# Quest for the descent of the German *E. coli* outbreak strain TY2482 - out of Africa? or out of Germany?

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## INTRODUCTION

The recent outbreak of the *Escherichia coli* infection in Germany reportedly has killed 35 people and sickened about 4000. Similar outbreaks were reported in 2001 and 2002 in Germany and Central Africa respectively. In order to detect all possible connections among these three outbreak strains and to extract the most virulent genes responsible for the increased pathogenicity of the present German strain, whole genome sequence data of the two isolates (*E. coli* TY_2482 & LB226692) were analyzed.
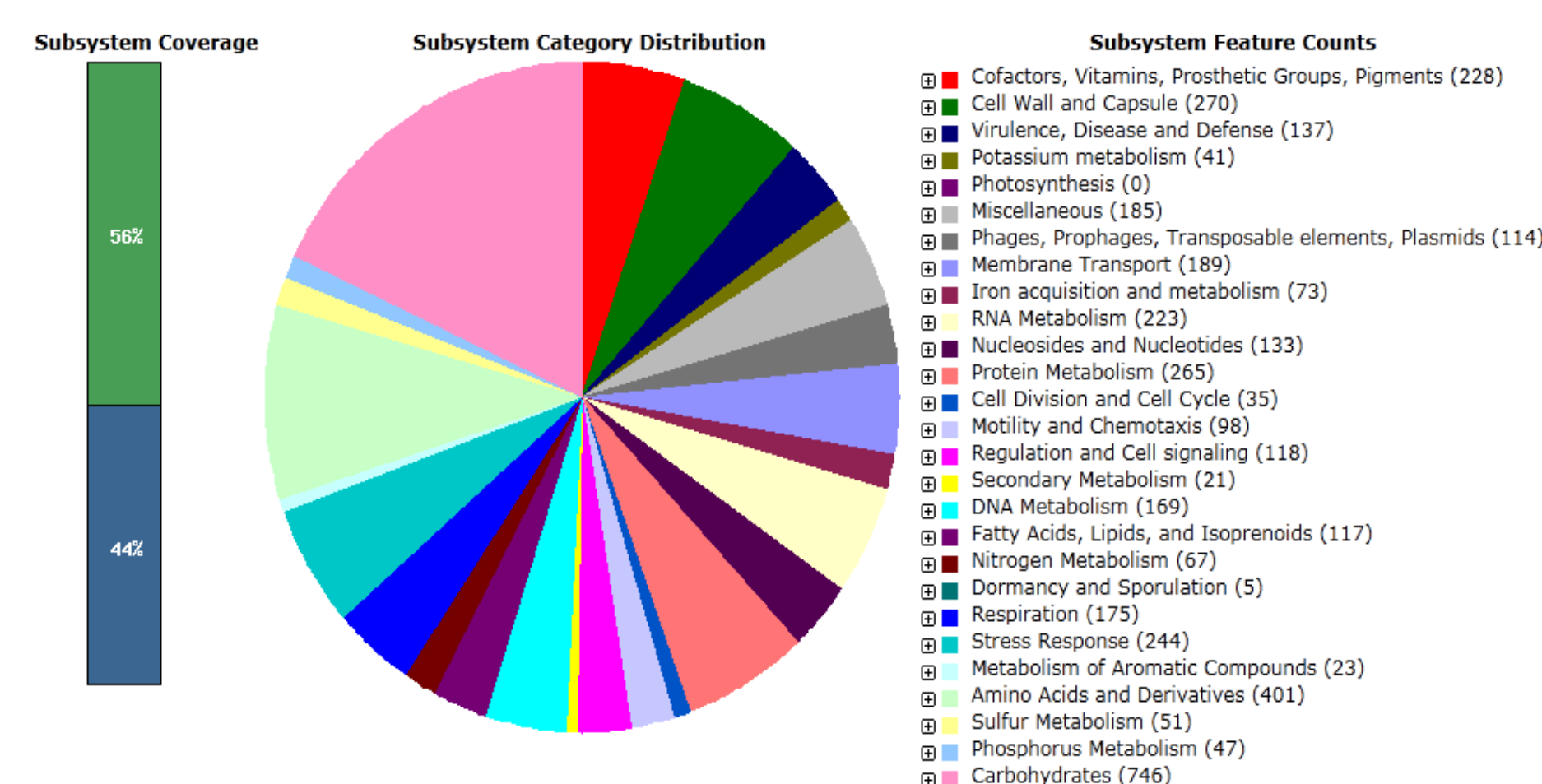
## Assembled contigs of outbreak strain *E. coli*_TY_2482

**RAST**   **MAUVE Alignment**   **BLAST Analysis**



**Fig1. The RAST generated subsystems category distribution for *E.coli* TY_2482**
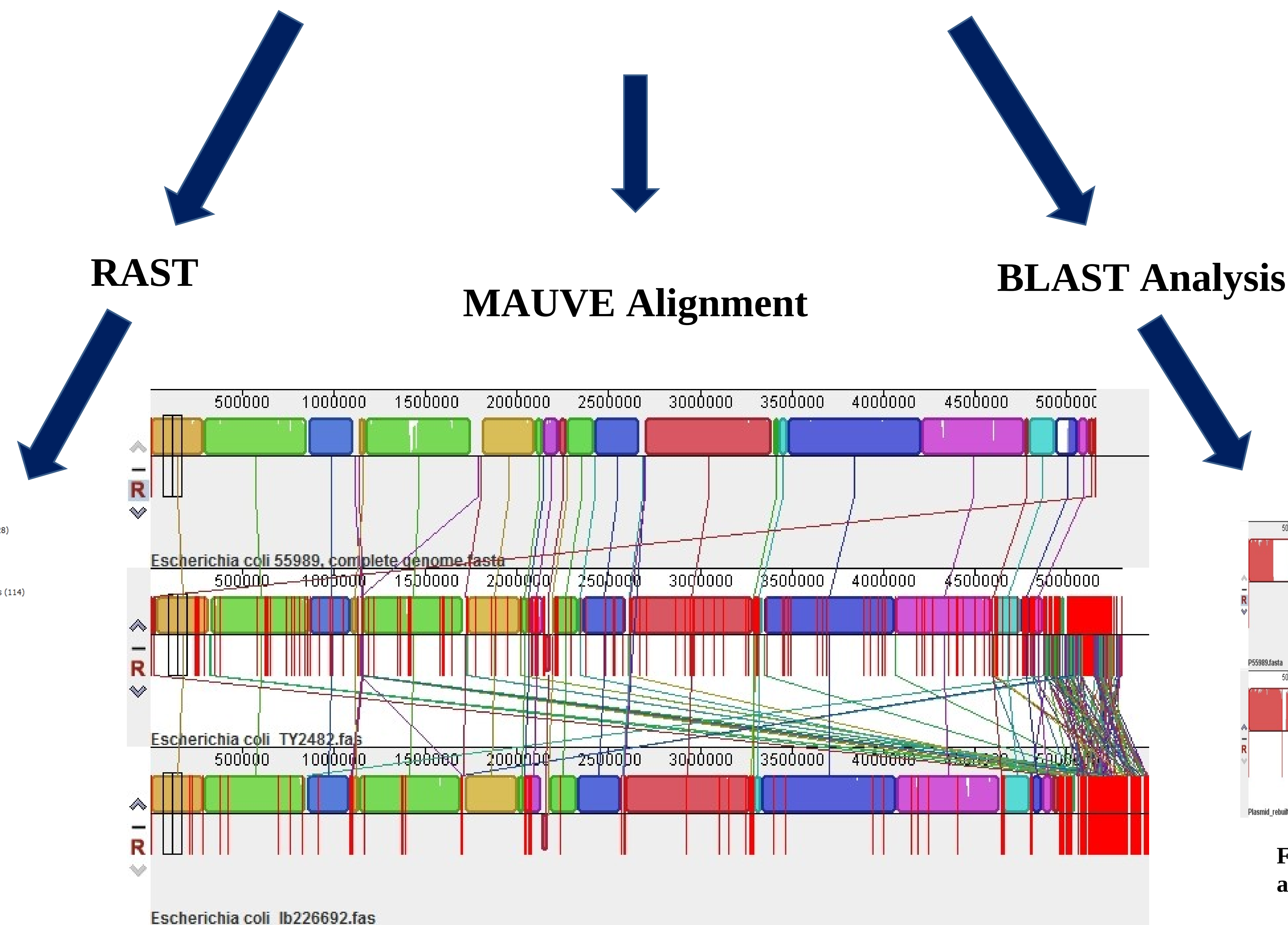


**Fig2. Mauve alignment of *E. coli* 55989 Vs *E. coli* TY_2482 Vs *E. coli* LB226692**
**In red: The regions highlighted in red in the above alignment are specific to the two strains TY-2482 & LB266692.**

## IMPORTANT FINDINGS

• The *E. coli* isolate TY-2482 genome size is 5299150bp with a G+C content of 51.63% and a coding percentage of 86.8%.
• The two outbreak *E. coli* isolates TY-2482 and LB226692 are genetically similar to 'African' strain (*E. coli* 55989).
• The *E. coli* 55989 plasmid sequences were also found in the contigs of TY-2482.
• *E. coli* TY-2482 also contained stx2 subunits A & B which correlates with the presence of Shiga toxin. Our analysis also confirmed the presence of tellurite resistance gene in the 2011 outbreak strain.
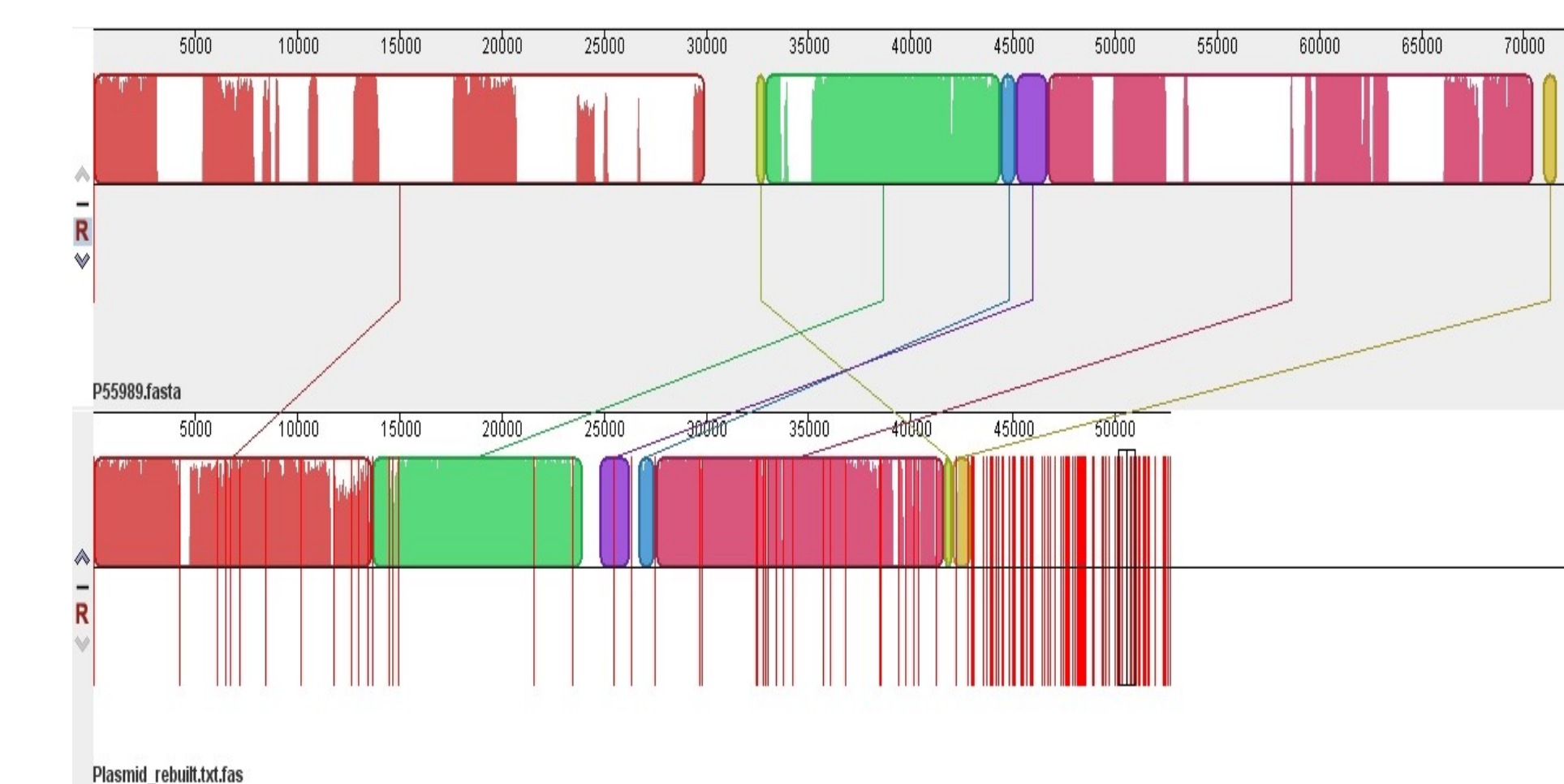• LEE flanking regions were found in the TY-2482 genome.



**Fig3. Mauve alignment: *E.coli* 55989p Vs BLASTn analyzed raw extracted plasmid of *E. coli* TY_2482**

## METHODOLOGY

• The curated assembly data of TY-2482 available in public domain ( ftp://ftp.genomics.org.cn/pub/Ecoli_TY-2482 ) was used for analysis.
• The annotation was performed using RAST (Rapid Annotation using Subsystem Technology) (Fig. 1).
• The mauve alignments were generated for the following pairs of sequences
*E. coli* 55989 Vs *E. coli* TY-2482 Vs *E. coli* TY-2482 (Fig. 2)
*E. coli* 55989 vs raw plasmid (Fig. 3)*
(*Each contig of the 513 contigs were aligned against *E. coli* 55989 (taxid:585055). Raw plasmid sequences were manually extracted from these alignment data)
• The sequences coding for stx2, tellurite resistance genes as well as the locus of enterocyte effacement (LEE) flanking regions were analyzed.

## REFERENCES

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6. @*BGI_Events* on twitter

## CONCLUSION

Analysis of the two genomes (2011 outbreak strains) with the EAEC 55989 suggests a strong clonality. Further, it is possible that the *E. coli* TY_2482 isolate (2011) could be an EAEC by makeup, as also observed for isolate 55989. Interestingly, We could locate a homologue of tellurite resistance gene in *E. coli* 55989 genome, although we failed to find shiga toxin encoding co-ordinates which could have been missing due to mistakes in sequencing/annotation of the strain 55989. Finally, it is tempting to suggest that the strain *E. coli* TY_2482 or its predecessor was endemic to Germany and that it could have emerged in Central Africa (2002) and therefore might have acquired a pandemic potential.

## ACKNOWLEDGEMENTS