RESEARCH

Dual host-parasite transcriptomes of apicomplexan Eimeria falciformis and its natural mouse host

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Abstract

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Keywords: Parasite, apicomplexa, RNA-seq, transcriptome, life-cycle, interaction

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Introduction

Text and results for this section, as per the individual journal's instructions for authors.

Results

A dual transcriptomics experiment

We performed mRNA sequencing of caecum tissue from mice infected with the apicomplexan parasite *E. falciformis*. Oocysts and sporozoites were included as "environmental" stages and processed "*in vitro*". To follow the life cycle of the parasite, we compare different time-points after infection.

We additionally used different mouse strains which display different immunocompetence in infection trials measured by oocyst output to assess the influence of host immunocompetence on parasite development (figure 1a,b). In these experiments we analysed mice lacking the Recombination activating gene 1, Rag1, and compared them to the parental C57BL/6 mouse line. Rag1 knock-out mice lack adaptive immune response due to the absence of mature B and T lymphocytes. All three mouse strains were used for infections of both naive mice and previously infected animals (onward referred to as "challenged").

Basic phenotyping showed differences in oocyst numbers between the immunocompetent (C57BL/6) and immunodeficient (Rag1-/-) host strain in infection of naive mice and in challenge infections. Immunocompetent NMRI mice were infected with a higher dosis of sporulated oocysts, and a drastic reduction of oocysts in faeces was seen in challenged mice compared to naive mice (Figure 1a). Oocyst numbers in faeces peaked on days 8-9 and all mice had cleared the infection by day 14. Development of *E. falciformis* intestinal stages is reflected by the percentage of parasite reads sequenced per time-point post infection (Figure 1b) and this was confirmed by quantitative reverse transcription PCR (RT qPCR) of parasitic 18S (Figure 1c).

We thus use dual RNA-seq to analyse the life cycle of *E. falciformis* under the influence of host immune responses at early stages of infection. We used an experimental design which allows to compare infections at 5 days post infection (dpi) for all experimental conditions (NMRI, C57BL/6 and Rag1-/- mouse strains in naive and challenge infection). In addition, additional time-points 3 dpi and 7 dpi were analysed from NMRI mice (Figure 1d).

Parasite and host dual transcriptomes can be assessed in parallel

In this RNA-seq experiment, each replicate sample was enriched for caecum epithelial tissue which was pooled from three mice. mRNA was extracted and sequencing libraries prepared. Two biological replicates were used for all but two conditions (with one and three replicates, respectively). These libraries were sequenced on several lanes of Illumina GAIIX (13 samples) and HiSeq machines (14 samples) and mapped to both mouse and parasite genomes simultaneously to avoid spurious assignments of reads in ultra conserved genomic regions. As samples and individual replicates were sequenced in batches to different depth and using different instrumentation (Table 1) we performed quality controls (additional files xyz). These confirm the absence of batch effects influencing analysis and quality of results.

Total numbers of sequenced reads as well as reads mapped to either the *E. falciformis* genome or the mouse genome are indicated in Table 1 for all replicates. The number of total read mappings for individual replicates ranged from 11,479,260 (sample NMRI_sporozoites_rep2) to 145,033,326 (NMRI_2ndInf_5dpi_rep1). At the latest time-point samples, 7 dpi, the overall mRNA output of the sampled caecum tissue is dominated by parasite material with proportional mRNA abundance of 77% (in NMRI_1stInf_7dpi_rep2) and 92% (in NMRI_1stInf_7dpi_rep1). (Figure 1b).

Exclusion of samples with uncertain infection status

A maximum of 86% (sample NMRI_1stInf_7dpi_rep1) and a minimum of 0.0326% (sample NMRI_2ndInf_3dpi_rep2) of mapped reads could be assigned to the *E. falciformis* genome in samples considered infected (Table 1). We excluded samples NMRI_2nd_3dpi_rep1 and NMRI_2nd_5dpi_rep2 due to low parasite contribution to the overall transcriptome. Technically, this exclusion made it possible to obtain read counts in agreement with a negative binomial distribution (see additional file x). It is also likely that the number of reads in the excluded samples would have been insufficient to fully normalise these datasets to those with the highest parasite contributions. From a biological point of view, both excluded are samples from challenge infection and we assume that the infection was cleared or reduced to a non-detectable level. One sample (NMRI_1stInf_0dpi_rep1) was excluded because the uninfected control showed unexpected mapping of reads to the *E. falciformis* genome. We consider the three excluded samples to display an uncertain state of infection.

The mouse transcriptome changes in the course of infection

Statistical testing for differential expression between infected and uninfected mice revealed changes in mRNA abundance becoming more pronounced (involving more genes) at later time-points post infection (especially at 7 dpi; Table 2).

The observed changes between controls and 7 dpi were in agreement with previously published microarry data. Fold-Change data obtained from *E. falciformis* infected mice at 6 dpi on Agilent microarrays (Schmidt et al 2012) or 7 dpi (our RNAseq data) against uninfected controls show a strong correlation (Spearman's $\rho = 0.74$; $Figure 2a$). $Considering both biological (e.g. exact time-points) and technical differences between the two methods this comparison confirms the adequacy of using dual RNA-seq for assessing the host transcriptome.$

For mouse, 325 mRNAs were considered differently abundant (DA; FDR¡1%) between controls and 3 dpi, 1,804 mRNAs between controls and 5 dpi and 2,711 mRNAs between controls and 7 dpi. This lead to a combined set of 3,453 genes responding to infection (Figure 2bi). DA mRNAs early in infection (3 dpi and 5 dpi) were not simply a subset of genes DA later in infection (7 dpi), but instead, the transcriptional profile of the mouse changes throughout the time-points tested here. To further validate this pattern of a distinct response in early infection we performed hierarchical clustering on the (union of) mouse genes DA between different time-points post infection (Figure 2c).

By hierarchical clustering of mouse samples, three main sample clusters formed, "main clusters" (dendrogram of columns at top of Figure 2c). Rag1-/- mice cluster with control samples, and there is no clear distinction between infected and non-infected Rag1-/- samples, confirming the immune deficiency phenotype in Rag1-/-. Control samples are defined by high abundance of transcripts in gene cluster 3 (yellow, clusters of rows on the left) and partly high abundance in cluster 4 (red). Immunodeficient Rag1-/- samples share this profile with control samples in gene cluster 4, and this cluster has low abundance in (most) other infection samples. This suggests that these are genes which become down-regulated in immune competent mice upon infection. Three samples of challenged mice from 3, 5, and 7 dpi display high abundance of transcripts in gene cluster 6 (blue). The same genes have a low abundance in two naive, immune competent mouse samples from 5 dpi. Genes in cluster 6 are therefore particularly interesting for investigating the role of adaptive immunity in this infection (although sample NMRI_2ndInf_5dpi_rep1 has a different profile).

Transcripts in gene clusters 3 and 4 are lowly abundant among all samples in the middle main cluster. Among those samples, the NMRI mouse samples display a trend towards high abundance in clusters 1, 2, 5 (green) and 7. Especially in the two late infection samples (7 dpi) a high transcript abundance is seen in clusters 1 and 5. The leftmost main sample cluster containing immunocompetent 5 dpi samples is characterized by low transcript abundance in cluster 6, and high abundance in cluster 7.

The pronounced changes later in infection reflect the expected onset of an adaptive immune response. This is underlined by enriched Gene Ontology, GO, terms in gene clusters with pronounced profiles late in infection (Figure 2c). Terms such as "antigen binding" and "immunoglobulin receptor binding" (molecular function, MF), and "immune system process" and "adaptive immune response" (biological process, BP) are highly enriched in Cluster 5 and confirm an activated adaptive immune response at this time-point.

Particular "regulation of cell death" and "regulation of apoptotic process" (BP)

"UDP-N-acetylglucosamine-lysosomal-enzyme" (MF)

General changes upon infection are a down-regulation of genes involved "lipid modification" or more detailed "phosphatidylinositol phosphorylation". These changes are similarly pronounce in the immunocompetent strains and Rag1-/- immunodefficient animals (cluster 3 of fibure 2c) (see supplementary table X). The presence of these changes immunocompromised animals invite to the speculation that those genes are independent of a potential later adaptive immune response.

Changes not detectable in Rag1-/- immunodefficient animals (cluster 3 of fibure 2c) but otherwise observed in general infection are characterised by and enrichment to genes involved in "positive regulation of calcineurin-NFAT", "blood coagulation" and "inositol phosphate-mediated signaling" (see supplementary table X). The absence of these changes in Rag1-/- mice allow us to speculate that those genes might be involved in a early onset of adaptive immune responses.

We detected further differences between infections of naive and challenge infected mouse hosts, especially at 7 dpi. These genes are characterized by...

The life cycle of E. falciformis is characterized by major changes in mRNA abundance

Table 2 lists pairwise sample comparisons and number of genes with differently abundant mRNAs per comparison. For *E. falciformis* no mRNAs are significantly differently abundant between first and second infection.

We applied hierarchical clustering on *E. falciformis* mRNAs which were differently abundant at different time-points post infection, including comparisons with oocysts and sporozoites. Changes throughout the intracellular life cycle in the host can be clearly categorised into an early (3 and 5 dpi) and late (7dpi) phase. Mouse immune status has no influence of clustering of parasite samples. Sporozoites show expression profiles similar to early infection stages while oocysts show a distinct mRNA abundance profile (MDS plot).

Parasite gene clusters shown on the left side (colour-coded and numbered 1 - 7) can be used to characterise clusters of samples. The one 7 dpi and 3 dpi sample in the rightmost sample sub-cluster differ from the three 7 dpi samples in the left sub-cluster in main cluster 1 (five samples). The two sub-clusters of samples have distinct profiles in gene clusters 2 and 7 (mint green and purple). Also genes in cluster 6 (blue) appear characteristic for the left sub-cluster; these transcripts display a below average abundance in these three 7 dpi samples.

The early infection sample cluster is characterised by a high abundance of transcripts in clusters 3 (yellow) and 6, and a below average abundance in clusters 1 (pink), 2, and 5 (green). Sporozoite samples have highly abundant transcripts in cluster 4 (red) and low abundance of transcripts in gene cluster 7. The latter is shared with oocyst samples. The oocyst samples, in addition, have low abundance of transcripts in gene clusters 2, 3, 4, 6 (and 7) and highly abundant transcripts in clusters 1 and 5.

Taken together, sample and gene clustering indicates that genes in clusters 2, 6 and 7 might be useful to characterise assumed gametocytes in 7 dpi samples. Genes in cluster 4 are candidates for sporozoite specific genes, and clusters 1 and 5 for oocyst specific genes in E. falciformis.

GO term enrichments in heatmap clusters

The annotations referred to here are inferred from orthologs in other *Eimeria* spp. or in *T. gondii*

Preparation for invasion in oocysts

The mRNA profile in the oocyst stage is mainly determined by highly abundant genes in cluster 4. Overrepresented GO-terms in this cluster are enriched by ortholog genes to peptidases, microneme localized proteins reported to be involved in invasion, genes associated with adhesion in protozoans (and with clotting in higher eukaryotes), and genes that are annotated to be involved in amino acid biosynthesis. Aminopeptidase N ('related' annotation) is the reported ortholog for three genes with abundant mRNAs in oocysts. In humans, this enzyme has been reported to cleave peptides bound to major histocompatibility complex, MHC, II (UniProt reference if we want to keep this... but does any secretion happen from oocysts...? Or is this too far-fetched to be interesting?).

A Thrombospondin type 1 domain-containing protein ortholog is highly abundant in cluster 4 (high abundance in oocysts). Thrombospondin type 1 domains have been reported in *E. tenella* microneme localizing proteins, MIC, e.g. MIC4 (Tomley01) In *E. tenella* MIC4 mRNA was reported in sporozoites where it localizes to the apical end, and in late schizonts and late oocyst stages, when sporozoites are forming. (Tomley01). For the same gene, the *T. gondii* annotation is Sushi domain-containing protein, which is also the ortholog annotation of another gene in this cluster. In the related malaria parasite *P. falciparum* the apical sushi protein, ASP, (which has a sushi domain) localizes to micronemes in merozoites but not other stages (OKeeffe05). Limulus clotting factor C, Coch-5b2 (Cochlin) and Lgl1, LCCL, (syn. F5/8 domain) domains are associated discoidin lectin domains and thereby with adhesion. (Pfam entries for 'LCCL domain' and 'Discoidin domain', May 2016). Taken together, this indicates that the thrombospondin and sushi-domain genes (EfaB_MINUS_4114.g412 and EfaB_PLUS_1425.g183) are involved in sporozoite invasion in *E. falciformis* and that the mRNAs are transcribed and available before excystation. A role in merozoite re-invasion in *E. falciformis* is not indicated by our data. The LCCL domain annotation and thrombospondins role in higher eukaryotes also indicates that adhesion or preparation for adhesion is important in oocysts. We suggest (speculate...?) that the thrombospondin annotated ortholog and the LCCL domain-containing protein (EfaB_MINUS_11233.g986) are involved in cell adhesion in *E. falciformis*.

Amino acid biosynthesis in oocysts

High abundance of aminotransferase mRNAs indicate amino acid biosynthesis or preparation for the same in oocysts (cluster 4). We identify D-3-phosphoglycerate dehydrogenase and alanine dehydrogenase orthologs, which are enzymes contributing to L-serine and L-alanine production, respectively. A putative *Eimeria* spp. cystathionine beta-synthase, CBS, in this cluster also indicates de novo cysteine production. Alkyl sulfatase mRNA is also abundant in oocysts. Generally, this enzyme enables an organism to exploit organic sulfur to produce and incorporate inorganic sulfur into the amino acids cysteine and methionine, when no inorganoc sulfur is available.

'Embryonic development' Nicalin 1, patched family protein (hedgehog)

Oocysts contain mRNA for fatty acid catabolism

MmgE/PrpD is overrepresented in oocysts. The enzyme is important for propionate catabolism in the 2-methylcitric acid cycle and has been shown to be used by the intestinal intracellular bacterium *Salmonella typhimurium* to generate pyruvate (Horswill99). Propionate is one of two most abundant small-chain fatty acids in the gut along with butyrate. Both fatty acids are largely produced as degradation products from food by commensal bacteria (Sun13). Sharing the intestines as a niche with *S. typhimurium* it is possible that also *E. falciformis* uses Mmg/PrpD to exploit available propionate for pyruvate production.

Oocyst highly abundant mRNAs are downregulated in sporozoites

Interestingly, the genes described above which are thought to be involved in amino acid biosynthesis and invasion are highly abundant in oocysts but are underrepresented in schizont stages (day 3 and day 5 samples) and even in sporozoites. An average abundance was detected on day 7 for these genes, indicating a role in either gametes or early oocyst formation. This pattern supports the suggestion that these specific mRNAs (cluster 4) for invasion and biosynthetic processes are prepared (and possibly expressed) in the oocyst stage but are no longer detectable in the cell at the timepont when the protein is assumed to be in use (sporozoites and merozoite stages). Therefore, correlating mRNA prevalence with biological function at the timepoint when mRNAs are detected must be done with care.

Down in sporozoites and oocysts –¿ cluster 3.....

Oocysts: profile for 3, 5, 6:

Sporozoites: 3 and 5

Day 7: 5 and 7

Specific genes.... Enolase 2, encoded by Eno2, is among the downregulated genes in oocysts and sporozoites. In *T. gondii* the paralog Eno1 is strongly associated with the cyst (bradyzoite) stage and Eno2 is associated with tachyzoite stages (kibe05). It is therefore expected that this mRNA is underrepresented in oocysts and our data also show that the same is true in sporozoites for *E. falciformis*. (TK: If important we could look specifically for Eno1 in cluster 4).

Down in sporozoites and oocysts –¿ cluster 3.....

Motility-related mRNAs indicate gamete development on day 7

Two clusters contain genes with mRNAs highly abundant on day 7 p.i; cluster 1 and 2. Dynein, kinesin and tubulin are annotations highly represented among orthologs of genes in both these clusters. The annotations indicate an important role for motility at this timepoint, probably reflecting development of microgametes. In addition, in cluster 2, there are two 'EF-hand domain containing proteins' annotations as well as caltractin, centrin-1, and troponin annotations. Caltractin and centrin-1 are associated with the centrosome and structure and function of microtubuli in mammals, and troponin is linked to muscle function (UniProt). Also potentially linked to motility is the occurence of growth arrest specific protein 8, Gas8, which in the mouse has been reported to be highly expressed in the testes and important for mouse sperm function (Yeh02).

Other genes among the 38 indicate carbon fixation (glycolysis/gluconeogenesis) or conversions of nucleoside phosphates. In addition, a Ras family protein, RNA polymerase II transcription initiation factor and Sec23 and Sec24 were among orthologs identified in *E. falciformis* cluster 2.

In cluster 1, carbon metabolism genes are represented by 6-phosphogluconate dehydrogenase and glycogen phosphorylase family protein 1. UDP-glucose 4-epimerase and amiloride-sensitive amine oxidase are reported as upregulated in gametocytes in *E. tenella* by RNA-seq (Walker15) and suggested by those authors to play a role in cyst wall synthesis.

Microneme proteins highly expressed on day 7 p.i.

Unintuitively for a protozoan organism, seven out of eight GO biological process terms in cluster 1 are associated with wound healing and blood coagulation. An explanation is offered by some of the orthologs to the three *E. falciformis* genes responsible for these terms. In protozoa, e.g., other *Eimeria* spp. and *Toxoplasma gondii* orthologs are annotated as 'Micronemal protein MIC4, related' (E. tenella) and more generally for several other protozoa, 'PAN domain containing proteins'. The PAN domain is found in the plasminogen/hepatocyte growth factor family and in coagulation factor XI family (REF), explaining why terms related to blood coagulation are enriched by these genes. Later publications on *T. gondii* (Marchant12) also associate PAN domains and proteins in apicomplexan parasites with micronemes and therefore invasion. In our case, this is peculiar, since the enrichment appears on day 7 p.i.. A possible role at this timepoint is suggested by work on the fungi *Sclerotinia sclerotiorum* where Yu et al. reported an important role for PAN domain proteins in cell wall integrity (Yu12). This role for MIC proteins has to our knowledge not been investigated in apicomplexan parasites. The PAN domain domain has also been reported to be common in nematodes such as *Caenorhabditis elegans*, however the function is not understood. (Thordai99) The other two GO terms in the cluster of day seven upregulated genes are DNA replication and DNA replication initiation, which most likely reflects late stage schizogony or gamete formation. Six genes contribute to this enrichment and orthologs are either annotated as DNA replcation licencing factors, DNA polymerases or minichromosome maintenance proteins 2/3/5/7, Mcm2/3/5/7.

Gene and sample patterns by hierarchical clustering

Samples (columns) cluster into two major clusters where day 7 p.i. samples form one group distinct from other samples. In the second group, oocsts and sporozoites are distinct and sporozoites cluster most closely with day 3 and 5 p.i. samples. Day 3 and 5 p.i. samples also cluster into two groups, of which one contains all NMRI day 5 p.i. samples. Apart from this, the two day 3 and 5 p.i. sample clusters have no obvious patters.

For gene clusters (rows), the two groups with high mRNA abundance on day 7 p.i. (cluster 1 and 2) do not cluster most closely with each other, but with the cluster for high mRNA abundance in oocysts (cluster 1 association) and with the cluster for high mRNA abundance in sporozoites (cluster 2 association).

Evolutionary conservation of expression changes in E. falciformis

For comparison of changes in the lifecycle of *E. falciformis* with the economically important chicken parasite *E. tenella* and the model apicompomplexan *Toxoplasma gondii* we downloaded expresson datasets from ...

Oocysts, Sproozoites

Discussion

In our analysis we demonstrate which biological processes are dominant in different life cycle stages of *E. falciformis* in the mouse. The RNAseq transcriptome provided here allows for detailed analysis of genes involved in those processes, providing candidates for life stage specific marker in *Eimeria* spp. research.

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1 Methods

1.1 Mice and infection procedure

Three strains of mice were used in our experiments: NMRI (Charles River Laboratories, Sulzfeld, Germany), C57BL/6 (), and Rag1-/- on C57BL/6 background (gift from Susanne Hartmann, FU?). Animal procedures were performed according to the German Animal Protection Laws as directed and approved by the overseeing authority Landesamt fuer Gesundheit und Soziales (Berlin, Germany). Animals where infected as described by Schmid et al., (Schmid12), but tapwater was used instead of PBS for administration of oocysts. Briefly, NMRI mice were infected two times, which will be referred to as first and second infection. For the first infection, 150 sporulated oocysts were administered in 100 L by oral gavage. During the first infection of 60 mice, all animals were weighed every day. On day zero, before infection, as well as on day three, five and seven days post infection, dpi, caeca from 3-4 sacrificed mice per time point were collected. Epithelial cells were isolated as described in Schmid et al.(schmid12). For challenge infection, mice recovered for four weeks before second infection. Recovery was monitored by weighing and visual inspection of fur. For the second infection, 1500 sporulated oocysts were applied by oral gavage. Three mice were used as non-second infection control, referred to as day 0, second infection.

1.2 Oocyst purification for infection and sequencing

Sporulated oocysts were purified by flotation from feces stored in potassium dichromate and administered orally in 100 uL tapwater. One *E. falciformis* isolate, *E. falciformis* Bayer Haberkorn 1970, was used for all infections and parasite samples. The strain is maintained through passage in NMRI mice in our facilities as described elsewhere (schmid12).

1.3 Sporozoite isolation

Sporozoites were isolated from sporocysts by excystment. For this, sporocysts were incubated at 37C in DMEM containing 0.04% tauroglycocholate (MP Biomedicals) and 0.25% trypsin (Applichem) for 30 min. Sporozoites were purified by the method of Schmatz et al (schmatz–).

1.4 RNA extraction

Total RNA was isolated from infected epithelial cells, sporozoites and sporulated oocysts using Trizol according to the manufacturer's protocol (Invitrogen). High quality *what is the meaning of 'high quality' here?* RNA was used to produce an mRNA library using the Illumina's TruSeq RNA Sample Preparation guide. *stolen from genome paper* Sporozoites were stored in 1 mL Trizol until RNA-isolation. Total RNA was isolated using the PureLink RNA Mini Kit (Invitrogen) and reverse transcribed into cDNA.

1.5 Sequencing, sequence quality assessment and alignment

cDNA samples were sequenced by either GAIIX or Illumina Hiseq 2000 as specified in SI xx (both unstranded). A fastq_quality_filter (FASTQ-toolkit, version 0.0.14, available at https://github.com/agordon/fastx_toolkit.git) was applied to Illumina Hiseq 2000 samples after replacing "N" bases by "." annotation. A phred score of 10 was applied. We further set q = 60. These settings require that nine out of ten bases or more are correct in at least 60% of the bases for each read.

1.6 Alignment and reference genomes

We used the published *Mus musculus* mm10 assembly (Genome Reference Consortium Mouse Build 38, GCA_000001635.2) as reference genome including annotations for mouse data. The *E. falciformis* genome (Heitlinger14) was downloaded from ToxoDB (Gajria07). For the alignment, the mouse and parasite genome files were merged into a dual reference genome, and files including mRNA sequences from both species were aligned against the dual reference genome using TopHat2 (version 2.0.14, Trapnell09) with -G specified, and a Bowtie2 (version 1.1.2, Langmead12) index of the dual genome. Single-end and pair-end sequence samples were aligned separately with library type 'fr-unstranded' specified for pair-end samples. Import into R was enabled by the R package Ballgown, which requires bam files to be processed by Tablemaker (Frazee15), in our case used with -qW -G specified. Tablemaker in turn makes use of Cufflinks (version 2.1.1, Trapnell10).

1.7 Differential mRNA abundance, data normalisation and sample exclusions

Count data was normalized using the R-package edgeR (version 3.14.0; cite) with the upperquartile normalisation method. Briefly, genes with zero coverage in all samples (libraries) are removed and normalisation factors are calculated for the 75% quantile for each library. This normalisation is suitable for read densities following a negative binomial distribution. Two samples contradicted this assumption (parasite data) for later modelling and both mouse and parasite data from these samples were excluded from further analysis: NMRI_1st_3dpi_rep1 and NMRI_2nd_5dpi_rep1 (SI ...). The method then fits a generalized linear model (GLM with a negative binomial link function) for each gene (glmFit) and then performs likelihood ratio tests for models w or w/o focal factor (glmLRT).

1.8 Selection of differentially abundant mRNAs nad hierarchical clustering

A selection of differently abundant mRNAs are used for hierarchical clustering of *E. falciformis* life cycle relevant genes. In each comparison (see Table 3), the union of

the at most 500 genes differentially abundant with lowest FDR (¡0.05) are selected. In the next step, the 500 mRNAs from each comparison (or less) are joined. For *E. falciformis* time p.i. comparison, this resulted in 1618 unique genes selected as differently expressed . The 22 genes in the NMRI vs C57BL/6 comparison are not included in the *E. falciformis* life cycle analysis. The same comparisons for mouse yielded 8052 genes in total and 1313 unique ones. In heatmaps, all samples, i.e. also samples which themselves did not have any significantly different mRNAs according to our selection, were included in hierarchical clustering. Scale bar in heatmaps show 0 as mean mRNA abundance for each gene (row). Up (green) and down-regulation (brown) denote number of standard deviations from 0, i.e., row mean. Hierarchical clustering was performed using with Euclidean distances, using complete linkage ('complete', R package base).

1.9 Differentially abundant mRNAs used for hierarchical clustering

All analyses were performed in R (cite R-core). Complete scripts are available at https://github.com/derele/Ef_RNAseq.git tagged as version 1.0.

Table 1 Genes used for hierarchical clustering of mRNAs differently abundant depending on time p.i..

Data description	*E. falciformis* genes	Mouse genes
Sum of 1st infection NMRI sample differences (including oocysts and sporozoites if appl.)	4935	8052
Used in hierarchical clustering (heatmap)	1618	1313

Competing interests
The authors declare that they have no competing interests.

Author's contributions
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Figures

Figure 1 Experimental design and outcome of a dual RNAseq experiment read sequences per mouse read sequences for each experimental condition. The more advanced the infection is, the higher the ratio of parasite reads is, reflecting parasite replication between day zero and day seven. .....compare 1st and 2nd ..... patterns between Rag and NMRI/C57BL/6? ..... Values are mean of replicates (n=2, if * n=1) on log10 scale. Each sample (replicate) consists of mRNA from three different mice.

figure 1 label cotribution of mouse vs. parasite transcripts to the overall transcriptional output of the analysed tissue for all samples.

Figure 2 *E. falciformis* mRNAs with significantly different abundance at different times p.i. in NMRI mice (see Table 2). Samples cluster according to expected developmental state of the parasite, without distinguishing between first and challenge infection. Hierarchical clustering was set to apply seven gene clusters.

1.10 Parasite development reflected in mouse data

Figure 3 Mouse mRNAs with significantly different abundance at different times p.i. in NMRI mice (see Table 2). Samples cluster according to expected developmental state of the parasite, without distinguishing between first and challenge infection. Rag1-/- mouse samples cluster together. Hierarchical clustering was set to apply four gene clusters.

When clustering mouse mRNAs which were different in time p.i. comparisons in Table 2, three out of four samples from day 7 p.i. (NMRI only) cluster together. These samples are characterized by gene cluster 3 (up) as well as 2 and 4 (down). The fourth day 7-sample (challenge infection, second replicate) clusters with day 3 and 5 samples. Upon visual inspection of this sample in gene cluster 4, it diplays a profile similar to non-infected mice. The same sample is abnormal in the parasite profile (Figure 1). NMRI and C57BL/6 uninfected samples (0dpi) cluster together, defined by gene clusters 4 (up), and 1 (down). Rag1-/- day 0 samples are however less pronounced in gene cluster 1. Day 3 and 5 samples cluster together, with Rag1-/- forming a separate group and Rag1-/- non-infected most distant in this sample cluster.

Sample*	Sequencing method	batch	total reads	reads mapping Mouse	reads mapping *E. falciformis*	Percentage ** *E. falciformis*	detected *E. falciformis* genes
NMRI_2ndInf_0dpi_rep1	GAII	2	108,937,797	70,489,674	247	0.0004	1
Rag_1stInf_0dpi_rep1	hiseq	3	25,362,793	18,853,850	443	0.0023	2
C57BL6_1stInf_0dpi_rep1	hiseq	3	35,731,249	25,119,348	457	0.0018	2
C57BL6_1stInf_0dpi_rep2	hiseq	3	47,085,959	34,377,133	608	0.0018	2
Rag_1stInf_0dpi_rep2	hiseq	3	46,556,156	35,233,327	676	0.0019	2
NMRI_2ndInf_0dpi_rep2	hiseq	3	58,122,244	40,794,245	3,406	0.0083	51
NMRI_2ndInf_3dpi_rep1	hiseq	3	57,934,016	40,544,287	4,803	0.0118	95
NMRI_2ndInf_5dpi_rep2	hiseq	3	63,965,539	48,289,181	10,941	0.0227	407
NMRI_1stInf_0dpi_rep1	GAII	1	82,364,585	55,176,243	17,954	0.0325	701
NMRI_2ndInf_3dpi_rep2	hiseq	3	65,548,826	46,171,909	29,548	0.0640	1,580
NMRI_2ndInf_7dpi_rep2	hiseq	3	67,487,466	51,722,265	40,091	0.0775	1,836
Rag_1stInf_5dpi_rep1	hiseq	3	38,651,359	29,982,453	63,024	0.2098	2,548
Rag_1stInf_5dpi_rep2	hiseq	3	34,779,832	25,297,803	99,000	0.3898	2,828
C57BL6_1stInf_5dpi_rep1	hiseq	3	40,904,388	29,319,604	185,969	0.6303	4,173
Rag_2ndInf_5dpi_rep1	hiseq	3	50,049,848	37,093,621	192,856	0.5172	4,167
C57BL6_1stInf_5dpi_rep2	hiseq	3	29,511,368	18,062,349	215,696	1.1801	3,823
C57BL6_2ndInf_5dpi_rep1	hiseq	3	35,148,432	25,660,184	262,909	1.0142	4,563
NMRI_1stInf_3dpi_rep1	GAII	1	73,236,430	49,993,358	394,384	0.7827	5,220
NMRI_1stInf_3dpi_rep2	GAII	2	160,709,694	117,791,044	413,051	0.3494	4,862
NMRI_1stInf_5dpi_rep2	GAII	2	119,902,722	76,419,774	794,570	1.0290	5,333
NMRI_2ndInf_5dpi_rep1	GAII	2	230,773,955	143,186,486	1,846,840	1.2734	5,533
NMRI_2ndInf_7dpi_rep1	hiseq	3	70,366,762	41,467,146	8,634,201	17.2335	5,875
NMRI_1stInf_5dpi_rep1	GAII	2	76,702,168	47,037,087	8,669,701	15.5631	5,700
NMRI_sporozoites_rep2	GAII	0	19,551,681	8,656	11,470,604	99.9246	5,513
NMRI_1stInf_5dpi_rep3	GAII	0	191,099,180	83,735,624	27,839,458	24.9513	5,784
NMRI_1stInf_7dpi_rep1	GAII	1	66,505,514	3,310,666	39,400,884	92.2488	5,932
NMRI_sporozoites_rep1	GAII	1	67,325,397	4,334	43,774,401	99.9901	5,825
NMRI_oocysts_rep1	GAII	1	68,859,802	3,805	49,653,065	99.9923	5,695
NMRI_oocysts_rep2	GAII	0	151,090,783	18,524	71,019,860	99.9739	5,777
NMRI_1stInf_7dpi_rep2	GAII	1	139,749,046	21,699,324	73,539,445	77.2159	5,943

* sample names are given as a) mouse strain b) first or challenge infection c) days post infection (dpi) and d) replicate number seperated by undersocre .

** percentag mapping *E. falciformis* is given as percentage in total mapping reads

2 mRNA abundance differences between different experimental groups

Table 2 mRNA abundance differences between different experimental groups.

Day post infection comparisons	*Ef* genes different (FDR≤1%)	Mouse genes different (FDR≤1%/5%)
NMRI 0 vs NMRI 3	NA	274
NMRI 0 vs NMRI 5	NA	1736
NMRI 0 vs NMRI 7	NA	2802
NMRI 3 vs NMRI 5	111	1
NMRI 3 vs NMRI 7	1385	1407
NMRI 5 vs NMRI 7	1895	873
C57BL/6 0 vs C57BL/6 5	NA	914
Rag1-/- 0 vs Rag1-/- 5	NA	45
Day post infection, parasite relevant comparisons		
Oocysts vs NMRI 3	3310	NA
Oocysts vs NMRI 5	3605	NA
Oocysts vs NMRI 7	3085	NA
Oocysts vs sporozoites	3421	NA
Sporozoites vs NMRI 3	1663	NA
Sporozoites vs NMRI 5	1605	NA
Sporozoites vs NMRI 7	2473	NA
First and second infection comparisons		
NMRI 3 1st vs NMRI 3 2nd	0	5
NMRI 5 1st vs NMRI 5 2nd	0	1
NMRI 7 1st vs NMRI 7 2nd	0	902
C57BL/6 1st vs C57BL/6 2nd (day 5)	0	mouse
Rag1-/- 1st vs Rag1-/- 2nd (day 5)	0	mouse

Additional Files

Additional file 1 — Raw and normalized counts
Raw counts of reads mappins to the *E. falciformis* and mouse genome for individual samples in our study. Normalized counts for seperately for the host and parasite mappings (three compressed csv files).

Additional file 2 — Results of statistical tests (edgeR)
Focal contrast, fold-changes, likelihood ratio in/excluding this difference in models, p-values , and false discovery rates (adjusted p-values) are given for all tested contrasts (one compressed csv file).

Additional file 3 — Additional methods and resuts
Document containing additonal figures and summary tables (pdf).

Additional file 4 — Results of enrichment analyses (topGO)
Tables listing all tested gene sets and resulting significatn GO terms.