

Draft Genome Sequence of *Enterobacter hormaechei* subsp. *steigerwaltii* Strain BEI01

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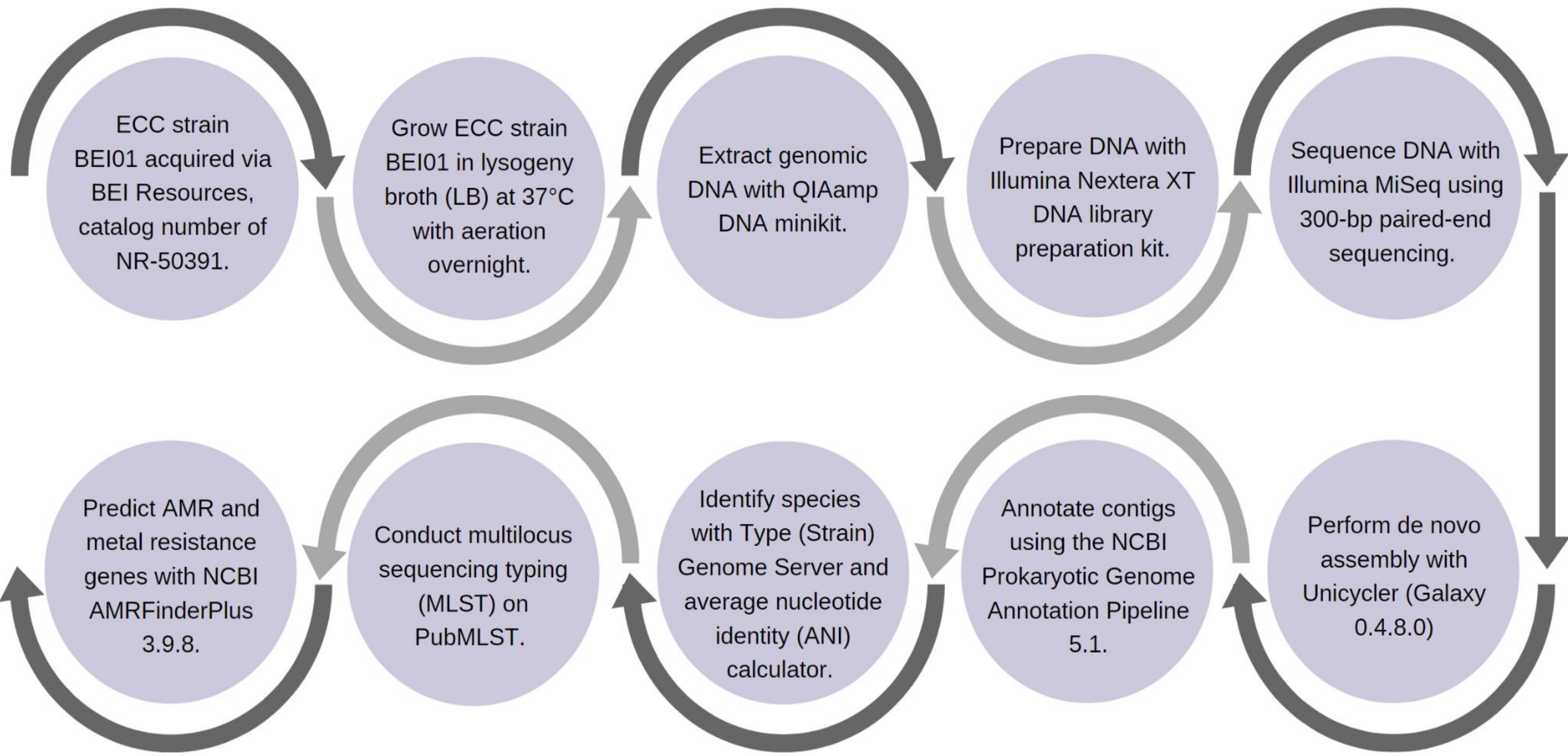
AIM

To report the draft genome sequence of *Enterobacter hormaechei* subsp. *steigerwaltii* strain BEI01

INTRODUCTION

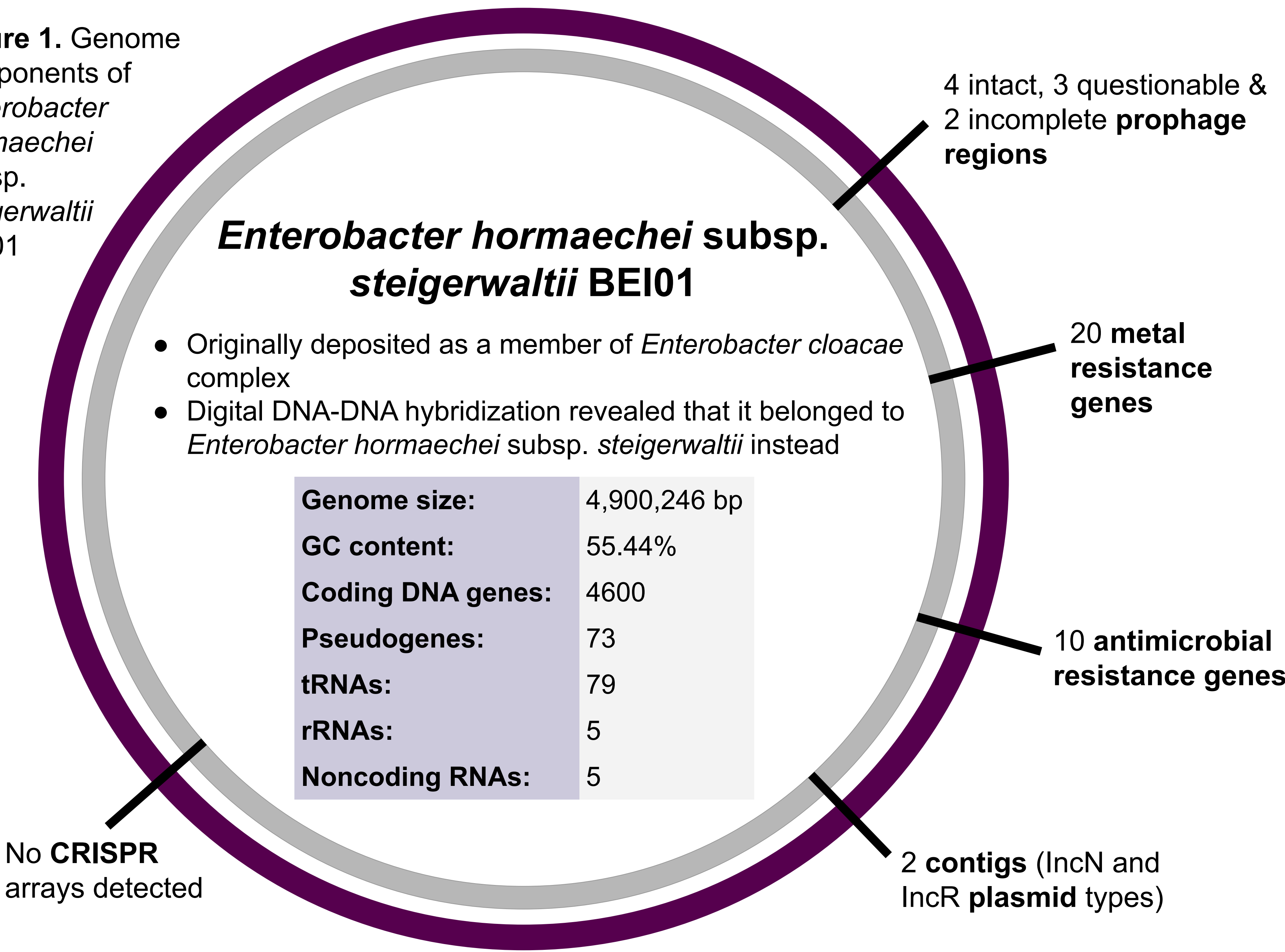
- Enterobacter cloacae* complex (ECC) comprises six different species—*E. cloacae*, *E. asburiae*, *E. kobei*, *E. hormaechei*, *E. ludwigii*, and *E. nimipressuralis*, that can cause a range of nosocomial infections
- As part of the *Enterobacteriaceae* family, the *Enterobacter cloacae* complex (ECC) can acquire antimicrobial resistance (AMR), resulting in multidrug-resistant isolates
- Species identification of these opportunistic pathogens allows better molecular epidemiology study of its transmission and AMR
- Draft genome sequence revealed the bacterium to be a multidrug-resistant strain with remarkable antimicrobial and metal resistance genes

METHODS



RESULTS

Figure 1. Genome components of *Enterobacter hormaechei* subsp. *steigerwaltii* BEI01



Class	Gene(s)
Antimicrobial resistance genes	
Aminoglycoside	<i>aadA1</i> , <i>aac(6')-Ib'</i>
Beta-lactam	<i>bla</i> _{ACT-17'} , <i>bla</i> _{KPC-2'} , <i>bla</i> _{OXA-9'} , <i>bla</i> _{TEM}
Fosfomycin	<i>fosA</i>
Phenicol	<i>catA</i>
Quinolone	<i>oqxB</i>
Trimethoprim	<i>drfA14</i>
Metal resistance genes	
Arsenic	<i>arsC</i> , <i>arsB</i> , <i>arsA</i> , <i>arsD</i> , <i>arsR</i>
Mercury	<i>merE</i> , <i>merD</i> , <i>merA</i> , <i>merC</i> , <i>merP</i> , <i>merT</i> , <i>merR</i>
Silver	<i>silE</i> , <i>silS</i> , <i>silR</i> , <i>silC</i> , <i>silF</i> , <i>silB</i> , <i>silA</i> , <i>silP</i>
Others	
Acid resistance	<i>asr</i>
Efflux pump	<i>fieF</i>
Siderophore	<i>iroN</i>

Table 1: List of antimicrobial resistance genes and metal resistance genes present in *Enterobacter hormaechei* subsp. *steigerwaltii* BEI01

DISCUSSION AND CONCLUSION

- Enterobacter hormaechei* subsp. *steigerwaltii* BEI01 contains 10 antimicrobial resistance genes (ARG) against 6 classes of antimicrobials, and 20 metal resistance genes (MRG) against 3 different metals (Table 1)
- Presence of *bla*_{KPC-2} highlights that the isolate belongs to sequence type 93, a global clone of carbapenemase-producing *Enterobacter* species (1)
- The MRG are also located in close proximity to ARG
- Close proximity of MRG and ARG might be of significance due to metals being used in agriculture (2), or found in metal-polluted urban soils (3), hence selection pressure for metal-resistant bacteria living in these environments may also indirectly select for the ARG
- Further investigation needed for MRG and their role in co-selection of ARG, and their potential role in allowing bacteria to persist in the hospital or the natural environment

REFERENCES

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