INTRODUCTION

Background: Shiga toxin-producing Escherichia coli (STEC) O157:H7 causes gastrointestinal disease in humans that may lead to the development of haemolytic uraemic syndrome (STEC-HUS) due to the action of Shiga toxin (Stx). The stx gene is located on a bacteriophage and can be divided into subtypes. Severe disease is significantly associated with STEC strains carrying the Stx2a subtype. In the UK, the burden of severe gastrointestinal disease caused by STEC O157:H7 can be attributed to strains belonging to one of three evolutionary sub-lineages; I/II, Ic and Ib. From 1983 until the mid-1990s, lineage I/IIa was most commonly associated with clinical disease; lineage Ic was dominant from 1996 until 2010; and lineage Ib emerged in 2010.

Objectives: To investigate whether the stx2a encoding by each lineage over time is located on the same bacteriophage.

Impact: Analysis of the stx2a encoding bacteriophage will provide insight on how highly pathogenic STEC strain emerge.

METHODS

Historically relevant strains of STEC O157:H7 from each sub-lineage and STEC O157:H7 strain 9000 (a publically available sequence) were sequenced using the MinION Platform to analyse the stx-encoding bacteriophage.

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<td>PT2/123</td>
<td>PT12</td>
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<td>1996-2012</td>
<td>2012-2018</td>
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Table 1: Characteristics of UK isolates sequenced in this study

Sequences were assembled and annotated, and the stx-encoding bacteriophage were identified and aligned for comparison with relevant reference strains

RESULTS

- Easyfig comparisons (Figure 3) showed both conserved regions and regions of variation between the of stx2a-encoding bacteriophage from each of the three lineages. In sub-lineages I/II and Ic, the stx-bacteriophage insertion (SBI) site of the stx2a-encoding bacteriophage was argW, whereas in sub-lineage Ib the SBI site was sbcA.
- Easyfig comparisons (Figure 4) revealed that the stx2a-encoding phage from the recently emerged sub-lineage Ib and the stx2c-encoding phage from sub-lineages I/IIa and Ic were highly conserved. The site for the stx2c-encoding bacteriophage from sub-lineages the stx2c-encoding phage from sub-lineages I/IIa and Ic was sbcA.

CONCLUSIONS

- This data indicate that bacteriophage can acquire either stx2a or stx2c.
- Furthermore, this data provides evidence that there are a variety of different stx2a-encoding bacteriophages circulating in the UK, and that the stx2a-encoding bacteriophage present in the strains belonging to sub-lineage I/IIa that caused the early outbreaks of STEC-HUS was not the same stx2a-encoding bacteriophage subsequently acquired by strains belonging to lineages Ic or Ib.

REFERENCES