Identification of antimicrobial resistance genes in multidrug-resistant clinical Bacteroides fragilis isolates by whole genome shotgun sequencing

Bacteroides fragilis constitutes the most frequent anaerobic bacterium causing bacteremia in humans. The genetic background for antimicrobial resistance in B. fragilis is diverse with some genes requiring insertion sequence (IS) elements inserted upstream for increased expression. To evaluate whole genome shotgun sequencing as a method for predicting antimicrobial resistance properties, one meropenem resistant and five multidrug-resistant blood culture isolates were sequenced and antimicrobial resistance genes and IS elements identified using ResFinder 2.1 (http://cge.cbs.dtu.dk/services/ResFinder/) and a custom BLAST database. Combinations of cfxA, cepA, cfrA, nimA, nimD, nimE, nimJ, tetQ, ermB, ermF, bexB, linAn2 and mefEn2 genes were identified in the six isolates. blaOXA-347, an open reading frame predicted to be a β-lactamase (Cheng et al., 2012), was identified in one strain. Full length IS elements were identified directly upstream of four genes, but in most cases contigs terminated 100–150 bases upstream of the gene in question. Even though partial IS elements were identified in these short sequences, certain identification could not be ascertained. Full antiobiograms for B. fragilis from genetic data will most likely require complete or nearly complete genomes. Current approaches to this are laborious and/or costly. Emerging technologies such as nanopore based single DNA strand sensing could perhaps provide a solution in the future.