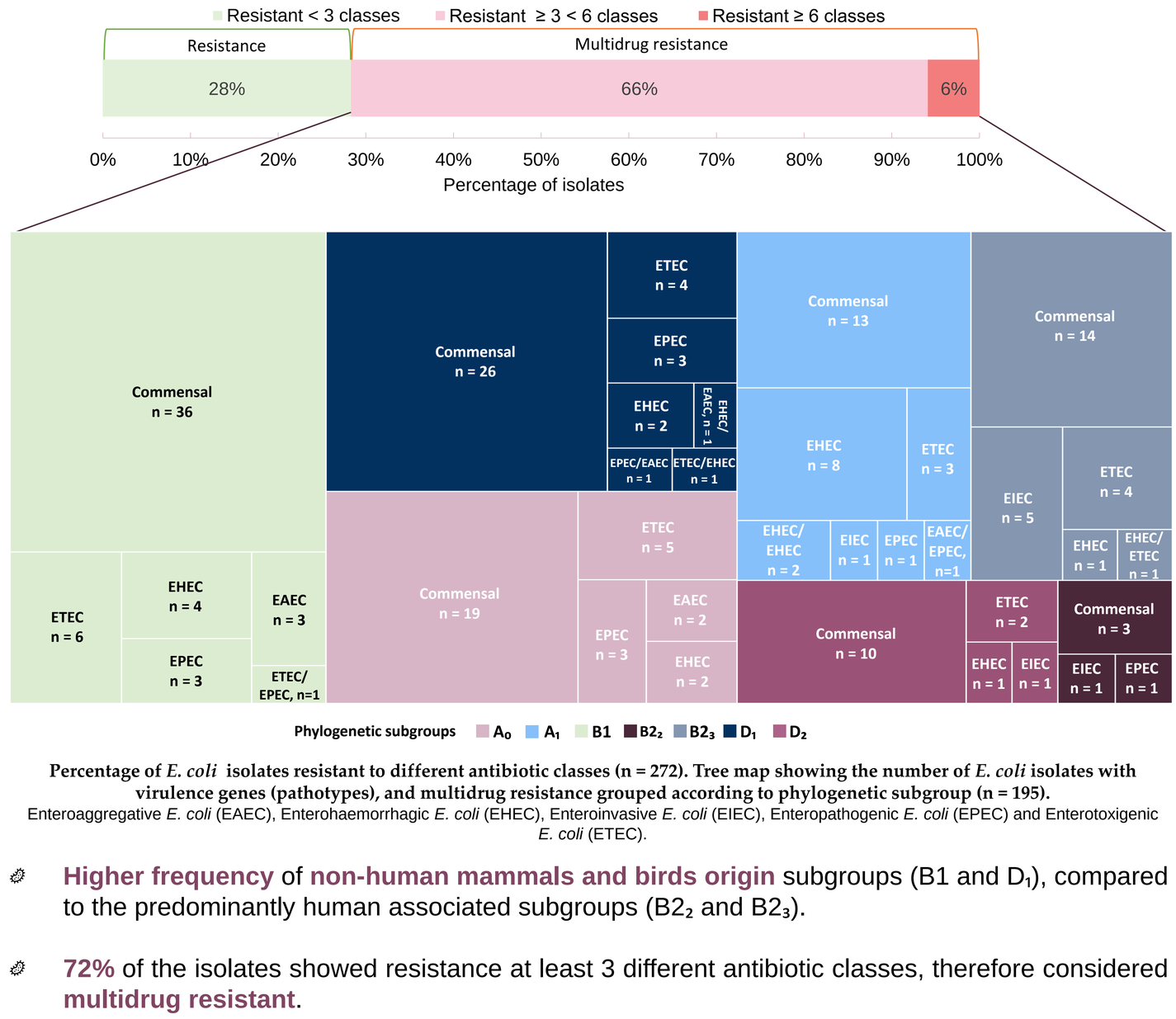


Results



Hierarchical clustering and heatmap of the antibiotic resistance profile of *E. coli* isolates according to the aquatic environmental source. Isolates with 100% of similarity were clustered together. Thicker vertical lines divided the 9 different antibiotic classes used.

From left to right: Cephalosporins – Ceftazidime 30 µg, Cefotaxime 5 µg, Cefoxitin 30 µg , Cephalothin 30 µg; Aminoglycosides – Amikacin 30 µg, Kanamycin 30 µg, Gentamicin 10 µg, Tobramycin 10 µg; Tetracyclines – Tetracycline 30 µg; Macrolides - Erythromycin 15 µg; Fluoroquinolones – Nalidixic acid 30µg, Ciprofloxacin 5 µg; Miscellaneous agents – Streptomycin 10 µg, Nitrofurantoin 300 µg, Trimethoprim – sulfamethoxazole 25 µg, Chloramphenicol 30 µg, Rifampicin 5 µg; Monobactams - Aztreonam 30 µg; Carbapenems – Imipenem 10 µg, Ertapenem 10 µg and Penicillins – Ampicillin 10 µg, Amoxicillin – clavulanic acid 30 µg.



Percentage of *E. coli* isolates resistant to different antibiotic classes (n = 272). Tree map showing the number of *E. coli* isolates with virulence genes (pathotypes), and multidrug resistance grouped according to phylogenetic subgroup (n = 195).
Enteroaggregative *E. coli* (EAEC), Enterohaemorrhagic *E. coli* (EHEC), Enteroinvasive *E. coli* (EIEC), Enteropathogenic *E. coli* (EPEC) and Enterotoxigenic *E. coli* (ETEC).

- **Higher frequency** of **non-human mammals and birds origin** subgroups (B1 and D_1), compared to the predominantly human associated subgroups ($B2_2$ and $B2_3$).
- **72%** of the isolates showed resistance at least 3 different antibiotic classes, therefore considered **multidrug resistant**.
- Among **Diarrheagenic *E. coli* isolates 75%**, exhibited **multidrug resistance**.
- Phylogenetic subgroup **A1** (non-humam mamals and humans), and group **B1** showed **higher virulence** and **multidrug resistance rates**.

Conclusions

- The outcomes highlighted the circulation of pathogenic and antibiotic-resistant *E. coli* in recreational waters. Moreover, non-human mammals and birds appear to play a key role in fecal contamination rather than sewage.
- This study emphasizes the importance of additional monitoring parameters to improve public health risk management to guarantee the safety of recreational water users.

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References

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Acknowledgments

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