Poster C-22

Comparative Genomic Profiling of an Emerging Pathogen using a 7 Genomes Escherichia coli Microarray

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Short Abstract: Shiga toxin-producing E. coli have emerged as important food borne pathogens. In this study, we characterize the novel strain, D1, encoding a shiga-toxin lamboid bacteriophage. Our analyses indicated that D1 is a K-12 like strain and that its ?3538 phage element most likely originates from the E. coli 3538 strain.

Long Abstract:

Background

The species Escherichia coli is a complex group of bacteria comprising several intestinal and extra-intestinal pathogroups as well as commensal bacteria that are normal inhabitants of the intestinal tract of all warm-blooded animals and humans. Of the intestinal pathogens, Shiga toxin-producing E. coli (STEC) have emerged as an important food borne pathogen world wide and can be the causative agent of diarrhea, hemorrhagic colitis and hemolytic uremic syndrome. Healthy ruminants such as cattle and sheep are regarded as the primary reservoir of STEC, harboring a variety of STEC that is regarded as non-pathogenic or pathogenic to humans depending on their content and combination of pathogenicity factors.

Shiga toxin-producing E. coli have emerged as an important food borne pathogen world wide. Shiga-toxin encoding genes are located on lamboid bacteriophages and evidence for the transduction of these phages between E. coli strains have been shown previously, and again recently by feeding sheep with E. coli O157:H7 strain 3538. This latter experiment resulted in the isolation of a transductant, E. coli O173 strain D1 from sheep feces. However, little is known about host specificity of these phages and similarities and differences of E. coli donor and recipient strains taking part in the transduction event.

Approach

In this study, we characterize the two unsequenced strains, D1 and 3538. For this, we describe the design and use of a high density oligonuclotide microarray covering seven sequenced E. coli genomes plus several sequenced E. coli plasmids, bacteriophages, pathogenicity islands and virulence genes. We evaluate its performance and demonstrate its use for hybridization of genomic DNA in order to compare the two E. coli strains with known sequenced E. coli strains; focusing on whole genome strain comparisons and the transduction of bacteriophage 3538 (stx2::cat) from E. coli O157:H7 strain 3538 to E. coli O173 strain D1. Recent advances in analysis of genomic DNA hybridization data were exploited. In particular, we used the physical mapping of probes in partitioning the probes

into present and absent chromosomal segments.

Results

Analysis of common virulence genes, phage elements and whole genome comparisons, indicated that D1 is a K-12 like strain and that its 3538 phage element most likely originates from the E. coli 3538 strain with which it shares a substantial proportion of phage elements. Moreover, results from our strain comparison support the idea of a common E. coli backbone, which we estimate to approximately 4 Mbp.

Analyses of validation experiments proved that results using our custom designed microarray were representative of the true biology. Segmentation approaches improved the analysis.