Abstract

Eimeria is an apicomplexan parasite causing disease coccidiosis that is most prominent in poultry farming industry. This thesis is aimed to develop new molecular tools and resolve issues that would be a valuable contribution in the field from both research and industry perspective. Because immunity to *Eimeria* is strictly species-specific, it is important to know and recognize correctly all species that parasitize the host. Traditional diagnostic approaches rely on classical methods such as oocyst morphology determination under the microscope, measurement of prepatent period or in-vivo assessment of lesions caused by this parasite. However, diagnostics of individual species using these methods is very time-consuming and it is often unreliable, especially when mixture of multiple species whose parameters overlap is analyzed. Methods utilizing conventional PCR to distinguish species already exist, however, they lack advantages offered by quantitative real-time PCR (qPCR). The first aim of this thesis was to develop qPCR assays for detection and quantification of seven *Eimeria* species which infect chicken utilizing single-copy non-polymorphic targets in order to ensure maximal specifity and coverage of all strains of each species. Usefulness of this method was demonstrated by analysis of field samples. Another aim was to resolve status of *Eimeria mivati* that was considered doubtful species. We have analyzed small ribosomal subunit (18S) sequences of single-oocyst derived strains of *E. mitis* and we have found that two types of 18S co-exist within single genome that correspond to sequences of *E. mitis* and *E. mivati*. This implies that *E. mitis* and *E. mivati* represent the same species. The phenomenon of two types of 18S within single genome was not observed in *Eimeria* until now and it has important implications for diagnostics and vaccine production. The last aim was related to turkey coccidia *E. adenoeides* where we encountered two strains that differed in oocyst morphology to the extent never described before. We have resolved their status by molecular phylogenetics using 18S gene and cross-immunity tests.