The study of shared bacterial and fungal microbiota of human and pets as a possible source of antibiotic resistance

Summary:

The microbiological aspect of the pet and owner relationship focuses on the microorganisms forming the microbiome. The sharing of the household by the owner and the pet is reflected in the two-way communication of the microbiota. The aims of the dissertation is to determine the microbial spectrum of bacteria and yeasts that can be cultivated *in vitro* in standard laboratory conditions. Antibiotic treatment in the last year could influence colonization by resistant microorganisms, therefore the abundance of shared bacterial and yeast species showing the same antimicrobial resistance phenotype between owners and their pets were monitored with respect to behavioral models.

A total of 1156 samples were obtained from 120 owners´ households and 80 control group participants without pet. Nasal mucosa, intertoe space, axillae, and auditory cannula swabs were collected from 145 owners and nasal mucosa and auditory cannula samples from 128 pets. 320 samples from the same anatomical locations like in owners were also provided to a control group of 80 people who have no contact with any animal for more than 1 year. All owners filled in a questionnaire with a statement regarding their relationship to pets and previous antibiotic therapy. Bacterial and yeast isolates were identified by standard laboratory methods and confirmed by MALDI–TOF MS. Based on the obtained data, hypotheses about the communication between the owners´ and pets´ microbiota were evaluated with comparison to non-owners´ microbiota.

Contact Index (CI) was introduce for expression of the intensity of contact between the owner and the pet, with scales 1–8 points. The values CI≤4 expresses a less close relationship and CI>4 a closer relationship. CI>4 was examined in 88.23 % (n=128). 26.56 % (n=34) of pets, 31.03 % (n=45) of owners and 31.25% (n=25) of non-owners were treated by antibiotics. A total of 176 microbial species (137 bacteria and 39 yeasts) were isolated. The richest microbial biodiversity was found in the pets´ nasal mucosa (n=96). The same resistance phenotype was found in 21.67 % of households (n=26) in 16 microbial species. The species abundance of microorganisms isolated from the owners and the control group did not differ significantly. Neither did the time of sharing one household between the owner and pet show any effect on the species abundance of microorganisms in the owner. There was no statistically significant influence of the CI of the householder on the abundance of bacterial and yeast isolates of microorganisms, and even on the sharing of resistant bacterial and yeast isolates.

Methicillin-resistant *Staphylococcus aureus* strain (MRSA) was the most frequently shared strain by owners and pet. Previous ATB therapy significantly affected the quantity of yeasts isolated in humans (owners and non-owners), whereas this effect was not observed in pets. Finally, the effect of ATB therapy over the last year was observed in at least one of the pairs (pet, owner) on the occurrence of strains of microorganisms with identical phenotypic resistance. In the control group, methicillin-resistant isolates (MRSA, MRSP) were also found in 9 cases (*S. aureus* in 8 cases and *S. pseudintermedius* in 1 case).

The microbial abundance of the owners and non-owners did not differ significantly. Even the time of sharing the household had no influence on the microbial abundance. There was no statistically significant influence of CI on microbial abundance, nor on the sharing of resistant isolates. Methicillin-resistant *Staphylococcus aureus* strain was most often shared between owner and pet (n=4). Previous ATB therapy significantly influenced the abundance of isolated yeast in human (owners and non-owners). This influence was not proven in the pets. ATB therapy also seems to have an impact on the occurrence of shared microorganisms with the same resistance phenotype.

Keywords: pets, owners, shared microbiota, antibiotic resistance