

**Conclusions:** *L. animalis* and *L. reuteri* isolated from canine feces possess potential characteristics allowing the LAB to survive in the gastrointestinal tract. The LAB have great antimicrobial activity and do not produce any harmful enzyme. These results suggested that the canine fecal LAB could be used as valuable probiotics in the companion animal industry.

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### Prevalence and Characterization of *Campylobacter jejuni* Isolates from Dairy Cattle Farms in Korea

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**Introduction:** *Campylobacter* spp. are common food borne pathogens that cause human enteritis in several industrialized nations, with *Campylobacter jejuni* accounted for 80-90% of human infections. Recent study suggested that human *C. jejuni* infections originated from cattle is the second highest and contaminated milk have been identified as source of large outbreaks, therefore the significance of *Campylobacter jejuni* in cattle farms should be concerned. Subtyping isolates from different sources may generate epidemiological linkage information which may be useful in disease control and provide information for risk assessment in the future study. Among these, pulsed-field gel electrophoresis (PFGE) is a well-known gold standard for subtyping *Campylobacter* as it is highly discriminatory, while *flaA* typing is considered an easy, rapid and commonly used genotypic method for *Campylobacter*. The objectives of this study are to determine the prevalence of *C. jejuni* among the dairy cattle farms in Korea, identify the possible farm management variables that affect the farm prevalence, and investigate the genetic relatedness between *C. jejuni* isolates using PFGE and *flaA* typing method.

**Materials and Methods:** Samples from 15 dairy cattle farms which were located in Gyeonggi-do, Korea were collected during 2012-2013. All farms were visited once or twice, except farm S which was visited 4 times. During each visit, stool samples and bedding samples were collected. The farm management variables- density of the lactating herd, hygiene level of the sawdust, stamping out policy and the main feed of each farm were recorded. The farm variables were analyzed using Fisher's exact test to identify the prevalence differences of *C. jejuni* between farms. After identification of *C. jejuni* using multiplex PCR targeting *cj0414* and 16S rRNA gene, 42 cattle farm isolates from this study and 14 isolates from various sources were sub-typed using PFGE and *flaA* typing to study their epidemiological relationship. The band profiles were analysed with Bionumerics ver. 6.6.

**Results:** The farm prevalence of *C. jejuni* was 60.0% (9/15) and the individual prevalence was 23.5% (70/298). The Fisher's exact test results of 15 farms showed that high animal density

(3/3, 100%) ( $P= 0.18$ ) and low hygiene level of sawdust (6/7, 85.7%) ( $P= 0.08$ ) appeared to be the possible factors that affect the presence of *C. jejuni* in the farms. Nineteen PFGE patterns, 19 *flaA* patterns and 29 composite types were detected based on the 90% similarity criterion. The discriminatory index of PFGE and *flaA* typing was 0.9143 and 0.9239, respectively. PFGE, *flaA* typing and composite results showed that the cattle isolates had similar patterns between farms and different sources (human and chicken isolates).

**Conclusions:** In conclusion, cattle can act as the reservoir for human campylobacteriosis and *C. jejuni* genotypes were diverse within a farm. Intervention strategies should develop in cattle farms to possibly reduce the burden of human campylobacteriosis contributes to the public. The inclusion of more isolates from various origins and the evaluation of pathogenic genes are expected in the future study to provide more information on the genetic relatedness between isolates from different sources.

#### References

- [1] Ribot EM, C Fitzgerald, K Kubota, B Swaminathan, and TJ Barrett, 2001. Rapid pulsed-field gel electrophoresis protocol for subtyping of *Campylobacter jejuni*. J Clin Microbiol, 39: 1889-1894.

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### Risk Assessment of H5N1 Highly Pathogenic Avian Influenza Virus into Korea through Migratory Wild Birds

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**Introduction:** Since 2003, highly pathogenic avian influenza (HPAI) outbreaks occurred 5 times in Korea and 4 of them were caused by H5N1 serotype. This study is to qualitatively estimate the probabilities of release of H5N1 HPAI virus into the Korea through migratory wild bird.

**Materials and Methods:** Based on framework set out by the World Organization for Animal Health (International Office of Epizootics., 2004), risk assessment scenario tree was developed to determine the risk of HPAI introduction into Korea by wild birds. Probability and numbers of birds were expressed qualitatively as *negligible, very low, low, medium, high, and very high* (Fao, 2009). Probabilities and values of numbers were combined to estimate the probability of H5N1 release in Korea.

**Results:** Twelve species of wild migratory birds were selected as high risk species according to the surveillance result of avian influenza virus positive in the Korean wild birds. Although predicted probabilities of release of H5N1 per individual bird per year were *low, very low, and negligible* in most of wild birds, probability of release H5N1 in Korea was *high* for Mallard and Baikal Teal species because of their *high* numbers migrating to Korea. All possible high risk species identified in Korea had common inhabits in China, Hong