

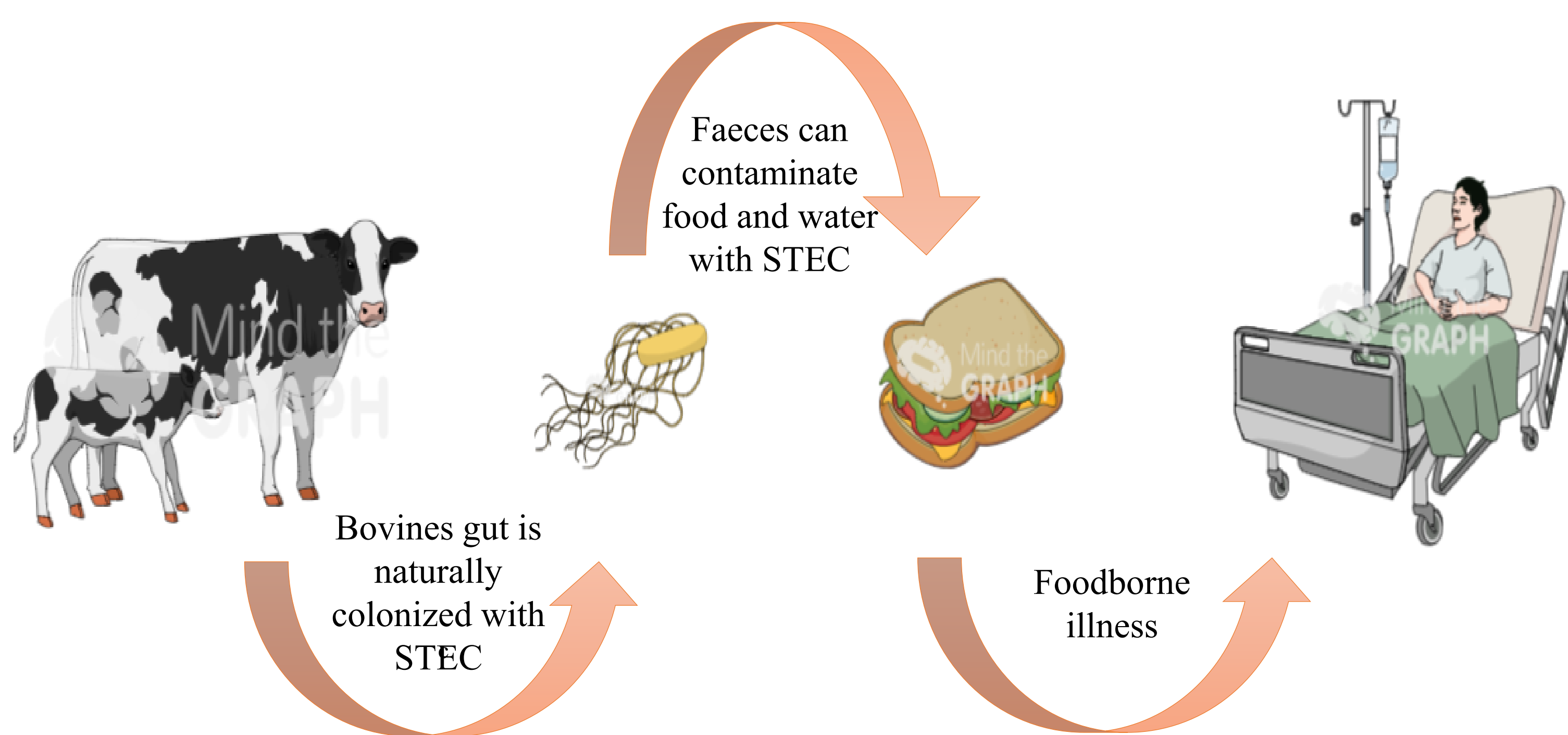
PREVALENCE OF SHIGATOXIGENIC *Escherichia coli* IN BOVINE CATTLE: A SURVEY IN THE NORTH REGION OF PORTUGAL

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INTRODUCTION

- Shiga toxin-producing *Escherichia coli* (STEC) strains are food-borne pathogens;
- STEC are transmitted to humans through many different routes, but mainly through consumption of contaminated foods;
- The most common STEC serotype causing human diseases is *E. coli* O157:H7, but other serotypes are associated with severe diseases;
- Ruminants, especially **cattle**, are a major reservoir for O157 and non-O157 STEC;



- STEC strains are characterized by the production of Shiga toxins (Stx) that are encoded by two genes *stx1* and/or *stx2*;
- Intimin protein (*eae* gene) is a virulence factor associated with severe outcomes of STEC-associated diseases.

OBJECTIVES

To assess the prevalence of STEC in dairy cattle faeces in the North of Portugal and to determine the genetic pool of STEC virulence genes: *stx1* and *stx2* and *eae*.

METHODS

- Samples:** faecal specimens were collected from the rectum of healthy dairy cattle (n=329):
 - Adult lactating cows (n=194);
 - Heifers (n=135), ages 6 to 18 months;
- Period and local:** between March and June 2019, at milk farms (n=17) - North of Portugal;
- Samples were enriched and analysed by real time PCR (qPCR) to detect the presence of *stx1*, *stx2* and *eae* in accordance to ISO/TS 13136:2012(E);
- Conventional PCR was used to detect *stx* subtypes (*stx1a*, *stx1c*, *stx1d*, *stx2a*, *stx2b*, *stx2c*, *stx2d*, *stx2e*, *stx2f*, and *stx2g*) according to the guidelines of the VTEC European Union Reference Laboratory;

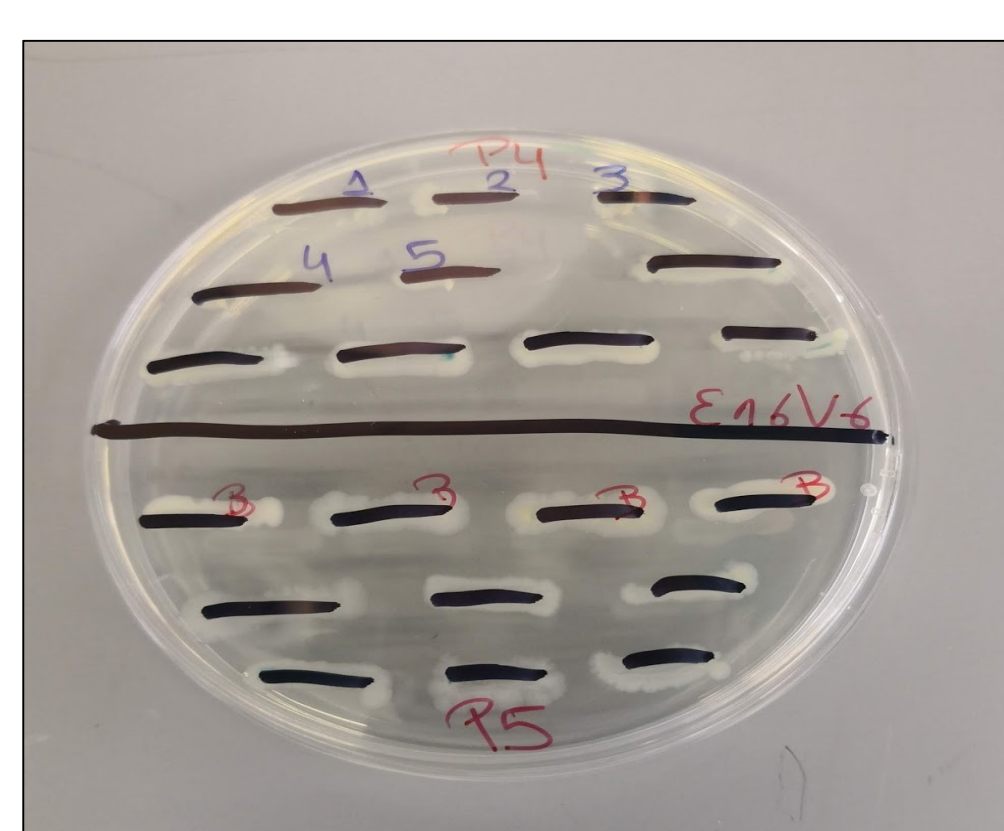
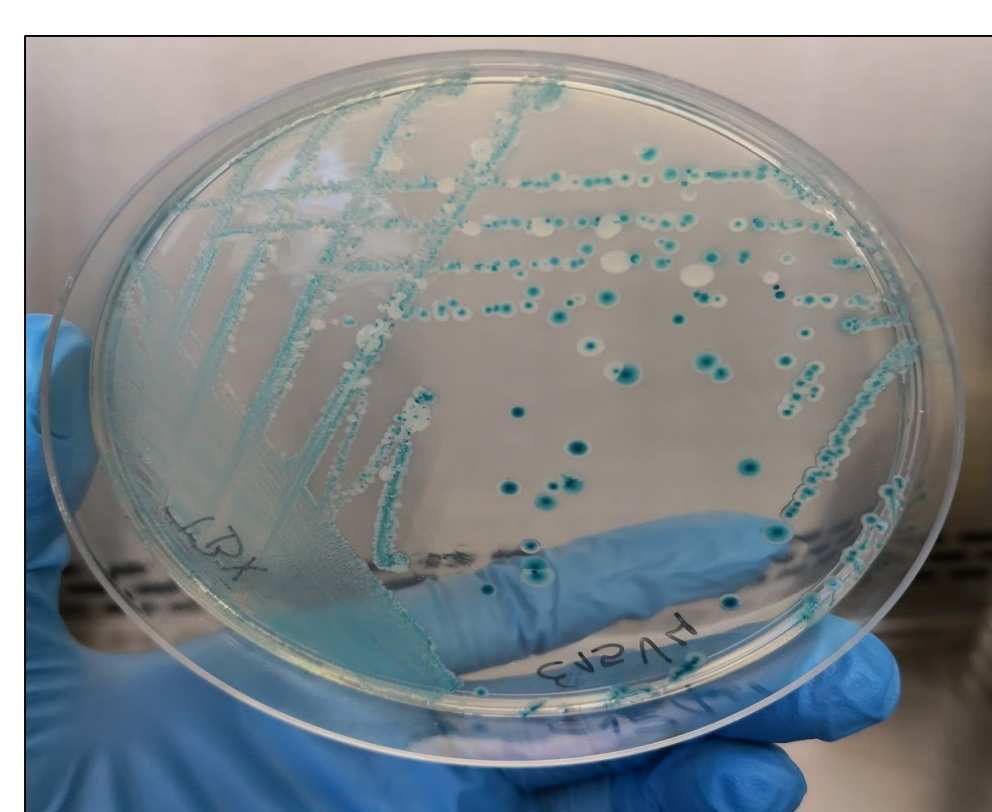


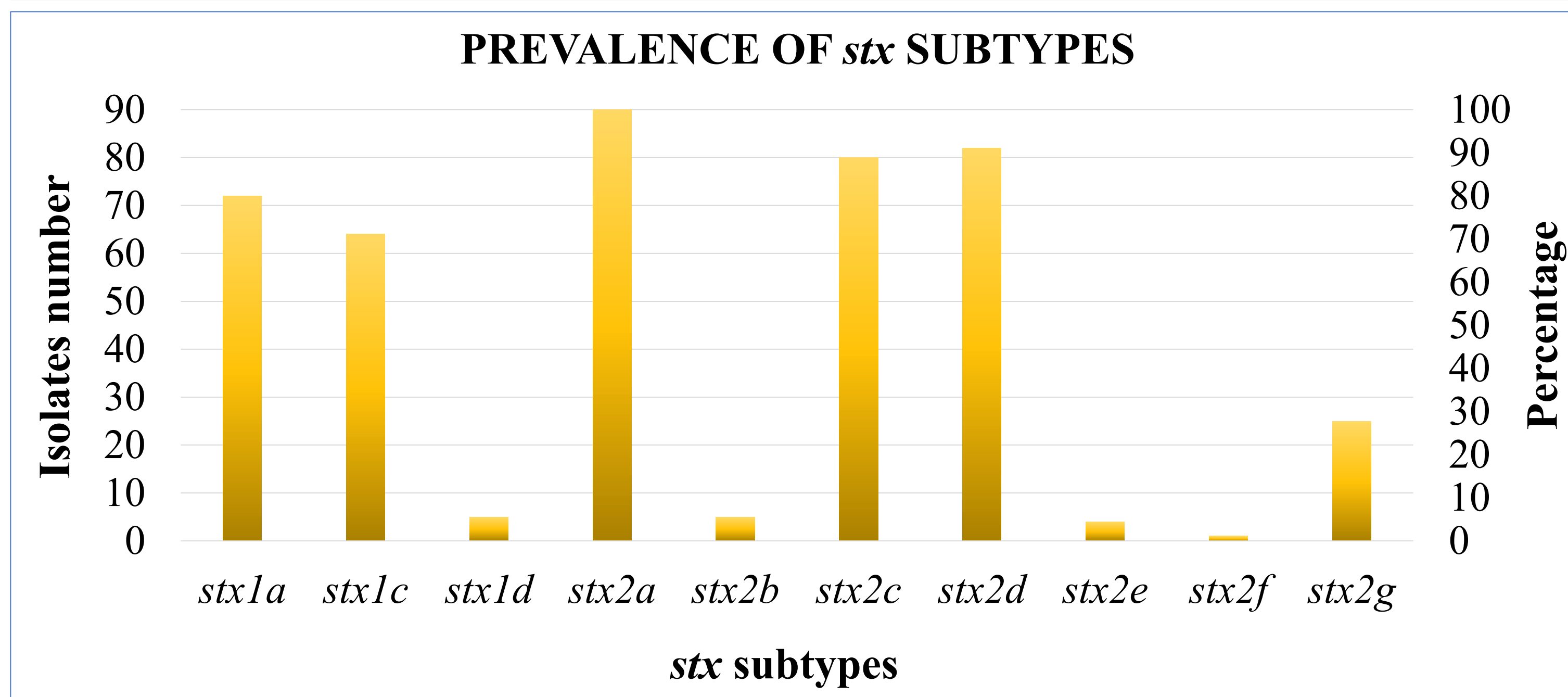
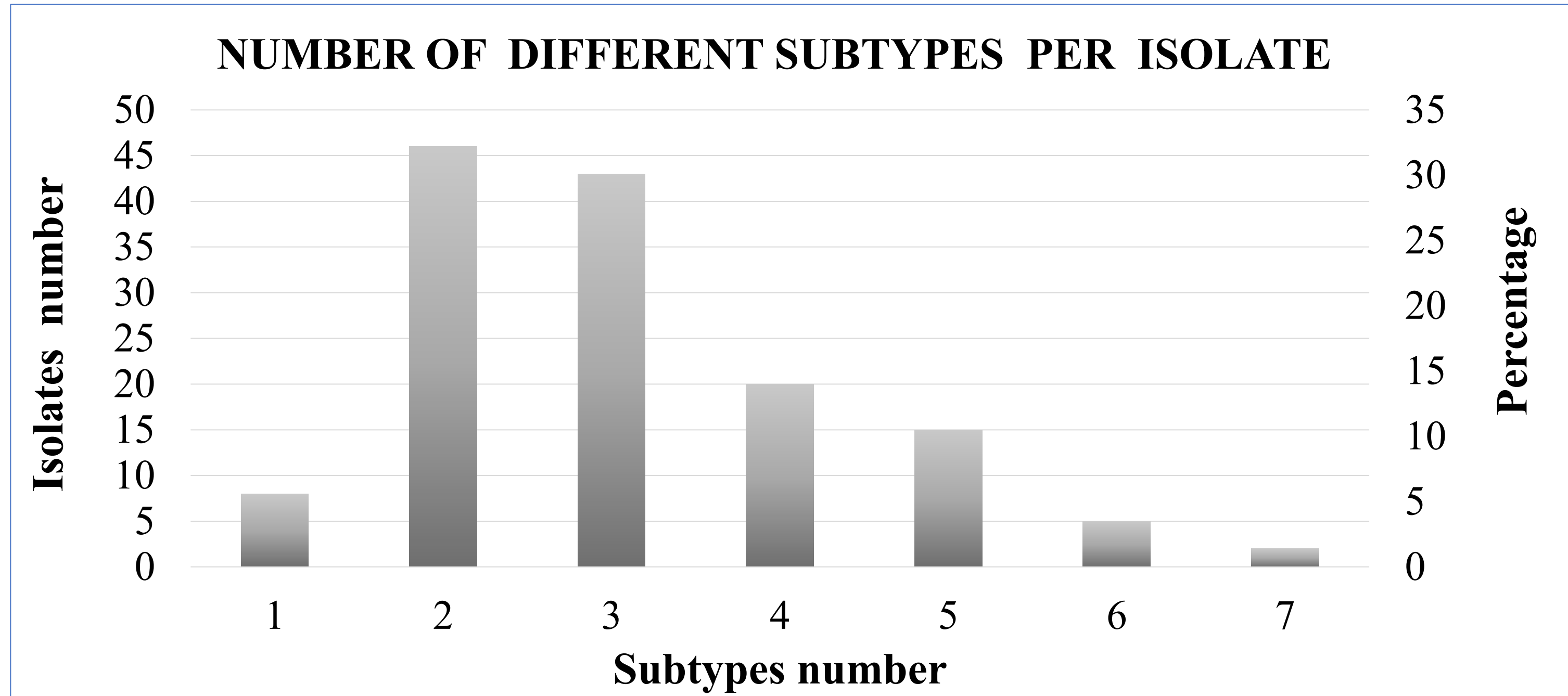
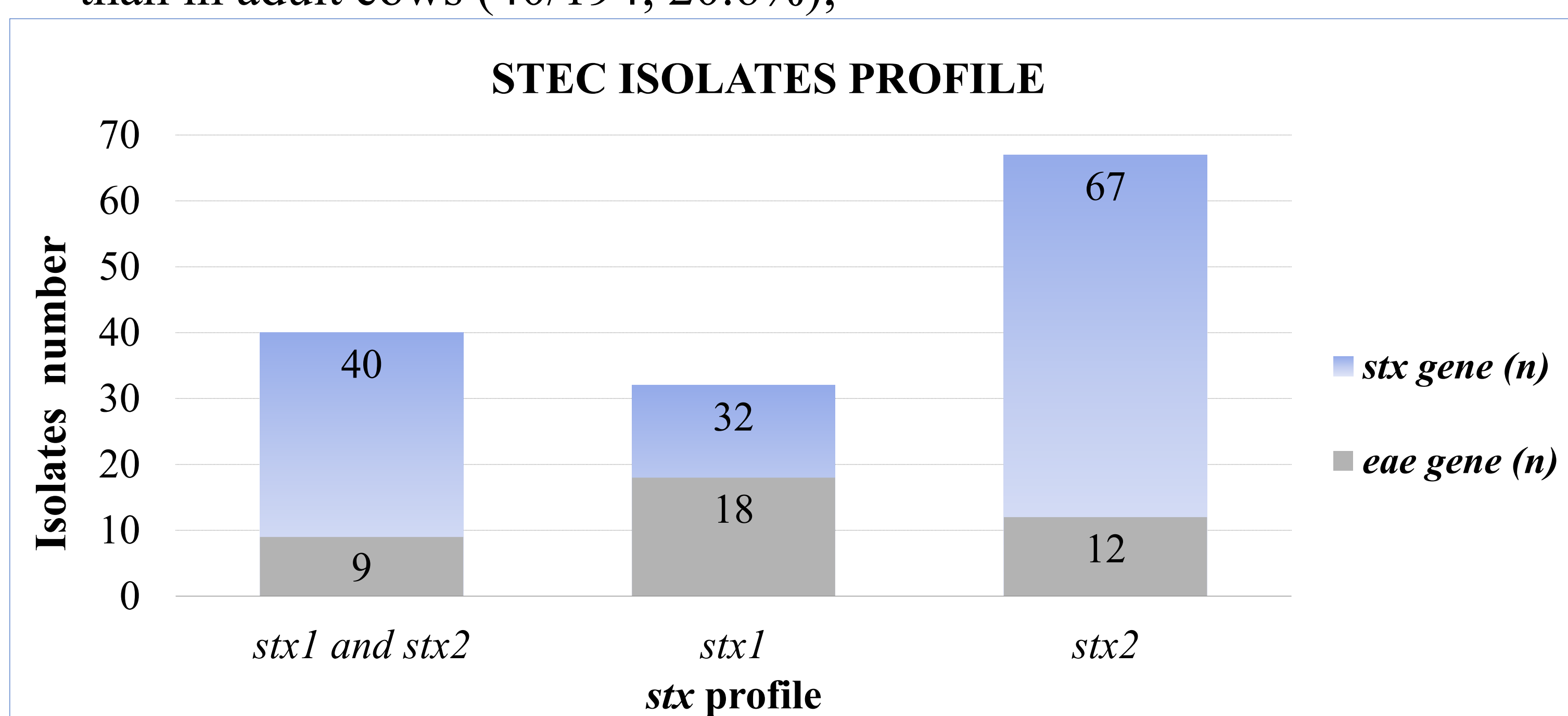
Figure 1 - *Escherichia coli* on the selective medium TBX (top image) and point inoculation on Nutrient Agar showing two pools of *E. coli* colonies from a STEC suspect sample (bottom image).



Figure 2 - Image of a milk farm, farm number 7, enrolled in the study.

RESULTS

- A total of **139** isolates were recovered from 108 positive animals (dairy cows and heifers) with a prevalence of 32,8%.
- STEC prevalence was significantly higher in heifers (68/135; 50.4%) than in adult cows (40/194; 20.6%);



- Subtypes *stx1a* and *stx1c* occurred alone or in combination with other subtypes;
- Stx1d* was only found in combination with *stx1a* and *stx1c*;
- No strains carried *stx2b* and *stx2d* alone;
- For the isolates carrying *stx1* and *stx2* simultaneously, the most common combination was *stx1a*, *stx1c*, *stx2a*, *stx2c* and *stx2d*.

CONCLUSION

- STEC prevalence in dairy cattle is high;
- A diverse combination of Shiga-toxin genes was found on isolates;
- Strains producing subtype Stx1a, Stx2a, Stx2c, or Stx2d were common and these toxins are often associated with development of human serious disease;
- Future strategies are needed to mitigate the presence of STEC in cattle and then reduce the possible contamination of food and, thus, humans.

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