

Microbiota becomes one of the most important subjects in biological research and numerous studies revealed that microbiota plays a broad spectrum of essential roles in different organisms. This master thesis focuses on the bacterial part of microbiota contained in mucosal tissues of wild house mice (*Mus musculus musculus*). Male and female samples were collected by nasal and oral cavity lavages, vaginal mucosa lavages and from urine and stool. We aimed to detect quantitative, qualitative and sex-specific differences in bacterial populations between mucosal tissues with particular focus on bacterial cycling in vaginal mucosa during the estrous cycles. Bacterial abundances were estimated by qPCR whilst bacterial diversity was detected by targeted metagenomic sequencing of the hypervariable region of the 16S rRNA gene. Significant differences were detected in bacterial abundances and alpha diversity between particular mucosal tissues. Stool samples contained the highest number of bacteria, while samples from the nasal mucosa and urine contained low amount of bacteria. The highest alpha diversity was discovered in stool samples, the least alpha diversity was found in the urine. Mucosal tissues also varied based on the bacterial composition on the level of particular genera. Detailed analysis of estrous cycles revealed significant changes in microbiota. High bacterial load and low alpha diversity was detected during proestrus and estrus – represented e.g. by the genus *Rodentibacter* – whilst the load rapidly decreased in metestrus and diestrus. However, no other sex-specific differences between particular tissues were detected in this study.