

The house dust mites (HDM; *Dermatophagoides farinae* and *Dermatophagoides pteronyssinus*) obtain nutrients from the debris of the skin, hairs and nails, that get off the human and animal body. These debris are covered by microorganisms and the microorganisms are the key factor in the survival of HDM in human-made environments.

In this study we made manipulative experiments with the extract from spent growth medium (SPGM). SPGM is the medium after mite cultivation, composed from mite feces, debris of the diet, dead mite bodies and microorganisms. The extract from SPGM (one and three-month-old mite cultures) was used as the source of microorganism to transfer them into diet of *D. farinae* a *D. pteronyssinus*.

The composition of the bacterial and fungal microbiomes differed between the HDM species, but the SPGM extract addition into diet influenced only the bacterial profile of *D. farinae*. In the *D. farinae* microbiome of specimens on SPGM-treated diets compared to those of the control situation, the *Lactobacillus* spp. profile decreased, while the *Cardinium*, *Staphylococcus*, *Acinetobacter*, and *Sphingomonas* profiles increased. The addition of SPGM extract decreased the microbial respiration in the microcosms with and without mites in almost all cases. Adding SPGM did not influence the population growth of *D. farinae*, but it had a variable effect on *D. pteronyssinus*. The results indicated that the HDM are marginally influenced by the microorganisms in their feces.