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Collaboration on Colistin resistant E. coli

1 message

Clinton Moodley <clintonmoodley@yahoo.com> Tue, Jan 29, 2019 at 5:07 PM
To: Katie Lennard <katieviljoen@gmail.com>
Cc: Clinton Moodley <Clinton.Moodley@nhls.ac.za>

Hi Katie,

Thanks for the great input at our meeting today. So excited to be working together again!

Just wanted to give you a brief heads-up on the **E. coli** project data, which you will use to setup and test the new pipeline. I may be over-simplifying, but please let me know if you need more detail.

In 2016 a new resistance element for the antibiotic Colistin was described. Resistance to this antibiotic was until then usually due to a chromosomal mutation and was rather uncommon. This drug is reserved for high level resistant infections in humans but is widely used in cattle as a prophylactic drug to prevent infection. Due to an increase in number or resistant bacteria to colistin, researchers in China investigated a potentially new resistance element and describe the **mcr**-1 colistin resistance gene (Liu **et al**., paper attached). What was so interesting about this gene is that it is found on a plasmid. Plasmids are extrachromosomal DNA molecules which can be shared between closely related bugs. This is really important, since it has allowed this new resistance element to spread rapidly from animals to humans. Since the first report of the element, there have been several reports of it around the world, with about 7 genotypes described already, and it has been observed in other bacteria like **Klebsiella**. Another interesting fact is that the resistance element is present on different plasmids. This means it is recombined into an existing plasmid when it's taken up. The plasmid backbones can have other resistance elements on them already, making the bacteria multidrug resistant. The plasmid backbones are usually unique to the location where they are identified.

After the first report of mcr-1 we started to collect **E. coli** at GSH which were resistant to colistin. We collected isolates for about a year in 2016 as part of an honours project. We collected and screened all the resistant isolates for the **mcr**-1 and **mcr**-2 genes using conventional PCR. We identified 17 isolates which were mcr-1 positive (all mcr-2 negative) and proceeded to do Illumina WGS on all of them. At this stage I've done preliminary data analyses, but on an isolate for isolate basis. We would like to publish this as an investigation of emergence and spread, but need to complete the bioinformatics on the isolates. This would be in line with the needs for the project we discussed today and will require the same workflow. I used a number of tools at http://www.genomicepidemiology.org/ for my preliminary data analysis. The isolates do not appear to be clonal over the period, but there is some overlap. The most important feature is the plasmids the resistance elements are found on, since these may be similar, even thought the genome is different between the strains, as the plasmid can be transferred between cells.

Things we would need to get from the pipeline:

1. QC, trim and filter
2. Mapping to reference to generate partial genomes, and plasmid assemblies (spades and plasmidspades?)
3. Annotation of all contigs
4. Identification of all resistance elements present (arg-annot or resfinder)
5. Phylogenetic tree of all genomes
6. Plasmid map of all plasmids (resistance element on plasmids which is our primary objective)
7. Plasmid typing

The raw reads can be found on the Med Micro server(http://athena.medmicro.uct.ac.za:5000/)in the File Station /MedMicro/Clinton/E. coli/original_data

The reference I used for the genome mapping was Escherichia coli MG1655. I struggled with the plasmid since its doesn't seem to map to any of the published sequences. We may need to use plasmid spades or similar to generate de novo contigs and annotate?

Happy to meet to chat if you need to.

Regards,

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