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**COINFECTIONS IN CASES OF SMEDI FROM DIAGNOSTIC TRANSMITTALS IN GERMANY**

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**Background and Objectives**

SMEDI displays a reproductive disorder associated with different pathogens like PPV1, PCV2 and others. Less is known about the prevalence and effect of coinfections with different pathogens in such cases. In the present study we examined fetuses from SMEDI litters for the presence of pathogen specific DNA of PPV1, PCV2, PCV3 and Leptospira spp. to evaluated the effect and prevalence of coinfections with the before mentioned pathogens in German SMEDI cases.

**Material and Methods**

In total 158 / 358 fetuses from diagnostic transmittals, selected by systematic random sampling (four fetuses per litter), from 40 SMEDI-affected litters of 18 different farms were examined for PPV1, PCV2, PCV3 and Leptospira spp. by real-time PCR. Epidemiological data were collected by a questionnaire from the corresponding farmers.

**Results**

In 94.4% of all farms and in 77.5% of all litters specific pathogen DNA was detected in different amounts and combinations. PPV1-, PCV2- or PCV3-DNA was present each in 16.7% of the farms as the only detectable pathogen. PPV1+PCV2 coinfection was detected in 33.3% of the farms, PCV2+PCV3+Leptospira spp. coinfection was present in 11.1% of the farms and no pathogen DNA was detected in 5.6% of the farms. The detection of Leptospira spp. in fetuses was significantly associated with a PCV2 coinfection (OR: 26.3; $p < 0.001$). Fetal maceration was associated with Leptospira spp. detection (OR: 8.6; $p = 0.003$), whereas mummification ($p = 0.047$), reduced crown-rump length ($p < 0.001$), and bodyweight ($p = 0.001$) of fetuses were significantly associated with PPV1 and PCV2 coinfection.

**Discussion and Conclusion**

The present study shows that coinfections with different pathogens appear regularly in SMEDI cases. Interaction of pathogens might lead to an enhanced negative effect on the development of fetuses (in terms of PCV2 + PPV1 coinfection) or possibly bilateral promote infections (in terms of PCV2 and Leptospira spp.). Molecular biological examinations in SMEDI affected herds should cover a broad range of pathogens to obtain an etiological diagnosis. Moreover, the phenotypical appearance of SMEDI-fetuses should be taken into consideration to increase the probability of pathogen detection.