

Occurrence of virulence-associated genes in *Arcobacter butzleri* and *Arcobacter cryaerophilus* isolates within the Czech Republic

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Bacteria of the *Arcobacter* genus, originating mainly from food and water, are dreaded germs for humans as well as animals. However, the virulence of these bacteria has not been fully elucidated yet. This study looked at the occurrence of eight virulence-associated factors (*ciaB*, *cj1349*, *pldA*, *irgA*, *hecA*, *tlyA*, *mviN*, *hecB*) in a total of 80 isolates of *A. butzleri* and 22 isolates of *A. cryaerophilus*. A polymerase chain reaction using specific primers was used to detect these virulence-associated genes. The presence of all genes in the isolates of *A. butzleri* (98.8% *ciaB*, 95.0% *cj1349*, 98.8% *pldA*, 22.5% *irgA*, 31.3% *hecA*, 95.0% *tlyA*, 97.5% *mviN*, 38.8% *hecB*), and *A. cryaerophilus* (95.5% *ciaB*, 0.0% *cj1349*, 9.1% *pldA*, 0.0% *irgA*, 0.0% *hecA*, 31.8% *tlyA*, 90.9% *mviN*, 0.0% *hecB*) was monitored. Among the tested isolates, there were 13 isolates (12.7%) of *A. butzleri*, in which the presence of all eight virulence-associated genes was recorded in the genome. In contrast, in one *A. cryaerophilus* strain, none of the observed genes were detected. The presence of *ciaB* and *mviN* genes was significantly more frequent in *A. cryaerophilus* isolates than other genes ($P < 0.05$). In general, more virulence-associated genes have been detected in *A. butzleri* isolates compared to *A. cryaerophilus*. The most common gene combination (*ciaB*, *cj1349*, *pldA*, *tlyA*, *mviN*) was detected in case of 39 isolates. In 50.0% of *A. butzleri* isolates derived from clinical samples, all eight virulence-associated genes were significantly more frequently detected ($P < 0.05$). The *tlyA* gene was significantly

more frequent occurred in *A. butzleri* isolates from meat and water samples, and *irgA* and *hecB* genes in clinical samples. Therefore, our study provides information about occurrence of virulence-associated genes in genome of *Arcobacter*-isolates. Our results indicate high incidence of virulence-associated genes in *Arcobacter* genomes and hence potentially pathogenic properties of the studied strains.

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