# *Eimeria falciformis* BayerHaberkorn1970 and wild derived isolates from house mice: differences in parasite lifecycle, pathogenicity and host immune reactions

Al Klifeh, E.1,2; Balard, A.1,2; Jarquín-Diaz V.H.1,2; Weyrich, A.3; Wibbelt, G.4; Heitlinger, E1,2.

1 Research Group Ecology and Evolution of molecular Parasite-Host Interactions, Leibniz Institute for Zoo and Wildlife Research, Alfred-Kowalke-Straße 17, 10315 Berlin, Germany.

2 Humboldt University, Institute for Biology, Dept. Molecular Parasitology, Philippstraße 13, 10115 Berlin, Germany.

3 Department Evolutionary Genetics, Leibniz Institute for Zoo and Wildlife Research, Alfred-Kowalke-Straße 17, 10315 Berlin, Germany.

3 Department Wildlife Diseases, Leibniz Institute for Zoo and Wildlife Research, Alfred-Kowalke-Straße 17, 10315 Berlin, Germany.

Species of *Eimeria* (Apicomplexa:Coccidia) differ in the timing of lifecycle progression and resulting infections differ in host immune reactions and pathology they induce. *Eimeria* infections in house mice are used as models e.g. for basic immunology and the most commonly used isolates have been passaged in laboratory mice for over 50 years. We questioned in how far such isolates are are still representative for infections in natural systems.

Here we compare the “laboratory isolate” *E. falciformis* BayerHaberkorn1970 with the wild derived isolate *E. falciformis* Brandenburg88*.* We contrast this with the wild derived isolate of *E. ferrisi* Brandenburg64. We compare for all three isolates parasite lifecycle progression, cytokine gene expression in the spleen and immune cell infiltration at the site of infection as a measure of host immune response, as well as host weight loss as a measure of pathogenicity.

While parasite lifecyle progression and pathogenicity are species-specific for *E. falciformis* *vs.* *E. ferrisi*, host cytokines are expressed at significantly higher level in the spleen of mice infected with the *E. falciformis* laboratory isolate than in both wild derived isolates, irrespective of the species. Differences in histopathology are observable between all three isolates: The *E. falciformis* laboratory isolate is inducing the strongest inflammation and immune cell infiltration followed by the wild derived *E. falciformis* isolate. E ferrisi Brandenburg64 is inducing milder histological changes than both *E. falciformis* isolates.

It can be speculated that the serial passaging of *E. falciformis* BayerHaberkorn1970 has resulted in evolutionary divergence of this isolate rendering it more virulent in NMRI mice. More generally, our results show that caution is needed when findings from experimental infection with laboratory strains should be integrated with observations in natural systems.

**Introduction**

Maintenance of parasite life cycles via serial passaging is a cornerstone of experimental parasitology. Parasites are propagated under defined and controlled conditions with the aim to provide infective stages for experiments (Lucius et al, 2017). The procedure allows the parasite to evolve due to mutation and genetic drift or adaptation to the passaging host and environment (Ebert, 1998; Burke, 2012). Genetic drift is promoted by the use of small inocula during passaging and drift can act while diversity of a parasite isolate is reduced intentionally to obtain a clonal strain. In clonal strains mutation and drift can continue to act (Farrell et al, 2014). Considering adaptive evolution, an important part of the passaging environment is given by living hosts (Elena and Lenski, 2003), which usually have low genetic diversity (e.g., clonal or inbred lines, cultures), are immunologically naive due to the absence of previous infections (Mackinnon ‎and Read 2004) and lack co-infections with other parasites (Abolins et al, 2017). Procedures for serial passaging of parasites typically collect infective stages at a particular time after infection and use the obtained inoculum to infect new animals or use haphazard infections in dense environments. Iteration of such a static routine likely differs from natural parasite environments with different timing of infections and variable transmission. In most cases both the biotic (host) and abiotic passaging environment thus differs profoundly from the environment experienced by the parasite during its life cycle under natural conditions. To summarize, parasite laboratory isolates might experience both neutral and adaptive evolutionary processes. As a consequence they might not be representative for analogues in natural systems.

Serial passage leads in most cases to higher virulence (enhanced growth and reproduction of the parasite and larger impact on the host) in the host type used for the process (reviewed by Ebert, 1998). This can be due to low genetic diversity in host populations (for example inbred lines) used for passage, reducing fitness trade-offs associated with specialization and promoting the expansion of more virulent pathogens. This phenomenon has been demonstrated in systems including the apicomplexan parasites Plasmodium spp. in rodents (Mackinnon and Read, 1999 and ‎2004; Barclay et al, 2014). These studies collectively show adaptation to the passage host to increase parasite virulence.

Contrary, but still consistent with this, passage of highly virulent isolates of the apicomplexan parasite Eimeria spp. can lead to attenuation of virulence when only the first oocystes committing to sexual reproductions are selected ([Shirley](https://www.ncbi.nlm.nih.gov/pubmed/?term=Shirley MW%5BAuthor%5D&cauthor=true&cauthor_uid=3375582) and [Bellatti](https://www.ncbi.nlm.nih.gov/pubmed/?term=Bellatti MA%5BAuthor%5D&cauthor=true&cauthor_uid=3375582) 1988, [McDonald](https://www.ncbi.nlm.nih.gov/pubmed/?term=McDonald V%5BAuthor%5D&cauthor=true&cauthor_uid=6877863) and [Ballingall](https://www.ncbi.nlm.nih.gov/pubmed/?term=Ballingall S%5BAuthor%5D&cauthor=true&cauthor_uid=6877863) 1983, Matsubayashi et al, 2016). These attenuated strains are called “precocious lines” and are the basis for live vaccines used in the poultry industry (Shirley and Long, 1990). Given the practical implications of this phenomenon, numerous experiments focused on changes in parasite life history, virulence and host response that arise as a consequence of attenuation. It is clear from these experiments that *Eimeria* spp. respond quickly to selection pressure. In contrast only a few studies attempt to correlate enhanced virulence after serial passaging of *Eimeria* with physiological (e.g. immune-) responses in the passaging host (Ref).

Species of the genus *Eimeria* have usually a small host range, often infecting a single host species (Hashimoto et al, 2014; Hnida and Duszynski, 1999; Kvičerová and Hypša, 2013; Vrba and Pakandl, 2015) and reside at specific sites within the intestines of their hosts (Chapman et al, 2013; Haberkorn, 1970; Owen, 1975). All species have a direct life cycle with asexual expansion and sexual reproduction within epithelial cells of the gastrointestinal tract before transmission stages (oocysts) are released. Diploid oocysts become infective after reductive divisions (sporulation) in the environment (Cacho et al, 2012; Canning and Anwar, 1968).

*Eimeria* spp. are widespread in diverse host species including all vertebrates. Infection causes damage in the intestinal mucosa resulting in malabsorption of nutrients and weight loss (Chapman et al, 2013; Haberkorn, 1970). Coccidiosis in livestock is a focus of veterinary research due to its economic impact (Brake et al, 1997; Cacho et al, 2012; Gadde et al, 2009; Laurent et al, 2001; Swaggerty et al, 2011). *Eimeria* species capable of natural infection of the mouse (*Mus musculus*) have been proposed as a model for e.g. host immune response against *Eimeria* (Heitlinger et al, 2014; Schmid et al, 2014). Serial passaging of laboratory isolates of *Eimeria* is usually conducted by collecting oocysts at the day of peak shedding. Oocysts are sporulated in an aqueous solution of potassium dichromate and inocula are used for new infections two to six months later, before infectivity decreases. The isolate *E. falciformis* BayerHaberkorn1970 has been isolated in 1960 (Haberkorn 1970) and has been propagated in laboratories (first at Bayer animal health, then at the institute for molecular parasitology of the Humboldt University at Berlin) since. In nearly 60 years since its isolation *E. falciformis* BayerHaberkorn1970 has likely become the most commonly used laboratory isolate of rodent *Eimeria* (Ehret et al, 2017; Mahrt and Shi 1988; Pogonka et al, 2010; Schito et al, 1996; Schmid et al, 2014, 2012; Stange et al, 2012; Steinfelder et al, 2005). In the present study we compared infection of mice (NMRI) with this laboratory isolate of *E. falciformis,* a wild derived isolate of *E. falciformis* (novel isolate Brandenburg88) and *E. ferrisi* Levine and Evens, 1965 (novel isolate Brandenburg64). We assessed similarities and differences in proliferation of tissue stages, oocyst shedding and in the host pathological changes and immune response between he two different *Eimeria* species. We used these differences as a background to compare the laboratory isolate of *E. falciformis* with the novel field isolate of the same species.

## RESULTS

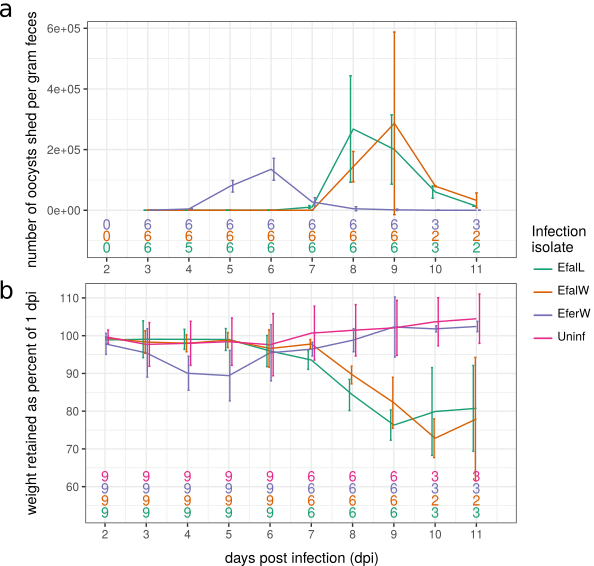
### Dynamics of infection and body weight loss differ between *Eimeria* species, including novel wild-derived isolates

Genotyping showed two novel isolates we obtained form individual house mice captured in the federal state of Brandenburg (Germany) to belong to the species *E. falciformis* and *E. ferrisi*. For all tested markers (the mitochondrial Cytochrom C oxidase subunit I (COI); the nuclear small ribosomal subunit (18S); and the open reading frame 470 (ORF470) from the apicoplast genome) the Brandenburg88 and Brandenburg64 isolate have between 99% and 100% identity in comparison with the available sequences from *E. falciformis* and *E. ferrisi*, respectively.

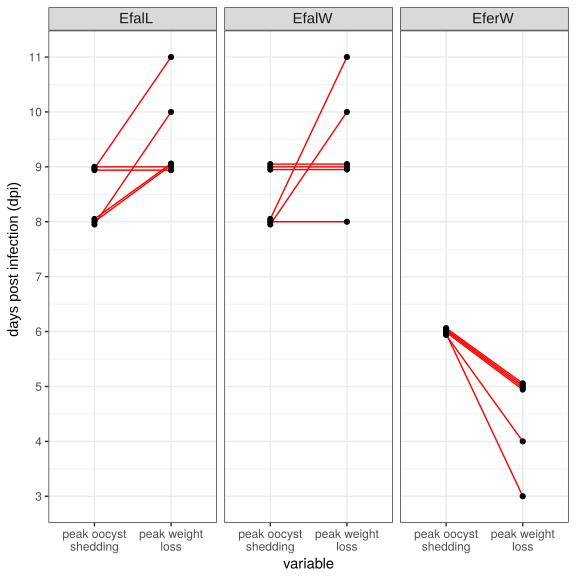
We infected mice with these novel *Eimeria* isolates as well as the laboratory isolate E.falciformis BayerHaberkorn1970 and followed the progression of infection by measuring parasite reproduction and host body weight loss. We assessed parasite reproduction via oocyst shedding from two to eleven days after infection (dpi) (Figure 1a). The two *E. falciformis* isolates and *E. ferrisi* showed different infection dynamics in NMRI mice: oocyst shedding of *E. ferrisi* has a peak intensity at 6 dpi, which was drastically reduced on 7 dpi (n = 12, U = 2.91, p = 0.002) and fell below detection levels on 10 dpi. Oocyst shedding of *E. falciformis* has a peak intensity at 8 dpi for the laboratory isolate BayerHaberkorn1970 (EfalL) and at 9 dpi for a recently derived isolate Brandenburg88 (EfalW). The oocyst numbers declined after this peak in both isolates, but shedding is still detectable at 11 dpi when we sacrificed the last mice. For the two *E. falciformis* isolates we observed no difference in shedding intensity of oocysts at the peak day (n = 12, U = 0.24, p = 0.846) and peak oocyst abundance did not differ significantly between *E. ferrisi* and both *E. falciformis* strains (EferW *vs.* EfalW, n = 12, U = 0.32, p= 0.777; EferW *vs.* EfalL, n = 12, U = 0.96, p= 0.37).

The period of patency (oocyst shedding) was characterized by body weight loss in infected mice in all infections (Figure 1b). Infections with *E. ferrisi* coincided with significant weight loss at 4 dpi (n = 18, U = -2.43, p = 0.013) and 5 dpi (n = 18, U = - 2.52, p = 0.010) in comparison to the control group. Infection with *E. falciformis* was accompanied by significant weight loss at 8 and 9 dpi in both EfalL (both dpi, n = 12, U = -2.89, p = 0.002) and EfalW (8dpi, n = 12, U = -2.41, p = 0.013; 9dpi, n = 12, U = -2.89, p = 0.002) isolates as compared to the control group. Weight losses in infections with *E. ferrisi* at their maximum (at 5 dpi) were, however, significantly lower compared to weight loss in infections with *E. falciformis* at their maximum (9 dpi; EferW vs. EfalW, n = 15, U = -2.0, p = 0.049; EferW vs. EfalL, n = 15, U = -2.59, p = 0.007).

Oocyst shedding and weight loss show different relative timing in *E. falciformis* compared to *E. ferrisi*. In infections with both isolates of *E. falciformis* weight loss coincides with or follows upto two days after oocyst shedding, in infections with *E. ferrisi* weight loss precedes peak oocyst shedding by one day or more (Figure 2).



**Figure 1 – Parasite life cycle progression and pathogenicity assessed as host weight loss during the infection-** Dynamics of parasite reproduction and host weight loss differ between the species *E. falciformis* and *E. ferrisi*. a) Oocyst shedding of *Eimeria* spp. from experimentally infected mice (NMRI) is displayed from 1 to 11 days post infection (dpi). Mice were infected with 200 sporulated oocyst of *E. ferrisi* Brandenburg64 (a recently derived isolate; EferW), *E. falciformis* BayerHaberkorn1970(a classical laboratory isolate; EfalL) or and *E. falciformis* Brandenburg88 (a recently derived isolate, EfalW). b) Body weight loss of the same three groups of mice is depicted as percentage of body weight retained compared to 1 dpi. The number of mice (n) is given at the bottom of the plot, it is reduced at the end of the experiment, because mice were sacrificed for collection of tissue samples. Lines indicate the mean for each group, error bars give the standard deviation.



**Figure 2** **– Relative timing of host weight loss and parasite reproduction differ between the species *E. falciformis* and *E. ferrisi* for individual hosts** - The peak of the host’s weight loss precedes the peak of oocyst shedding in infections with E. ferrisi, while in infections with E. falciformis the hosts lost most weight either on the day or after the day parasites most oocysts were shed. Points depict the peak day of both oocyst shedding and weight loss respectively and red lines connect both measurement from the same mouse. All mice sacrificed at 9dpi or later are assessed. For underlying experimental procedures see Figure 1. For *E. falciformis* infections the day of maximal wight loss could have been potentially even later if some mice (n=3 for each isolate) were not sacrificed at 9dpi.

**Intensity of tissue stages of *Eimeria spp.***

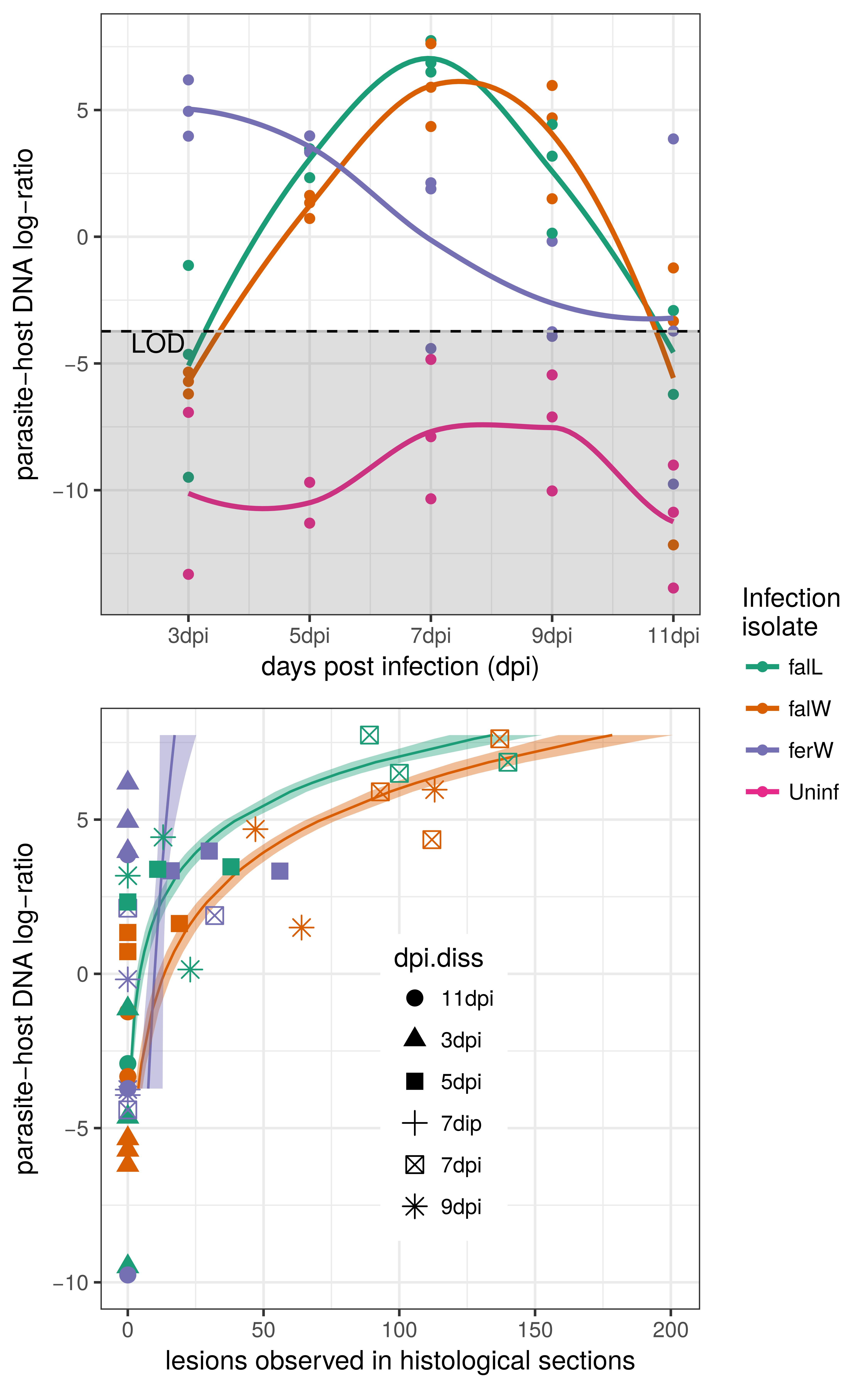
*Eimeria* infections in our study result in a transient presence of parasite stages in epithelial cells of the caecum. We quantified the intensity of infection by a quantitative PCR (qPCR) assay using gDNA from caecal tissue. By specifically amplifying genes for the parasite (Cytochrome C-oxidase subunit I; COI) and the host (nuclear *cdc42* gene), we analysed the ratio of parasite DNA to host DNA. We report this ratio on a native (log2) scale of measurement and further call it the parasite-host DNA log-ratio (Figure 3a). The analysis of infected (*E. ferrisi* n =15; *E. falciformis*, EfalW n = 14, EfalL n = 14) and control samples (n = 13) allows us to estimate a limit of detection (LOD; mean + 2 standard deviations of the negative controls) for the assay at a parasite-host DNA log-ratio of -3.73. This corresponds to roughly eight *Eimeria* COI molecules for 100 copies of the mouse nuclear genome. We measured th highest value for an individual negative control sample at a parasite-host DNA log-ratio of -4.84. Maximum values for parasite-host DNA log-ratio (observed in the EfalL isolate) were 7.74 indicating a ratio of 214 parasite COI mDNA copies for each copy of the mouse genome in crude tissue at this point.

At 3 dpi *E. ferrisi* has the highest value of parasite-host DNA log-ratio (6.19), while most infections with *E. falciformis* were still below the limit of detection (all EfalW and for two out of three EfalL). For *E. falciformis* (both isolates) parasite-host DNA log-ratio increased to values well above zero (equal numbers of parasite mitochondrial and host nuclear DNA copies) at 5 dpi and highest values were reached at 7 dpi. Again the amount of DNA measured for *E. falciformis* (at this peak intensity) was similar to that of *E. ferrisi* (at 3 dpi, its peak). At 11 dpi the parasite-mouse DNA log-ratio was reduced to values below zero for all samples, and for most samples below the limit of detection (except for one *E. ferrisi* outlier-sample, for which a value of 3.86 was measured).

To test how this parasite-host DNA log-ratio predicts visible parasite tissue stages we counted these in histological sections. In a generalized linear model (Table 1) the parasite-host DNA log-ratio is a significant predictor for the number of tissue stages (Figure 3b). The prediction based on the parasite-host DNA log-ratio is different for both isolates of *E. falciformis*, meaning that a lower number of tissue stages are found for similar parasite-host DNA log-ratio in EferW. For *E. ferrisi* the prediction is still lower. The model fit is poor for *E. ferrisi*, however, and inspections of Figure 3b makes clear that for this species parasite presence coincides with tissue stages only at 5 dpi.

**Table 1** – A generalized linear model predicts tissue lesions with the amount of parasite DNA relative to host DNA (parasite-host DNA log-ratio).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | Lesion score | | |
|  |  | *Prediction* | *CI* | *p* |
| (Intercept) |  | 4.43 | 3.18 – 6.03 | <.001 |
| P-H ratio |  | 1.55 | 1.48 – 1.64 | <.001 |
| Infection isolate | | | | |
| Inf. EfalW |  | 3.03 | 2.09 – 4.46 | <.001 |
| Inf. EferW |  | 2.23 | 1.45 – 3.42 | <.001 |
| P-H ratio : Inf.EfalW |  | 0.90 | 0.84 – 0.95 | <.001 |
| P-H ratio : Inf.EferW |  | 0.69 | 0.63 – 0.76 | <.001 |
| Observations |  | 33 | | |



**Figure 3 – The relative amount of parasite *vs.* host DNA (parasite-host DNA log-ratio) estimates the intensity of parasite caecum tissue stages.** a) The parasite-host DNA log-ratio was calculated from the difference in cycle of threshold (Ct) values of qPCRs performed on a single copy nuclear gene (Cdc42) of the host and on a mitochondrial (COI) gene of the parasite. Lines are drawn using local polynomial regression fitting (a “loess smoother”). b) Predictions of parasitic tissue stages from these qPCR data are shown for all parasite isolates at different times after infections. Lines here represent predictions from a generalized linear model, shaded areas 95% confidence intervals of these predictions. For *E. falciformis* (EfalW and EfalL) this model provides better fit than for *E. ferrisi* (EferW).

**Differences in immune gene expression between the laboratory and wild-derived isolates**

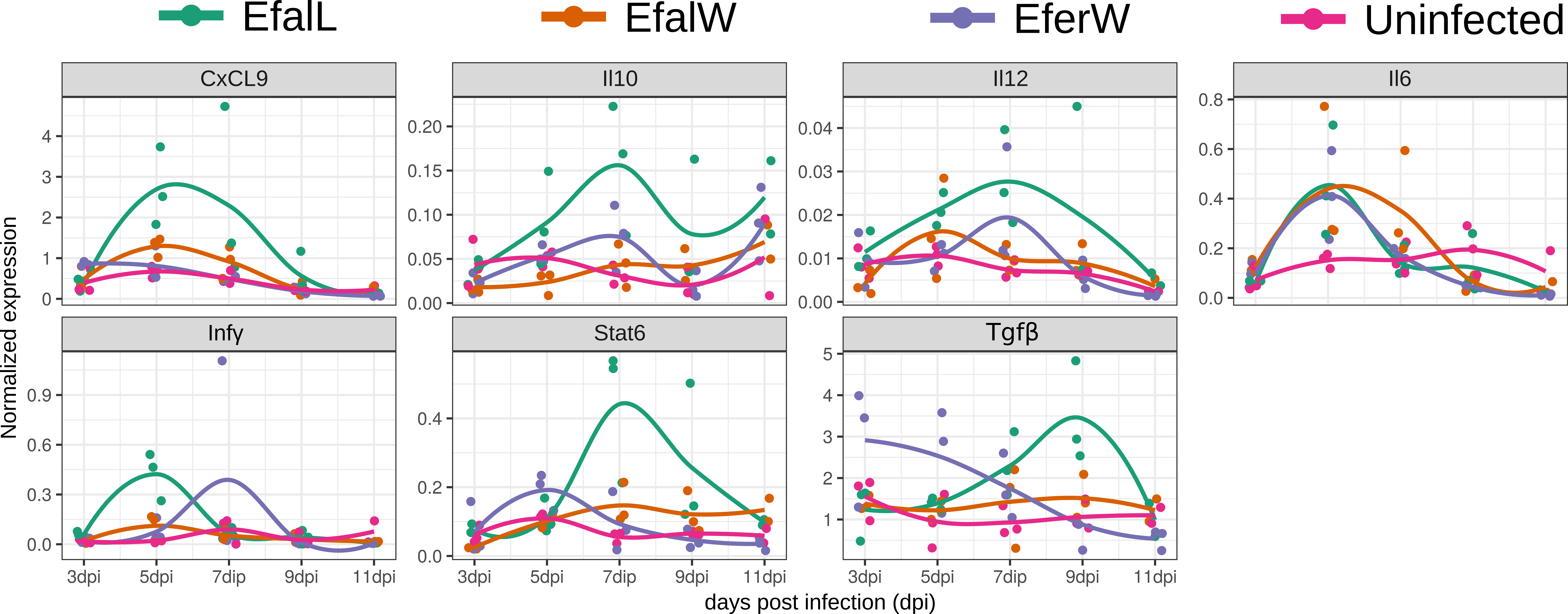
To characterize the immune response of NMRI mice against the *Eimeria* isolates we assessed gene expression of relevant cytokines in the spleen. Expression levels for most genes differ significantly between uninfected controls and mice infected with the laboratory isolate *E. falciformis* BayerHaberkorn1970 (EfalL) (Figure 4). We used linear mixed effect models with dpi as random effect to “pool” information over multiple dpi, effectively increasing sample sizes (Table 2). Mice infected with EfalL show significantly higher expression levels of chemokine 9 (CxCl9), interleukins 10 and 12 (Il10 and Il12), tumour growth factor beta (Tgfβ), and signal transducer and activator of transcription 6 (Stat6). We did not detect significant expression differences between control and EfalL infected mice for interleukin 6 (Il6) and interferon gamma (Ifnγ).

For both wild-derived strains *E. falciformis* (EfalW) and *E. ferris**i* (EferW), in contrast, expression levels for any of the examined genes do not differ significantly between uninfected and infected mice. Expression in infections with the laboratory isolate (EfalL) is significantly elevated also compared to infections with both wild derived parasite isolates (EferW and EfalW) (Table 2).

Some genes show (according to the model outlined above) non-significant differences in gene expression profiles over the course of infection. This includes differences between infections with different parasite isolates (Figure 4). We did not analyse these differences on individual days statistically due to the low sample sizes, but give a description of our observations. Il6 shows elevated levels of expression for all infection groups compared to controls at 5 dpi. Expression levels for Ifnγ seem elevated only at 5 dpi and only in infections with the *E. falciformis* laboratory isolate (EfalL). Both cases of potential elevations in expression fail to be detected as significant over controls in our mixed effect models, likely because they are transient and diminished already at 7 dpi. Il10, Il12, Stat6 and CxCl9 show elevated expression levels at multiple days of infection for the EfalL compared to all other infection groups (and were thus significant in our model). Tgfβ shows elevated expression levels early in infection with EferW (3 and 5 dpi) and late in infections with EfalL (7 and 9 dpi). Taken together these observations add detail on the individual cytokines and underline our general finding of differences between wild-derived and laboratory isolates of *E. falciformis*.

In summary expression of genes relevant for immune responses does not differ significantly from uninfected controls during infection with wild derived isolates of both *E. falciformis* (EfalW) and *E. ferrisi* (EferW). In contrast, most genes are expressed at significantly higher levels in infections with the laboratory isolate of *E. falciformis* compared to uninfected controls but also to all other infections including those with the wild derived *E. falciformis* (EfalW) isolate*.*

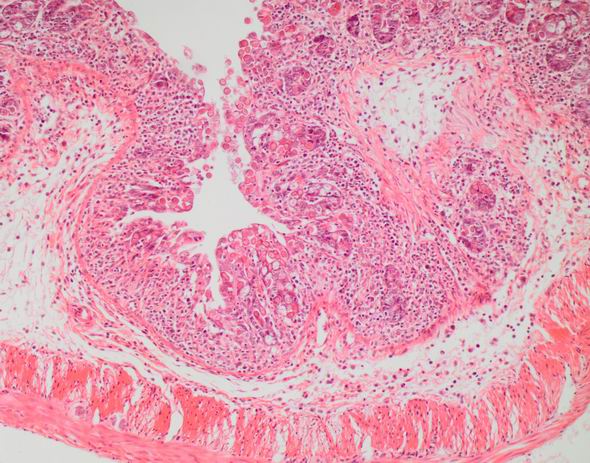
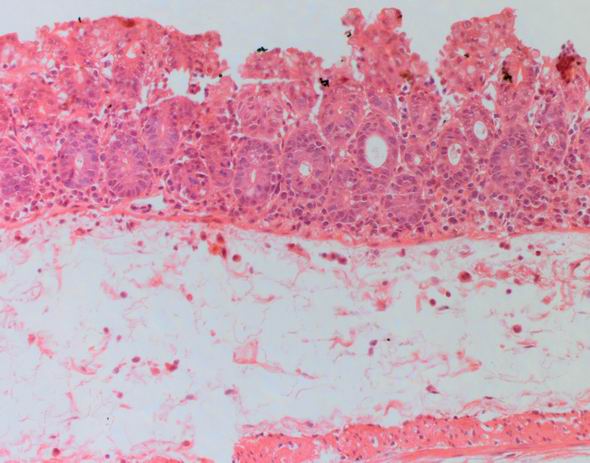
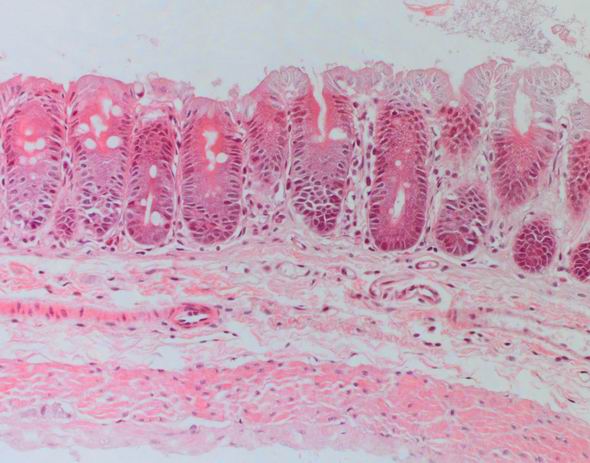
**Table 2** – Generalized linear mixed effect models show gene expression differences between wild (EfalW) and laboratory (EfalL) isolates of *Eimeria falciformis.* This table is submitted as separate file.

**Figure 4** – Hosts infected with wild and laboratory isolate of *E. falciformis* show different patterns of gene expression in the spleen. Mice were sacrificed at different time points post infection and mRNA expression was assessed using quantitative PCRs. Dots indicate normalized expression values for individual mice. Lines are drawn using local polynomial regression fitting (a “loess smoother”).

**Inflammatory cell infiltration differs between *E. falciformis* isolates**

To link our observation of gene expression in the spleen with independent measures of immune response and pathological changes, we performed a histological scoring of inflammatory cell infiltration (Table 3, Figure 5). Uninfected mice did not show inflammatory cell infiltration, besides a few (n= xx) exceptions with very low numbers of infiltrating KIND\_OF cells.

In mice infected with the laboratory isolate of *E. falciformis* (EfalL) a relatively high score of inflammation was observed already during pre-patency (at 5 dpi). The extent of immune infiltration remained high until 9 dpi and declined towards 11 dpi. In contrast, in caeca of mice infected with the wild derived isolate of *E. falciformis* (EfalW) only low numbers of inflammatory cells were found in the pre-patent period. Infiltration consisted mainly of lymphocytes and plasma cells at this stage of infection. Inflammation then increased at 7 dpi onwards, and during this period, eosinophilic granulocytes were also detected. Infiltration was marked at 9 dpi before decreasing slightly towards 11 dpi.



The quality of the observed infiltration was the same in both infections with wild derived and laboratory isolate of *E. falciformis*. Infiltrations are consistently characterised by both KIND\_OF cells, KIND\_OF cells and the presence of eosinophils.

In infections with *E. ferrisi* a milder inflammatory response was detected on 3 dpi and 5 dpi, with the latter being relatively (to other dpi of *E. ferrisi* infection) stronger followed by a subsequent decline towards 7 dpi. We used an inflammation score of mice sacrificed at different days during the infection (Table 3) in mixed effect models. Overall inflammation was significantly lower in *E. ferresi* infected mice than in those infected with *E. falciformis* (glmm; EfalL *vs.* EferW p = 0.001; EfalW *vs*. EferW p = 0.014).

**Table 3 - Score for the relative severity of leukocyte infiltration in sections from the mid-part of the caecum from NMRI mice infected with Eimeria spp.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Treatment¹ | Relative severity of leukocyte infiltration in caecum1 | | | | |
| 3dpi | 5dpi | 7pdi | 9dpi | 11dpi |
| ***E. ferrisi* (EferW)** | 2, 1, 1 | 1, 2, 2 | 1, 2, 1 | 1, 1, 1 | 0, 0, 0 |
| ***E.falciformis* (EfalW)** | 0, 1, 1 | 1, 0, 1 | 2, 2, 2 | 3, 2, 3 | 2, 2 |
| ***E.falciformis* (EfalL)** | 1, 2, 1 | 3, 3, 3 | 3, 3, 2 | 3, 3, 2 | 1, 1 |

1Leukocyte infiltration was scored on a 0 to 3 scale, where 0 represent no infiltration and 1, 2, 3 represented low, moderate, or high infiltration, respectively. One section from each caecum sample was used for scoring. Each section was subdivided into three low magnification fields, and infiltration revealed a mixture of mononuclear and KIND\_OF cells. A numerical score was assigned to each section by averaging three low magnification fields. For each infection group and dpi values for three or two mice are reported.

**Discussion**

Infections are increasingly studied in combinations of natural systems and laboratory settings to understand the evolution of pathogens and the immune system. Natural parasites of the house mouse can play an important role when bridging this research with experimental immunology. We here study Eimeria spp., natural parasites of the house mouse. We evaluated whether the “laboratory isolate” Eimeria falciformis BayerHaberkorn1970 (Haberkorn, 1970) differs from wild derived isolates of the same species and of *E. ferrisi* concerning infection dynamics, pathogenicity and the immune reactions it induces. We found not only expected differences in parasite life cycle progression between Eimeria species (E. falciformis vs. E. ferrisi), but also differences between the wild derived and laboratory isolate of E. falciformis. The laboratory isolate of E. falciformis induces relatively stronger immune reactions and pathologic changes in NMRI mice than newly derived isolates of both E. ferrisi and E. falciformis.

Between the two E. falciformis isolates BayerHaberkorn1970 (EfalL) and Brandenburg88 (EfalW) we observed only slight differences in the length of the pre-patent period (time until oocyst shedding, starting at 6 vs. 7 dpi). These results are in agreement with previous reports from the same host (NMRI mice) and the BayerHaberkorn1970 isolate (Ehret et al, 2017; Schmid et al, 2014, 2012; Stange et al, 2012). The pre-patent period for the wild derived E. falciformis isolate (7 dpi) corresponds to that reported for the parasite isolate E. falciformis var praghensis (Kasai et al, 1991; Mesfin et al, 1978), but Mahrt and Shi (1988) and Schito et al, (1996) demonstrated slightly longer pre-patent periods (7 or 8 dpi) also in other E. falciformis infections.

The output of oocysts in our study (for all isolates) was similar or only slightly lower than in previous reports (Ehret et al, 2017; Schmid et al, 2014). Our observation regarding the lifecycle progression of E. ferrisi, agree with the initial description of the life cycle in Mus musculus (Ankrom et al, 1975). E. ferrisi is characterized by a – especially when compared to *E. falciformis* – short life cycle with patency at 3 dpi. It is also noteworthy that the oocyst output of this species did not differ significantly when compared to that of both E. falciformis isolates (Figure 1). This data establishes *E. ferrisi* Brandenburg64 as a parasite isolate with low pathogenicity and high parasite reproduction. It invites comparisons of host-parastite interactions with more pathogenic isolates and could be attactive an alternative infection model with less impact on the host (i.e. allowing shorter experiments more compliant with welfare of host animals).

Pathogenicity assessed by maximal weight loss during infections with *E. falciformis* was more severe in the present study compared to previous experiments (Ehret et al, 2017; Schmid et al, 2012; Stange et al, 2012). A potential reason for such a relatively high pathogenicity could – as in any experimental *Eimeria* infection – be an underestimation when adjusting the number of sporulated oocysts for the inoculum. As observed by Haberkorn (1970) higher dosed inocula lead to enhanced pathology, while the extent and timing of oocyst shedding are not impacted. Importantly, we here developed a method to assess the intensity of intestinal stages relative to the number host cells (parasite-host DNA log-ratio). This allows us to argue for the consistency of infectious doses: the tissue intensity attained by all three strains used in our experiment was not significantly different, and the tissue intensity of the two *E. falciformis* was very similar throughout the infection. We can conclude that we report results from a strong infection relative to previous studies, which was consistent between innocula of different strains.

This allows us to compare weight loss as an indication of pathogenicity between strains and to relate this to parasite reproduction: in *E. falciformis* infections maximal weight loss was observed at 9 dpi, while infections with *E. ferrisi* induced a significantly lower maximal weight loss at 5 dpi. These observations can be either due to fewer or faster cycles of asexual merogony of the parasite. Lines of poultry *Eimeria* with an abbreviated life cycle (so called “precocious lines”) show low oocyst output and are less pathogenic to their host (McDonald and Ballingall, 1983; Shirley and Bellatti, 1988; Shirley and Harvey, 2000; Shirley and Long, 1990). *E. ferrisi*, in contrast, attains substantial oocyst output, but shares low pathology with such precocious lines. This suggests that short phases of asexual expansion might be associated with low pathogenicity in *Eimeria* infections independent of total oocyst shedding. Parasite fitness for “naturally precocious” species of *Eimeria* might be high, while simultaneously host fitness is affected relatively little by infections.

Integrating weight loss dynamics with parasite lifecycle progression and comparing the two isolates of E. falciformis and that of E. ferrisi shows that E. ferrisi induces most weight loss before the peak of its oocyst shedding, while both E. falciformis isolates impact the host after the peak of their oocyst shedding (Figure 2). These differences suggest that mechanisms underlying pathogenesis might be different between the two parasite species. Histology indicates that weight loss coincides with immune cell influx in E. falciformis infections (Figure5). This influx differed slightly in timing starting at 5 dpi in the E. falciformis laboratory isolate and 7dpi in the wild derived isolate. Such influx of immune cells into the tissue might be associated with immuno-pathology (Baskin et al, 2009; Brant et al, 2014; Stange et al, 2012). As an alternative or additional cause of pathogenicity sexual reproduction of E. falciformis might directly cause an exhaust of epithelial cell which burst when oocysts are released into the lumen (Kasai et al, 1991). Infections with *E. ferrisi* were characterised by yet lower immune cell infiltration and weight loss coincided with the peak abundance of endogenous stages at 3 dpi (Figure 2), suggesting that parasite proliferation causes pathology in host infected with this species. It can thus be speculated whether it is simply the extraction of energy of E. ferrisi for its own growth causing pathology in this system.

Cellular infiltrations within the mucosa during experimental infections with *Eimeria* have been observed in many host species including mice (Gadde et al, 2009; Laurent et al, 2001; Mesfin et al, 1978; Muñoz-Caro et al, 2016; Rose et al, 1992). Schmid et al. (2014) demonstrated by immunohistochemical analyses that *E. falciformis* infection in the caecum of NMRI mice leads to tissue infiltration with lymphocytes and macrophages. These changes are accompanied by elevated expression of Infγ and the production of the major chemokines CxC subfamily at the site of infection. Inflammatory infiltrates were also slightly more prominent in our experiment in the laboratory isolate of *E. falciformis (*EfalL) than in closely related wild derived *E. falciformis* isolate (EfalW) and we thus asked whether systemic immune response differs between infections.

To address whether and how more systemic immune responses are induced, we measured the expression of cytokines in the spleen. Seven markers for different immune response pathways were selected: CxCL9 is a major immune-regulator, INFγ represents the innate pro-inflammatory response (Mosmann et al, 1986). IL12is a marker for Th1-type response against intracellular parasites, STAT6 for a Th2-type response. IL6 is a marker for the Th17pathway in the mucosal barrier tissues and, finally, IL10 and TGFβ have anti-inflammatory roles (reviewed in Terner *et al*, 2014, Stenger and Röllingho 2001). All these chemokines play a role for leukocyte attraction to the site of infection (Lillehoj, 1998; Pogonka et al, 2010; Rose, 1974) and are involved in controlling the expansion of *Eimeria* in mouse models (Laurent et al, 2001; Lowenthal et al, 1997; Yun et al, 2000). It is unclear, however, whether they are unregulated in the spleen upon *Eimeria* infection, indicating a more systemic response.

In the spleens of mice infected with the laboratory isolate of *E. falciformis* we observed elevated mRNA levels of the pro-inflammatory Th1 cytokine Il12. The Il12/Ifnγ axis is crucial for the activation of cellular immune responses against intracellular parasites including Eimeria (Cacho et al, 2012; Chow et al, 2011; Ehigiator et al, 2007; Heinzel et al, 1991; Kulkarni et al, 2011; Lillehoj, 1998; Michailowsky et al, 2001; Ovington and Smith, 1992; Rose et al, 1992; Schmid et al, 2014; Ehret et al, 2017). Our analysis didn’t detect Ifnγ itself as significantly unregulated, as an elevated expression was only detectable early after infection (at 3dpi). We, however, observed significantly increased expression of the anti-inflammatory Th1 cytokines Il10 and Tgfβ. IL10 can counteract Ifnγ and is also expressed in spleens of *Eimeria*-infected chicken (Rothwell et al, 2000). Il10 expression in the spleen could be indicative for an attempt to balance inflammation during infection. A failure to established this inflammatory balance can lead to pronounced inflammation and immunopathology (Inagaki-Ohara et al, 2006). In addition, we observed significantly elevated expression of Stat6 and the major regulatory chemokine CxCL9, which can be induced downstream of INFγ (Djamiatun et al, 2017; Hirako et al, 2016; Schmid et al, 2014) and are involved in recruitment and activation of effector T lymphocytes in the spleen as well as in non-lymphoid organs such as intestine in disease models including *E. falciformis* infections (Hardison et al, 2006; Khan et al, 2001; Schmid et al, 2014).

Few studies have assessed systemic immune response via expression of cytokines in the spleen during *Eimeria* infections. Steinfelder et al, (2005) showed that proliferated KIND\_OF cells from spleen of *E. falciformis* infected mice released IFNγ and IL4 and likely contribute to the development of a systemic humoral response in infected mice. E. tenellaantigen has been shown to induce IFNγ release in spleen cells of from immunized chickens (Prowse & Pallister, 1989). Similarly, Byrnes et al, 1993 illustrated that splenic macrophages can produce IL1 and TNFα during the primary infection of E. tenella and E. maxima. The expression of Toll-like receptors (TLR3, TLR15), signal adaptor (MyD88) (Zhou et al, 2014) and IFNy (Rothwell et al, 2000) has been detected in the spleen of chickens as a response to infection with E. tenella. Taken together our data indicates a systemic immune response against *E. falciformis* BayerHaberkorn detectable in the spleen based on elevated mRNA levels of cytokines previously associated with in *Eimeria* infections.

Infection with the laboratory isolate of E. falciformis lead to significantly higher expression levels of cytokines in the spleen compared to both wild-derived isolates. In contrast, the wild derived isolates of E. falciformis and E. ferrisi did not induce significant expression changes over control levels in our mixed effect model analysis.

In spite of the overall non-significant changes, stints of elevated expression (failing to be significant in an analysis over different time points) seem plausible for Il6 in the spleen during infections with all three *Eimeria* isolates. IL6 is expressed during the initial stage of inflammation at the site of infection, where it has a role in stimulating the intestinal epithelial proliferation and repair after injury (Kuhn et al, 2014). It can be transported as a protein through the bloodstream to the liver and spleen (Hienrich et al, 1990), where it promotes specific differentiation of naïve CD4+ T cells (Tanaka et al, 2014). In experimental infections of mice with *E. falciformis* marked induction of Il6 transcription between 5 and 7 dpi has been reported at the site of infection (Ehret et al, 2017). Enhanced expression in the spleen might suggest that the immune modulatory role of IL6 in the spleen during *Eimeria* infections could be augmented by elevated mRNA expression within this organ.

Similarly, Tgfβ expression levels seemed elevated in the spleen early during infection with E. ferrisi (3 and 5 dpi) and late in infections with the *E. falciformis* laboratory isolate (7 and 9 dpi; only in the latter significantly though). The simultaneous elevation of Il6 expression levels, may indicate the involvement of a Th17 pathway to control the infection events. Tgfβ and Il6 play crucial roles in the generation of IL17 from naïve CD4+ T cells of mouse (Sehrawat and Rouse, 2017; Korn et al, 2009). IL17 in turn contributes to both immunopathology and parasite restriction during infection with *E. falciformis* (Stange, 2013). These exceptions only underline the fact that a systemic immune response was hardly detectable, using gene expression in the spleen, in infections with wild derived *Eimeria* isolates.

The apparent differences in immune response of the wild-derived and the laboratory isolate of *E. falciformis* invite speculation about their origin. Unfortunately, we do not know the infection phenotype (pathogenicity and induced immune reactions) of *E. falciformis* BayerHaberkorn directly after its isolation. It is plausible, however, that the pathology before serial passaging resembled that observed for our wild derived isolate. The consequences of serial passaging could then be seen as the result of an accidental evolutionary experiment (Ebert, 1998).

Independent of the ultimate reasons for the difference in immunogenicity, we conclude that the infections with the laboratory isolate E. falciformis might not be representative for parasite-host interaction in their original ecological and evolutionary context. *Eimeria* is one of the most relevant parasites for wildlife immunology and we recommend to isolate strains of the parasite from the natural system with minimal passaging prior to infection experiments.

**3. Material and Methods**

**3.1. Isolation of *E. falciformis* Brandenburg88 (EfalW) and *E. ferrisi* Brandenburg64 (EferW)**

The pure inocula of *E. falciformis* Brandenburg88 (EfalW) and *E. ferrisi* Brandenburg64 (EferW) wild derived isolates were produced by a single passage through NMRI mice preceding the reported experiment. Briefly, sporulated oocysts of *Eimeria* for each isolate were recovered from faecal samples obtained by trapping individual wild house mice in the federal state of Brandenburg (Germany). The last part of the full name of novel isolates corresponds to a running number used for mice caught during field sampling. The mouse yielding the isolate *E. falciformis* Brandenburg88 had been caught at 13.84 52.2678 DD, the mouse yielding *E. ferrsi* Brandenburg64 at 13.4642 52.4164 DD.

Isolates were identified through amplification and sequence comparison of three genetic markers (small ribosomal subunit 18S, Cytochrome c Oxidase I COI and Open Reading Frame 470 ORF470). Sequences from *E. falciformis* Brandenburg88 (MH751942, MH755305, MH755336) and *E. ferrisi* Brandenburg64 (MH751927, MH777469, MH755326) were deposited in the NCBI Genbank. These isolates have between 99% and 100% of identity in comparison with the available sequences from *E. falciformis* and *E. ferrisi*.

From flotations of these fecal samples 300 and 600 oocysts for *E. ferrisi* Brandenburg64 and *E. falciformis* Brandenburg88, respectively, were inoculated into 16 weeks old female NMRI mice. All mice were reared individually in wire cages in isolation cabinets and provided with food and water *ad libitum*. The faeces from those mice were collected daily. Oocysts in faeces were harvested using flotation (see below). They were then placed in 2% potassium dichromate and incubated at 25 °C for 4 days to permit oocyst sporulation. Sporulated oocysts were examined repeatedly under the light microscope and were then stored at 4 °C for about 1 month prior to use. The inoculum of *E. falciformis* BayerHaberkorn was prepared simultaneously using the same protocol.

**3.2. Genotyping of newly derived isolates**

- PCR protocol

- sequencing

**3.2. Infection protocol, oocyst counting and sample collection**

60 female NMRI mice (10 to 12 weeks old) were randomly assigned to one of four groups, including a control group that was not inoculated. Oocyst concentrations of three different inocula were adjusted by counting the total number of oocysts in 10µl directly on a standard microscope slide. Using these inocula the remaining 45 mice (15 per group) were inoculated via oral gavage with 0.1 ml of inoculum containing a single dose of 200 sporulated oocysts.

Faeces were collected every day of the experiment, weighted and stored in 2% solution of potassium dichromate. For flotation the the fecal material was homogenized, centrifuged at 3175g and the pellet was washed with distilled water. Oocysts were recovered from the sediment by 2 successive flotations in saturated NaCl solution each followed by washing. After the last washing 2ml of PBS was added to the pellet and 10µl of the solution were loaded into a “Neubauer-improved chamber”.

The pellet was washed twice with physiological NaCl solution and after the last washing 2ml of 2% potassium dichromate solution were added to the pellet. 10µl of the resulting solution was loaded into a “Neubauer-improved chamber”. Oocysts were counted in eight grid squares. Then the number of oocysts per gram faeces was obtained according to the (0.1µl) volume per grid square: *Concentration (oocyst/g) = total #of oocyst / #squares counted \** *10.000 ml-1 \* 2ml / g (faeces).*

During the 11 days of the experiment the body weight of mice was recorded. From each group three mice were sacrificed on 3, 5, 7, 9, and 11 dpi. Immediately after death the viscera were exenterated and spleen and caeca removed. Caecal contents were gently removed with physiological NaCl solution and the tissue was cut longitudinally into two pieces. One piece was transferred into a 1.5ml tube containing RNAlater® (Life Technologies; Carlsbad, CA, USA) and stored for 4h at 4°C before being transferred to−20 °C. The second piece of caecum tissue was fixed in 4% formalin and stored at room temperature for histological examination.

**3.3. Quantification of *Eimeria* load in infected mouse caecum tissue**

For DNA extraction frozen caecum tissue was manually homogenized by grinding in liquid N2. Genomic DNA was extracted using innu PREP DNA Mini Kit® (Analytika jena) according to the manufacturer’s protocol incorporating proteinase K digestion. Purified DNA stored at -20 °C until subjected to qPCR for host and parasite DNA quantification.

Primers used in this study to amplify the mitochondrial COI region of *Eimeria* spp. are Eim-COI-forward 5’TGTCTATTCACTTGGGCTATTGT3’ and Eim-COI-reverse5’GGATCACCGTTAAATGAGGCA 3’ and target a region in the COI divergent from the host version of the gene. For host genomic DNA amplification we used a primer targeting the *Mus*-*cdc42* gene with the sequence: *Mus*-*cdc42-*forward 5’CTCTCCTCCCCTCTGTCTTG3’ and *Mus*-*cdc42-*reverse 5’TCCTTTTGGGTTGAGTTTCC3’.

60 DNA samples were added for qPCR to Multiplate™ 96-Well PCR plates (BioRad), with reactions performed in duplicate for each sample. Each plate also contained a non template control and a plate control sample (ddH2O). All pipetting steps took place in a clean and sterile flow box, designated for working with DNA. The qPCR mixture of 10 μL was prepared using the iQ™ SYBR® Green PCR Kit (Bio-Rad): 5 μL of 2X iQ™ SYBR® Green Master Mix, 0.3 μL of 20 μM forward and reverse primers, and 4 μL of 10ng/μL template DNA. The thermal cycling protocol was set as follows: initial denaturation for 15 minutes at 95°C, followed by 40 cycles of 15 seconds at 95°C, 30 seconds annealing at 60°C for Eim-COI primer or 58°C for *Mus*-*cdc42,* and 30 seconds at 68°C and measuring the fluorescence signal at the end of every step.

qPCR amplifications and analysis were performed using Bio-Rad CFX96, Thermalcycler1000 system, which determined the cycle of quantification (Cq). To assess the validity of our protocol we examined assay specificity, efficiency and repeatability on three separate RT-PCR amplifications. To confirm the specificity of the assay a melting curve was generated during RT-PCR by adding a stepwise temperature increase from of 65.0°C to 95.0°C, with 0.5°C increment after amplification. After calculating mean Cp between technical replicates, the abundance of *Eimeria* relative to host DNA was estimated as the ∆Cq between mouse and parasite DNA. As a log of a ratio is equivalent to subtractions between log values, this represents a log(2)-ratio between mouse host (*Mus*-*cdc42*) and *Eimeria* parasite (Eim-COI) DNA copies.

**3.4. RNA extractions and reverse transcription**

Before RNA isolation, frozen spleen tissue was homogenized by grinding after addition of liquid nitrogen. Total RNA was isolated using the PureLink™ RNA Mini Kit ([Thermo Fisher Scientific](https://www.google.de/url?sa=t&rct=j&q=&esrc=s&source=web&cd=1&cad=rja&uact=8&ved=0ahUKEwi__puD3IfYAhXGKlAKHYjaDEAQFgg4MAA&url=https%3A%2F%2Fwww.thermofisher.com%2Forder%2Fcatalog%2Fproduct%2F12183018A&usg=AOvVaw0FVD2VXdCZI8KVSaguQkxK)). Briefly, frozen homogenized sample was transferred with a sterile scalpel blade into tubes with 1ml lysis solution with 1% 2-Mercaptoethanol and 1.4 mm zirconium oxide beads (Peqlab GmbH, Erlangen, Germany). Subsequently samples were homogenized at room temperature (RT) using a Precellys® 24 tissue homogenizer twice at 6,000 rpm for 20 sec interrupted by a 30 sec cooling break. All further steps took place in a clean and sterile flow box, designated for RNA extraction only to eliminate most of the aerosol which developed during the shaking. All samples were centrifuged for 1 min at maximum speed (13,400 rpm) (Eppendorf) to eliminate the foam. The pure supernatant was collected and mixed with 1:1 ratio of 70% EthO. Afterwards, 600 µl of the previous mixture was added onto the Spin Filter in a 2.0 ml tube and centrifuged at 13,400 rpm for 30 sec. The filter binds all double stranded genomic DNA (gDNA), whereas single stranded RNA remains in solution. To get red of gDNA, an on-column DNA digestion was accomplished by PureLink DNase Set ([Thermo Fisher Scientific](https://www.google.de/url?sa=t&rct=j&q=&esrc=s&source=web&cd=1&cad=rja&uact=8&ved=0ahUKEwi__puD3IfYAhXGKlAKHYjaDEAQFgg4MAA&url=https%3A%2F%2Fwww.thermofisher.com%2Forder%2Fcatalog%2Fproduct%2F12183018A&usg=AOvVaw0FVD2VXdCZI8KVSaguQkxK)) according to the manufacturer protocol. To purify the RNA a washing solutions were added to the samples on the column and were centrifuged at 13,400 rpm for 30 sec.

After RNA isolation, the synthesis of complementary DNA (cDNA) was performed using the RevertAid H Minus First Strand cDNA Synthesis Kit (Thermo Fisher Scientific, Braunschweig, Germany). The Kit included the genetically engineered RevertAid™ H Minus M-MuLV Reverse Transcriptase (200 U/µl) which lacks the ribonuclease H activity to prevent RNA digestion. This prevents degradation of RNA in RNA-DNA hybrids during synthesis of the first strand cDNA.

Nuclease-free H2O was added to 1µg template RNA to a total volume of 22 µl and 10 µl 0.1 pg/µl. 2 µl Oligo (dT)18 primer (100 µM, 0.5 µg/µl) were added to synthesize only RNAs with 3’-poly(A) tails. To denature potential secondary structures, the mixture was heated to 65°C for 5 min using the 2720 Thermal Cycler (Applied Biosystems) and rapidly cooled on ice afterwards to prevent renaturation. Subsequently, the reverse transcriptase mix was added.

The reaction was carried out by incubation for 60 min at 42°C followed by heating (termination) at 70°C for 10 min. two separated cDNA synthesis reaction was carried out for each individual sample. Thereby resulting first strand cDNA was then pooled from which aliquots was then drawn for subsequent gene expression study.

**3.5. Gene expression quantification**

To make an overall measure of the function of the immune response during the infection, we measured the expression levels of eight genes of interest, along with three reference genes. Genes of interest were CxCL9, Il10, Il12, Tgfβ, Stat6, Il6, Infγ and Tnfα. The primers targeting these genes are given in Table 3.

Table 3: Primer-pairs used for qPCR analysis of gene expression.

|  |  |  |  |
| --- | --- | --- | --- |
| Gene | Primer Sequence (5´- 3´) | Amplicon size(nt) | Source |
| *Mm*CDC42-F  *Mm*CDC42-R | CTCTCCTCCCCTCTGTCTTG  TCCTTTTGGGTTGAGTTTCC | 96 | This study |
| *Mm*Ppia-F  *Mm*Ppia-R | ACCGTGTTCTTCGACATCAC  ATGGCGTGTAAAGTCACCAC | 198 | This study |
| *Mm*Ppib-F  *Mm*Ppib-R | CAAAGACACCAATGGCTCAC  TGACATCCTTCAGTGGCTTG | 161 | Ehret et al, 2017 |
| *Mm*IFNg-F  *Mm*IFNg-R | ACAGCAAGGCGAAAAAGGATG  TGGTGGACCACTCGGATGA | 106 | Primer Bank  ID 145966741c2 |
| *Mm*IL6-F  *Mm*IL6-R | TAGTCCTTCCTACCCCAATTTCC  TTGGTCCTTAGCCACTCCTTC | 88 | Primer Bank  ID 13624311a1 |
| *Mm*IL10-F  *Mm*IL10-R | CCCATTCCTCGTCACGATCTC  TCAGACTGGTTTGGGATAGGTTT | 110 | Primer Bank  ID 6680389a1 |
| *Mm*IL12-F  *Mm*IL12-R | ATGGCTGCTGCGTTGAGAA  AGCACTCATAGTCTGTCTTGGA | 108 | Primer Bank  ID 6680399a1 |
| *Mm*TGFb-F  *Mm*TGFb-R | TACGTCAGACATTCGGGAAGCAGT  AAAGACAGCCACTCAGGCGTATCA | 186 | This study |
| *Mm*CXCL9  *Mm*CXCL9 | GGAGTTCGAGGAACCCTAGTG  GGGATTTGTAGTGGATCGTGC | 82 | Primer Bank  ID 162287427c1 |
| *Mm*STAT6  *Mm*STAT*6* | CTCTGTGGGGCCTAATTTCCA  CATCTGAACCGACCAGGAACT | 135 | Primer Bank  ID 6678155a1 |
| *Mm*TNFa  *Mm*TNFa | CATCTTCTCAAAATTCGAGTGACAA  CCTCCACTTGGTGGTTTGCT | 63 | This study |

A total of 60 cDNA samples were split between PCR plates (Multiplate™ 96-Well, BioRad) with reactions performed in duplicate for each sample. If the standard deviation of Cq values between duplicates was > 0.4, corresponding samples were repeated (as described in Weyrich et al, 2010). Each plate contained a non-template control sample and negative controls.

The qPCR mixture of 10 μL was prepared using the iQ™ SYBR® Green PCR Kit (Bio-Rad): 5 μL of 2X iQ™ SYBR® Green Master Mix, 3 μL of 10 μM forward and reverse primers, and 4 μL of 10ng/μL template cDNA. qPCR amplifications were performed using Bio-Rad CFX96, Thermalcycler1000 system as follows: initial denaturation for 15 minutes at 95°C, followed by 40 cycles of 15 seconds at 95°C, 30 seconds at 60°C and 30 seconds at 68°C with a measuring of the fluorescence signal at the end of every step. The cycle of quantification (Cq) was determined by the amplification plot in CFX96-Bio-Rad software. Finally, a melting curve was generated to confirm the specificity of the reaction by adding a cycle of 65.0°C to 95.0°C in 0.5°C increments.

Accurate normalization with a set of most stably expressed reference genes which are often specific for tissue and experimental conditions is essential for the production of reliable data in RT-PCR experiments (Axtner et al, 2009; Weyrich et al, 2010). To select the most stable reference genes for relative-quantification of genes of interest, we tested four candidate genes: *Gabdh*6, *Cdc42*, *Ppia and* *Ppip*, using 16 randomly selected cDNAs from spleen samples. Analysis of the gene stability measure was performed using qbase+ (Biogazelle) implemented in the Bio-Rad CFX96 Thermalcycler1000, resulted *in Cdc42*, *Ppia* and *Ppip* (Table 3) as the most stable reference genes for this study. For the three reference genes, normalization factors (NF) were calculated using the geometric mean of the corresponding expression values for all spleen cDNAs (Vandesompele et al, 2002). Relative expression values for each tested sample of each gene of interest were then calculated using the ∆Cq method, adjusted for the amplification efficiencies of each primer pair and standardized against the normalization factors (NF) of each sample.

An increase in the expression of TNFα of was detected in all experimental groups, including the non-infected control group, around 5 dpi. Melting curves for this cytokine indicated a non-specific amplification artefact as likely reason for this and the data was thus excluded from further reports.

### 3.6. Histological examination and scoring

Formalin fixed samples from the mid-part of the caeca were processed routinely,embedded in paraffin and sectioned with 4 μm thickness. Tissue slides were stained with hematoxylin and eosin and were examined at 100- 200- and 400-times magnification by light microscopy. The cellular infiltration in response to the Eimeria infection was obtained by qualitatively assessing the extent and nature of leukocyte infiltration in the intestinal wall based on the morphological characteristic of each cell type. A numerical score was assigned with 0 representing no leukocyte infiltration and 1, 2, and 3 mild, moderate, or severe infiltration, respectively.

A further score was based on the detection of characteristic *Eimeria* developmental stages (Goodwin, 1996). We used photographs of the caecum slides at 400-times magnification (Cell® image analysis) to count micro- and macrogamonts in 6 high power fields per section.

**3.7. Statistical analyses and visualisation**

All statistical analyses and visualisations were performed in R (R Development Core Team, 2008). An “exact” version of the Mann-Whitney U-tests available in the package “coin” was used to account for ties in all comparisons of weight loss or oocyst shedding. A generalized linear model of the poisson family (log-link) was used to predict histological lesions with the parasite-host DNA log-ratio and parasite isolate used for infection allowing for different intercept and slopes for each isolate.

Linear mixed effect models (function “lmer” of the package lme4) were used to test for differences in gene expression. For each gene (as response variable) these models used the infecting *Eimeria* isolate as only fixed effect and the time of infection (dpi) as a random intercept. Similarly, linear mixed effect models for leukocyte infiltration scores (as response variable) were used with infection isolate as fixed effect and dpi as a random intercept. For visualisations the package ggplot2 was used, including the default “loess” smoother as indicated in figure legends.

**Ethics statement**

All animal procedures in this investigation were performed according to the German Animal Protection Laws as directed and approved by the overseeing authority Landesamt für Gesundheit und Soziales (Berlin, Germany) under permit number H0098/04.

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