Pooling of porcine fecal samples for quantification of Lawsonia intracellularis by real-time polymerase chain reaction

Procedures in which biological specimens are mixed and tested as 1 sample (pooling) have been applied for various biological specimens and laboratory examinations. The objective of the current study was to investigate agreement between laboratory testing of fecal pools and theoretical values obtained by averaging test results from individual fecal samples in relation to a quantitative polymerase chain reaction (qPCR) test for Lawsonia intracellularis. Ten diarrheic and 10 normal fecal samples were submitted from each of 43 Danish swine herds (n = 860 fecal samples). Pools (n = 43), each containing 20 individual fecal samples from the same herd, were prepared in the laboratory by pooling 10% fecal phosphate buffered saline solutions. All pools and individual fecal samples were subjected to qPCR testing for L. intracellularis. The theoretical number of L. intracellularis in the pools was calculated as the mean number of bacteria from the 20 individual fecal samples contributing to each pool. Agreement between the laboratory testing of pools and theoretical calculations based on individual sample results was evaluated. Pooling resulted in fewer L. intracellularis–positive herds (41.9%) compared with testing 20 fecal samples (53.5%). Agreement between the laboratory and the theoretical pools for dichotomized test results was 100% (95% confidence interval: 91.8–100%). For the quantitative test results, Lin concordance correlation coefficient was 0.997. The mean difference between the laboratory testing and the theoretical values was not different from zero (mean difference = 0.039 log10 bacteria/g feces; P = 0.26)

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