MLST clustering of Campylobacter jejuni isolates from patients with gastroenteritis, reactive arthritis and Guillain-Barre syndrome

Aims: To determine the diversity and population structure of Campylobacter jejuni (C. jejuni) isolates from Danish patients and to examine the association between multi-locus sequence typing types and different clinical symptoms including gastroenteritis (GI), Guillain-Barre syndrome (GBS) and reactive arthritis (RA).

Methods and Results: Multi-locus sequence typing (MLST) was used to characterize 122 isolates, including 18 from patients with RA and 8 from patients with GBS. The GI and RA isolates were collected in Denmark during 2002-2003 and the GBS isolates were obtained from other countries. In total, 51 sequence types (STs) were identified within 18 clonal complexes (CCs). Of these three CCs, ST-21, ST-45 and ST-22 clonal complexes accounted for 64 percent of all isolates. The GBS isolates in this study significantly grouped into the ST-22 clonal complex, consistent with the PubMLST database isolates. There was no significant clustering of the RA isolates.

Conclusions: Isolates from Denmark were found to be highly genetically diverse. GBS isolates grouped significantly with clonal complex ST-22, but the absence of clustering of RA isolates indicated that the phylogenetic background for this sequela could not be reconstructed using variation in MLST loci. Possibly, putative RA-associated genes may vary, by recombination or expression differences, independent of MLST loci.

Impact of the Study: MLST typing of C. jejuni isolates from Danish patients with gastroenteritis confirmed that the diversity of clones in Denmark is comparable to that in other European countries. Furthermore, a verification of the grouping of GBS isolates compared to RA isolates provides information about evolution of the bacterial population resulting in this important sequela.