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DETECTION OF *BRACHYSPIRA HYODYSENTERIAE* IN A CARRION CROW (*CORVUS CORONE*)

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Background & Objectives

The role of corvid birds in the epidemiology of *Brachyspira (B.) hyodysenteriae* causing swine dysentery in pigs has been questioned. Therefore, we examined crows living close to *B. hyodysenteriae* positive pigs for the presence of *B. hyodysenteriae* and analysed isolates with molecular methods.

Material & Methods

Intestinal swabs of four young crows (*Corvus corone*) and faecal swabs from pigs living in two neighbouring *B. hyodysenteriae* positive free-ranging pig herds (herd A and B; 10 swabs/ herd) were sampled. The 24 samples were analysed by *Brachyspira* specific culture, and the isolates were identified by *nox*- polymerase chain reaction specific for *Brachyspira* spp. followed by restriction fragment length polymorphism. *B. hyodysenteriae* isolates were typed using multi-locus sequence typing (MLST).

Results

Eight samples from herd A and six from herd B as well as one crow sample were positive for *B. hyodysenteriae*. The eight isolates from herd A and one isolate from herd B belonged to sequence type (ST) ST196. The remaining five porcine isolates from herd B as well as the corvid isolate were grouped into ST66.

Discussion & Conclusion

This is the first description of *B. hyodysenteriae* in crows and its molecular relationship to *B. hyodysenteriae* from pigs from the same area. This emphasizes that crows should be considered as a potential vector spreading *B. hyodysenteriae* into pig herds. Further studies are now necessary to elucidate the actual role and impact of crows in the epidemiology of *B. hyodysenteriae*.

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