Trichomonads is a group of anaerobic single-celled eukaryotes currently classified in the kingdom Excavata (phylum Parabasalia), although does not share any of typically excavate features (the characteristic arrangement of the cytoskeleton and the ventral feeding groove). The taxonomy is based only on the molecular-phylogenetic analyses.

Genus *Tetratrichomonas* contains probably the highest number of known species within the phylum Parabasalia, parasites and commensals of numerous vertebrate and invertebrate hosts. According to phylogenetic methods the genus has been divided into group A and B. This thesis is focused on the group A, which is split into 12 lineages (lineage 1 – 10, novel lineage 2, lineage LP). During our survey we discovered a new lineage - called sheep lineage, related to this group. Its position in group A is still unclear. Morphological differences between lineages have more or less confirmed the position of other lineages in phylogeny based taxonomy tree, which has been published previously.

In this work, the differences between lineages have been described detailly. It is obvious that almost all lineages or groups of lineages are distinguishable from each other on the basis of morphological characters (size and shape of the body, the number of anterior flagella, parabasal body size, height of microtubular axostyle-pelta komplex, thickness of costa) and form a single species, morfospecies. Based on described features some lineages have been assigned to already described species. Lineages 1 and 2, which were morfologically indistinguishable, were assigned to species *Tetratrichomonas ovis*. Lineages 4 and 5, which shared common morphological features correspond to the description of *Tetratrichomonas brumpti*. Lineage 7 has been assigned to *Tetratrichomonas buttreyi*, which has been isolated from pigs. According to our opinion lineage 10 could match with the description of "*Tetratrichomonas ovis*", respectively *Tetratrichomonas pavlovi*. The newly discovered sheep lineage can be related to *Tetratrichomonas didelphidis*, respectively *Tetratrichomonas guttula*, however its classification is very uncertain and will require further analysis.