

Genomic characterization of weaning-associated porcine *Escherichia coli* in Belgium

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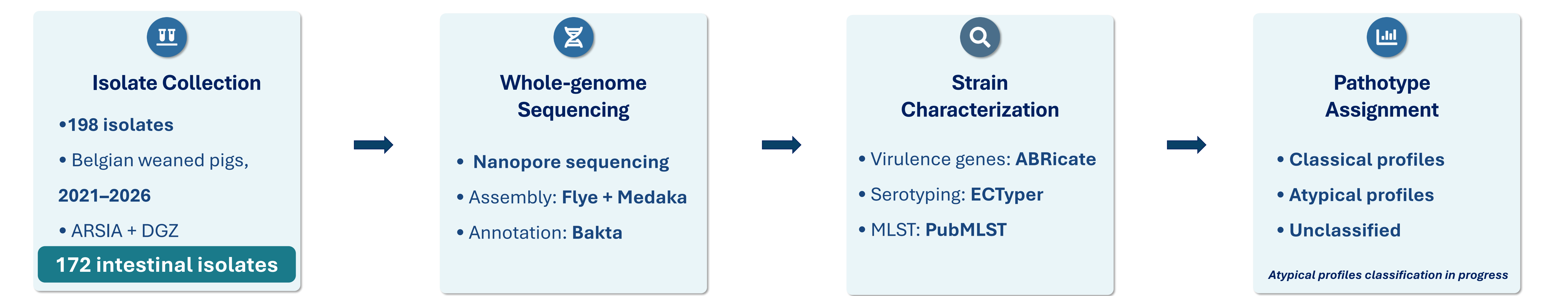
INTRODUCTION



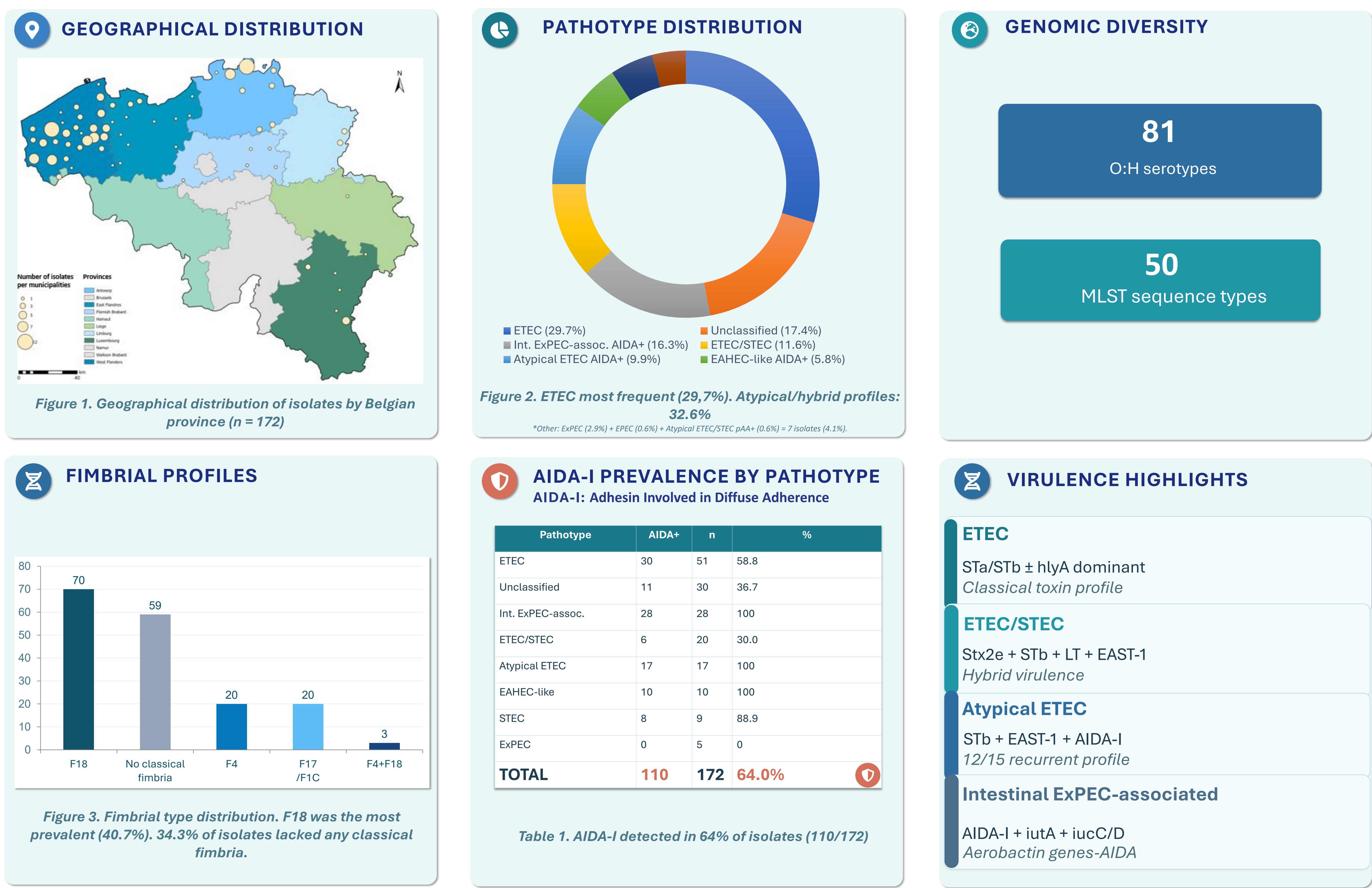
OBJECTIVE

To characterize the genomic and virulence diversity of weaning-associated porcine *E. coli* circulating in Belgium

MATERIALS & METHODS



RESULTS



CONCLUSION & PERSPECTIVES

- ETEC was the predominant pathotype, but a substantial proportion of isolates displayed atypical or hybrid virulence profiles, highlighting the complexity of the current *E. coli* population
- Weaning-associated porcine *E. coli* circulating in Belgium exhibit a high level of genomic diversity, with 81 O:H serotypes and 50 MLST sequence types identified
- AIDA-I was widely distributed across multiple pathotypes, suggesting a broader role in porcine *E. coli* populations than traditionally recognize
- These findings provide an updated overview of the genomic and virulence diversity of weaning-associated *E. coli* in Belgium and support further investigations into antimicrobial resistance and the classification of emerging atypical pathotypes

NEXT STEPS

AMR profile identification of the strains