



Microarray characterization of *Campylobacter jejuni* genes involved in colonization and antimicrobial resistance of broiler chickens.

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Introduction : *Campylobacter jejuni* is a pathogen transmitted by chicken and knowledge on the distribution of the genes involved its colonization is still sparse. This study objective was to evaluate the prevalence and distribution of some of these genes in bacteria isolated from slaughtered Canadian chickens recovered within two distinct periods of time.

Methods : A 70-mer oligonucleotide microarray (253 probes) was designed, based on *C. jejuni* rm1221 genome, to detect 227 genes and their variants associated with antimicrobial resistance (AR) (n=37) and chicken colonization (23 involved in envelope biosynthesis, 19 pathogenesis, 29 chemotaxis/mobility, 7 detoxification, 14 metabolism, 54 transport and binding of nutrients, 5 regulatory, 24 hypothetical, 11 unclassified and 5 control). It was used to screen 57 chicken strains collected from different farms (n = 16 in 2003 and n = 9 in 2008) that were compared according to the similarity of the hybridization patterns obtained.

Results : Among the strains, 93 probes were always positive and mainly associated with transport and binding of nutrients. Genes involved in pathogenesis, such as *ciaB* and *jlpa* were present in all strains. Other probes (n = 12), mostly associated with AR, were always negative. For most probes (n = 142, such as *ggT* 10 % and *cj1371* 66%), we observed a variable prevalence (2% to 98%). It could reflect the variation in chicken colonization in the field and illustrate the genetic variability of these strains. Among the AR genes, those associated with efflux and β -lactamases were the most prevalent along with *tetO* (67%) and *aphA3* (16%). The dendrogram showed that strains clustered together according to their sampling origin and not with the period even though some probes were time specific.

Conclusions : This study assessed the prevalence and distribution of genes associated with chicken colonization and AR, showing that most of these are stable in time.