Comparative transcriptomics reveal conserved impacts of rearing density on immune response of two important aquaculture species

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Abstract

Background: Infectious diseases represent an important barrier to sustainable aquaculture development. Rearing density can substantially impact fish productivity, health and welfare in aquaculture, including growth rates, behaviour and, crucially, immune activity. Given the current emphasis on aquaculture diversification, stress-related indicators broadly applicable across species are needed.

Results: Utilising an interspecific comparative transcriptomic (RNAseq) approach, we compared gill gene expression responses of Atlantic salmon (Salmo salar) and Nile tilapia (Oreochromis niloticus) to rearing density and Saprolegnia parasitica infection. Salmon reared at high-density showed increased expression of stress-related markers (e.g. c-fos and hsp70), and downregulation of innate immune genes. Upon pathogen challenge, only salmon reared at low density exhibited increased expression of inflammatory interleukins and lymphocyte-related genes. Tilapia immunity, in contrast, was impaired at low-density. Using overlapping gene ontology enrichment and gene ortholog analyses, we found that density-related stress similarly impacted salmon and tilapia in key immune pathways, altering the expression of genes vital to inflammatory and Th17 responses to pathogen challenge.

Conclusions: Given the challenges posed by ectoparasites and gill diseases in fish farms, this study underscores the importance of optimal rearing densities for immunocompetence, particularly for mucosal immunity. Our comparative transcriptomics analyses identified density stress impacted immune markers common across different fish taxa, providing key molecular targets with potential for monitoring and enhancing aquaculture resilience in a wide range of farmed species.

Background

Sustainable aquaculture development continues to be at the forefront of priorities for meeting protein demands of a growing human population (1, 2) and therefore remains the fastest growing food sector (3). A staggering 598 aquatic species are commercially cultured worldwide today, up by 26.7% in the last 10 years alone (3), vastly outweighing the diversity of terrestrial animal production (4). Arguably one of the greatest challenges to the current level of farmed aquatic species diversity and future diversification of aquaculture is to identify and reliably assess the optimum conditions for each species' health, welfare, and productivity.

Rearing density is considered one of the pivotal factors determining aquaculture productivity and profitability (5–7). While overcrowding and/or under-stocking can significantly impact overt measures of fish performance such as growth rate (8, 9), size uniformity (10), and aggressive/unwanted behaviours (11–13), it can also adversely affect less obvious physiological parameters such as stress levels (9, 14), circulating hormones (14, 15), and flesh quality/composition (16). It is increasingly apparent that suboptimal rearing densities have negative consequences for fish immunity (17–19) and thus increase susceptibility to pathogens (10, 20). Infectious disease is currently one of the greatest barriers to sustainable aquaculture intensification (21), and a substantial economic burden on the industry (22). Therefore, it is important to know if the underlying effects of rearing density on fish health are conserved

across fish species, and whether broadly applicable key stress indicators can be applied for management of density-related stress in aquaculture.

RNAseq methods have proved valuable tools for assessing the wider impacts of environmental stressors and pathogens on animal health at the functional genomic level (23–25). Interspecific comparative transcriptomics (comparison of gene expression responses across multiple species) has, as yet, been little used in the context of aquaculture. However, the utility of interspecific comparative transcriptomics to address fundamental questions in fish biology and evolution (26, 27), and reveal key species differences in response to shared pathogens in vertebrates (28, 29), indicates its potential value as a tool for refining aquaculture practices.

Nile tilapia (*Oreochromis niloticus)* and Atlantic salmon (*Salmo salar)* are two of the most important farmed finfish species worldwide, accounting for 8% and 4% of global annual production, respectively (3). Suboptimal rearing densities have been shown to negatively affect salmon and tilapia welfare (30–32), health (33, 34) and productivity (35). Salmon tend to experience greater stress at high rearing densities (31, 36). Conversely, tilapia show increased aggression, and are therefore considered more stressed, at low densities (20, 32). For both tilapia and salmon production, outbreaks of *Saprolegnia parasitica*a fungal-like pathogen that parasitizes the skin, fins and gills of fish (37)—are a substantial economic burden (37–39), with limited effective treatment options approved for aquaculture (37).

This study compares the impact of rearing density on the functional genomic responses of salmon and tilapia to *Saprolegnia parasitica* challenge, utilising an interspecific comparative transcriptomic (RNAseq) approach. We assess the commonalities of density-specific pathogen responses of these two key—yet highly divergent (ca. 225 MYA; (40))—aquaculture species, with the aim of identifying stress-related transcriptomic-level markers broadly applicable across the diversity of cultured fish.

Results

This study first examines Atlantic salmon (*Salmo salar)* transcriptome-wide expression responses to rearing density and infection challenge. This data was then analysed alongside comparable, previously reported data (20) on Nile Tilapia (*Oreochromis niloticus)* to assess commonalities of density-specific immune responses across divergent fish species, which respond differently to stocking-density.

Salmon transcriptomic responses to rearing density and Saprolegnia challenge

No salmon developed visible signs of *Saprolegnia* infection (i.e. mycelial growths or lesions) during the current experiment. Illumina RNAseq achieved an average 31.6 million reads per sample (range 29.3 to 32.1 million). In the gills, comparison of healthy salmon at high and low density (i.e. unchallenged controls) gene expression found 1,163 genes significantly differentially expressed. We found significant enrichment of genes with higher expression in low-density salmon (568 genes) for 124 biological process

GO terms including several immune-related functions such as “innate immune response” (GO:0045087, e.g. *hck)*„ “neutrophil mediated immunity” (GO:0002446, e.g. *rac2)*„ and “dendritic cell differentiation” (GO:0097028, e.g. *lyn)*.. These genes were also enriched for “cortisol metabolic process” (GO:0034650, e.g. *hsd11b2)*.. Genes with higher expression in healthy high-density salmon (compared to healthy low-density fish, 595 genes) were enriched for 93 biological process GO terms including a number related to physiological stress such as osmotic (e.g. GO:0042538, GO:0042539) and starvation responses (e.g. GO:0042594). This gene set also included hormonal responses, including “response to growth hormone” (GO:0060416), “thyroid hormone transport” (GO:0070327), and “response to estradiol” (GO:0032355). Full lists of differentially expressed genes and GO terms are provided in Supplementary File S1.

Comparison of gill tissues in healthy (unchallenged control) and *Saprolegnia*-challenged salmon at high and low density revealed 1,859 and 1,649 differentially expressed genes respectively. Genes exhibiting increased expression in *Saprolegnia*-challenged salmon at both densities were highly enriched for GO terms related to immune functions including “inflammatory response” (GO:0006954), “lymphocyte chemotaxis” (GO:0048247), “T cell proliferation” (GO:0042098), and “cellular response to interleukin–1” (GO:0071347). Enrichment of downregulated genes in *Saprolegnia*-challenged salmon (59 GO terms) was predominantly developmental processes (e.g. GO:0048706 embryonic skeletal system development, GO:0050793 regulation of developmental process, GO:0048538 thymus development). However, this gene set also included immune (GO:0045624 positive regulation of T-helper cell differentiation, GO:0072679 thymocyte migration) and circadian rhythm functions (GO:0032922 circadian regulation of gene expression, GO:0045475 locomotor rhythm). Upregulated expression specific to high-density challenged salmon was rich in GO terms related to mast cell responses, including mast cell mediator production (e.g. leukotriene: GO:0006691, prostaglandin: GO:0001516), chemotaxis (GO:0071624) and activation (GO:0033004, GO:0043303). In contrast, genes found only to be significantly increased in low-density challenged salmon were enriched for adaptive immune functions including lymphocyte differentiation and aggregation (GO:0030098, GO:0071593), T helper cell development (GO:0045064, GO:0072540), and B cell chemotaxis (GO:0035754). Full lists of differentially expressed genes and GO terms are provided in Supplementary File S1.

Interspecific comparison of density and Saprolegnia transcriptomic responses

Impact of density on uninfected salmon and tilapia

Comparison of functional enrichment of differential expression between high- and low-density treatments in unchallenged (healthy) salmon and tilapia reveal a small number of biological processes shared between these species (Supplementary File S2), including “innate immune response” (GO:0045087) in genes showing higher expression in high-density tilapia and low-density salmon. Using a reciprocal best hit approach, we found 21,745 1:1 orthologs between published salmon and tilapia transcriptomes, of

which 13,364 were expressed in gill tissues of both species. Twenty-three gene orthologs were found to be differentially expressed between healthy high- and low-density fish in both species (Table 1), including several genes involved in regulation of transcription *(dlx3, mef2d, npas2, med12)*..

Saprolegnia responses in salmon and tilapia

To assess overlap of functional responses to challenge with *Saprolegnia,* we compared differential expression GO term enrichment between salmon (unchallenged control vs *Saprolegnia* challenged) and tilapia (20). All GO terms found to be shared among salmon and tilapia treatment groups are summarized in Table 2. For the purposes of this study, we focussed our attention to those related to immunity. Salmon challenged with *Saprolegnia* (though no visible signs of saprolegniasis) showed increased expression of genes associated with “immune response” (GO:0006955) at both densities. In contrast, this GO term was enriched in genes with decreased expression in tilapia at both densities challenged with *Saprolegnia* (and exhibiting signs of saprolegniasis). Increased expression of genes involved in Fcε receptor signalling (GO:0038095) was found at both densities in both species (Table 2). Mast cell degranulation genes (GO:0043303) were upregulated in *Saprolegnia*-challenged tilapia in both density treatments, but only observed in high-density salmon (Table 2). Genes with increased expression in low-density salmon and high-density tilapia shared GO enrichment for “T-helper 2 cell differentiation” (GO:0045064), “T-helper 17 cell lineage commitment” (GO:0072540), “myeloid dendritic cell differentiation” (GO:0043011), “defence response to protozoan” (GO:0042832), and “isotype switching” (GO:0045190) (Table 2).

Examining expression patterns of 1:1 gene orthologs, we found 41 genes with significantly higher expression in *Saprolegnia*-challenged salmon and tilapia. These included genes involved in antigen presentation (*ap1m1, ap1s2, ap1s3),*, neutrophil activity (*lect2, serpinb1)* and inflammation (*il1rap)* (Table 3). Twenty-two genes were found to have increased expression in challenged fish in both species at only low densities, including two tumor necrosis factor superfamily members involved in immune responses (*tnfsf9, tnfsf15)*.. Mucin genes also exhibited similar responses with density in both species; *muc5ac* had higher expression at low density, whilst “integumentary mucin” (XP_014011243.1) was significantly lower in expression in high density challenged fish of both species. Several genes exhibited contrasting density-specific *Saprolegnia* challenge responses (22 increased in high-density salmon/low-density tilapia, 21 increased in low-density salmon/high-density tilapia) were related to T helper cell activity/maintenance (e.g. *il17c, lag3, tnfaip8l2, batf;* Figure 1).

An alternative to looking at the overlap of individual gene differential expression and gene ontology enrichment, is to examine cross-species preservation of weighted gene co-expression networks (28, 41). WGCNA of expressed tilapia genes with salmon 1:1 orthologs (n = 13,364) found 18 genes modules, of which 4 were associated with *Saprolegnia*-challenge status and significantly preserved in salmon (Supplementary File S2). By defining gene co-expression networks (13 modules) in salmon, six modules were significantly associated with *Saprolegnia* status and were preserved in tilapia (Supplementary File S2). Although in both species single gene modules were found to be associated with density and *Saprolegnia* (Supplementary File S2), neither were significantly preserved in the other species.

Discussion

Rearing density is a critical factor for intensive aquaculture productivity, with suboptimal conditions known to impact fish, from growth (8, 9) and quality (16) to health (17, 19) and welfare (9, 30, 31, 42). Here, we used a transcriptome-wide approach to assess the effect of rearing density on pathogen responses in Atlantic salmon, revealing suppression of immunologically-important gill gene expression responses at high density. Strikingly, we identified conserved disruption of Th_{17} responses in salmon and Nile tilapia (43) when subject to density stress. This study highlights the potential of interspecific comparative transcriptomics to identify broadly-applicable indicators of fish health.

In our study, comparison of expression profiles of unchallenged (i.e. “healthy”) salmon reared at high and low densities revealed a substantial number of differentially expressed genes in the gills (n = 1,163). High density salmon (four-fold higher than “low-density” treatment, though still within recommended welfare limits (44)) had increased expression of key markers for stress in vertebrates including *c-fos* (45–47) and *hsp70* (48, 49). Previous studies on the effects of rearing density on immunity in salmonids have primarily focussed on levels of serum antibodies (typically IgM) or antibody-producing cells, with suppression generally found at higher densities (8, 36). In addition, non-specific innate immune markers such as serum lysozyme activity have been shown to be influenced by rearing density (42). Here, we found that salmon raised at high density had lower expression of genes related to immune responses including neutrophil (e.g. *rac2)*„ dendritic cell (e.g. *cd209, ctss)*„ and B cell immunity (e.g. *lyn, cd22, blnk)* plus inflammatory interleukins (*il−12, il−17)* (Supplementary File S1). A previous study of rainbow trout head-kidney gene expression during crowding stress also showed increased *hsp70* stress marker expression, but found different immune gene suppression (*lyzII, tnf−1α, il−1β, il−8 and ifn-γ1)* (18). This suggests that crowding stress in salmonids may result in tissue-specific suppression of immune factors, which must be considered for their potential impacts on disease susceptibility. Clearly overcrowding in salmonids has a wider impact on their immune system expression than previously reported. The effects of crowding stress on immune health caused by high rearing densities may explain in part the failure of supportive breeding in salmon conservation (50–52).

We found over 1,500 genes differentially expressed in the gills of *Saprolegnia*-challenged and control (sham-challenged) fish at both densities, although no salmon at either density showed visual signs of saprolegniasis (e.g. mycelial growth). Fish at both densities exhibited expression profiles indicating initiation of inflammatory (particularly interleukin−1β mediated) responses and lymphocyte migration (Supplementary File S1), in line with previous studies of salmonids (53–55). A previous targeted immune gene study of *Saprolegnia*-challenged Atlantic salmon also showed differential expression profiles in gills despite an absence of visible signs of infection (53). Our results, however, indicate a far wider impact of sublethal *Saprolegnia* challenge; in addition to altered expression of immune genes, we found disruption of expression related to a wide range of physiological processes including development and circadian functioning (Supplementary File S1). Disruption of circadian rhythms is increasingly recognised as detrimental to vertebrate health (56), yet we are only beginning to consider this in the context of teleost immunity in aquaculture (20, 57, 58). Furthermore, *Saprolegnia* species are considered ubiquitous in

freshwaters (37) and our results suggest that in aquaculture facilities even sublethal levels of *Saprolegnia parasitica* (or other related pathogenic species) may substantially impact fish health and productivity.

A key factor to *Saprolegnia* virulence is the pathogens' ability to suppress fish adaptive immunity such as T helper cell responses and immunoglobulin production (53). While we found transcriptomic evidence of adaptive immunosuppression at both densities (e.g. downregulation of T helper cell differentiation, Supplementary File S1), the extent of suppression appeared to be density-specific. Genes upregulated in response to *Saprolegnia* found only in salmon reared at the lower density included those important to lymphocyte development and migration (including both B and T cells). In contrast, infection responses of fish raised at high density suggest a greater reliance on mast cells (Supplementary File S1), mediators of acute inflammation and non-specific antimicrobial production in teleosts (59, 60). Given the dramatic impact Saprolegniasis has on salmon aquaculture, accounting for at least 1 in 10 reported mortalities (61), our findings highlight the potential importance for optimal rearing densities to mitigate against this devastating fish pathogen.

The great diversity of fish species now cultured (3) poses a challenge to identify biomarkers broadly applicable to monitor optimal husbandry conditions and/or fish health and welfare status in aquaculture. Cortisol is most commonly used as an indicator of stress in fish and is widely implicated in suppression of immunity (62). Cortisol levels do not, however, necessarily correlate with immune function and parasite susceptibility (63), and cortisol effects on immune levels can be inconsistent (62). Our approach to uncover common biomarkers for the impacts of suboptimal husbandry conditions and their effects on fish immunity, was to compare the full transcriptional responses of two highly divergent fish species to density and pathogen challenge. Examining gene ontology (GO) enrichment in density responses from our salmon data and a previous, comparable study of Nile tilapia (20) revealed a number of GO terms shared between healthy salmon and tilapia (Supplementary File S2). Importantly, we found low-density tilapia and high-density salmon both have lower expression of genes classed as GO term "innate immune response", indicating a broad-scale signal of innate immune suppression due to density-dependent stress. Although we found only a small number of salmon-tilapia gene orthologs sharing differential expression due to density alone (Table 1), these included a homolog of *dok1,* a known negative regulator of inflammatory pathways and innate lymphocytes in vertebrates (64, 65). This gene had higher expression in high-density salmon and low-density tilapia, further indicating that suboptimal rearing density suppresses innate immune levels.

Comparing expression responses to *Saprolegnia* between salmon and tilapia revealed an upregulation of genes related to Fcε receptor signalling in both species at both densities (Table 2). Moreover, "mast cell degranulation" was found in upregulated genes of both densities of *Saprolegnia*-challenged tilapia, and high-density salmon (Table 2). Mast cells release mediators thought to be critical in responses against the fungal-like pathogen *Saprolegnia* (53). There is increasing recognition for the involvement of mast cells in fungal infections in other vertebrates (66), and more generally their importance in fish immune systems (60). We propose this cell set should be considered more closely for understanding innate

resistance/susceptibility to saprolegniasis, particularly in salmonids where their functioning appears to be impacted by rearing density.

We found intriguing conservation in the impacts of rearing density on immune responses of fish. At the rearing density least stressful for each species (salmon; low-density, tilapia; high-density), we found expression patterns consistent with enhanced T helper cell activity. GO term enrichment for Th_2 cell differentiation and Th_{17} cell lineage commitment were found in genes with increased expression in both these groups. In addition, *batf*a transcription factor crucial to Th_{17} cell differentiation (67) - was significantly upregulated in response to *Saprolegnia* challenge only at these “non-stressful” densities (Figure 1). In contrast, the “stressed” fish density groups (high-density salmon, low-density tilapia) both exhibited increased expression of *lag3,* a negative regulator of T cell expansion (68), whose activity has been implicated in reduced parasite clearance in other vertebrates (69). Moreover, these fish also had increased expression of *tnfaip8l2 (*Table 3), a suppressor of inflammation that is typically downregulated (i.e. to induce inflammation) during pathogen challenge in vertebrates including fish (70, 71). Taken together, these results indicate suboptimal rearing densities can disrupt beneficial Th_{17}/inflammatory transcriptional responses to pathogens, and these genes provide potential new markers for measures of health under different rearing densities, across a wide range of teleost species. Interestingly, in mammals, Th_{17} responses are increasingly recognised for their importance in mucosal (72) and vaccine-induced immunity (73). This appears to hold true for fish (74), which raises the question as to whether optimising rearing densities in aquaculture may in turn increase vaccine efficacy.

Conclusions

Rearing density of Atlantic salmon can significantly impact their immune status with suboptimal rearing density broadly suppressing gill innate immune gene expression, but also key adaptive immune responses to pathogen challenge. In addition, we found density-driven disruption of Th_{17} responses—key to mucosal immunity—to be similar between Atlantic salmon and Nile tilapia, suggesting these genes may be useful transcriptional indicators of rearing density impacted immunity across a broad range of fish species. We propose maintaining fish at suitable densities may not only improve natural immunocompetence, but could improve vaccination efficacy, and recommend this as a valuable line of future research for mitigating disease in aquaculture. As the species diversity of aquaculture increases, whilst disease remains a barrier to sustainable intensification of the industry, the key molecular targets identified here have the potential for monitoring and enhancing aquaculture resilience across the range of farmed species.

Methods

Salmon rearing conditions

Salmon fry (average weight = 2.55 g, average standard length = 6.52 cm), obtained from Landcatch Natural Selection (10 families; 1:1 crosses), were maintained in a re-circulating aquaculture system in CSAR, Swansea University (water temperature 10.5 ± 0.5 °C, pH 7.5 ± 0.2). Fry were fed with a commercial salmon feed (Nutraparr, Skretting, UK) and kept under a 12:12h photoperiod. Water oxygen saturation (>90%), ammonia (<0.02 mg/L), nitrite (<0.01 mg L^{-1}) and nitrate (<15 mg L^{-1}) were maintained within an appropriate range. The density experiment was conducted for 16 weeks. Fry were randomly assigned to low- and high-density groups, within two replicate 260 L tanks per treatment. Each low-density tank contained 130 fish (initial density 1.3 g L^{-1}, final density 3.6 g L^{-1}), and each high-density tank contained 520 fish (initial density 5.1 g L^{-1}, final density 14.6 g L^{-1}). These densities fall within current farming practices and UK welfare recommendations (up to 30 g L^{-1} for 5 to 30 g juvenile fish (44)). All experiments were performed with the approval of the Swansea Animal Welfare and Ethical Review Body (Approval Number IP–1415–2), and infection challenges were approved by Cardiff University Animal Ethics Committee and conducted under UK Home Office License PPL 302876.

Saprolegnia challenges

Saprolegnia parasitica maintenance and zoopsore production followed Ellison et al (43) and zoospore suspensions were equilibrated to 10.5 °C before use (75). Fish were simultaneously challenged with *S. parasitica* within their treatment groups to avoid the masking effects of acute stress due to confinement and individual isolation (76). The exposure trials were conducted in 22L tanks, with 2 replicate tanks per group containing 96 fish/tank (4 fish L^{-1}, 29.2 g L^{-1}) for high density groups (2 control tanks, 2 Saprolegnia-challenge tanks), and 24 fish/tank (1 fish L^{-1}, 7.3 g L^{-1}) for low density groups (2 control tanks, 2 Saprolegnia-challenge tanks).

Following Ellison et al (43), all fish were net shaken to facilitate infection (77) and live zoospores were added directly to high-density aquaria to achieve a concentration of 5×10^6 zoospores L^{-1}. A mixture of 1:3 live:heat-killed zoospores was added directly to each low-density aquarium to achieve a concentration of 5×10^6 zoospores L^{-1}, controlling for equivalent 1) number of infective zoospores per individual and 2) concentration of organic matter between density treatment groups. Water and zoospore solutions were changed every 6 h during 24 h exposure period and fish in unchallenged control groups received the same handling and maintenance regime.

Fish were visually inspected hourly (under red light during dark periods) throughout the experiment and those challenged with *S. parasitica* from both density groups displayed signs of lethargy (reduced swimming activity, increased resting on the bottom of the tank) ~12 h after infection, but there were no signs of mycelial growth. At 24 h post-exposure, six fish per treatment tank (high/low density, challenged/sham-challenged, 2 tank replicates) were euthanised with an overdose of Phenoxyethanol (0.5 ml L^{-1}) and samples of gill tissues (all arches) were immediately preserved in RNAlater and stored at − 80 °C until RNA extraction. Gill tissues were chosen as they are one of the primary sites of infection of *S. parasitica (*54), and critical to fish mucosal immunity and antibody-producing cell production (78).

Salmon transcriptome sequencing and gene expression analyses

RNA extractions, Illumina TruSeq library preparation, Illumin NextSeq sequencing, raw sequence read quality assessment and preparation followed Ellison et al. (43). Raw reads are available at the NCBI Short Read Archive under Accession Number PRJNA552428. Trimmed reads were mapped to the *Salmo salar* genome (International Cooperation to Sequence the Atlantic Salmon Genome, version 2) using HISAT2 version 2.0.5 (80) and quantified using RSEM version 1.2.30 (81). Transcripts were filtered to include only those with at least two counts per million mapped reads (TPM) in at least two individuals. Differential expression tests were performed using the R package limma (82), comparing 1) high- and low-density control (uninfected) fish, and 2) infected and uninfected (control) fish. Potential tank effects were explicitly accounted using the duplicateCorrelation function (82). Overlap of differentially expressed genes between salmon treatment groups were determined using Venny version 2.1 (83). Gene ontology (GO) functional enrichment tests (with FDR correction) were carried out via the R package TopGO (84) to detect significantly overrepresented biological processes of groups of differentially expressed genes shared/unique to particular treatment groups.

Interspecific comparisons of gill transcriptomic responses to Saprolegnia challenge

To examine the similarity of rearing density impacts on transcriptomic responses to pathogen challenge across divergent fish species, we compared salmon gene expression profiles to those previously characterised in Nile tilapia (*Oreochromis niloticus)* by Ellison et al. (2018, 24 h sample data only). For this, we used three methods: 1) overlap of GO term enrichment of differentially expressed genes using the full transcriptome of both species, 2) overlap of differentially expressed 1:1 gene orthologs, and 3) preservation of weighted gene co-expression networks defined using 1:1 gene orthologs. These two datasets were broadly comparable as in both 1) “high-density” rearing treatments were 4 times that of the “low-density” treatments (4 fish L^{-1} and 1 fish L^{-1} respectively), 2) the same tissue (gill) was studied, 3) tissue samples were taken 24 h post-*Saprolegnia* exposure, and 4) the same *S. parasitica* isolate, inoculation dose and challenge procedures were used.

Biological processes GO term lists from functional enrichment tests comparing healthy and *Saprolegnia*-infected tilapia at 24 h post-exposure were compared to those in salmon using Venny version 2.1 (83). We performed a reciprocal best-hit analysis to identify 1:1 gene orthologs between the two species. We used BLASTP with an E-value threshold of 1×10^{-6} to search all protein sequences from one species against the other (85). Only sequences that were the reciprocal best hit between both species were retained for further analyses.

Weighted gene co-expression networks (gene modules) were defined and correlated with treatments following methods of Ellison et al. (2018) in tilapia and salmon using only genes with a 1:1 ortholog in

the other species. To assess the degree to which gene modules were conserved in the other species, module preservation statistics were computed using the modulePreservation function (500 permutations) (41, 86). Network module preservation statistics quantify how density and connectivity patterns of modules defined in a reference data set are preserved in a test data. A $Z_{summary}$ score of 2.0 to 10.0 was considered weak to moderately preserved, and $Z_{summary}$ above 10.0 was considered highly preserved among species (41, 86).

List Of Abbreviations

FDR: false discovery rate

GO: gene ontology

MYA: million years ago

RNAseq: RNA sequencing

Th_2: T helper cell type 2

Th_{17}: T helper cell type 17

TPM: transcripts per million mapped reads

WGCNA: weighted gene coexpression network analysis

Declarations

Ethics approval & consent to participate: All experiments were performed with the approval of the Swansea Animal Welfare and Ethical Review Body (Approval Number IP–1415–2), and infection challenges were approved by Cardiff University Animal Ethics Committee and conducted under UK Home Office License PPL 302876. Consent to participate: not applicable.

Consent for publication: Not applicable.

Availability of data and materials: All sequence data have been submitted to the NCBI Sequence Read Archive (Accession: PRJNA552428) and will be made publicly available upon acceptance of this manuscript for publishing. All other data are available as additional files with this article.

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

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Tables

Table 1. Summary of Atlantic salmon and Nile tilapia gene orthologs that exhibit density-specific expression in response to rearing density. Shaded boxes indicate the treatment group (H = high-density 4 fish/L, L = low-density 1 fish/L) with higher expression.

Gene	Function	Salmon		Tilapia	
		H	L	H	L
dihydropyrimidinase-related	axon repair/development, cell migration, filipodia				
large neutral amino acids transporter small subunit 4-like	amino acid transport				
aquaporin FA-CHIP-like	ammonium, CO_2, water transport				
complement decay-accelerating factor-like	cell adhesion, motility, angiogenesis				
GTP-binding 2	GTPase activity				
ras-related and estrogen-regulated growth inhibitor	GTPase activity				
inositol-trisphosphate 3-kinase C	inositol phosphate biosynthetic process				
egl nine homolog 2-like	oxidation-reduction				
death-associated kinase 3	protein kinase				
transmembrane protease serine 4-like	proteolysis				
neuronal PAS domain-containing 2-like	regulation of transcription				
homeobox DLX-3	regulation of transcription				
myocyte-specific enhancer factor 2D	regulation of transcription				
mediator of RNA polymerase II transcription subunit 12	regulation of transcription				
endothelin B receptor-like	vasoconstriction, cartilage development				
PDZ and LIM domain 4	zinc ion binding, protein binding				
docking 1-like	insulin receptor binding				
transmembrane 268-like	unknown				
poly [ADP-ribose] polymerase 9	NAD+ ADP-ribosyl transferase activity				
claudin-4-like	structural molecule activity				
aldehyde dehydrogenase family 3 member B1-like	aldehyde metabolic process				
non-lysosomal glucosylceramidase	axonogenesis				

nucleotide exchange factor SIL1	binding				

Table 2. Summary of Gene Ontology (GO) term enrichment overlap of differentially expressed genes compared between control (sham-challenged) and *Saprolegnia*-challenged Atlantic salmon and Nile tilapia. Arrows indicate treatment groups (H = high-density 4 fish/L, L = low-density 1 fish/L, HL = both densities) in which significant enrichment was found. Arrow direction indicates direction of expression (↓ = decreased expression, ↑ = increased expression).

Salmon			Tilapia			GO biological process
HL	H	L	HL	H	L	
↓	↓	↓	↓	↓	↓	regulation of Rho protein signal transduction
↑	↑		↑	↑		spliceosomal snRNP assembly
	↑		↓	↓	↑	regulation of apoptotic process
↑			↑	↑	↑	fructose metabolic process
↓	↓		↓		↓	peptidyl-tyrosine phosphorylation
↓		↓	↓	↑		DNA replication
↓		↓	↓		↓	protein phosphorylation
	↓		↓	↓	↑	regulation of cell growth
↑	↑		↑			isoprenoid biosynthetic process
	↑	↑			↓	spermine biosynthetic process, embryonic neurocranium morphogenesis
	↑		↑	↑		protein peptidyl-prolyl isomerization, protein folding, glycolytic process, pentose-phosphate shunt, oxidation-reduction process
	↑		↑↓			protein methylation
	↑		↑		↑	Arp2/3 complex-mediated actin nucleation
	↑		↓		↑	cellular response to xenobiotic stimulus
↑↓					↓	cell cycle
↑	↓			↓		determination of ventral identity
↑		↑		↑		rRNA modification
↑		↑	↑			defence response to Gram-negative bacterium
↑		↓	↓			convergent extension involved in gastrulation
↑			↑	↑		pseudouridine synthesis
↑			↑		↑	fructose 2,6-bisphosphate metabolic process
↑			↓		↓	immune response
↓		↓		↓		locomotor rhythm
↓		↓			↓	embryonic skeletal system development, transmembrane receptor protein tyrosine kinase signalling pathway
↓			↓	↓		regulation of ARF protein signal transduction

↓			↓		↓	protein kinase C-activating G protein-coupled receptor signalling pathway, retinal ganglion cell axon guidance
	↓	↑		↓		regulation of transcription by RNA polymerase II
	↓	↓		↓		positive regulation of GTPase activity, negative regulation of transcription (DNA-templated)
	↓	↓			↓	negative regulation of angiogenesis
	↓		↓	↓		cell adhesion
	↓		↓		↓	axon guidance
		↑	↑	↑		ribosome biogenesis, nucleoside metabolic process
		↑		↑	↑	protein O-linked mannosylation
		↓	↑	↑		DNA recombination
		↓	↓	↓		signal transduction
	↑			↑		proton transport
	↑		↑			mast cell degranulation, response to lipopolysaccharide, peptidyl-lysine methylation, galactose metabolic process, proton-transporting ATP synthase complex assembly
	↑		↓			embryonic digestive tract morphogenesis, proepicardium development, regulation of vascular endothelial growth factor receptor signalling pathway
	↑			↓		regulation of alternative mRNA splicing via spliceosome
	↑				↑	fucosylation, RNA phosphodiester bond hydrolysis, intestinal cholesterol absorption, peptide cross-linking
	↑				↓	stabilization of membrane potential
↑				↑		spliceosomal complex assembly, mRNA transport, exonucleolytic trimming, positive regulation of cell division
↑			↑			Fc-epsilon receptor signalling pathway, viral entry into host cell, maturation of LSU-rRNA, asparagine biosynthetic process, nuclear import, isocitrate metabolic process, regulation of translational initiation, histone mRNA metabolic process, cyclooxygenase pathway, mitotic sister chromatid cohesion, ribosomal subunit export from nucleus
↑			↓			cell migration involved in gastrulation, spermatid development, cell chemotaxis

↑			↓	positive regulation of gene expression, positive regulation of ERK1 and ERK2 cascade, gastric inhibitory peptide signalling pathway
↑			↑	carbohydrate phosphorylation, melanosome transport, phospholipid transport
↑			↓	NADP biosynthetic process
↓			↑	regulation of skeletal muscle cell differentiation, adherens junction assembly
↓		↓		positive regulation of cell proliferation, negative regulation of canonical Wnt signalling, fibroblast growth factor receptor signalling, smoothened signalling pathway, dorsal root ganglion development, positive regulation of transcription
↓			↓	phosphate ion transmembrane transport, endothelial cell chemotaxis
↓			↓	de novo' actin filament nucleation, lipoprotein metabolic process
	↓	↑		regulation of stress fiber assembly
	↓	↓		proteolysis, heart development, retinol metabolic process, response to axon injury, homophilic cell adhesion via plasma membrane
	↓		↓	regulation of cell proliferation, mesenchyme migration, somatic muscle development, inactivation of MAPK activity, positive regulation of protein kinase A signalling, angiogenesis, actin filament organization
	↓		↑	phagocytosis, protein autophosphorylation, reverse cholesterol transport, negative regulation of ERK1 and ERK2 cascade, Rho protein signal transduction
	↓		↓	Roundabout signalling pathway, notochord morphogenesis, regulation of calcineurin-NFAT signalling, calcium ion import
		↑	↑	T-helper 2 cell differentiation, T-helper 17 cell lineage commitment, myeloid dendritic cell differentiation, defence response to protozoan, isotype switching, rRNA methylation, hematopoietic stem cell differentiation, ribonucleoside monophosphate biosynthetic process, fatty acid biosynthetic process, threonine catabolic process
		↑	↑	regulation of defence response to virus by virus
		↑	↓	NLS-bearing protein import into nucleus, regulation of RNA splicing
		↓	↑	peptidyl-diphthamide biosynthetic process, 'de novo' CTP biosynthetic process
		↓	↓	regulation of protein localization, retinoic acid catabolic process

↓	↑	regulation of Rho guanyl-nucleotide exchange factor activity, regulation of ephrin receptor signalling, cytoplasmic microtubule organization, peripheral nervous system myelin maintenance, Kit signalling pathway, drug transmembrane transport
↓	↓	positive regulation of non-canonical Wnt signalling pathway, negative regulation of vascular endothelial growth factor receptor signalling pathway, reelin-mediated signalling pathway, histone H4-K16 acetylation, positive regulation of Wnt signalling pathway

Table 3. Summary of gene orthologs sharing differential expression between control (sham-challenged) and *Saprolegnia*-challenged Atlantic salmon and Nile tilapia. Arrows indicate treatment groups (H = high-density 4 fish/L, L = low-density 1 fish/L) in which significant enrichment was found. Arrow direction indicates direction of expression (↓ = decreased expression, ↑ = increased expression).

Salmon		Tilapia		ID	Gene
H	L	H	L		
↑			↑	XP_013995411.1	growth differentiation factor 15
↑			↑	XP_014004629.1	interleukin-17C
↑			↑	XP_014009356.1	lymphocyte activation gene 3
↑			↑	XP_014056305.1	tumor necrosis factor alpha-induced protein 8-like 2
	↑	↑		XP_003455658.1	basic leucine zipper transcriptional factor ATF-like
	↓	↓		XP_014027980.1	perforin-1
↑		↑		XP_014068485.1	stimulator of interferon genes
↓		↓		XP_014011243.1	integumentary mucin
	↑		↑	XP_014015941.1	tumor necrosis factor ligand superfamily member 15-like
	↑		↑	XP_014001973.1	tumor necrosis factor receptor superfamily member 9-like
	↑		↑	XP_014064920.1	mucin-5AC-like
↑	↑	↑	↑	NP_001117024.1	interleukin 1 receptor accessory protein
↑	↑	↑	↑	XP_014036616.1	leukocyte elastase inhibitor
↑	↑	↑	↑	XP_014067437.1	leukocyte cell-derived chemotaxin 2 precursor
↑	↑	↑	↑	XP_014071691.1	AP-1 complex subunit mu-1
↑	↑	↑	↑	XP_014047427.1	AP-1 complex subunit sigma-2
↑	↑	↑	↑	NP_001134642.1	AP-1 complex subunit sigma-3

Figures

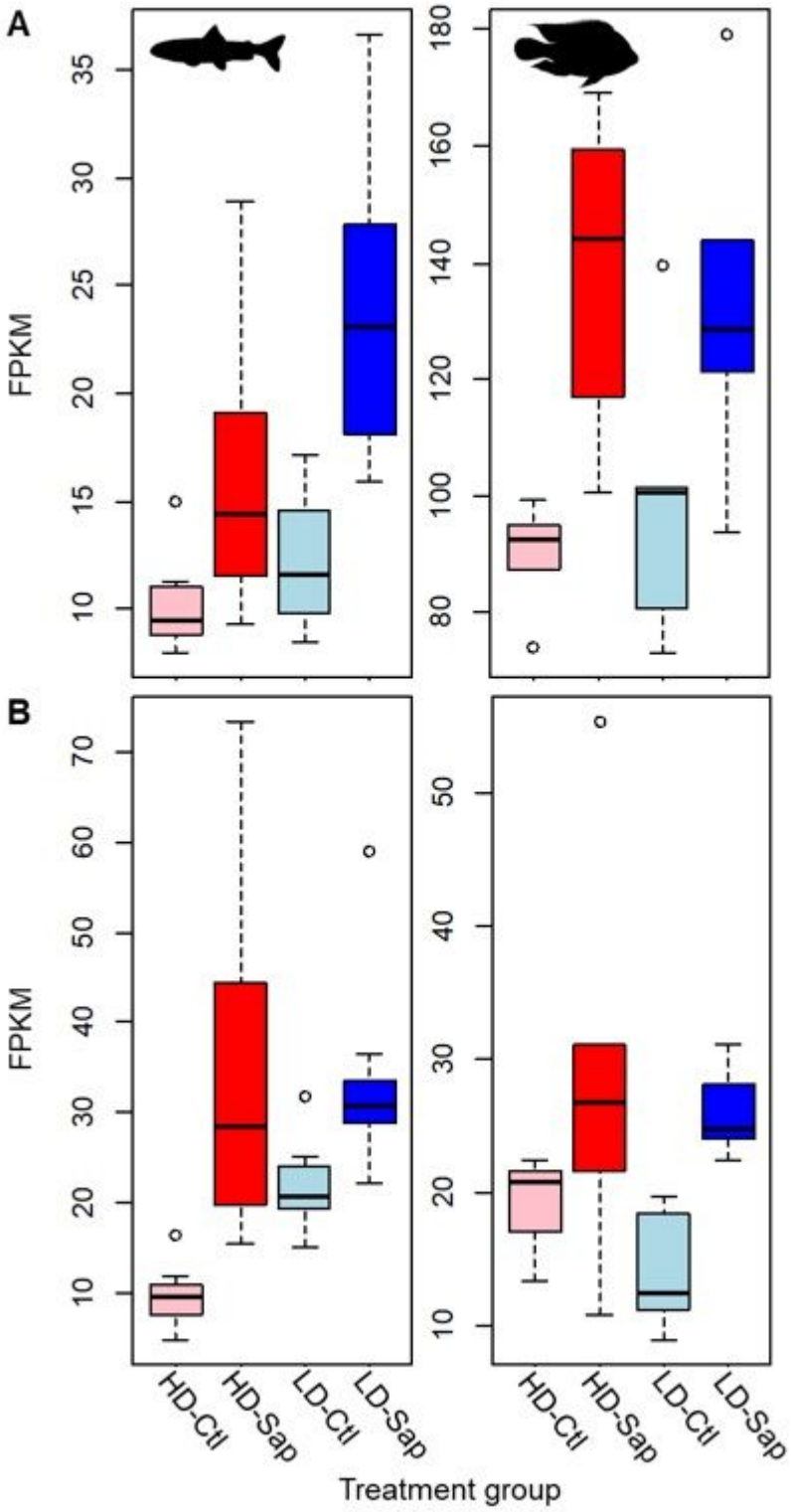

Figure 1

Boxplots of A) batf, and B) il17c gene expression (FPKM; Fragments Per Kilobase of transcript per Million mapped reads) in Atlantic salmon (left, n = 8; 4 per tank) and Nile tilapia (right, n = 5 fish per group). Colours indicate density treatment (red = high-density; “HD”, blue = low-density; “LD”) and colour intensity Saprolegnia status (light = sham-challenged; “Ctl”, dark = Saprolegnia-challenged; “Sap”). Shown in the

boxplots are minimum, first quartile, median, third quartile, and maximum values. Extreme values are shown by closed circles.

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