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## Veterinarni Medicina

**Prevalence of antibiotic resistance genes in faecal samples from cattle, pigs and poultry**

Faldynova M, Videnska P, Havlickova H, Sisak F, Juricova H, Babak V, Steinhauser L, Rychlik I:

Veterinarni Medicina, 58 (2013): 298-304

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Antibiotic resistant bacteria can be easily isolated from the faeces of cattle, pigs or poultry. However, whether the production of different farm animals is associated with a higher or lower prevalence of antibiotic resistance is not clear. In this study we therefore used real time PCR for the quantification of antibiotic gene prevalence in the DNA purified from the faeces of farm animals. First we showed that experimental streptomycin therapy of 12-week-old chickens and 46-week-old hens significantly increased the relative prevalence of *strA* and *sul2* genes though this did not necessarily indicate an absolute increase of *strA*-encoding

gene prevalence in the DNA purified from the faeces of cattle, pigs and laying hens. The lowest prevalence of *strA*, *aadA*, *sul1*, *sul2*, *tet(A)*, *tet(B)*, *tet(G)* and *cat* genes was recorded in the intestinal contents of laying hens. In cattle and pig faecal samples, an intermediate prevalence of antibiotic resistance genes was observed with *strA* and *sul2* dominating by two logs over the remaining six tested genes. The differences in *strA* and *sul2* prevalence between cattle and pig microbiota were not significant whilst the prevalence of *strA* and *sul2* in laying hen microbiota was significantly lower than in the other two species. Cattle and pig production systems may therefore represent a more important reservoir of antibiotic resistant bacteria than laying hens.

### **Keywords:**

real time PCR; antibiotic resistance; farm animals; chicken; pig; cattle

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