PLASMID DYNAMICS CONVERTS STRAINS INTO DIFFERENT PATHOGENS

Hanna Skarin and Bo Segerman, National Veterinary Institute (SVA), Uppsala, Sweden

Conclusion

This study shows that toxin plasmids have been exchanged between strains belonging to Clostridium botulinum group III, Clostridium novyi and Clostridium haemolyticum1. The presence of toxin genes on the plasmids is also unstable. This makes the pathogenesis of these species unpredictable. It further poses an increased risk for a negative detection as they are identified upon their toxin genes.

The aim

In this study we have explored the genetic relationship between the three species C. botulinum C. novyi and C. haemolyticum and we have especially looked for plasmid interactions and the exchange of pathogenic traits.

Introduction

A close genetic relationship exists between C. botulinum group III, C. novyi and C. haemolyticum and a collective genotypic name have been proposed for the three species; C. novyi sensu lato. Strains of these species carry most of their toxin genes on plasmids or bacteriophages. The toxin genes are responsible for the different diseases: botulism, gas gangrene and black disease, and bacillary hemoglobinuria, respectively.

Results

The genomes of C. novyi sensu lato were divided into four different lineages on the basis of the overall genomic sequence similarity (Figure 1). Three lineages contained strains of more than one species. An unusually large plasmidome was discovered. Patterns of interactions could be distinguished within and between plasmids. This dynamic process appears to be primarily driven by phages. Some plasmids or bacteriophages were present in more than one species and lineage, for example the phages encoding the botulinum neurotoxin or the novyi alpha-toxin. Most of the toxin genes were localized on the plasmidome and their locations were also highly variable (Figure 2).

Method

Strains of C. botulinum group III, C. novyi and C. haemolyticum were sequenced using the Roche 454 and Illumina MiSeq technology. Genome and plasmid comparisons were made using the software program Gegenees2.

References


Figure 1. Average whole genome similarity of C. novyi sensu lato genomes. Four lineages were identified (I-IV).

Figure 2. Toxin gene dynamics in the plasmidome of C. novyi sensu lato. Striped boxes illustrate a varying presence within the plasmid group. PG= plasmid group, bont = the botulinum neurotoxin gene.